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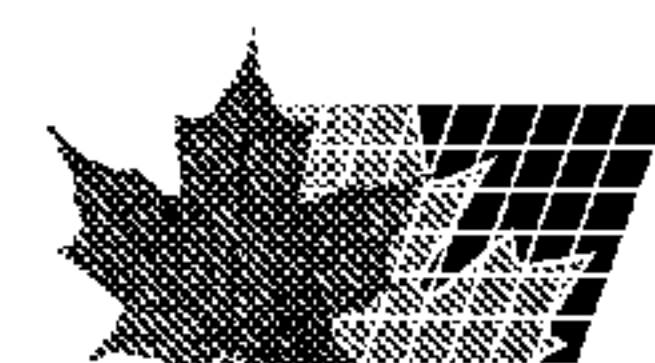
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(57) **Abrégé/Abstract:**

This invention relates generally to a plant cell with enhanced nitrogen use efficiency and/or increased biomass production as compared to a corresponding non-transformed wild type plant cell by increasing or generating one or more activities of polypeptides associated with enhanced nitrogen use efficiency in plants.



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(57) Abstract: This invention relates generally to a plant cell with enhanced nitrogen use efficiency and/or increased biomass production as compared to a corresponding non-transformed wild type plant cell by increasing or generating one or more activities of polypeptides associated with enhanced nitrogen use efficiency in plants.

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Plants with increased yield

[0000.1.1.1] This application incorporates by reference EP 07117448.6 filed on September 18, 2007 and EP 08161134.5 filed on July 25, 2008.

5

[0001.1.1.1] The present invention pertains to the field of molecular biology, plant genetics, plant physiology and developmental biology. More specifically, the present invention disclosed herein provides plant cells comprising nucleic acids enhancing or improving one or more traits of a transgenic plant, plants comprising such cells, progeny, seed and pollen derived from such plants, and methods of making and methods of using such plant cell(s) or plant(s), progeny, seed(s) or pollen. Particularly, said improved trait(s) are manifested in an increased yield, preferably by improving one or more yield-related trait(s).

15 [0002.1.1.1] Under field conditions, plant performance, for example in terms of growth, development, biomass accumulation and seed generation, depends on a plant's tolerance and acclimation ability to numerous environmental conditions, changes and stresses. Since the beginning of agriculture and horticulture, there was a need for improving plant traits in crop cultivation. Besides increasing yield by applying technical advances in crop planting, breeding strategies foster crop properties to withstand biotic and abiotic stresses, to increase nutrient use efficiency and to alter other crop specific yield parameters. The intrinsic growth and development characteristics of plants are improved, tolerance to biotic and abiotic stresses are introduced to maintain yield under environmental stress conditions and to extend acreage under different climatic situations. Crops with better nutrient use efficiency are developed to reduce fertilizer input and also to extend acreage into regions with nutrient poor soil.

30 Plants are sessile organisms and consequently need to cope with various environmental stresses. Biotic stresses such as plant pests and pathogens on the one hand, and abiotic environmental stresses on the other hand are major limiting factors of plant growth and productivity (Boyer, Plant Productivity and Environment, Science 218, 443-448 (1982); Bohnert et al., Adaptations to Environmental Stresses, Plant Cell 7 (7), 1099-1111 (1995)), thereby limiting plant cultivation and geographical distribution. Plants exposed to the different stresses typically have low yields of plant material, seeds, fruit and other products. Crop losses and crop yield losses of e.g. major crops such as rice, maize (corn), oil seed rape (including winter oil seed rape and canola), cotton, soybean and wheat caused by these stresses represent a significant economic and political factor and contribute to food shortages, particularly in many underdeveloped countries.

40

Conventional means for crop and horticultural improvements today utilize selective breeding techniques to identify plants with desirable characteristics. Such conventional

techniques, however, have several drawbacks. Very often plants contain heterogeneous genetic components that may not always result in the desirable trait being passed on from parent plants, particularly not without other negative impacts. Thus, particularly complex traits such as yield and stress phenomena make genetic optimization by traditional breeding approaches difficult, costly and time-consuming. On the contrary, advances in molecular biology have allowed modifying the germplasm of plants in a specific way. The modification of a single gene, for example, resulted in several cases in a significant increase in e.g. stress tolerance (Wang et al., 2003) and other yield-related traits. As different plants have to resist different kinds and strengths of stress in different cultivation areas there is still a need to identify genes which show various combinations of stress resistance to produce optimal yield. There is still a need to identify genes which have the overall capacity to improve yield of plants.

[0003.1.1.1] The present invention provides transgenic plant nuclei and/or transgenic plant cells comprising one or more nucleic acid(s) which enhances or improves one or more trait(s) of a transgenic plant, plants comprising such cells, progeny, seed and pollen derived from such plants, and methods of making and methods of using such plant cell(s) or plant(s), progeny, seed(s) or pollen. Particularly, said improved trait(s) are manifested in an increased yield.

In one embodiment, the present invention provides a method for producing such transgenic plant cell(s) or plant(s) with increased yield by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxyphosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that

regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reduc-
 tase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes pro-
 tein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster as-
 sembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific
 5 metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic
 recombination protein , membrane protein, metal ion transporter, microsomal beta-
 keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein,
 mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of
 the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis
 10 protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras
 guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac sub-
 family of Ras-like proteins, Nuclear cap-binding protein complex subunit , nuclear fu-
 sion protein precursor, nuclear pore complex subunit, origin recognition complex sub-
 unit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl
 15 cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phospho-
 glucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase,
 Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline
 dehydrogenase, protein component of the large ribosomal subunit, protein involved in
 shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosyn-
 20 thesis, protein kinase, protein necessary for structural stability of L-A double-stranded
 RNA-containing particles, protein required for maturation of ribosomal RNAs, protein
 translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 pro-
 tein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repres-
 sor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal
 25 protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase,
 short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal
 transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint
 complex subunit, splicing factor, Stationary phase protein , subunit of cytoplasmic
 phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) com-
 30 plex of the cis-Golgi , threonine ammonia-lyase, transcription elongation factor, tran-
 scription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3),
 transmembrane protein with a role in cell wall polymer composition, transport protein,
 ubiquitin regulatory protein , UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE
 binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase,
 35 yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-
 protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein,
 yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein,
 yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein,
 ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein,
 40 ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein,
 ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-
 protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein,

YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease.

In a further embodiment, the activity is increased by increasing the amount and/or activity of one or more protein(s) having an activity selected from the group consisting of

2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidylyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydrolyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothienoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribo-

- somal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein , subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi , threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein , UDP-N-acetylglucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease; and wherein such one or more protein(s) each comprises a polypeptide as depicted in table II, column 5 or 7.
- Said increased yield in accordance with the present invention can typically be achieved by enhancing or improving, in comparison to a non-transformed starting or wild-type plant, one or more yield-related traits of a plant. Such yield-related traits of a plant the improvement of which results in increased yield comprise, without limitation, the increase of the intrinsic yield capacity of a plant, improved nutrient use efficiency, and/or increased stress tolerance.

According to the present invention, yield-related traits concerning an increase of the intrinsic yield capacity of a plant may be manifested by improving the specific (intrinsic) seed yield (e.g. in terms of increased seed/ grain size, increased ear number, increased seed number per ear, improvement of seed filling, improvement of seed composition, embryo and/or endosperm improvements, or the like); modification and improvement of inherent growth and development mechanisms of a plant (such as plant

height, plant growth rate, pod number, pod position on the plant, number of internodes, incidence of pod shatter, efficiency of nodulation and nitrogen fixation, efficiency of carbon assimilation, improvement of seedling vigour/early vigour, enhanced efficiency of germination (under stressed or non-stressed conditions), improvement in plant architecture, cell cycle modifications, photosynthesis modifications, various signaling pathway modifications, modification of transcriptional regulation, modification of translational regulation, modification of enzyme activities, and the like); and/or the like.

According to the present invention, yield-related traits concerning an improvement or increase in nutrient use efficiency of a plant may be manifested by improving a plant's general efficiency of nutrient assimilation (e.g. in terms of improvement of general nutrient uptake and/or transport, improving a plant's general transport mechanisms, assimilation pathway improvements, and the like), and/or by improving specific nutrient use efficiency of nutrients including, but not limited to, phosphorus, potassium, and nitrogen.

According to the present invention, yield-related traits concerning an improvement or increase of stress tolerance of a plant may be manifested by improving or increasing a plant's tolerance against stress, particularly abiotic stress. In the present application, abiotic stress refers generally to abiotic environmental conditions a plant is typically confronted with, including conditions which are typically referred to as "abiotic stress" conditions including, but not limited to, drought (tolerance to drought may be achieved as a result of improved water use efficiency), heat, low temperatures and cold conditions (such as freezing and chilling conditions), salinity, osmotic stress, shade, high plant density, mechanical stress, oxidative stress, and the like.

According to the present invention, the improvement of yield-related traits relating to an increase of the intrinsic yield capacity of a plant and/or to a plant's tolerance to abiotic stress(es) is a particularly preferred embodiment for enhancing or improving yield of said plant.

[0004.1.1.1] The term "yield" as used herein generally refers to a measurable produce from a plant, particularly a crop.

Yield and yield increase (in comparison to a non-transformed starting or wild-type plant) can be measured in a number of ways, and it is understood that a skilled person will be able to apply the correct meaning in view of the particular embodiments, the particular crop concerned and the specific purpose or application concerned.

In the preferred embodiments of the present invention described herein, an increase in yield refers to increased biomass yield, increased seed yield, and/or increased yield

regarding one or more specific content(s) of a whole plant or parts thereof or plant seed(s).

5 In preferred embodiments, "yield" refers to biomass yield comprising dry weight biomass yield and/or fresh weight biomass yield, each with regard to the aerial and/or underground parts of a plant, depending on the specific circumstances (test conditions, specific crop of interest, application of interest, and the like). In each case, biomass yield may be calculated as fresh weight, dry weight or a moisture adjusted basis, and on the other hand on a per plant basis or in relation to a specific area (e.g. biomass
10 yield per acre/ square meter/ or the like).

In other preferred embodiments, "yield" refers to seed yield which can be measured by one or more of the following parameters: number of seed or number of filled seed (per plant or per area (acre/ square meter or the like)); seed filling rate (ratio between number of filled seeds and total number of seeds); number of flowers per plant; seed biomass or total seed weight (per plant or per area (acre/square meter or the like); thousand kernel weight (TKW; extrapolated from the number of filled seeds counted and their total weight; an increase in TKW may be caused by an increased seed size, an increased seed weight, an increased embryo size, and/or an increased endosperm); or
15 other parameters allowing to measure seed yield. Seed yield may be determined on a dry weight or on a fresh weight basis, or typically on a moisture adjusted basis, e.g. at 15.5 percent moisture.
20

In further preferred embodiments, yield refers to the specific content and/or composition of a harvestable product, including, without limitation, an enhanced and/or improved sugar content or sugar composition, an enhanced or improved starch content and/or starch composition, an enhanced and/or improved oil content and/or oil composition (such as enhanced seed oil content), an enhanced or improved protein content and/or protein composition (such as enhanced seed protein content), an enhanced
25 and/or improved vitamin content and/ or vitamin composition, or the like.
30

In a preferred meaning according to the present application, "yield" as described herein may also refer to the harvestable yield of a plant, which largely depends on the specific plant/ crop of interest as well as its intended application (such as food production, feed
35 production, processed food production, biofuel, biogas or alcohol production, or the like) of interest in each particular case. Thus, yield may also be calculated as harvest index (expressed as a ratio of the weight of the respective harvestable parts divided by the total biomass), harvestable parts weight per area (acre, square meter, or the like); and the like.
40

Preferably, the preferred enhanced or improved yield characteristics of a plant described herein according to the present invention can be achieved in the absence or presence of stress conditions.

- 5 The meaning of “yield” is, thus, mainly dependent on the crop of interest and the intended application, and it is understood, that the skilled person will understand in each particular case what is meant from the circumstances of the description.

[0005.1.1.1] In a preferred embodiment of the present invention, plant yield is in-
10 creased by increasing one or more of yield-related traits selected from one or more improvements concerning the nutrient use efficiency of a photosynthetic active organism, especially a plant. An improvement or increase in nutrient use efficiency of a plant may be manifested by improving a plant's general efficiency of nutrient assimilation (e.g. in terms of improvement of general nutrient uptake and/or transport, improving a
15 plant's general transport mechanisms, assimilation pathway improvements, and the like), and/or by improving specific nutrient use efficiency of nutrients including, but not limited to, phosphorus, potassium, and nitrogen.

The term “nutrient deficiency” refers to conditions where the respective photosynthetic
20 organism, especially a plant, lacks of nutrient, like phosphorus, potassium or nitrogen; especially the term “nitrogen deficiency” refers to conditions where the respective photosynthetic organism, especially a plant, lacks of or nitrogen.

In a preferred embodiment the present invention relates to the manipulation of the ni-
25 trogen use efficiency in photosynthetic active organisms, preferably in plants. In particular, the present invention relates to a process for the enhanced nitrogen uptake and/or nitrogen utilization, in photosynthetic active organisms, especially in plants. Also the present invention relates to a process for enhanced biomass production, especially under nitrogen limited conditions, in photosynthetic active organisms, especially in
30 plants.

[0006.1.1.1] In particular, this invention relates to plant cells and/or plants tailored
to grow under conditions of nitrogen deficiency, and/or to plant cells and/or plants
showing increased yield when grown under non-nitrogen-deficiency conditions.

35

[0007.1.1.1] The invention also deals with methods of producing and screening for
and breeding such plant cells and/or plants.

[0008.1.1.1] Plant nutrition is essential to the growth and development of plants
40 and therefore also for quantity and quality of plant products. Because of the strong influence of the efficiency of nutrition uptake as well as nutrition utilization on plant yield

and product quality, a huge amount of fertilizer is poured onto soils to optimize plant growth and quality.

5 Plant growth is primarily limited by three nutrients - phosphorous, potassium and nitrogen. Therefore nitrogen (N) is one of the major nutritional elements required for plant growth, which is usually the rate-limiting element in plant growth. Nitrogen is part of numerous important compounds found in living cells, like amino acids, proteins (e.g. enzymes), nucleic acids, and chlorophyll. 1.5% to 2% of plant dry matter is nitrogen and approximately 16% of total plant protein. Thus, the availability of nitrogen has a
10 major impact on amino acid synthesis as well as amino acid composition, accumulation of amino acids, on protein synthesis and accumulation thereof, and based thereupon it is a major limiting factor for plant growth and yield (Frink C.R., Proc. Natl. Acad Sci. USA 96, 1175 (1999)).

15 [0009.1.1.1] Plants can utilize a wide range of nitrogen species including volatile ammonia (NH_3), nitrogen oxides (NO_x), mineral nitrogen, like nitrate (NO_3^-) and ammonium salts (NH_4^+), urea and urea derivatives, and organic nitrogen (amino acids, peptides, and the like). Some plants are able to utilize atmospheric nitrogen by symbiotic bacteria or certain fungi. However, in most agricultural soils, nitrate (NO_3^-) is the most
20 important source of nitrogen (Crawford N.M., Glass A.D.M., Trends in Plant Science, 3 389 (1998); Hirsch R.E., Sussman M.R., TIBTech 17, 356 (1999)). Nevertheless also ammonium NH_4^+ plays an important, probably underestimated role, because most plants preferentially take up NH_4^+ when both forms are present - even if NH_4^+ is present at lower concentrations than NO_3^- (von Wiren N. et al., Curr. Opin. Plant Biol. 3, 254
25 (2000)).

[0010.1.1.1] Because of the high nitrogen requirements for crop plants, nitrogen fertilization is a major worldwide agricultural investment, with 80 million metric tons of nitrogen fertilizers (as nitrate and/or ammonium) applied annually (Frink C.R., Proc.
30 Natl. Acad Sci. USA 96, 1175 (1999)). There are also negative environmental consequences for the extensive use of nitrogen containing fertilizers in crop production since the crops retain only about two-thirds of the applied nitrogen. Therefore high inputs of fertilizer are followed by large outputs by leaching, gaseous losses and crop removal. The unabsorbed nitrogen can subsequently leach into the soil and contaminate water
35 supplies (Frink C.R., Proc. Natl. Acad Sci. USA 96, 1175 (1999)). Because of the high leaching losses of nitrogen from agricultural ecosystems to surface water and groundwater, nitrogen is also recognized as a pollutant. Nitrogen leaching, namely as nitrate from agricultural lands, affects drinking water quality and causes eutrophication of lakes and coastal areas. Abundant use of nitrogen containing fertilizers can further lead
40 to final deterioration of soil quality, to environmental pollution and health hazards.

- [0011.1.1.1] Because of the high costs of nitrogen fertilizer in relation to the revenues for agricultural products, and additionally its deleterious effect on the environment, it is desirable to develop strategies to reduce nitrogen input and/or to optimize nitrogen uptake and/or utilization of a given nitrogen availability while simultaneously maintaining optimal yield, productivity and quality of photosynthetic active organisms, preferably cultivated plants, e.g. crops. Also it is desirable to obtain "existing" yield of crops with lower fertilizer input and/or higher yield on soils of similar or even poorer quality.
- 10 [0012.1.1.1] For efficient nitrogen uptake and utilization, complex processes associated with absorption, translocation, assimilation, and redistribution of nitrogen are required to operate effectively. Differences in nitrogen absorption between genotypes have been demonstrated for several species by different researchers (Chang S.C., Robison D.J., Sci. World J., Suppl. 2, 407 (2001)). Considerable evidence of genotypic differences in nitrogen uptake has also been reported for maize and canola (Weisler et al., Sci. World J., Suppl. 2, 61 (2001); Gallais A., Hirel B., J. Exper. Bot. 55, 295 (2004)).
- 20 [0013.1.1.1] Plants absorb nitrate via transporters localized to the root epidermal and cortical cell plasma membrane over a wide nitrate concentration range using several different transport mechanisms, including constitutive and nitrate-inducible high-affinity transport systems, as well as nitrate-inducible low-affinity transporters (Stitt M., Curr. Opin. Plant Biol. 2, 178 (1999)). In addition nitrate uptake in plants is highly regulated and coordinated with other transport and metabolic pathways (Crawford N.M. Plant Cell 7, 859 (1995)), and a number of nitrate uptake and assimilation-related genes have been identified and characterized (Forde B.G., Ann. Rev. Plant Biol 53, 203 (2002)). Once in the root cell cytoplasm, nitrate may be stored in the vacuole for later use, transported into the xylem and translocated to the shoot for assimilation and/or storage, released back into the rhizosphere, or reduced to nitrite and then to ammonia via nitrate reductase (NR) and nitrite reductases (NiR). The reduction of nitrate to nitrite and then to ammonia enables the assimilation of nitrogen into amino acids via the GOGAT pathway (Stitt M., Curr. Opin. Plant Biol. 2, 178 (1999)). In order to be incorporated into amino acids, nucleic acids, and other compounds, NO_3^- must be reduced to NH_4^+ . NR (nitrate reductase) is the first enzyme in the process of NO_3^- reduction to NH_4^+ . It is a substrate-inducible enzyme and is thought to be the most limiting step in nitrogen assimilation.
- 30 [0014.1.1.1] The in-situ rate of NO_3^- reduction is controlled primarily by the rate of NO_3^- uptake, rather than by alterations in nitrate reductase activity (NRA) or limitations in reducing power. Thus, NO_3^- uptake appears to be of primary importance in nitrogen assimilation in NO_3^- -fed plants. Genetic variation in NRA is well documented in several species. NRA is affected by factors such as environmental conditions and plant devel-

opmental stages, as well as plant part, such as roots and tops. Furthermore, in vivo and in vitro assays usually give different results. Variable results were found by several researchers in their efforts to relate NRA to grain yield and N-related traits such as total reduced plant nitrogen, grain nitrogen content, grain nitrogen concentration, and nitrogen harvest index.

[0015.1.1.1] Beneath NO_3^- plants can take up nitrogen also in the form of ammonium. Although the average NH_4^+ concentrations in soil are often 10 to 1000 times lower than those of NO_3^- (Marschner H.L., "Mineral Nutrition in Higher Plants", London, Academic Press, 1995), the difference in soil concentrations does not necessarily reflect the uptake ratio of each nitrogen source. Plants take up NH_4^+ preferentially when both forms - NO_3^- as well as NH_4^+ - are available, possibly because its assimilation requires less energy since NO_3^- has to be reduced prior to assimilation (Bloom et al., Plant Phys. 1294-1301 (1992)).

[0016.1.1.1] Ammonium uptake systems have been characterized in different organisms, including yeast and plants. The yeast *Saccharomyces cerevisiae* contains three MEP genes for ammonium transporters, which are all controlled by nitrogen, being repressed in the presence of an nitrogen source that is readily metabolized, such as NH_4^+ (Marini et al., Mol. Cell Biol. 17, 4282 (1997)). Plant genes encoding ammonium transport systems have been cloned by complementation of a yeast mutant, homology searches in databases and heterogonous hybridizations (von Wiren N. et al., Curr. Opin. Plant Biol., 3, 254 (2000)). Experimental evidence of the physiological function of NH_4^+ transporters mainly rely on correlations between ammonium transporter expression and influx of labeled ammonium. The situation is complicated by the fact, that in *Arabidopsis* but also in other plants ammonium transporters are present in gene families, the members of which have different expression patterns and physiological characteristics. Although DE 43 37 597 claims sequences for plant ammonium transporters and their use for manipulation of the nitrogen metabolism and plant growth under certain conditions, any evidence for positive effects on nitrogen assimilation or plant growth under certain conditions through ectopic expression of the plant ammonium transporters are missing.

[0017.1.1.1] Usually the first step in the assimilation of inorganic nitrogen into organic form involves the reaction of glutamate with ammonium to form glutamine being catalyzed by glutamine synthase. Glutamine thus formed may transfer in turn its amino function of the amido group to aspartate to form asparagine being catalyzed by asparagine synthase. The steady flow of nitrogen from ammonia to asparagine depends upon the recycling of glutamate, alpha-ketoglutarate and aspartate, being catalyzed by glutamine-2-oxoglutarate aminotransferase and aspartate aminotransferase. Glutamine and asparagine represent the major long distance "nitrogen transport compounds" in plants. These are abundant in phloem sap but they have somewhat different roles in

plant nitrogen metabolism since glutamine is more metabolic active based on the fact that it can directly transfer its amino function of the amido group to a number of substrates, whereas asparagine is more efficient in “nitrogen transport and storage”.

- 5 [0018.1.1.1] In order to describe the efficiency of the complete pathway of nitrogen, starting with the uptake from the soil, assimilation of nitrogen, transport and accumulation of N-containing compounds within the photosynthetic organism, influencing biomass and yield, different approaches are known. And in the light of the importance of optimal nitrogen use different strategies have been followed for plant optimizations.
- 10 [0019.1.1.1] In some cases enzymes of the nitrogen assimilation pathway, like of glutamine synthetase, asparagine synthetase and asparaginase, were overexpressed. Although initially unsuccessful like the overexpression of a cytosolic glutamine synthetase gene in Lotus (Vincent R. et al., *Planta* 201, 424 (1997)), recent documents
- 15 show at least some success. WO 95/09911 describes the overexpression of glutamine-synthetase, asparagine-synthetase and asparaginase in transgenic plant for application in enhanced nitrogen-fixation and improved yield. Chichkova et al. reported in *J. Exp. Bot.*, 52, 2079 (2001) that transgenic tobacco plants that overexpress alfalfa NADH-glutamate-synthase have higher carbon and nitrogen content, but not a specific enrichment in nitrogen in comparison to carbon. In another case, the overexpression of a
- 20 nitrogen assimilation gene, in this case the *Escherichia coli* glutamate-dehydrogenase, did not lead to a relative increase in nitrogen content, but rather to a significant increase in fresh weight and dry weight. In another case, overexpression of the ASN1 gene enhances the nitrogen status in seeds of *Arabidopsis* (Lam H. et al., *Plant*
- 25 *Physiol.* 321, 926 (2003)). In seeds of those overexpressing lines the authors observed the elevation of soluble seed protein contents, elevation of total protein contents from acid-hydrolyzed seeds and a higher tolerance of young seedlings when grown under nitrogen-limiting conditions.
- 30 [0020.1.1.1] A different interesting approach was followed by Yanagisawa et al., *PNAS* 101, 7833 (2004). The authors used hereby the transcription factor Dof1. The overexpression of this regulatory factor induced the up-regulation of genes encoding enzymes for carbon skeleton production, a marked increase of amino acid contents, and a reduction of the glucose level in transgenic *Arabidopsis*. Elementary analysis
- 35 revealed that the nitrogen content increased in transgenic plants (approximate to 30%), indicating a promotion of net nitrogen assimilation. Most significantly, the Dof1 transgenic plants exhibit improved growth under low-nitrogen conditions. Although looking promising, this approach likely has the drawback, that it relies on a plant transcription factor and the complex corresponding signaling cascade which both might be the subject of different internal regulatory and feedback mechanism modifying or even diminishing the desired effect at least under certain conditions.
- 40

[0021.1.1.1] Therefore, there is still a need for photosynthetic active organisms, especially plants, that are capable to use nitrogen more efficiently so that less nitrogen is required for the same yield or higher yields may be obtained with current levels of nitrogen use. In addition, there is still a need for photosynthetic active organism, especially plants, that show an increase in biomass and/or yield.

[0022.1.1.1] Accordingly, it is also an object of this invention to develop an inexpensive process for an enhanced nitrogen up-take and/or transport and/or assimilation and/or utilisation in a photosynthetic active organism, which are reflected alone or altogether in an increased nitrogen use efficiency (NUE) and/or a process for an increased biomass production and/or yield under conditions of limited nitrogen supply.

It was found that this object is achieved by providing a process according to the present invention described herein.

It is further an object of this invention to provide plant cells and/or plants, which show an enhanced NUE, and/or exhibit under conditions of limited nitrogen supply an increased biomass production and/or yield, as compared to a corresponding non-transformed wild type plant cell and/or plant.

It was found that this object is achieved by providing plant cells and/or plants according to the present invention described herein.

[0023.1.1.1] In one embodiment of the present invention, these traits are achieved by a process for the enhanced nitrogen utilization (= nitrogen use efficiency (NUE)) in a photosynthetic active organism, preferably a plant, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In an embodiment thereof, the term "enhanced NUE" means that the photosynthetic active organism, preferably a plant, exhibits a generally enhanced yield (as defined hereinabove) under normal conditions or under low nutrient conditions, especially an enhanced biomass yield per unit of nitrogen available from the surrounding medium, soil or environment, including nitrogen fertilizer, on which the photosynthetic active organism, preferably a plant, is grown, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In an embodiment thereof, the term "enhanced NUE" means that the photosynthetic active organism, preferably a plant, exhibits an enhanced dry biomass yield per unit of nitrogen available from the surrounding medium, soil or environment, including nitrogen fertilizer, on which the photosynthetic active organism, preferably a plant, is grown, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In an embodiment thereof, the term “enhanced NUE” means that the photosynthetic active organism, preferably a plant, exhibits an enhanced aerial dry biomass yield per unit of nitrogen available from the surrounding medium, soil or environment, including nitrogen fertilizer, on which the photosynthetic active organism, preferably a plant, is grown, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In an embodiment thereof, the term “enhanced NUE” means that the photosynthetic active organism, preferably a plant, exhibits an enhanced underground dry biomass yield per unit of nitrogen available from the surrounding medium, soil or environment, including nitrogen fertilizer, on which the photosynthetic active organism, preferably a plant, is grown, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In another embodiment thereof, the term “enhanced NUE” means that the photosynthetic active organism, preferably a plant, exhibits an enhanced fresh weight biomass yield per unit of nitrogen available from the surrounding medium, soil or environment, including nitrogen fertilizer, on which the photosynthetic active organism, preferably a plant, is grown, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In an embodiment thereof, the term “enhanced NUE” means that the photosynthetic active organism, preferably a plant, exhibits an enhanced aerial fresh weight biomass yield per unit of nitrogen available from the surrounding medium, soil or environment, including nitrogen fertilizer, on which the photosynthetic active organism, preferably a plant, is grown, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In an embodiment thereof, the term “enhanced NUE” means that the photosynthetic active organism, preferably a plant, exhibits an enhanced underground fresh weight biomass yield per unit of nitrogen available from the surrounding medium, soil or environment, including nitrogen fertilizer, on which the photosynthetic active organism, preferably a plant, is grown, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In another embodiment thereof, the term “enhanced NUE” means that the photosynthetic active organism, preferably a plant, exhibits an enhanced yield of harvestable parts of a plant per unit of nitrogen available from the surrounding medium, soil or environment, including nitrogen fertilizer, on which the photosynthetic active organism, preferably a plant, is grown, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In an embodiment thereof, the term “enhanced NUE” means that the photosynthetic active organism, preferably a plant, exhibits an enhanced yield of dry harvestable parts of a plant per unit of nitrogen available from the surrounding medium, soil or environment, including nitrogen fertilizer, on which the photosynthetic active organism, preferably a plant, is grown, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In an embodiment thereof, the term “enhanced NUE” means that the photosynthetic active organism, preferably a plant, exhibits an enhanced yield of dry aerial harvestable parts of a plant per unit of nitrogen available from the surrounding medium, soil or environment, including nitrogen fertilizer, on which the photosynthetic active organism, preferably a plant, is grown, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In an embodiment thereof, the term “enhanced NUE” means that the photosynthetic active organism, preferably a plant, exhibits an enhanced yield of underground dry harvestable parts of a plant per unit of nitrogen available from the surrounding medium, soil or environment, including nitrogen fertilizer, on which the photosynthetic active organism, preferably a plant, is grown, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In another embodiment thereof, the term “enhanced NUE” means that the photosynthetic active organism, preferably a plant, exhibits an enhanced yield of fresh weight harvestable parts of a plant per unit of nitrogen available from the surrounding medium, soil or environment, including nitrogen fertilizer, on which the photosynthetic active organism, preferably a plant, is grown, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In an embodiment thereof, the term “enhanced NUE” means that the photosynthetic active organism, preferably a plant, exhibits an enhanced yield of aerial fresh weight harvestable parts of a plant per unit of nitrogen available from the surrounding medium, soil or environment, including nitrogen fertilizer, on which the photosynthetic active organism, preferably a plant, is grown, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In an embodiment thereof, the term “enhanced NUE” means that the photosynthetic active organism, preferably a plant, exhibits an enhanced yield of underground fresh weight harvestable parts of a plant per unit of nitrogen available from the surrounding medium, soil or environment, including nitrogen fertilizer, on which the photosynthetic active organism, preferably a plant, is grown, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In a further embodiment, the term “enhanced NUE” means that the photosynthetic active organism, preferably a plant, exhibits an enhanced yield of the crop fruit per unit of nitrogen available from the surrounding medium, soil or environment, including nitrogen fertilizer, on which the photosynthetic active organism, preferably a plant, is grown, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In an embodiment thereof, the term “enhanced NUE” means that the photosynthetic active organism, preferably a plant, exhibits an enhanced yield of the fresh crop fruit per unit of nitrogen available from the surrounding medium, soil or environment, including nitrogen fertilizer, on which the photosynthetic active organism, preferably a plant, is grown, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In an embodiment thereof, the term “enhanced NUE” means that the photosynthetic active organism, preferably a plant, exhibits an enhanced yield of the dry crop fruit per unit of nitrogen available from the surrounding medium, soil or environment, including nitrogen fertilizer, on which the photosynthetic active organism, preferably a plant, is grown, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In an embodiment thereof, the term “enhanced NUE” means that the photosynthetic active organism, preferably a plant, exhibits an enhanced grain dry weight per unit of nitrogen supplied, as compared to a corresponding non-transformed wild type photosynthetic active organism, in analogy to Reynolds, M.P., Ortiz-Monasterio J.J., and McNab A. (eds.), 2001, “Application of Physiology in Wheat Breeding, Mexico, D.F.:CIMMYT, which is incorporated by reference.

In a further embodiment, the term “enhanced NUE” means that the photosynthetic active organism, preferably a plant, exhibits an enhanced yield of seeds per unit of nitrogen available from the surrounding medium, soil or environment, including nitrogen fertilizer, on which the photosynthetic active organism, preferably a plant, is grown, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In an embodiment thereof, the term “enhanced NUE” means that the photosynthetic active organism, preferably a plant, exhibits an enhanced yield of fresh weight seeds per unit of nitrogen available from the surrounding medium, soil or environment, including nitrogen fertilizer, on which the photosynthetic active organism, preferably a plant, is grown, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In an embodiment thereof, the term “enhanced NUE” means that the photosynthetic active organism, preferably a plant, exhibits an enhanced yield of dry seeds per unit of nitrogen available from the surrounding medium, soil or environment, including nitrogen fertilizer, on which the photosynthetic active organism, preferably a plant, is grown, as compared to a corresponding non-transformed wild type photosynthetic active organism.

[0024.1.1.1] In another embodiment of the present invention, these traits are achieved by a process for an increased biomass production and/or yield under conditions of limited nitrogen supply, in a photosynthetic active organism, preferably plant, as compared to a corresponding non-transformed wild type photosynthetic active organism.

In an embodiment thereof, the term “increased biomass production” means that the photosynthetic active organism, especially a plant, exhibit an increased growth rate under conditions of limited nitrogen supply, compared to the corresponding wild-type photosynthetic active organism. An increased growth rate may be reflected inter alia by an increased biomass production of the whole plant, or by an increased biomass production of the aerial parts of a plant, or by an increased biomass production of the underground parts of a plant, or by an increased biomass production of parts of a plant, like stems, leaves, blossoms, fruits, seeds.

In an embodiment thereof, increased biomass production includes higher fruit yields, higher seed yields, higher fresh matter production, and/or higher dry matter production.

In another embodiment thereof, the term “increased biomass production” means that the photosynthetic active organism, preferably plant, exhibits a prolonged growth under conditions of limited nitrogen supply, as compared to the corresponding non-transformed wild type photosynthetic active organism. A prolonged growth comprises survival and/or continued growth of the photosynthetic active organism, preferably plant, at the moment when the non-transformed wild type photosynthetic active organism shows visual symptoms of deficiency and/or death.

[0025.1.1.1] In one embodiment of the invention the enhanced NUE is determined and quantified according to the following method:

Transformed plants are grown in pots in a growth chamber (Svalöf Weibull, Svalöv, Sweden). In case the plants are *Arabidopsis thaliana* seeds thereof are sown in pots containing a 1:1 (v:v) mixture of nutrient depleted soil (“Einheitserde Typ 0”, 30% clay, Tantau, Wansdorf Germany) and sand. Germination is induced by a four day period at 4°C, in the dark. Subsequently the plants are grown under standard growth conditions.

In case the plants are *Arabidopsis thaliana*, the standard growth conditions are: photo-period of 16 h light and 8 h dark, 20 °C, 60% relative humidity, and a photon flux density of 200 $\mu\text{E}/\text{m}^2\text{s}$. Plants are grown and cultured. In case the plants are *Arabidopsis thaliana* they are watered every second day with a N-depleted nutrient solution. The N-depleted nutrient solution e.g. contains beneath water

mineral nutrient	final concentration
KCl	3.00 mM
MgSO ₄ x 7 H ₂ O	0.5 mM
CaCl ₂ x 6 H ₂ O	1.5 mM
K ₂ SO ₄	1.5 mM
NaH ₂ PO ₄	1.5 mM
Fe-EDTA	40 μM
H ₃ BO ₃	25 μM
MnSO ₄ x H ₂ O	1 μM
ZnSO ₄ x 7 H ₂ O	0.5 μM
Cu ₂ SO ₄ x 5 H ₂ O	0.3 μM
Na ₂ MoO ₄ x 2 H ₂ O	0.05 μM

but no other N-containing salt.

10 After 9 to 10 days the plants are individualized. After a total time of 29 to 31 days the plants are harvested and rated by the fresh weight of the aerial parts of the plants, preferably the rosettes.

[0026.1.1.1] In another embodiment of the present invention, plant yield is increased by increasing one or more of yield-related traits selected from one or more stress tolerance(s). During its life-cycle, a plant is generally confronted with a diversity of environmental conditions. Any such conditions which may, under certain circumstances, have an impact on plant yield, are herein referred to as "stress" condition. Environmental stresses may generally be divided into biotic and abiotic (environmental) stresses. For the sake of completeness, it is mentioned that unfavorable nutrient conditions are sometimes also referred to as "environmental stress". As will be appreciated by the skilled artisan, the present invention does also contemplate solutions for this kind of environmental stress. This topic is described and dealt with in detail in the paragraphs hereinabove referring to increased nutrient use efficiency.

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In a particularly preferred embodiment of the present invention, yield-related traits which can be improved by the present invention are stress tolerance(s).

In a preferred embodiment of the present invention, plant yield is increased by increasing one or more of yield-related traits selected from one or more abiotic stress tolerance(s).

- 5 Generally, the term "increased tolerance to stress" can be defined as survival of plants, and/or higher yield production, under stress conditions as compared to a non-transformed wild type or starting plant.

10 For the purposes of the description of the present invention, the terms "enhanced tolerance to abiotic stress", "enhanced resistance to abiotic environmental stress", "enhanced tolerance to environmental stress", "improved adaptation to environmental stress" and other variations and expressions similar in its meaning are used interchangeably and refer, without limitation, to an improvement in tolerance to one or more abiotic environmental stress(es) as described herein and as compared to a corresponding (non-transformed) wild type (or starting) plant.

15 [0027.1.1.1] In a preferred embodiment of the present invention, plant yield is increased by increasing one or more of yield-related traits selected from one or more abiotic stress tolerance(s). In a particularly preferred embodiment of the present invention, said yield-related trait is increased water use efficiency of a plant and/ or increased tolerance to drought conditions.

20 Drought, heat, cold and salt stress have a common theme important for plant growth and that is water availability. Plants are typically exposed during their life cycle to conditions of reduced environmental water content. Most plants have evolved strategies to protect themselves against these conditions of low water or desiccation. However, if the severity and duration of the drought conditions are too great, the effects on plant development, growth and yield of most crop plants are profound. Continuous exposure to drought causes major alterations in the plant metabolism. These great changes in metabolism ultimately lead to cell death and consequently yield losses.

25 Developing stress-tolerant plants is a strategy that has the potential to solve or mediate at least some of these problems (McKersie and Leshem, 1994. Stress and Stress Coping in Cultivated Plants, Kluwer Academic Publishers). However, traditional plant breeding strategies to develop new lines of plants that exhibit resistance (tolerance) to these types of stress are relatively slow and require specific resistant lines for crossing with the desired line. 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 drought, cold and salt tolerance and/or resistance are complex in nature and involve multiple mechanisms of cellular adaptation and numerous metabolic pathways (McKersie and Leshem, 1994. Stress and Stress Coping in Cultivated Plants, Kluwer Aca-

demic Publishers). This multi-component nature of stress tolerance and/or resistance has not only made breeding for tolerance and/or resistance largely unsuccessful.

5 Plants are exposed during their life cycle also to heat, cold and salt stress. The protection strategies are similar to those of drought resistance. Since high salt content in some soils results in less available water for cell intake, its effect is similar to those observed under drought conditions. Likewise, under freezing temperatures, plant cells loose water as a result of ice formation that starts in the apoplast and withdraws water from the symplast (McKersie and Leshem, 1994. Stress and Stress Coping in Cultivated Plants, Kluwer Academic Publishers). Physiologically these stresses are also interconnected and may induce similar cellular damage. For example drought and salt stress are manifested primarily as osmotic stress, leading to the disruption of homeostasis and ion distribution in the cell (Serrano et al., 1999; Zhu, 2001a; Wang et al., 2003). Oxidative stress, which frequently accompanies high temperature, salinity or drought stress, may cause denaturation of functional or structural proteins (Smirnoff, 1998). As a consequence these abiotic stresses often activate similar signaling pathways (Shinozaki and Ymaguchi-Shinozaki, 2000; Knight and Knight, 2001; Zhu 2001b, 2002) and cellular responses, e.g. the production of certain stress proteins, antioxidants and compatible solutes (Vierling and Kimpel, 1992; Zhu et al., 1997; Cushman and Bohnert, 2000).

At the moment many genetical and biotechnological approaches are known in order to obtain plants growing under conditions of low water availability.

25 These approaches are generally based on the introduction and expression of genes in plant cell coding for different enzymes as disclosed for example in WO 2004/011888, WO 2006/032708, US 20050097640, US 20060037108, US 20050108791, Serrano et al. (Scientia Horticulturae 78, 261-269 (1999)) and many others.

30 For example the overexpression of antioxidant enzymes or ROS-scavenging enzymes is one possibility to engineer tolerance, e.g. transgenic alfalfa plants expressing Mn-superoxide dismutase tend to have reduced injury after water-deficit stress (McKersie et al., Plant Physiol. 111, 1177-1181(1996)). These same transgenic plants have increased biomass production in field trials (McKersie et al., Plant Physiology 119, 839-847 (1999); McKersie et al., Plant Physiol. 111, 1177-1181 (1996)). Transgenic plants that overproduce osmolytes such as mannitol, fructans, proline or glycine-betaine also show increased resistance to some forms of abiotic stress and it is proposed that the synthesized osmolytes act as ROS scavengers (Tarczynski. et al. Science 259, 508-510 (1993); Sheveleva,. et al., Plant Physiol.115, 1211-1219 (1997)).

40

Generally the transformed and stress resistant plants cited exhibit slower growth and reduced biomass, due to an imbalance in development and physiology of the plant,

thus having significant fitness cost (Kasuga et al., 1999, Danby and Gehring et al., 2005). Despite maintaining basic metabolic function this leads to severe biomass and yield loss. Sometimes the root/shoot dry weight ratio increases as plant water stress develops. The increase is mostly due to a relative reduction in shoot dry weight. The
5 ratio of seed yield to above-ground dry weight is relatively stable under many environmental conditions and so a robust correlation between plant size and grain yield can often be obtained. These processes are intrinsically linked because the majority of grain biomass is dependent on current stored photosynthetic productivity by the leaves and stem of the plant. Therefore selecting for plant size, even at early stages of development,
10 opment, has been used as an indicator for future potential.

In some cases (US 20060037108) an increased biomass, mainly a greater shoot biomass was observed after a drought treatment by withholding water for 6 to 8 days.

- 15 There is still a need to identify genes expressed in stress tolerant plants that have the capacity to confer stress resistance to its host plant and to other plant species, especially to confer increased tolerance and/or resistance to environmental stress, preferably under conditions of water deficiency and confers increased biomass production.
- 20 It is an object of this invention to identify new methods to confer stress tolerance and/or resistance in plants or plant cells.

In preferred embodiments of the present invention, thus, abiotic environmental stress refers to drought and low water content, wherein drought stress means any environmental stress which leads to a lack of water in plants or reduction of water supply to
25 plants, including desiccation.

In a further embodiment of the invention the term "increased tolerance to abiotic stress" relates to an increased tolerance to water stress, which is produced as a secondary stress by low temperature and/or salt, and/or as a primary stress during drought or
30 heat.

In accordance with the present invention, in one embodiment, increased tolerance to drought conditions can be determinated and quantified according to the following
35 method:

Transformed plants are grown individually in pots in a growth chamber (York Industriekälte GmbH, Mannheim, Germany). Germination is induced. In case the plants are *Arabidopsis thaliana* sown seeds are kept at 4°C, in the dark, for 3 days in order to
40 induce germination. Subsequently conditions are changed for 3 days to 20°C/ 6°C day/night temperature with a 16/8h day-night cycle at 150 µE. Subsequently the plants are grown under standard growth conditions. In case the plants are *Arabidopsis*

- thaliana, the standard growth conditions are: photoperiod of 16 h light and 8 h dark, 20 °C, 60% relative humidity, and a photon flux density of 200 μ E. Plants are grown and cultured until they develop leaves. In case the plants are *Arabidopsis thaliana* they are watered daily until they were approximately 3 weeks old. Starting at that time drought
- 5 was imposed by withholding water. After the non-transformed wild type plants show visual symptoms of injury, the evaluation starts and plants are scored for symptoms of drought symptoms and biomass production comparison to wild type and neighboring plants for 5 - 6 days in succession.
- 10 Visual symptoms of injury stating for one or any combination of two, three or more of the following features:
- a) wilting
 - b) leaf browning
 - c) loss of turgor, which results in drooping of leaves or needles stems, and flowers,
 - 15 d) drooping and/or shedding of leaves or needles,
 - e) the leaves are green but leaf angled slightly toward the ground compared with controls,
 - f) leaf blades begun to fold (curl) inward,
 - g) premature senescence of leaves or needles,
 - 20 h) loss of chlorophyll in leaves or needles and/or yellowing.

[0028.1.1.1] In another preferred embodiment of the present invention, plant yield is increased by increasing one or more of yield-related traits selected from one or more abiotic stress tolerance(s). In a particularly preferred embodiment of the present inven-

25 tion, said yield-related trait is increased tolerance to heat conditions.

[0029.1.1.1] In a preferred embodiment of the present invention, plant yield is increased by increasing one or more of yield-related traits selected from one or more abiotic stress tolerance(s). In a particularly preferred embodiment of the present inven-

30 tion, said yield-related trait is increased low temperature tolerance, comprising freezing tolerance and/or chilling tolerance.

Environmental temperatures change within minutes to hours in the diurnal cycle, in hours to days as a result of changing weather, and over weeks to months as a result of

35 seasonal changes. Low temperatures impinge on a plethora of biological processes. They retard or inhibit almost all metabolic and cellular processes, with the typical Q_{10} for protein-dependent catalysis lying between 2 and 3. They impact on membrane-based processes, because low temperatures alter the physical properties of lipids and reduce membrane fluidity. At temperatures below zero, there is the additional danger of

40 ice formation. This typically takes place in the apoplast of a cell, leading to withdrawal of water and dehydration of the symplast. The response of plants to low temperature is

an important determinant of their ecological range. The problem of coping with low temperatures is exacerbated by the need to prolong the growing season beyond the short summer found at high latitudes or altitudes.

- 5 Most plants have evolved adaptive strategies to protect themselves against low temperatures. Generally, adaptation to low temperature may be divided into chilling tolerance, and freezing tolerance.

10 Chilling tolerance is naturally found in species from temperate or boreal zones and allows survival and an enhanced growth at low but non-freezing temperatures. Species from tropical or subtropical zones are chilling sensitive and often show wilting, chlorosis or necrosis, slowed growth and even death at temperatures around 10°C during one or more stages of development. Freezing tolerance allows survival at near zero to particularly subzero temperatures. It is believed to be promoted by a process termed cold-
15 acclimation which occurs at low but non-freezing temperatures and provides increased freezing tolerance at subzero temperatures. In addition, most species from temperate regions have life cycles that are adapted to seasonal changes of the temperature. For those plants, low temperatures may also play an important role in plant development through the process of stratification and vernalisation. It becomes obvious that a clear-
20 cut distinction between or definition of chilling tolerance and freezing tolerance is difficult and that the processes may be overlapping or interconnected.

The molecular basis of freezing tolerance has been intensively researched in Arabidopsis. Physiological changes during cold acclimation include changes in lipid composition to increase membrane fluidity, expression of proteins that modify the physical
25 characteristics of membranes, accumulation of compatible solutes like sucrose, raffinose and proline (Cook et al., Proc. Natl. Acad Sci. USA 101, 15243-15248 (2004)), detoxification of active oxygen species and altered leaf development to increase the levels of proteins involved in photosynthetic electron transport and carbon fixation.
30 Some of these changes are specific for low temperature, and others also occur in response to dehydration, mechanical stress.

Less is known about the molecular basis of chilling tolerance at different stages of plant development. Exposure of chilling-sensitive species to low temperatures has a negative
35 impact on seed germination rates as well as early seedling growth and interferes with photosynthesis of the growing plant which may result in photoinhibition. In particular, the process of seed germination strongly depends on environmental temperature and the properties of the seeds determine the level of activity and performance during germination and seedling emergence when being exposed to low temperature. Chilling
40 often delays leaf development and interferes with plastid biogenesis, leading to delayed greening, chlorosis and thickening or deformation of new leaves. Chilling temperatures inhibit respiration, phloem transport, and restrict the utilization of photoassimilate for

growth. As one result, sugars and other metabolites accumulate and cause osmotic imbalance.

5 Chilling tolerance is a major breeding trait because most major crops, particularly corn (maize), bean, rice, soy bean, cotton, tomato, banana, cucumber and potato, are chilling-sensitive.

10 Breeding of crops with improved adaption to abiotic environmental stresses, and particularly low temperature (i.e. chilling tolerance and/or freezing tolerance), will result in a better trait for stress tolerance and is expected to increase quality and yield of the respective crop. However, the genetic and molecular basis of chilling responses is poorly understood. Although genetic diversity has been identified, for example from landraces and related species that grow at light altitudes, and is being introduced into breeding lines, the genes responsible for the qualitative trait loci have not yet been
15 identified. Additionally, it becomes evident that stress tolerance in plants like low temperature, drought, heat and salt stress tolerance have a common theme important for plant growth, namely the availability of water. Plants are typically exposed during their life cycle to conditions of reduced environmental water content.

20 The protection strategies are similar to those of chilling tolerance. For example components of low temperature, drought, heat and salt stress are manifested as osmotic stress, leading to the disruption of homeostasis and ion distribution in the cell (Serrano et al., J Exp Bot 50, 1023–1036 (1999); Zhu J.K. Trends Plant Sci 6, 66–71 (2001a); Wang et al., 2003). Under freezing temperatures, plant cells lose water as a result of
25 ice formation that starts in the apoplast and withdraws water from the symplast (McKersie and Leshem, 1994. Stress and Stress Coping in Cultivated Plants, Kluwer Academic Publishers). Oxidative stress, which frequently accompanies low/high temperature, salinity or drought stress, may cause denaturation of functional or structural proteins (Smirnoff, Curr. Opin. Biotech. 9, 214–219 (1998)). As a consequence these
30 abiotic stresses often activate similar signaling pathways (Shinozaki and Ymaguchi-Shinozaki, 2000; Knight and Knight, 2001; Zhu J.K. Curr. Opin Plant Biol. 4, 401–406 (2001b), Zhu, Annu. Rev. Plant Biol. 53, 247–73 (2002)) and cellular responses, e.g. the production of certain stress proteins, anti-oxidants and compatible solutes (Vierling and Kimpel, 1992; Zhu et al., 1997; Cushman and Bohnert, 2000). For example, heat stress
35 shares transcriptional responses that are similar to response pathways induced by other abiotic stresses (e.g. Swindell et al., BMC Genomics, 8, 125 (2007)).

[0030.1.1.1] Developing stress-tolerant and/or resistant plants, particularly low
temperature tolerant and/or resistant plants, is a strategy that has the potential to solve
40 or mediate at least some of the existing problems (McKersie and Leshem, 1994. Stress and Stress Coping in Cultivated Plants, Kluwer Academic Publishers). However, traditional plant breeding strategies to develop new lines of plants that exhibit tolerance to

these types of stress are relatively slow and require specific resistant lines for crossing with the desired line. Limited germplasm resources for stress tolerance and incompatibility in crosses between distantly related plant species represent significant problems encountered in conventional breeding.

5

[0031.1.1.1] Additionally, the cellular processes leading to drought, low temperature and salt tolerance are complex in nature and involve multiple mechanisms of cellular adaptation and numerous metabolic pathways (McKersie and Leshem, 1994. Stress and Stress Coping in Cultivated Plants, Kluwer Academic Publishers). This multi-
10 component nature of stress tolerance has not only made breeding for tolerance largely unsuccessful, but has also limited the ability to genetically engineer stress tolerance plants using biotechnological methods.

[0032.1.1.1] The results of current research indicate that tolerance to low temperature is a complex quantitative trait. The lack of a mechanistic understanding makes it
15 difficult to design a transgenic approach to improve stress tolerance.

[0033.1.1.1] At the time the invention was made, a couple of genetical and biotechnological approaches are known in order to obtain plants growing under conditions
20 of low temperature. These approaches are generally based on the introduction and expression of genes in plant cells coding for different enzymes, as disclosed for example in WO 2007/044988, WO 2007/078280, WO 1992/013082, WO 2007/052376, WO 2006/137574.

[0034.1.1.1] The overexpression of antioxidant enzymes or ROS-scavenging enzymes is one possibility to engineer tolerance, e.g. transgenic alfalfa plants expressing Mn-superoxide dismutase tend to have reduced injury after water-deficit stress
25 (McKersie et al., Plant Physiol. 111, 1177–1181 (1996)). These same transgenic plants show increased yield in field trials (McKersie et al., 1999. Plant Physiology, 119, 839–
30 847 (1999.); McKersie et al., Plant Physiol. 111, 1177–1181 (1996)). Transgenic plants that overproduce osmolytes such as mannitol, fructans, proline or glycine-betaine also show increased tolerance to some forms of abiotic stress and it is proposed that the synthesized osmolytes act as ROS scavengers (Tarczynski et al., Science 259, 508–
35 510 (1993.); Sheveleva, et al., Plant Physiol. 115, 1211–1219 (1997)).

35

Nevertheless, the transformed and stress resistant plants cited above generally exhibit slower growth and reduced biomass, due to an imbalance in development and physiology of the plant, thus having significant fitness cost (Kasuga et al., Nature Biotech 17, 287–291(1999)). Despite maintaining basic metabolic function this leads to severe
40 biomass and yield loss. Sometimes the root/shoot dry weight ratio increase as plant water stress develops. The increase is mostly due to a relative reduction in shoot dry weight. The ratio of seed yield to above-ground dry weight is relatively stable under

many environmental conditions and so a robust correlation between plant size and grain yield can often be obtained. These processes are intrinsically linked because the majority of grain biomass is dependent on current stored photosynthetic productivity by the leaves and stem of the plant. Therefore selecting for plant size, even at early stages of development, has been used as an indicator for future yield potential.

Accordingly, for the purposes of the description of the present invention, improved or enhanced "chilling tolerance" or variations thereof refers to improved adaptation to low but non-freezing temperatures around 10 °C, preferably temperatures between 1 to 18 °C, more preferably 4-14 °C, and most preferred 8 to 12 °C; hereinafter called "chilling temperature.

For the purposes of the description of the present invention, improved or enhanced "freezing tolerance" or variations thereof refers to improved adaptation to temperatures near or below zero, namely preferably temperatures below 4 °C, more preferably below 3 or 2 °C, and particularly preferred at or below 0 (zero) °C or below -4 °C, or even extremely low temperatures down to -10 °C or lower; hereinafter called "freezing temperature.

More generally, "improved adaptation" to environmental stress like e.g. freezing and/or chilling temperatures refers to an improved plant performance, while plant performance refers to more yield, particularly with regard to one or more of the yield related traits as defined in more detail above.

Accordingly, for the purposes of the description of the present invention, the term "low temperature" with respect to low temperature stress on a plant, and preferably a crop plant, refers to any of the low temperature conditions as described herein, preferably chilling and/or freezing temperatures as defined above, as the context requires. It is understood that a skilled artisan will be able to recognize from the particular context in the present description which temperature or temperature range is meant by "low temperature".

In the present invention, enhanced tolerance to low temperature may, for example and preferably, be determined according to the following method:

Transformed plants are grown in pots in a growth chamber (e.g. York, Mannheim, Germany). In case the plants are *Arabidopsis thaliana* seeds thereof are sown in pots containing a 3.5:1 (v:v) mixture of nutrient rich soil (GS90, Tantau, Wansdorf, Germany) and sand. Plants are grown under standard growth conditions. In case the plants are *Arabidopsis thaliana*, the standard growth conditions are: photoperiod of 16 h light and 8 h dark, 20 °C, 60% relative humidity, and a photon flux density of 200 $\mu\text{mol}/\text{m}^2\text{s}$. Plants are grown and cultured. In case the plants are *Arabidopsis thaliana*

they are watered every second day. After 9 to 10 days the plants are individualized. Cold (e.g. chilling at 11 - 12 °C) is applied 14 days after sowing until the end of the experiment. After a total growth period of 29 to 31 days the plants are harvested and rated by the fresh weight of the aerial parts of the plants, in the case of Arabidopsis preferably the rosettes.

[0035.1.1.1] In another preferred embodiment of the present invention, plant yield is increased by increasing one or more of yield-related traits selected from one or more abiotic stress tolerance(s). In a particularly preferred embodiment of the present invention, said yield-related trait may also be increased salinity tolerance (salt tolerance), tolerance to osmotic stress, increased shade tolerance, increased tolerance to a high plant density, increased tolerance to mechanical stresses, and/or increased tolerance to oxidative stress.

[0036.1.1.1] In another preferred embodiment of the present invention, plant yield is increased by increasing yield in the absence of stress as well as the absence of nutrient deficiencies (= intrinsic yield).

[0037.1.1.1] Accordingly, in preferred embodiments, the present invention provides a method for producing a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing increased yield as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-

helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized
 5 to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor,
 15 nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase,
 20 protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator, translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein,
 35 ubiquitin regulatory protein, UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein,
 40 ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein,

ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease.

5 Furthermore, the present invention provides a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing increased yield as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activi-

10 ties selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, auto-

15 phagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T /

20 prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone

25 receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmo-

30 sensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombina-

35 tion protein, membrane protein, metal ion transporter, microsomal beta-ketoreductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras

40 guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex sub-

unit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl
 cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase,
 phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decar-
 boxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter,
 5 proline dehydrogenase, protein component of the large ribosomal subunit, protein in-
 volved in shmoo formation and bipolar bud site selection, protein involved in sphingol-
 ipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-
 stranded RNA-containing particles, protein required for maturation of ribosomal RNAs,
 protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type
 10 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome,
 repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribo-
 somal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydro-
 genase, short chain fatty acid transporter, signal recognition particle subunit (SRP54),
 signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle
 15 checkpoint complex subunit, splicing factor, Stationary phase protein , subunit of cyto-
 plasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle
 (TRAPP) complex of the cis-Golgi , threonine ammonia-lyase, transcription elongation
 factor, transcription factor, Transcriptional activator , translational elongation factor EF-
 3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport
 20 protein, ubiquitin regulatory protein , UDP-N-acetyl-glucosamine-1-P transferase, v-
 SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydro-
 genase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein,
 YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-
 protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-
 25 protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-
 protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-
 protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-
 protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein,
 YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-
 30 protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein,
 YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease.

In the preferred embodiments of the present invention, yield is increased by improving
 one or more of the yield-related traits as defined herein.

35

Accordingly, in an embodiment, the present invention provides a method for producing
 a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more
 of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from
 such plant cell and/or transgenic plant(s); each showing an increased nutrient use effi-
 40 ciency as compared to a corresponding non-transformed wild type plant cell or plant,
 especially a transgenic plant cell and/or plant with increased NUE and/or increased
 biomass production as compared to a corresponding non-transformed wild type plant

cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translo-

case protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short

5 chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein , subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi , threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein , UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-

15 protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein,

20 ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease.

Furthermore, in particularly preferred embodiments, the present invention provides a

25 transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing increased nutrient use efficiency as compared to a corresponding non-transformed wild type plant cell or plant, especially a transgenic plant cell and/or plant with increased NUE and/or increased biomass production as compared to a corresponding non-transformed wild type plant cell or plant,

30 by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein , autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-

35 protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidylyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling

40

network, cysteine transporter , cytochrome c oxidase subunit VIII, cytosolic catalase,
 cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-
 sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Fac-
 tor arrest protein , G protein coupled pheromone receptor receptor, gamma-glutamyl
 5 kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxy-
 lase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane
 protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcrip-
 tion activator that binds inositol/choline-responsive elements, hexose transporter, his-
 tidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-
 10 lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, in-
 heritance of peroxisomes protein, integral membrane protein localized to late Golgi
 vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine
 transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding
 transcriptional repressor, Meiotic recombination protein , membrane protein, metal ion
 15 transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space pro-
 tein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mito-
 chondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase,
 molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore
 protein, non-essential Ras guanine nucleotide exchange factor, non-essential small
 20 GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein
 complex subunit , nuclear fusion protein precursor, nuclear pore complex subunit, ori-
 gin recognition complex subunit, outer membrane usher protein, oxidoreductase, pep-
 tide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylser-
 ine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopanto-
 25 thenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potas-
 sium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribo-
 somal subunit, protein involved in shmoo formation and bipolar bud site selection, pro-
 tein involved in sphingolipid biosynthesis, protein kinase, protein necessary for struc-
 tural stability of L-A double-stranded RNA-containing particles, protein required for
 30 maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein,
 regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory
 subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation
 inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III
 subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recog-
 35 nition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein
 for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary
 phase protein , subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the
 transport protein particle (TRAPP) complex of the cis-Golgi , threonine ammonia-lyase,
 transcription elongation factor, transcription factor, Transcriptional activator , transla-
 40 tional elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall
 polymer composition, transport protein, ubiquitin regulatory protein , UDP-N-acetyl-
 glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in

Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease.

In other particularly preferred embodiments, the present invention provides a method for producing a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing an increased nutrient use efficiency, especially a transgenic plant cell and/or plant with increased NUE and/or increased biomass production, and an increased stress resistance, particularly abiotic stress resistance, especially an increased low temperature tolerance, in particular an increased tolerance to chilling, and/or an increased water use efficiency, in particular tolerance to drought conditions, as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidylyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol

acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein , membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras

5 guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit , nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase,

15 phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-

20 stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydro-

25 genase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein , subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi , threonine ammonia-lyase, transcription elongation

30 factor, transcription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein , UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein,

35 YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-

40 protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein,

YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease. Furthermore, in such other particularly preferred embodiments, the present invention provides a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived

5 from such plant cell and/or transgenic plant(s); each showing an increased nutrient use efficiency, especially a transgenic plant cell and/or plant with increased NUE and/or increased biomass production, and increased stress resistance, particularly abiotic stress resistance, especially an increased low temperature tolerance, in particular an increased tolerance to chilling, and/or an increased water use efficiency, in particular

10 tolerance to drought conditions, as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-

15 mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltrans-

20 ferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidylyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydro-

25 genase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-

30 loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, ly-

35 sine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mito-

40 chondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like

- proteins, Nuclear cap-binding protein complex subunit , nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomu-
- 5 tase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-
- 10 containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short
- 15 chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein , subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi , threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein , UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-
- 25 protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein,
- 30 ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease.
- 35 Thus, in the most preferred embodiments of the present invention, a method is provided for producing a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing an increased nitrogen use efficiency (NUE) and an increased low temperature tolerance,
- 40 particularly chilling tolerance, as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol

reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate
 kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-
 mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein,
 aromatic amino acid aminotransferase II, ARV1 protein , autophagy-specific phosphati-
 5 dylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-
 protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein,
 b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltrans-
 ferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex pro-
 10 tein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehy-
 drogenase (bifunctional), clathrin associated protein complex small subunit, component
 of the RAM signaling network, cysteine transporter , cytochrome c oxidase subunit VIII,
 cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydro-
 genase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase
 beta subunit, Factor arrest protein , G protein coupled pheromone receptor receptor,
 15 gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, gly-
 cine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit,
 golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-
 loop-helix transcription activator that binds inositol/choline-responsive elements, hex-
 ose transporter, histidine kinase osmosensor that regulates an osmosensing MAP
 20 kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier
 protein dehydratase, inheritance of peroxisomes protein, integral membrane protein
 localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, ly-
 sine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophos-
 pholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein ,
 25 membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochon-
 drial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal pro-
 tein of the large subunit, mitochondrial ribosomal protein of the small subunit, mito-
 chondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol
 transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide
 30 exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like
 proteins, Nuclear cap-binding protein complex subunit , nuclear fusion protein precur-
 sor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane
 usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase,
 PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomu-
 35 tase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphori-
 bosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydro-
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 formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis,
 protein kinase, protein necessary for structural stability of L-A double-stranded RNA-
 40 containing particles, protein required for maturation of ribosomal RNAs, protein translo-
 case protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein ser-
 ine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1

transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint

5 complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator, translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein,

10 ubiquitin regulatory protein, UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein,

15 yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein,

20 YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease. Furthermore, in such most preferred embodiments, the present invention provides a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such

25 plant cell and/or transgenic plant(s); each showing increased nitrogen use efficiency (NUE) and an increased low temperature tolerance, particularly chilling tolerance, as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal

30 protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein,

35 B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling

40 network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Fac-

tor arrest protein , G protein coupled pheromone receptor receptor, gamma-glutamyl
 kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxy-
 lase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane
 protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcrip-
 5 tion activator that binds inositol/choline-responsive elements, hexose transporter, his-
 tidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-
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 10 transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding
 transcriptional repressor, Meiotic recombination protein , membrane protein, metal ion
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 tein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mito-
 chondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase,
 15 molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore
 protein, non-essential Ras guanine nucleotide exchange factor, non-essential small
 GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein
 complex subunit , nuclear fusion protein precursor, nuclear pore complex subunit, ori-
 gin recognition complex subunit, outer membrane usher protein, oxidoreductase, pep-
 20 tide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylser-
 ine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopanto-
 thenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potas-
 sium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribo-
 somal subunit, protein involved in shmoo formation and bipolar bud site selection, pro-
 25 tein involved in sphingolipid biosynthesis, protein kinase, protein necessary for struc-
 tural stability of L-A double-stranded RNA-containing particles, protein required for
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 regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory
 subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation
 30 inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III
 subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recog-
 nition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein
 for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary
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 ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-

- protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease.
- 10 Thus, in the most preferred embodiments of the present invention, a method is provided for producing a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing an increased nitrogen use efficiency (NUE) and an increased water use efficiency, particularly tolerance to drought conditions, as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidylyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondon-

drial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine-threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator, translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein, UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease. Furthermore, in such most preferred embodiments, the present invention provides a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing increased nitrogen use efficiency

(NUE) and an increased water use efficiency (WUE) particularly tolerance to drought conditions, as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S

5 ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein,

10 B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidylyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling

15 network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase,

20 glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydrolyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi

25 vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore

30 protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothienoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for struc-

40

tural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein , subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi , threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein , UDP-N-acetylglucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease.

Thus, in the most preferred embodiments of the present invention, a method is provided for producing a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing an increased nitrogen use efficiency (NUE), an increased low temperature tolerance, particularly chilling tolerance, and an increased water use efficiency, particularly tolerance to drought conditions, as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein , autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall

endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine-threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase, transcription elongation factor, tran-

scription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3),
 transmembrane protein with a role in cell wall polymer composition, transport protein,
 ubiquitin regulatory protein , UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE
 binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase,
 5 yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-
 protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein,
 yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein,
 yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein,
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 10 ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein,
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 YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease.
 15 Furthermore, in such most preferred embodiments, the present invention provides a
 transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of
 such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such
 plant cell and/or transgenic plant(s); each showing increased nitrogen use efficiency
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 20 increased water use efficiency (WUE) particularly tolerance to drought conditions, as
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 25 ductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase pro-
 moting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid ami-
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 plex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein,
 B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-
 30 protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-
 1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cyti-
 dylyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional),
 clathrin associated protein complex small subunit, component of the RAM signaling
 network, cysteine transporter , cytochrome c oxidase subunit VIII, cytosolic catalase,
 35 cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-
 sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Fac-
 tor arrest protein , G protein coupled pheromone receptor receptor, gamma-glutamyl
 kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxy-
 40 lase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane
 protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcrip-
 tion activator that binds inositol/choline-responsive elements, hexose transporter, his-
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lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding
 5 transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore
 10 protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopanto-
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 20 maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III
 25 subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase,
 30 transcription elongation factor, transcription factor, Transcriptional activator, translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein, UDP-N-acetylglucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-
 35 protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-
 40 protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein,

YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease.

Accordingly, in an embodiment, the present invention provides a method for producing

5 a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing an increased nutrient use efficiency as compared to a corresponding non-transformed wild type plant cell or plant, especially a transgenic plant cell and/or plant with increased NUE and/or increased

10 biomass production as compared to a corresponding non-transformed wild type plant cell or plant, and increased yield in the absence of stress as well as the absence of nutrient deficiencies, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate

15 kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein,

20 b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidylyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII,

25 cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit,

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40 transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide

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5 PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis,

10 protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine-threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of

15 the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator, translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein, UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase,

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35 Furthermore, in particularly preferred embodiments, the present invention provides a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing increased nutrient use efficiency as compared to a corresponding non-transformed wild type plant cell or plant, especially a

40 transgenic plant cell and/or plant with increased NUE and/or increased biomass production as compared to a corresponding non-transformed wild type plant cell or plant, and increased yield in the absence of stress as well as the absence of nutrient defi-

ciencies, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translo-

- case protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein , subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi , threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein , UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease.
- In other particularly preferred embodiments, the present invention provides a method for producing a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing an increased nutrient use efficiency, especially a transgenic plant cell and/or plant with increased NUE and/or increased biomass production, and an increased stress resistance, particularly abiotic stress resistance, especially an increased low temperature tolerance, in particular an increased tolerance to chilling, and/or an increased water use efficiency, in particular tolerance to drought conditions, and increased yield in the absence of stress as well as the absence of nutrient deficiencies, as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein , autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-

protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidylyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmo-sensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle

(TRAPP) complex of the cis-Golgi , threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein , UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease.

Furthermore, in such other particularly preferred embodiments, the present invention provides a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing an increased nutrient use efficiency, especially a transgenic plant cell and/or plant with increased NUE and/or increased biomass production, and an increased stress resistance, particularly abiotic stress resistance, especially an increased low temperature tolerance, in particular an increased tolerance to chilling, and/or an increased water use efficiency, in particular tolerance to drought conditions, and increased yield in the absence of stress as well as the absence of nutrient deficiencies, as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein , autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter , cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein , G protein coupled pheromone receptor receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, gly-

cine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit,
 golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-
 loop-helix transcription activator that binds inositol/choline-responsive elements, hex-
 ose transporter, histidine kinase osmosensor that regulates an osmosensing MAP
 5 kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier
 protein dehydratase, inheritance of peroxisomes protein, integral membrane protein
 localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, ly-
 sine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophos-
 pholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein ,
 10 membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochon-
 drial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal pro-
 tein of the large subunit, mitochondrial ribosomal protein of the small subunit, mito-
 chondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol
 transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide
 15 exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like
 proteins, Nuclear cap-binding protein complex subunit , nuclear fusion protein precur-
 sor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane
 usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase,
 PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomu-
 20 tase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphori-
 bosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydro-
 genase, protein component of the large ribosomal subunit, protein involved in shmoo
 formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis,
 protein kinase, protein necessary for structural stability of L-A double-stranded RNA-
 25 containing particles, protein required for maturation of ribosomal RNAs, protein translo-
 case protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein ser-
 ine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1
 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of
 the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short
 30 chain fatty acid transporter, signal recognition particle subunit (SRP54), signal trans-
 ducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint
 complex subunit, splicing factor, Stationary phase protein , subunit of cytoplasmic
 phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) com-
 plex of the cis-Golgi , threonine ammonia-lyase, transcription elongation factor, tran-
 35 scription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3),
 transmembrane protein with a role in cell wall polymer composition, transport protein,
 ubiquitin regulatory protein , UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE
 binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase,
 yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-
 40 protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein,
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 yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein,

ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein,
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Thus, in the most preferred embodiments of the present invention, a method is provided for producing a transgenic plant cell nucleus; a transgenic plant cell; plant(s)
 10 comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing an increased nitrogen use efficiency (NUE) and increased yield, in the absence of stress as well as the absence of nutrient deficiencies, and an increased low temperature tolerance, particularly chilling tolerance, as compared to a corresponding non-transformed
 15 wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein,
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 25 cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase
 30 beta subunit, Factor arrest protein, G protein coupled pheromone receptor receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP
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deficiencies, and an increased low temperature tolerance, particularly chilling tolerance, as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal

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40

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 5 oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase,
 dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease,
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 sensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol
 acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral mem-
 15 brane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein,
 isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprote-
 ase, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombina-
 tion protein , membrane protein, metal ion transporter, microsomal beta-keto-
 reductase, mitochondrial intermembrane space protein, mitochondrial protein, mito-
 20 chondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the
 small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis pro-
 tein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras
 guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac sub-
 family of Ras-like proteins, Nuclear cap-binding protein complex subunit , nuclear fu-
 25 sion protein precursor, nuclear pore complex subunit, origin recognition complex sub-
 unit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl
 cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase,
 phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decar-
 boxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter,
 30 proline dehydrogenase, protein component of the large ribosomal subunit, protein in-
 volved in shmoo formation and bipolar bud site selection, protein involved in sphingol-
 ipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-
 stranded RNA-containing particles, protein required for maturation of ribosomal RNAs,
 protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type
 35 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome,
 repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribo-
 somal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydro-
 genase, short chain fatty acid transporter, signal recognition particle subunit (SRP54),
 signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle
 40 checkpoint complex subunit, splicing factor, Stationary phase protein , subunit of cyto-
 plasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle
 (TRAPP) complex of the cis-Golgi , threonine ammonia-lyase, transcription elongation

factor, transcription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein , UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease.

Furthermore, in such most preferred embodiments, the present invention provides a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing increased nitrogen use efficiency (NUE) and increased yield, in the absence of stress as well as the absence of nutrient deficiencies, and an increased water use efficiency (WUE) particularly tolerance to drought conditions, as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein , autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter , cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein , G protein coupled pheromone receptor receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase

cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein
 dehydratase, inheritance of peroxisomes protein, integral membrane protein localized
 to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, ly-
 sine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophos-
 5 pholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein ,
 membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochon-
 drial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal pro-
 tein of the large subunit, mitochondrial ribosomal protein of the small subunit, mito-
 chondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol
 10 transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide
 exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like
 proteins, Nuclear cap-binding protein complex subunit , nuclear fusion protein precur-
 sor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane
 usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase,
 15 PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomu-
 tase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphori-
 bosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydro-
 genase, protein component of the large ribosomal subunit, protein involved in shmoo
 formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis,
 20 protein kinase, protein necessary for structural stability of L-A double-stranded RNA-
 containing particles, protein required for maturation of ribosomal RNAs, protein translo-
 case protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein ser-
 ine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1
 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of
 25 the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short
 chain fatty acid transporter, signal recognition particle subunit (SRP54), signal trans-
 ducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint
 complex subunit, splicing factor, Stationary phase protein , subunit of cytoplasmic
 phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) com-
 30 plex of the cis-Golgi , threonine ammonia-lyase, transcription elongation factor, tran-
 scription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3),
 transmembrane protein with a role in cell wall polymer composition, transport protein,
 ubiquitin regulatory protein , UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE
 binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase,
 35 yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-
 protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein,
 yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein,
 yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein,
 ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein,
 40 ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein,
 ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-
 protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein,

YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease.

Thus, in the most preferred embodiments of the present invention, a method is provided for producing a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing an increased nitrogen use efficiency (NUE), an increased yield, in the absence of stress as well as the absence of nutrient deficiencies, an increased low temperature tolerance, particularly chilling tolerance, and an increased water use efficiency, particularly tolerance to drought conditions, as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidylyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide

exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase,

5 PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis,

10 protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine-threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of

15 the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator, translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein, UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase,

25 yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein,

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35 Furthermore, in such most preferred embodiments, the present invention provides a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing increased nitrogen use efficiency (NUE), an increased yield in the absence of stress as well as the absence of nutrient

40 deficiencies, an increased low temperature tolerance, particularly chilling tolerance and an increased water use efficiency (WUE) particularly tolerance to drought conditions, as compared to a corresponding non-transformed wild type plant cell or plant, by in-

creasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidylyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydrolyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothienoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein,

regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein , subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi , threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein , UDP-N-acetylglucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease.

Among these particularly preferred embodiments of the present invention, the preferred increased nutrient use efficiency achieved in accordance with the methods of the present invention, and shown by the transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s), which are provided by the present invention, is increased nitrogen use efficiency (NUE).

[0038.1.1.1] In the preferred embodiments of the present invention described above, it is even more preferred the increase or generation of one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylyate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein , autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin syn-

thase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter , cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, 5 dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein , G protein coupled pheromone receptor receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding 10 protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmo-sensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, 15 isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein , membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the 20 small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit , nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, 25 outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, 35 repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein , subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle 40 (TRAPP) complex of the cis-Golgi , threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator , translational elongation factor EF-

3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein, UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease is effected by one or more nucleic acid sequences as shown in table I, column 5 or 7, by one or more proteins each comprising a polypeptide encoded by one or more nucleic acid sequences as shown in table I, column 5 or 7, and/or by one or more protein(s) each comprising a polypeptide as depicted in table II, column 5 or 7.

[0039.1.1.1] For the purpose of the description of the present invention the proteins having an activity selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidylyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster as-

sembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein,

5 mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac sub-family of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fu-

10 sion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter,

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20 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle

25 checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator, translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport

30 protein, ubiquitin regulatory protein, UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-

35 protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-

40 protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease, polypeptides encoded by one or more nucleic acid sequences encoded by one or more

nucleic acid sequences as shown in table I, column 5 or 7, and/or the polypeptides as depicted in table II, application no. 1, column 5 or 7 are named as "NUE related protein" NUERP.

- 5 [0040.1.1.1] Thus, in preferred embodiments, the present invention provides a method for producing a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing increased yield as compared to a corresponding non-transformed wild type plant cell or plant, by
- 10 increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional),
- 20 clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydrolyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding
- 35 transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, ori-
- 40

gin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothienoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein , subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi , threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein , UDP-N-acetylglucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease, which is effected by one or more nucleic acid sequences as shown in table I, column 5 or 7, by one or more proteins each comprising a polypeptide encoded by one or more nucleic acid sequences as shown in table I, column 5 or 7, and/or by one or more protein(s) each comprising a polypeptide as depicted in table II, column 5 or 7. Furthermore, the present invention provides a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing increased yield as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltrans-

ferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidylyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-ketoreductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine-threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribo-

somal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator, translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein, UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease, which is effected by one or more nucleic acid sequences as shown in table I, column 5 or 7, by one or more proteins each comprising a polypeptide encoded by one or more nucleic acid sequences as shown in table I, column 5 or 7, and/or by one or more protein(s) each comprising a polypeptide as depicted in table II, column 5 or 7.

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In these preferred embodiments of the present invention, yield is increased by improving one or more of the yield-related traits as defined herein.

Thus, in particularly preferred embodiments, the present invention provides a method for producing a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing an increased nutrient use efficiency as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall

endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine-threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase, transcription elongation factor, tran-

scription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3),
 transmembrane protein with a role in cell wall polymer composition, transport protein,
 ubiquitin regulatory protein , UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE
 binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase,
 5 yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-
 protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein,
 yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein,
 yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein,
 ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein,
 10 ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein,
 ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-
 protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein,
 YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein,
 YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease,
 15 which is effected by one or more nucleic acid sequences as shown in table I, column 5
 or 7, by one or more proteins each comprising a polypeptide encoded by one or more
 nucleic acid sequences as shown in table I, column 5 or 7, and/or by one or more pro-
 tein(s) each comprising a polypeptide as depicted in table II, column 5 or 7. Further-
 more, in particularly preferred embodiments, the present invention provides a trans-
 20 genic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of
 such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such
 plant cell and/or transgenic plant(s); each showing increased nutrient use efficiency as
 compared to a corresponding non-transformed wild type plant cell or plant, by increas-
 ing or generating one or more activities selected from the group consisting of 2-
 25 dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal
 protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide re-
 ductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase pro-
 moting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid ami-
 notransferase II, ARV1 protein , autophagy-specific phosphatidylinositol 3-kinase com-
 30 plex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein,
 B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-
 protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-
 1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cyti-
 dylyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional),
 35 clathrin associated protein complex small subunit, component of the RAM signaling
 network, cysteine transporter , cytochrome c oxidase subunit VIII, cytosolic catalase,
 cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-
 sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Fac-
 tor arrest protein , G protein coupled pheromone receptor receptor, gamma-glutamyl
 40 kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxy-
 lase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane
 protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcrip-

tion activator that binds inositol/choline-responsive elements, hexose transporter, his-
 tidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-
 lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, in-
 heritance of peroxisomes protein, integral membrane protein localized to late Golgi
 5 vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine
 transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding
 transcriptional repressor, Meiotic recombination protein , membrane protein, metal ion
 transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space pro-
 tein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mito-
 10 chondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase,
 molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore
 protein, non-essential Ras guanine nucleotide exchange factor, non-essential small
 GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein
 complex subunit , nuclear fusion protein precursor, nuclear pore complex subunit, ori-
 15 gin recognition complex subunit, outer membrane usher protein, oxidoreductase, pep-
 tide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylser-
 ine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopanto-
 thenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potas-
 sium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribo-
 20 somal subunit, protein involved in shmoo formation and bipolar bud site selection, pro-
 tein involved in sphingolipid biosynthesis, protein kinase, protein necessary for struc-
 tural stability of L-A double-stranded RNA-containing particles, protein required for
 maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein,
 regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory
 25 subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation
 inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III
 subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recog-
 nition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein
 for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary
 30 phase protein , subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the
 transport protein particle (TRAPP) complex of the cis-Golgi , threonine ammonia-lyase,
 transcription elongation factor, transcription factor, Transcriptional activator , transla-
 tional elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall
 polymer composition, transport protein, ubiquitin regulatory protein , UDP-N-acetyl-
 35 glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in
 Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-
 protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein,
 ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-
 protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-
 40 protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-
 protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-
 protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-

- protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease, which is effected by one or more nucleic acid sequences as shown in
- 5 table I, column 5 or 7, by one or more proteins each comprising a polypeptide encoded by one or more nucleic acid sequences as shown in table I, column 5 or 7, and/or by one or more protein(s) each comprising a polypeptide as depicted in table II, column 5 or 7.
- 10 In other preferred embodiments, the present invention provides a method for producing a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing an increased NUE and/or in-
- 15 creased biomass production, and an increased stress resistance, particularly abiotic stress resistance, especially an increased low temperature tolerance, in particular an increased tolerance to chilling, and/or an increased water use efficiency, in particular tolerance to drought conditions, as compared to a corresponding non-transformed wild
- 20 type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate
- 25 kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphati-
- 30 dylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltrans-
- 35 ferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component
- 40 of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophos-

pholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein ,
 membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochon-
 drial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal pro-
 tein of the large subunit, mitochondrial ribosomal protein of the small subunit, mito-
 5 chondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol
 transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide
 exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like
 proteins, Nuclear cap-binding protein complex subunit , nuclear fusion protein precu-
 sor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane
 10 usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase,
 PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomu-
 tase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphori-
 bosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydro-
 genase, protein component of the large ribosomal subunit, protein involved in shmoo
 15 formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis,
 protein kinase, protein necessary for structural stability of L-A double-stranded RNA-
 containing particles, protein required for maturation of ribosomal RNAs, protein translo-
 case protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein ser-
 ine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1
 20 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of
 the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short
 chain fatty acid transporter, signal recognition particle subunit (SRP54), signal trans-
 ducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint
 complex subunit, splicing factor, Stationary phase protein , subunit of cytoplasmic
 25 phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) com-
 plex of the cis-Golgi , threonine ammonia-lyase, transcription elongation factor, tran-
 scription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3),
 transmembrane protein with a role in cell wall polymer composition, transport protein,
 ubiquitin regulatory protein , UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE
 30 binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase,
 yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-
 protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein,
 yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein,
 yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein,
 35 ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein,
 ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein,
 ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-
 protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein,
 YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein,
 40 YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease,
 which is effected by one or more nucleic acid sequences as shown in table I, column 5
 or 7, by one or more proteins each comprising a polypeptide encoded by one or more

nucleic acid sequences as shown in table I, column 5 or 7, and/or by one or more protein(s) each comprising a polypeptide as depicted in table II, column 5 or 7. Furthermore, in such other particularly preferred embodiments, the present invention provides a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more

5 of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing an increased NUE and/or increased biomass production, and an increased stress resistance, particularly abiotic stress resistance, especially an increased low temperature tolerance, in particular an increased tolerance to chilling, and/or an increased water use efficiency, in particular

10 tolerance to drought conditions, as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-

15 mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltrans-

20 ferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidylyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydro-

25 genase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-

30 loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, ly-

35 sine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mito-

40 chondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like

proteins, Nuclear cap-binding protein complex subunit , nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomu-

5 tase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-

10 containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short

15 chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein , subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi , threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein , UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-

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35 or 7, by one or more proteins each comprising a polypeptide encoded by one or more nucleic acid sequences as shown in table I, column 5 or 7, and/or by one or more protein(s) each comprising a polypeptide as depicted in table II, column 5 or 7.

40 In other preferred embodiments, the present invention provides a method for producing a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing an increased nitrogen use effi-

ciency and an increased low temperature resistance, particularly chilling tolerance, as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydrolyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothienoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for struc-

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transcription elongation factor, transcription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein , UDP-N-acetylglucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease, which is effected by one or more nucleic acid sequences as shown in table I, column 5 or 7, by one or more proteins each comprising a polypeptide encoded by one or more nucleic acid sequences as shown in table I, column 5 or 7, and/or by one or more protein(s) each comprising a polypeptide as depicted in table II, column 5 or 7.

In other preferred embodiments, the present invention provides a method for producing a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing an increased nitrogen use efficiency and an increased water use efficiency, particularly tolerance to drought conditions, as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein , autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter , cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein , G protein coupled pheromone receptor receptor, gamma-glutamyl

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 35 protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease, which is effected by one or more nucleic acid sequences as shown in
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 5 a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more
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 such plant cell and/or transgenic plant(s); each showing an increased nitrogen use effi-
 ciency and an increased low temperature resistance, particularly chilling tolerance, and
 an increased water use efficiency, particularly tolerance to drought conditions, as com-
 10 pared to a corresponding non-transformed wild type plant cell or plant, by increasing or
 generating one or more activities selected from the group consisting of 2-dehydro-3-
 deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein,
 adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase,
 Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting com-
 15 plex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II,
 ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein sub-
 unit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein,
 b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-
 protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase,
 20 chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidylyltransferase,
 chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated
 protein complex small subunit, component of the RAM signaling network, cysteine
 transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hy-
 droxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate
 25 lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G
 protein coupled pheromone receptor receptor, gamma-glutamyl kinase, glucoamylase,
 glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase,
 golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell
 wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds
 30 inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor
 that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine re-
 ductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes
 protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster
 assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-
 35 specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor,
 Meiotic recombination protein, membrane protein, metal ion transporter, microsomal
 beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial pro-
 tein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal pro-
 tein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosyn-
 40 thesis protein, myo-inositol transporter, non-essential kinetochore protein, non-
 essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the
 Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit,

nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein , subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi , threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein , UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease, which is effected by one or more nucleic acid sequences as shown in table I, column 5 or 7, by one or more proteins each comprising a polypeptide encoded by one or more nucleic acid sequences as shown in table I, column 5 or 7, and/or by one or more protein(s) each comprising a polypeptide as depicted in table II, column 5 or 7. Furthermore, in such even more preferred embodiments, the present invention provides a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing increased nitrogen use efficiency and an increased low temperature tolerance, particularly chilling tolerance, and an increased water use efficiency, particularly tolerance to drought conditions, as compared

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protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein , subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi , threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein , UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease, which is effected by one or more nucleic acid sequences as shown in table I, column 5 or 7, by one or more proteins each comprising a polypeptide encoded by one or more nucleic acid sequences as shown in table I, column 5 or 7, and/or by one or more protein(s) each comprising a polypeptide as depicted in table II, column 5 or 7.

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 dylyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional),
 5 clathrin associated protein complex small subunit, component of the RAM signaling
 network, cysteine transporter , cytochrome c oxidase subunit VIII, cytosolic catalase,
 cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-
 sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Fac-
 tor arrest protein , G protein coupled pheromone receptor receptor, gamma-glutamyl
 10 kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxy-
 lase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane
 protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcrip-
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 tidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-
 15 lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, in-
 heritance of peroxisomes protein, integral membrane protein localized to late Golgi
 vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine
 transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding
 transcriptional repressor, Meiotic recombination protein , membrane protein, metal ion
 20 transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space pro-
 tein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mito-
 chondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase,
 molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore
 protein, non-essential Ras guanine nucleotide exchange factor, non-essential small
 25 GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein
 complex subunit , nuclear fusion protein precursor, nuclear pore complex subunit, ori-
 gin recognition complex subunit, outer membrane usher protein, oxidoreductase, pep-
 tide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylser-
 ine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopanto-
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 subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recog-
 40 nition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein
 for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary
 phase protein , subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the

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5 provides a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing increased nutrient efficiency, especially increased nitrogen use efficiency and/or increased biomass production, and an increased yield in the absence of stress as well as the absence of nutrient

10 deficiencies, as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-

20 1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydrolyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine

35 transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein

40

complex subunit , nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopanto-

5 thenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for

10 maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary

15 phase protein , subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi , threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein , UDP-N-acetylglucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-

20 protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-

25 protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease, which is effected by one or more nucleic acid sequences as shown in table I, column 5 or 7, by one or more proteins each comprising a polypeptide encoded

30 by one or more nucleic acid sequences as shown in table I, column 5 or 7, and/or by one or more protein(s) each comprising a polypeptide as depicted in table II, column 5 or 7.

40 In other preferred embodiments, the present invention provides a method for producing a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing an increased nutrient effi-

ciency, especially an increased nitrogen use efficiency and/or increased biomass production, and an increased stress resistance, particularly abiotic stress resistance, especially an increased low temperature tolerance, in particular an increased tolerance to chilling, and/or an increased water use efficiency, in particular tolerance to drought

5 conditions, and increased yield in the absence of stress as well as the absence of nutrient deficiencies, as compared to the corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl

10 hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein,

15 B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase,

20 cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi

25 membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized

30 to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor,

40 nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomu-

tase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine-threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator, translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein, UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease, which is effected by one or more nucleic acid sequences as shown in table I, column 5 or 7, by one or more proteins each comprising a polypeptide encoded by one or more nucleic acid sequences as shown in table I, column 5 or 7, and/or by one or more protein(s) each comprising a polypeptide as depicted in table II, column 5 or 7. Furthermore, in such even more preferred embodiments, the present invention provides a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing increased nutrient efficiency, especially increased nitrogen use efficiency and/or increased biomass production, and an increased stress resistance, particular abiotic stress resistance, especially low temperature tolerance, in particular tolerance to chilling, and/or an increased water use efficiency, in particular tolerance to drought conditions, and an increased yield in the absence of stress as well as the absence of nutrient deficiencies, as compared to a

corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidylyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs,

protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein , subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi , threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein , UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease, which is effected by one or more nucleic acid sequences as shown in table I, column 5 or 7, by one or more proteins each comprising a polypeptide encoded by one or more nucleic acid sequences as shown in table I, column 5 or 7, and/or by one or more protein(s) each comprising a polypeptide as depicted in table II, column 5 or 7.

In other preferred embodiments, the present invention provides a method for producing a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing an increased nitrogen use efficiency and increased yield in the absence of stress as well as the absence of nutrient deficiencies, and an increased low temperature tolerance, particularly chilling tolerance, as compared to the corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein , autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein,

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 1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cyti-
 dylyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional),
 5 clathrin associated protein complex small subunit, component of the RAM signaling
 network, cysteine transporter , cytochrome c oxidase subunit VIII, cytosolic catalase,
 cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-
 sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Fac-
 tor arrest protein , G protein coupled pheromone receptor receptor, gamma-glutamyl
 10 kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxy-
 lase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane
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 15 lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, in-
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 transcriptional repressor, Meiotic recombination protein , membrane protein, metal ion
 20 transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space pro-
 tein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mito-
 chondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase,
 molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore
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 25 GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein
 complex subunit , nuclear fusion protein precursor, nuclear pore complex subunit, ori-
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 tide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylser-
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kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydrolyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothienoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator, translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein, UDP-N-acetylglucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-

protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease, which is effected by one or more nucleic acid sequences as shown in table I, column 5 or 7, by one or more proteins each comprising a polypeptide encoded by one or more nucleic acid sequences as shown in table I, column 5 or 7, and/or by one or more protein(s) each comprising a polypeptide as depicted in table II, column 5 or 7.

In other preferred embodiments, the present invention provides a method for producing a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing an increased nitrogen use efficiency and increased yield in the absence of stress as well as the absence of nutrient deficiencies, and an increased water use efficiency, particularly tolerance to drought conditions, as compared to the corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydrolyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi

vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothienoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator, translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein, UDP-N-acetylglucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease, which is effected by one or more nucleic acid sequences as shown in

table I, column 5 or 7, by one or more proteins each comprising a polypeptide encoded by one or more nucleic acid sequences as shown in table I, column 5 or 7, and/or by one or more protein(s) each comprising a polypeptide as depicted in table II, column 5 or 7. Furthermore, in such even more preferred embodiments, the present invention

5 provides a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing increased nitrogen use efficiency and an increased yield in the absence of stress as well as the absence of nutrient deficiencies, and an increased water use efficiency, particularly tolerance to

10 drought conditions, as compared to a corresponding non-transformed wild type plant cell or plant, by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase,

15 anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall

20 endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-

25 sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-

30 helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, ly-

35 sine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mito-

40 chondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like

proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine-threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator, translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein, UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease, which is effected by one or more nucleic acid sequences as shown in table I, column 5 or 7, by one or more proteins each comprising a polypeptide encoded by one or more nucleic acid sequences as shown in table I, column 5 or 7, and/or by one or more protein(s) each comprising a polypeptide as depicted in table II, column 5 or 7.

In other preferred embodiments, the present invention provides a method for producing a transgenic plant cell nucleus; a transgenic plant cell; plant(s) comprising one or more of such transgenic nuclei or plant cell(s); progeny, seed, and/or pollen derived from such plant cell and/or transgenic plant(s); each showing an increased nitrogen use effi-

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10 ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase,

15 chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G

20 protein coupled pheromone receptor receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor

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30 Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-

35 essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase,

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plex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine-threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54),

signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator, translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein, UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease, which is effected by one or more nucleic acid sequences as shown in table I, column 5 or 7, by one or more proteins each comprising a polypeptide encoded by one or more nucleic acid sequences as shown in table I, column 5 or 7, and/or by one or more protein(s) each comprising a polypeptide as depicted in table II, column 5 or 7.

[0041.1.1.1] In a preferred embodiment of the invention a photosynthetic active organism, especially a plant, shows an enhanced NUE.

[0042.1.1.1] In another preferred embodiment a photosynthetic active organism, especially a plant, shows increased biomass production and/or yield under conditions of limited nitrogen supply.

[0043.1.1.1] In another embodiment this invention fulfills the need to identify new, unique genes capable of effecting an increased yield in a plant upon expression or over-expression of endogenous and/or exogenous genes.

In preferred embodiments thereof, this invention fulfills the need to identify new, unique genes capable of effecting an increased yield in a plant upon expression or over-expression of one or more endogenous genes.

In preferred embodiments thereof, this invention fulfills the need to identify new, unique genes capable of effecting an increased yield in a plant upon expression or over-expression of one or more exogenous genes.

In another embodiment this invention fulfills the need to identify new, unique genes capable of effecting an increased nutrient efficiency, especially an increased NUE, and an increased stress resistance, particularly abiotic stress resistance, especially an increased low temperature tolerance, in particular an increased tolerance to chilling,
5 and/or an increased water use efficiency, in particular tolerance to drought conditions, in a plant upon expression or over-expression of endogenous and/or exogenous genes.

In preferred embodiments thereof, this invention fulfills the need to identify new, unique
10 genes capable of effecting an increased nutrient efficiency, especially an increased NUE, and an increased stress resistance, particularly abiotic stress resistance, especially an increased low temperature tolerance, in particular an increased tolerance to chilling, and/or an increased water use efficiency, in particular tolerance to drought conditions, in a plant upon expression or over-expression of one or more endogenous
15 genes.

In preferred embodiments thereof, this invention fulfills the need to identify new, unique genes capable of effecting an increased nutrient efficiency, especially an increased NUE, and an increased stress resistance, particularly abiotic stress resistance, especially an increased low temperature tolerance, in particular an increased tolerance to chilling, and/or an increased water use efficiency, in particular tolerance to drought conditions, in a plant upon expression or over-expression of one or more exogenous
20 genes.

25 In another embodiment this invention fulfills the need to identify new, unique genes capable of effecting an increased NUE, and an increased low temperature tolerance, in particular an increased tolerance to chilling, in a plant upon expression or over-expression of endogenous and/or exogenous genes.

30 In preferred embodiments thereof, this invention fulfills the need to identify new, unique genes capable of effecting an increased NUE, and an increased low temperature tolerance, in particular an increased tolerance to chilling, in a plant upon expression or over-expression of one or more endogenous genes.

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40 In another embodiment this invention fulfills the need to identify new, unique genes capable of effecting an increased NUE, and an increased water use efficiency, in par-

ticular tolerance to drought conditions, in a plant upon expression or over-expression of endogenous and/or exogenous genes.

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10 In preferred embodiments thereof, this invention fulfills the need to identify new, unique genes capable of effecting an increased NUE, and an increased water use efficiency, in particular tolerance to drought conditions, in a plant upon expression or over-expression of one or more exogenous genes.

15 In another embodiment this invention fulfills the need to identify new, unique genes capable of effecting an increased NUE, an increased low temperature tolerance, in particular an increased tolerance to chilling, and an increased water use efficiency, in particular tolerance to drought conditions, in a plant upon expression or over-expression of endogenous and/or exogenous genes.

20 In preferred embodiments thereof, this invention fulfills the need to identify new, unique genes capable of effecting an increased NUE, an increased low temperature tolerance, in particular an increased tolerance to chilling, and an increased water use efficiency, in particular tolerance to drought conditions, in a plant upon expression or over-expression of one or more endogenous genes.

25 In preferred embodiments thereof, this invention fulfills the need to identify new, unique genes capable of effecting an increased NUE, an increased low temperature tolerance, in particular an increased tolerance to chilling, and an increased water use efficiency, in particular tolerance to drought conditions, in a plant upon expression or over-expression of one or more exogenous genes.

30 In another embodiment this invention fulfills the need to identify new, unique genes capable of effecting an increased nutrient efficiency, especially an increased NUE, and an increased yield in the absence of stress as well as the absence of nutrient deficiencies, in a plant upon expression or over-expression of endogenous and/or exogenous genes.

40 In preferred embodiments thereof, this invention fulfills the need to identify new, unique genes capable of effecting an increased nutrient efficiency, especially an increased NUE, and an increased yield in the absence of stress as well as the absence of nutrient deficiencies, in a plant upon expression or over-expression of one or more endogenous genes.

5 In preferred embodiments thereof, this invention fulfills the need to identify new, unique genes capable of effecting an increased nutrient efficiency, especially an increased NUE, and an increased yield in the absence of stress as well as the absence of nutrient deficiencies, in a plant upon expression or over-expression of one or more exogenous genes.

10 In another embodiment this invention fulfills the need to identify new, unique genes capable of effecting an increased nutrient efficiency, especially an increased NUE, an increased stress resistance, particularly abiotic stress resistance, especially an increased low temperature tolerance, in particular an increased tolerance to chilling, and/or an increased water use efficiency, in particular tolerance to drought conditions, and an increased yield in the absence of stress as well as the absence of nutrient deficiencies, in a plant upon expression or over-expression of endogenous and/or exogenous genes.

20 In preferred embodiments thereof, this invention fulfills the need to identify new, unique genes capable of effecting an increased nutrient efficiency, especially an increased NUE, and an increased stress resistance, particularly abiotic stress resistance, especially an increased low temperature tolerance, in particular an increased tolerance to chilling, and/or an increased water use efficiency, in particular tolerance to drought conditions, and an increased yield in the absence of stress as well as the absence of nutrient deficiencies, in a plant upon expression or over-expression of one or more endogenous genes.

25 In preferred embodiments thereof, this invention fulfills the need to identify new, unique genes capable of effecting an increased nutrient efficiency, especially an increased NUE, and an increased stress resistance, particularly abiotic stress resistance, especially an increased low temperature tolerance, in particular an increased tolerance to chilling, and/or an increased water use efficiency, in particular tolerance to drought conditions, and an increased yield in the absence of stress as well as the absence of nutrient deficiencies, in a plant upon expression or over-expression of one or more exogenous genes.

35 In another embodiment this invention fulfills the need to identify new, unique genes capable of effecting an increased NUE, an increased low temperature tolerance, in particular an increased tolerance to chilling, and an increased yield in the absence of stress as well as the absence of nutrient deficiencies, in a plant upon expression or over-expression of endogenous and/or exogenous genes.

40 In preferred embodiments thereof, this invention fulfills the need to identify new, unique genes capable of effecting an NUE, an increased low temperature tolerance, in particu-

lar an increased tolerance to chilling, and an increased yield in the absence of stress as well as the absence of nutrient deficiencies, in a plant upon expression or over-expression of one or more endogenous genes.

- 5 In preferred embodiments thereof, this invention fulfills the need to identify new, unique genes capable of effecting an increased NUE, an increased low temperature tolerance, and an increased yield in the absence of stress as well as the absence of nutrient deficiencies, in a plant upon expression or over-expression of one or more exogenous genes.
- 10 In another embodiment this invention fulfills the need to identify new, unique genes capable of effecting an increased NUE, an increased water use efficiency, in particular tolerance to drought conditions, and an increased yield in the absence of stress as well as the absence of nutrient deficiencies, in a plant upon expression or over-expression of endogenous and/or exogenous genes.
- 15 In preferred embodiments thereof, this invention fulfills the need to identify new, unique genes capable of effecting an increased NUE, an increased water use efficiency, in particular tolerance to drought conditions, and an increased yield in the absence of stress as well as the absence of nutrient deficiencies, in a plant upon expression or
- 20 over-expression of one or more endogenous genes.
- In preferred embodiments thereof, this invention fulfills the need to identify new, unique genes capable of effecting an increased NUE, an increased water use efficiency, in particular tolerance to drought conditions, and an increased yield in the absence of
- 25 stress as well as the absence of nutrient deficiencies, in a plant upon expression or over-expression of one or more exogenous genes.
- In another embodiment this invention fulfills the need to identify new, unique genes capable of effecting an increased NUE, an increased low temperature tolerance, in
- 30 particular an increased tolerance to chilling, an increased water use efficiency, in particular tolerance to drought conditions, and an increased yield in the absence of stress as well as the absence of nutrient deficiencies, in a plant upon expression or over-expression of endogenous and/or exogenous genes.
- 35 In preferred embodiments thereof, this invention fulfills the need to identify new, unique genes capable of effecting an increased NUE, an increased low temperature tolerance, in particular an increased tolerance to chilling, an increased water use efficiency, in particular tolerance to drought conditions, and an increased yield in the absence of stress as well as the absence of nutrient deficiencies, in a plant upon expression or
- 40 over-expression of one or more endogenous genes.

In preferred embodiments thereof, this invention fulfills the need to identify new, unique genes capable of effecting an increased NUE, an increased low temperature tolerance, in particular an increased tolerance to chilling, an increased water use efficiency, in particular tolerance to drought conditions, and an increased yield in the absence of stress as well as the absence of nutrient deficiencies, in a plant upon expression or over-expression of one or more exogenous genes.

In another embodiment this invention fulfills the need to identify new, unique genes capable of conferring enhanced nutrient efficiency, especially enhanced NUE, to photosynthetic active organism, preferably plants, upon expression or over-expression of one or more endogenous and/or exogenous genes.

In another embodiment thereof this invention fulfills the need to identify new, unique genes capable of conferring enhanced nutrient efficiency, especially enhanced NUE, to photosynthetic active organism, preferably plants, upon expression or over-expression of one or more endogenous genes.

In another embodiment thereof this invention fulfills the need to identify new, unique genes capable of conferring enhanced nutrient efficiency, especially enhanced NUE, to photosynthetic active organism, preferably plants, upon expression or over-expression of one or more exogenous genes.

In another embodiment this invention fulfills the need to identify new, unique genes capable of conferring an increase of biomass production to photosynthetic active organism, preferably plants, upon expression or over-expression of one or more endogenous and/or exogenous genes.

In another embodiment thereof this invention fulfills the need to identify new, unique genes capable of conferring an increase of biomass production to photosynthetic active organism, preferably plants, upon expression or over-expression of one or more endogenous genes.

In another embodiment thereof this invention fulfills the need to identify new, unique genes capable of conferring an increase of biomass production to photosynthetic active organism, preferably plants, upon expression or over-expression of one or more exogenous genes.

In another embodiment this invention fulfills the need to identify new, unique genes capable of conferring an enhanced NUE in combination with an increase of biomass production to photosynthetic active organism, preferably plants, upon expression or over-expression of one or more endogenous and/or exogenous genes.

In another embodiment thereof this invention fulfills the need to identify new, unique genes capable of conferring an enhanced NUE in combination with an increase of biomass production to photosynthetic active organism, preferably plants, upon expression or over-expression of one or more endogenous genes.

5

In another embodiment this invention fulfills the need to identify new, unique genes capable of conferring an enhanced NUE in combination with an increase of biomass production to photosynthetic active organism, preferably plants, upon expression or over-expression of one or more exogenous genes.

10

Thus, in the most preferred embodiments of the present invention, this invention fulfills the need to identify new, unique genes capable of effecting an increased nitrogen use efficiency (NUE), optionally an increased low temperature tolerance, particularly chilling tolerance, optionally an increased water use efficiency, in particular tolerance to drought conditions, and optionally an increased yield in the absence of stress as well as the absence of nutrient deficiencies. In each of the above described preferred embodiments, it is preferred that said genes of the invention have the capacity of increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidylyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydrolyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding

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transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothienoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator, translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein, UDP-N-acetylglucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease. In these preferred embodiments of the present invention, it is even more preferred that the increase or generation of one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol

reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate
 kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-
 mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein,
 aromatic amino acid aminotransferase II, ARV1 protein , autophagy-specific phosphati-
 5 dylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-
 protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein,
 b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltrans-
 ferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex pro-
 10 tein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehy-
 drogenase (bifunctional), clathrin associated protein complex small subunit, component
 of the RAM signaling network, cysteine transporter , cytochrome c oxidase subunit VIII,
 cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydro-
 genase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase
 beta subunit, Factor arrest protein , G protein coupled pheromone receptor receptor,
 15 gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, gly-
 cine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit,
 golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-
 loop-helix transcription activator that binds inositol/choline-responsive elements, hex-
 ose transporter, histidine kinase osmosensor that regulates an osmosensing MAP
 20 kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier
 protein dehydratase, inheritance of peroxisomes protein, integral membrane protein
 localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, ly-
 sine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophos-
 pholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein ,
 25 membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochon-
 drial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal pro-
 tein of the large subunit, mitochondrial ribosomal protein of the small subunit, mito-
 chondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol
 transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide
 30 exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like
 proteins, Nuclear cap-binding protein complex subunit , nuclear fusion protein precur-
 sor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane
 usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase,
 PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomu-
 35 tase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphori-
 bosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydro-
 genase, protein component of the large ribosomal subunit, protein involved in shmoo
 formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis,
 protein kinase, protein necessary for structural stability of L-A double-stranded RNA-
 40 containing particles, protein required for maturation of ribosomal RNAs, protein translo-
 case protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein ser-
 ine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1

transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator, translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein, UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease is effected by one or more nucleic acid sequences as shown in table I, column 5 or 7, by one or more proteins encoded by one or more nucleic acid sequences as shown in table I, column 5 or 7, and/or by one or more protein(s) as depicted in table II, column 5 or 7. The need to identify such new, unique genes is particularly fulfilled by providing the NUERP encoding genes disclosed herein.

[0044.1.1.1] Accordingly, the present invention relates to a method for producing a transgenic photosynthetic active organism or a part thereof, preferably a plant cell, a plant or a part thereof, resulting in increased yield, preferably with enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type photosynthetic active organism or a part thereof, preferably a plant cell, a plant or a part thereof, which comprises

(a) increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-

protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidylyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network,

5 cysteine transporter , cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein , G protein coupled pheromone receptor receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit,

10 glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein , membrane protein, metal

20 ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit , nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase,

30 phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small

35 subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint

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- complex subunit, splicing factor, Stationary phase protein , subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi , threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein , UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease. in a photosynthetic active organism or a part thereof, preferably a plant cell, a plant or a part thereof,
- 20 and
- (b) growing the photosynthetic active organism or a part thereof, preferably a plant cell, a plant or a part thereof under conditions which permit the development of a photosynthetic active organism or a part thereof, preferably a plant cell, a plant or a part thereof, showing increased yield, preferably enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type photosynthetic active organism or a part thereof, preferably a plant cell, a plant or a part thereof.
- 25
- 30 [0045.1.1.1] In an further embodiment, the present invention relates to a method for producing a transgenic plant cell nucleus, a transgenic plant cell, a transgenic plant or a part thereof, resulting in increased yield as compared to a corresponding non-transformed wild type plant cell, a transgenic plant or a part thereof, which comprises
- (a) increasing or generating, in said plant cell nucleus, plant cell, plant or part thereof, one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein , autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-
- 35
- 40

protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine
 acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase
 3 complex protein, cholinephosphate cytidylyltransferase, chorismate mutase T /
 prephenate dehydrogenase (bifunctional), clathrin associated protein complex
 5 small subunit, component of the RAM signaling network, cysteine transporter ,
 cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxy-
 methyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phos-
 phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest
 protein , G protein coupled pheromone receptor receptor, gamma-glutamyl
 10 kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decar-
 boxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi
 membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-
 loop-helix transcription activator that binds inositol/choline-responsive elements,
 hexose transporter, histidine kinase osmosensor that regulates an osmosensing
 15 MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol
 acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral
 membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly
 protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific
 metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor,
 20 Meiotic recombination protein , membrane protein, metal ion transporter, micro-
 somal beta-keto-reductase, mitochondrial intermembrane space protein, mito-
 chondrial protein, mitochondrial ribosomal protein of the large subunit, mitochon-
 drial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase,
 molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kine-
 25 tochore protein, non-essential Ras guanine nucleotide exchange factor, non-
 essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear
 cap-binding protein complex subunit , nuclear fusion protein precursor, nuclear
 pore complex subunit, origin recognition complex subunit, outer membrane usher
 protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase,
 30 PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomu-
 tase/phosphomannomutase, phosphopantothienoylcysteine decarboxylase,
 Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter,
 proline dehydrogenase, protein component of the large ribosomal subunit, protein
 involved in shmoo formation and bipolar bud site selection, protein involved in
 35 sphingolipid biosynthesis, protein kinase, protein necessary for structural stability
 of L-A double-stranded RNA-containing particles, protein required for maturation
 of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regula-
 tory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory
 subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-
 40 dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit,
 RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid
 transporter, signal recognition particle subunit (SRP54), signal transducing MEK

- kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator, translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein, UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease;
- 20 (b) growing a plant cell, a plant or a part thereof under conditions, preferably in presence or absence of nutrient deficiency and/or abiotic stress, which permits the development of a plant cell, a plant or a part thereof, showing increased yield as compared to a corresponding non-transformed wild type plant cell, a transgenic plant or a part thereto,
- 25 and
- (c) selecting the plant cell, a plant or a part thereof, showing increased yield, preferably improved nutrient use efficiency and/or abiotic stress resistance, as compared to a corresponding non-transformed wild type plant cell, a transgenic plant or a part thereof which shows visual symptoms of deficiency and/or death under
- 30 said conditions.

- [0046.1.1.1] In an embodiment the present invention relates to a method for producing a transgenic photosynthetic active organism or a part thereof, preferably a plant cell, a plant or a part thereof with enhanced NUE and/or increased biomass production,
- 35 as compared to a corresponding non-transformed wild type photosynthetic active organism or a part thereof, preferably a plant cell, a plant or a part thereof, which comprises
- (a) increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S
- 40 ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor pro-

tein, aromatic amino acid aminotransferase II, ARV1 protein , autophagy-specific
 phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-
 protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-
 protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-
 5 protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaper-
 one, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase,
 chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associ-
 ated protein complex small subunit, component of the RAM signaling network,
 cysteine transporter , cytochrome c oxidase subunit VIII, cytosolic catalase, cyto-
 10 solic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-
 sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta sub-
 unit, Factor arrest protein , G protein coupled pheromone receptor receptor,
 gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit,
 glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor
 15 subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding
 protein, helix-loop-helix transcription activator that binds inositol/choline-
 responsive elements, hexose transporter, histidine kinase osmosensor that regu-
 lates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reduc-
 tase, hydroxymyristol acyl carrier protein dehydratase, inheritance of perox-
 20 isomes protein, integral membrane protein localized to late Golgi vesicles, iron
 sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter
 subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding tran-
 scriptional repressor, Meiotic recombination protein , membrane protein, metal
 ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane
 25 space protein, mitochondrial protein, mitochondrial ribosomal protein of the large
 subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-
 tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter,
 non-essential kinetochore protein, non-essential Ras guanine nucleotide ex-
 change factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like
 30 proteins, Nuclear cap-binding protein complex subunit , nuclear fusion protein
 precursor, nuclear pore complex subunit, origin recognition complex subunit,
 outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-
 prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase,
 phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine de-
 35 carboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen
 antiporter, proline dehydrogenase, protein component of the large ribosomal
 subunit, protein involved in shmoo formation and bipolar bud site selection, pro-
 tein involved in sphingolipid biosynthesis, protein kinase, protein necessary for
 structural stability of L-A double-stranded RNA-containing particles, protein re-
 40 quired for maturation of ribosomal RNAs, protein translocase protein, Regulatory
 CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phos-
 phatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription,

- Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator, translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein, UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease. in a photosynthetic active organism or a part thereof, preferably a plant cell, a plant or a part thereof,
- 25 (b) growing the photosynthetic active organism or a part thereof, preferably a plant cell, a plant or a part thereof together with non-transformed wildtype photosynthetic active organism or a part thereof, preferably a plant, under conditions of limited nitrogen supply,
- and
- 30 (c) selecting the photosynthetic active organism or a part thereof, preferably a plant cell, a plant or a part thereof, with enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type photosynthetic active organism or a part thereof, preferably a plant cell, a plant or a part thereof, after the non-transformed wild type photosynthetic active organism or a part thereof, preferably a plant cell, a plant or a part thereof, show visual symptoms of deficiency and/or death.
- 35

[0047.1.1.1] In one embodiment the present invention relates to a method for producing a transgenic photosynthetic active organism or a part thereof, preferably plant cell nucleus, a plant cell, a plant or a part thereof, resulting in increased yield, especially enhanced NUE and/or increased biomass production, as compared to a corre-

40

sponding non-transformed wild type photosynthetic active organism or a part thereof, preferably a plant cell, a plant or a part thereof, which comprises

- (a) increasing or generating the activity of a protein as shown in table II, application no. 1, column 3, preferably encoded by the nucleic acid sequences as shown in table I, application no. 1, column 5, in photosynthetic active organism or a part thereof, preferably a plant cell nucleus, a plant cell, a plant or a part thereof, and
- (b) growing the photosynthetic active organism or a part thereof, preferably a plant cell, a plant or a part thereof under conditions which permit the development of a plant showing increased yield, especially enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type photosynthetic active organism or a part thereof, preferably a plant.

- [0048.1.1.1] Accordingly, the present invention relates to a method for producing a transgenic plant cell, a plant or a part thereof, resulting in increased yield, especially enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof, which comprises
- (a) increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron

sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter
 subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding tran-
 scriptional repressor, Meiotic recombination protein , membrane protein, metal
 ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane
 5 space protein, mitochondrial protein, mitochondrial ribosomal protein of the large
 subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-
 tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter,
 non-essential kinetochore protein, non-essential Ras guanine nucleotide ex-
 change factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like
 10 proteins, Nuclear cap-binding protein complex subunit , nuclear fusion protein
 precursor, nuclear pore complex subunit, origin recognition complex subunit,
 outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-
 prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase,
 phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine de-
 15 carboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen
 antiporter, proline dehydrogenase, protein component of the large ribosomal
 subunit, protein involved in shmoo formation and bipolar bud site selection, pro-
 tein involved in sphingolipid biosynthesis, protein kinase, protein necessary for
 structural stability of L-A double-stranded RNA-containing particles, protein re-
 20 quired for maturation of ribosomal RNAs, protein translocase protein, Regulatory
 CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phos-
 phatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription,
 Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small
 subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain
 25 fatty acid transporter, signal recognition particle subunit (SRP54), signal trans-
 ducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint
 complex subunit, splicing factor, Stationary phase protein , subunit of cytoplasmic
 phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP)
 complex of the cis-Golgi , threonine ammonia-lyase, transcription elongation fac-
 30 tor, transcription factor, Transcriptional activator , translational elongation factor
 EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition,
 transport protein, ubiquitin regulatory protein , UDP-N-acetyl-glucosamine-1-P
 transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi trans-
 port, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein,
 35 ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein,
 ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-
 protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein,
 YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-
 protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein,
 40 YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-
 protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein,
 YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-

protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease in an organelle, especially the plastid, of a plant cell,

and

- 5 (b) growing the plant cell under conditions which permit the development of a plant showing increased yield, especially enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant.

- [0048.2.1.1] In another embodiment the present invention relates to a method for
10 producing a transgenic plant cell, a plant or a part thereof, resulting in increased yield, especially enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof, which comprises
- (a) increasing or generating one or more activities selected from the group consisting
15 of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific
20 phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase,
25 chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor receptor,
30 gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane
35
40

space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator, translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein, UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease in the cytosol of a plant cell,

and

- (b) growing the plant cell under conditions which permit the development of a plant showing increased yield, especially enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant.

5 [0049.1.1.1] In one embodiment the present invention relates to a method for producing a transgenic plant cell, a plant or a part thereof, resulting in increased yield, especially enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof, which comprises

10 (a) increasing or generating the activity of a protein as shown in table II, application no. 1, column 3, preferably encoded by the nucleic acid sequences as shown in table I, application no. 1, column 5 or 7, in an organelle, especially in the plastid, of a plant cell,

and

15 (b) growing the plant cell under conditions which permit the development of a plant showing increased yield, especially enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant.

20 [0049.2.1.1] In one embodiment the present invention relates to a method for producing a transgenic plant cell, a plant or a part thereof, resulting in increased yield, especially enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof, which comprises

25 (a) increasing or generating the activity of a protein as shown in table II, application no. 1, column 3, preferably encoded by the nucleic acid sequences as shown in table I, application no. 1, column 5 or 7, in the cytosol of a plant cell,

and

30 (b) growing the plant cell under conditions which permit the development of a plant showing increased yield, especially enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant.

35 [0050.1.1.1] In another embodiment the present invention is related to a method for producing a transgenic plant cell, a plant or a part thereof, resulting in increased yield, especially enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof, which comprises

40 (a) increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific

phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-
 protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-
 protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-
 protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaper-
 one, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase,
 chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associ-
 ated protein complex small subunit, component of the RAM signaling network,
 cysteine transporter , cytochrome c oxidase subunit VIII, cytosolic catalase, cyto-
 solic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydro-
 sphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta sub-
 unit, Factor arrest protein , G protein coupled pheromone receptor receptor,
 gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit,
 glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor
 subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding
 protein, helix-loop-helix transcription activator that binds inositol/choline-
 responsive elements, hexose transporter, histidine kinase osmosensor that regu-
 lates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reduc-
 tase, hydroxymyristol acyl carrier protein dehydratase, inheritance of perox-
 isomes protein, integral membrane protein localized to late Golgi vesicles, iron
 sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter
 subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding tran-
 scriptional repressor, Meiotic recombination protein , membrane protein, metal
 ion transporter, microsomal beta-keto-reductase, mitochondrial intermembrane
 space protein, mitochondrial protein, mitochondrial ribosomal protein of the large
 subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-
 tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter,
 non-essential kinetochore protein, non-essential Ras guanine nucleotide ex-
 change factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like
 proteins, Nuclear cap-binding protein complex subunit , nuclear fusion protein
 precursor, nuclear pore complex subunit, origin recognition complex subunit,
 outer membrane usher protein, oxidoreductase, peptide transporter, peptidyl-
 prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase,
 phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine de-
 carboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen
 antiporter, proline dehydrogenase, protein component of the large ribosomal
 subunit, protein involved in shmoo formation and bipolar bud site selection, pro-
 tein involved in sphingolipid biosynthesis, protein kinase, protein necessary for
 structural stability of L-A double-stranded RNA-containing particles, protein re-
 quired for maturation of ribosomal RNAs, protein translocase protein, Regulatory
 CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phos-
 phatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription,
 Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small

- subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein, subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi, threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator, translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein, UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease. in an organelle of a plant cell; or
- (b) increasing or generating the activity of a protein as shown in table II, application no. 1, column 3 encoded by the nucleic acid sequences as shown in table I, application no. 1, column 5 or 7, which are joined to a nucleic acid sequence encoding a transit peptide in a plant cell; or
- (c) increasing or generating the activity of a protein as shown in table II, application no. 1, column 3 encoded by the nucleic acid sequences as shown in table I, application no. 1, column 5 or 7, which are joined to a nucleic acid sequence encoding an organelle localization sequence, especially a chloroplast localization sequence, in a plant cell,
- and
- (d) growing the plant cell under conditions which permit the development of a plant showing increased yield, especially enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant.

[0051.1.1.1] In another embodiment, the present invention relates to a method for producing a transgenic plant cell, a plant or a part thereof, resulting in increased yield, especially enhanced nutrient efficiency, in particular enhanced NUE and/or increased biomass production, and optionally resulting in increased stress tolerance, especially abiotic stress tolerance, preferably low temperature tolerance and/or increased water

use efficiency, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof, which comprises

- (a) increasing or generating the activity of a protein as shown in table II, application no. 1, column 3 encoded by the nucleic acid sequences as shown in table I, application no. 1, column 5 or 7, in an organelle of a plant through the transformation of the organelle, or
 - (b) increasing or generating the activity of a protein as shown in table II, application no. 1, column 3 encoded by the nucleic acid sequences as shown in table I, application no. 1, column 5 or 7 in the plastid of a plant, or in one or more parts thereof through the transformation of the plastids;
- and
- (c) growing the plant cell under conditions which permit the development of a plant showing increased yield, especially enhanced nutrient efficiency, in particular enhanced NUE and/or increased biomass production, and optionally resulting in increased stress tolerance, especially abiotic stress tolerance, preferably low temperature tolerance and/or increased water use efficiency, as compared to a corresponding non-transformed wild type plant.

[0052.1.1.1] In principle the nucleic acid sequence encoding a transit peptide can be isolated from every organism such as microorganisms such as algae or plants containing plastids preferably chloroplasts. A "transit peptide" is an amino acid sequence, whose encoding nucleic acid sequence is translated together with the corresponding structural gene. That means the transit peptide is an integral part of the translated protein and forms an amino terminal extension of the protein. Both are translated as so called "preprotein". In general the transit peptide is cleaved off from the preprotein during or just after import of the protein into the correct cell organelle such as a plastid to yield the mature protein. The transit peptide ensures correct localization of the mature protein by facilitating the transport of proteins through intracellular membranes.

Preferred nucleic acid sequences encoding a transit peptide are derived from a nucleic acid sequence encoding a protein finally resided in the plastid and stemming from an organism selected from the group consisting of the genera *Acetabularia*, *Arabidopsis*, *Brassica*, *Capsicum*, *Chlamydomonas*, *Curubita*, *Dunaliella*, *Euglena*, *Flaveria*, *Glycine*, *Helianthus*, *Hordeum*, *Lemna*, *Lolium*, *Lycopersion*, *Malus*, *Medicago*, *Mesembryanthemum*, *Nicotiana*, *Oenothera*, *Oryza*, *Petunia*, *Phaseolus*, *Physcomitrella*, *Pinus*, *Pisum*, *Raphanus*, *Silene*, *Sinapis*, *Solanum*, *Spinacea*, *Stevia*, *Synechococcus*, *Triticum* and *Zea*.

[0053.1.1.1] Advantageously such transit peptides, which are beneficially used in the inventive process, are derived from the nucleic acid sequence encoding a protein selected from the group consisting of ribulose biphosphate carboxylase/oxygenase, 5-enolpyruvyl-shikimate-3-phosphate synthase, acetolactate synthase, chloroplast ribo-

somal protein CS17, Cs protein, ferredoxin, plastocyanin, ribulose biphosphate carboxylase activase, tryptophan synthase, acyl carrier protein, plastid chaperonin-60, cytochrome *c*₅₅₂, 22-kDa heat shock protein, 33-kDa Oxygen-evolving enhancer protein 1, ATP synthase γ subunit, ATP synthase δ subunit, chlorophyll-a/b-binding proteinII-1, 5 Oxygen-evolving enhancer protein 2, Oxygen-evolving enhancer protein 3, photosystem I: P21, photosystem I: P28, photosystem I: P30, photosystem I: P35, photosystem I: P37, glycerol-3-phosphate acyltransferases, chlorophyll a/b binding protein, CAB2 protein, hydroxymethyl-bilane synthase, pyruvate-orthophosphate dikinase, CAB3 protein, plastid ferritin, ferritin, early light-inducible protein, glutamate-1-semialdehyde 10 aminotransferase, protochlorophyllide reductase, starch-granule-bound amylase synthase, light-harvesting chlorophyll a/b-binding protein of photosystem II, major pollen allergen Lol p 5a, plastid ClpB ATP-dependent protease, superoxide dismutase, ferredoxin NADP oxidoreductase, 28-kDa ribonucleoprotein, 31-kDa ribonucleoprotein, 33-kDa ribonucleoprotein, acetolactate synthase, ATP synthase CF₀ subunit 1, ATP synthase CF₀ subunit 2, ATP synthase CF₀ subunit 3, ATP synthase CF₀ subunit 4, cytochrome f, ADP-glucose pyrophosphorylase, glutamine synthase, glutamine synthase 2, 15 carbonic anhydrase, GapA protein, heat-shock-protein hsp21, phosphate translocator, plastid ClpA ATP-dependent protease, plastid ribosomal protein CL24, plastid ribosomal protein CL9, plastid ribosomal protein PsCL18, plastid ribosomal protein PsCL25, DAHP synthase, starch phosphorylase, root acyl carrier protein II, betaine-aldehyde dehydrogenase, GapB protein, glutamine synthetase 2, phosphoribulokinase, nitrite reductase, ribosomal protein L12, ribosomal protein L13, ribosomal protein L21, ribosomal protein L35, ribosomal protein L40, triose phosphate-3-phosphoglycerate-phosphate translocator, ferredoxin-dependent glutamate synthase, glyceraldehyde-3-phosphate dehydrogenase, NADP-dependent malic enzyme and NADP-malate dehydrogenase. 25

[0054.1.1.1] More preferred the nucleic acid sequence encoding a transit peptide is derived from a nucleic acid sequence encoding a protein finally resided in the plastid and stemming from an organism selected from the group consisting of the species 30 *Acetabularia mediterranea*, *Arabidopsis thaliana*, *Brassica campestris*, *Brassica napus*, *Capsicum annuum*, *Chlamydomonas reinhardtii*, *Cururbita moschata*, *Dunaliella salina*, *Dunaliella tertiolecta*, *Euglena gracilis*, *Flaveria trinervia*, *Glycine max*, *Helianthus annuus*, *Hordeum vulgare*, *Lemna gibba*, *Lolium perenne*, *Lycopersion esculentum*, 35 *Malus domestica*, *Medicago falcata*, *Medicago sativa*, *Mesembryanthemum crystallinum*, *Nicotiana plumbaginifolia*, *Nicotiana sylvestris*, *Nicotiana tabacum*, *Oenothera hookeri*, *Oryza sativa*, *Petunia hybrida*, *Phaseolus vulgaris*, *Physcomitrella patens*, *Pinus tunbergii*, *Pisum sativum*, *Raphanus sativus*, *Silene pratensis*, *Sinapis alba*, *Solanum tuberosum*, *Spinacea oleracea*, *Stevia rebaudiana*, *Synechococcus*, *Synechocystis*, *Triticum aestivum* and *Zea mays*. 40

[0055.1.1.1] Even more preferred nucleic acid sequences are encoding transit peptides as disclosed by von Heijne et al. (Plant Molecular Biology Reporter, 9 (2), 104, (1991)), which are hereby incorporated by reference. Table V shows some examples of the transit peptide sequences disclosed by von Heijne et al. According to the disclosure of the invention especially in the examples the skilled worker is able to link other nucleic acid sequences disclosed by von Heijne et al. to the nucleic acid sequences shown in table I, application no. 1, columns 5 and 7. Most preferred nucleic acid sequences encoding transit peptides are derived from the genus *Spinacia* such as chloroplast 30S ribosomal protein PSrp-1, root acyl carrier protein II, acyl carrier protein, ATP synthase: γ subunit, ATP synthase: δ subunit, cytochrom f, ferredoxin I, ferredoxin NADP oxidoreductase (= FNR), nitrite reductase, phosphoribulokinase, plastocyanin or carbonic anhydrase. The skilled worker will recognize that various other nucleic acid sequences encoding transit peptides can easily isolated from plastid-localized proteins, which are expressed from nuclear genes as precursors and are then targeted to plastids. Such transit peptides encoding sequences can be used for the construction of other expression constructs. The transit peptides advantageously used in the inventive process and which are part of the inventive nucleic acid sequences and proteins are typically 20 to 120 amino acids, preferably 25 to 110, 30 to 100 or 35 to 90 amino acids, more preferably 40 to 85 amino acids and most preferably 45 to 80 amino acids in length and functions post-translationally to direct the protein to the plastid preferably to the chloroplast. The nucleic acid sequences encoding such transit peptides are localized upstream of nucleic acid sequence encoding the mature protein. For the correct molecular joining of the transit peptide encoding nucleic acid and the nucleic acid encoding the protein to be targeted it is sometimes necessary to introduce additional base pairs at the joining position, which forms restriction enzyme recognition sequences useful for the molecular joining of the different nucleic acid molecules. This procedure might lead to very few additional amino acids at the N-terminal of the mature imported protein, which usually and preferably do not interfere with the protein function. In any case, the additional base pairs at the joining position which forms restriction enzyme recognition sequences have to be chosen with care, in order to avoid the formation of stop codons or codons which encode amino acids with a strong influence on protein folding, like e.g. proline. It is preferred that such additional codons encode small structural flexible amino acids such as glycine or alanine.

[0056.1.1.1] As mentioned above the nucleic acid sequences coding for the proteins as shown in table II, application no. 1, column 3 and its homologs as disclosed in table I, application no. 1, columns 5 and 7 can be joined to a nucleic acid sequence encoding a transit peptide. This nucleic acid sequence encoding a transit peptide ensures transport of the protein to the respective organelle, especially the plastid. The nucleic acid sequence of the gene to be expressed and the nucleic acid sequence encoding the transit peptide are operably linked. Therefore the transit peptide is fused in frame to the nucleic acid sequence coding for proteins as shown in table II, application

no. 1, column 3 and its homologs as disclosed in table I, application no. 1, columns 5 and 7.

- 5 [0057.1.1.1] The term "organelle" according to the invention shall mean for example "mitochondria" or preferably "plastid" (throughout the specification the "plural" shall comprise the "singular" and vice versa). The term "plastid" according to the invention is intended to include various forms of plastids including proplastids, chloroplasts, chromoplasts, gerontoplasts, leucoplasts, amyloplasts, elaioplasts and etioplasts, preferably chloroplasts. They all have as a common ancestor the aforementioned proplastids.
- 10 [0058.1.1.1] Other transit peptides are disclosed by Schmidt et al. (J. Biol. Chem. 268 (36), 27447 (1993)), Della-Cioppa et al. (Plant. Physiol. 84, 965 (1987)), de Castro Silva Filho et al. (Plant Mol. Biol. 30, 769 (1996)), Zhao et al. (J. Biol. Chem. 270 (11), 6081(1995)), Römer et al. (Biochem. Biophys. Res. Commun. 196 (3), 1414 (1993)),
- 15 Keegstra et al. (Annu. Rev. Plant Physiol. Plant Mol. Biol. 40, 471(1989)), Lubben et al. (Photosynthesis Res. 17, 173 (1988)) and Lawrence et al. (J. Biol. Chem. 272 (33), 20357 (1997)). A general review about targeting is disclosed by Kermode Allison R. in Critical Reviews in Plant Science 15 (4), 285 (1996) under the title "Mechanisms of Intracellular Protein Transport and Targeting in Plant Cells."
- 20 [0059.1.1.1] Favored transit peptide sequences, which are used in the inventive process and which form part of the inventive nucleic acid sequences are generally enriched in hydroxylated amino acid residues (serine and threonine), with these two residues generally constituting 20 to 35 % of the total. They often have an amino-terminal
- 25 region empty of Gly, Pro, and charged residues. Furthermore they have a number of small hydrophobic amino acids such as valine and alanine and generally acidic amino acids are lacking. In addition they generally have a middle region rich in Ser, Thr, Lys and Arg. Overall they have very often a net positive charge.
- 30 [0060.1.1.1] Alternatively, nucleic acid sequences coding for the transit peptides may be chemically synthesized either in part or wholly according to structure of transit peptide sequences disclosed in the prior art. Said natural or chemically synthesized sequences can be directly linked to the sequences encoding the mature protein or via a linker nucleic acid sequence, which may be typically less than 500 base pairs, preferably
- 35 less than 450, 400, 350, 300, 250 or 200 base pairs, more preferably less than 150, 100, 90, 80, 70, 60, 50, 40 or 30 base pairs and most preferably less than 25, 20, 15, 12, 9, 6 or 3 base pairs in length and are in frame to the coding sequence. Furthermore favorable nucleic acid sequences encoding transit peptides may comprise sequences derived from more than one biological and/or chemical source and may include a nucleic acid sequence derived from the amino-terminal region of the mature protein,
- 40 which in its native state is linked to the transit peptide. In a preferred embodiment of the invention said amino-terminal region of the mature protein is typically less than 150

amino acids, preferably less than 140, 130, 120, 110, 100 or 90 amino acids, more preferably less than 80, 70, 60, 50, 40, 35, 30, 25 or 20 amino acids and most preferably less than 19, 18, 17, 16, 15, 14, 13, 12, 11 or 10 amino acids in length. But even shorter or longer stretches are also possible. In addition target sequences, which facilitate the transport of proteins to other cell compartments such as the vacuole, endoplasmic reticulum, golgi complex, glyoxysomes, peroxisomes or mitochondria may be also part of the inventive nucleic acid sequence. The proteins translated from said inventive nucleic acid sequences are a kind of fusion proteins that means the nucleic acid sequences encoding the transit peptide for example the ones shown in table V, preferably the last one of the table are joint to the nucleic acid sequences shown in table I, application no. 1, columns 5 and 7. The person skilled in the art is able to join said sequences in a functional manner. Advantageously the transit peptide part is cleaved off from the protein part shown in table II, application no. 1, columns 5 and 7 during the transport preferably into the plastids. All products of the cleavage of the preferred transit peptide shown in the last line of table V have preferably the N-terminal amino acid sequences QIA CSS or QIA EFQLTT in front of the start methionine of the protein mentioned in table II, application no. 1, columns 5 and 7. Other short amino acid sequences of an range of 1 to 20 amino acids preferable 2 to 15 amino acids, more preferable 3 to 10 amino acids most preferably 4 to 8 amino acids are also possible in front of the start methionine of the protein motioned in table II, application no. 1, columns 5 and 7. In case of the amino acid sequence QIA CSS the three amino acids in front of the start methionine are stemming from the LIC (= ligation independent cloning) cassette. Said short amino acid sequence is preferred in the case of the expression of E. coli genes. In case of the amino acid sequence QIA EFQLTT the six amino acids in front of the start methionine are stemming from the LIC cassette. Said short amino acid sequence is preferred in the case of the expression of S. cerevisiae genes. The skilled worker knows that other short sequences are also useful in the expression of the genes mentioned in table I, application no. 1, columns 5 and 7. Furthermore the skilled worker is aware of the fact that there is not a need for such short sequences in the expression of the genes.

Table V: Examples of transit peptides disclosed by von Heijne et al.

Trans Pep	Organism	Transit Peptide	SEQ ID NO:	Reference
1	Acetabularia mediterranea	MASIMMNKSVVLSKECAKPLATPK VTLNKRGFATTIATKNREMMVWQP FNNKMFETFSFLPP	17	Mol. Gen. Genet. 218, 445 (1989)
2	Arabidopsis thaliana	MAASLQSTATFLQSAKIATAPSRG SSHLRSTQAVGKSFGLETSSARLT CSFQSDFKDFTGKCSDAVKIAGFA	18	EMBO J. 8, 3187 (1989)

Trans Pep	Organism	Transit Peptide	SEQ ID NO:	Reference
		LATSALVVSGASAEGAPK		
3	Arabidopsis thaliana	MAQVSRICNGVQNPSLICNLSKSS QRKSPLSVSLKTQQHPRAYPISSS WGLKKSGMTLIGSELRLKVMSSV STAEKASEIVLQPIREISGLIKLP	19	Mol. Gen. Genet. 210, 437 (1987)
4	Arabidopsis thaliana	MAAATTTTTTSSSISFSTKPSPSS SKSPLPISRFSLPFSLNPNKSSSS SRRRGIKSSSPSSISAVLNTTTNV TTTPSPTKPTKPETFISRFAPDQP RKGA	20	Plant Physiol. 85, 1110 (1987)
5	Arabidopsis thaliana	MITSSLTCSLQALKLSSPFAHGST PLSSLKPNSEFPNHRMPALVPV	21	J. Biol. Chem. 265, 2763 (1990)
6	Arabidopsis thaliana	MASLLGTSSSAI- WASPSLSSPSSKPS SSPICFRPGKL FGSKLNAGIQI RPKKNRSRYHVSVMNVATEINSTE QVVGKFDSKKSARPVYPFAAI	22	EMBO J. 9, 1337 (1990)
7	Arabidopsis thaliana	MASTALSSAIVGTSFIRRSPAPISL RSLPSANTQSLFGLKSGTARGG RVVAM	23	Plant Physiol. 93, 572 (1990)
8	Arabidopsis thaliana	MAASTMALSSPAFAGKAVNLSPAA SEVLGSGRVTNRKTV	24	Nucl. Acids Res. 14, 4051 (1986)
9	Arabidopsis thaliana	MAAITSATVTIPSFTGLKLAVSSK PKTLSTISRSSSATRAPPKLALKS SLKDFGVIAVATAASIVLAGNAMA MEVLLGSDDGSLAFVPSEFT	25	Gene 65, 59 (1988)
10	Arabidopsis thaliana	MAAAVSTVGAINRAPLSLNGSGSG AVSAPASTFLGKKVTVSRFAQSN KKSNGSFKVLAVKEDKQTDGDRWR GLAYDTSDDQIDI	26	Nucl. Acids Res. 17, 2871 (1989)
11	Arabidopsis thaliana	MKSSMLSSTAWTSPAQATMVAPF TGLKSSASFPVTRKANNDITSITS NGGRVSC	27	Plant Mol. Biol. 11, 745 (1988)
12	Arabidopsis thaliana	MAASGTSATFRASVSSAPSSSSSQL THLKSPFKAVKYTPLPSSRSKSSS FSVSCTIAKDPPVLMAAGSDPALW QRPDSFGRFGKFGGKYVPE	28	Proc. Natl. Acad. Sci. USA, 86, 4604 (1989)
13	Brassica	MSTTFCSSVCMQATSLAATTRISF	29	Nucl. Acids

Trans Pep	Organism	Transit Peptide	SEQ ID NO:	Reference
	campestris	QKPALVSTTNLSFNLRRSIPTRFS ISCAAKPETVEKVSKIVKKQLSLK DDQKVVAE		Res. 15, 7197 (1987)
14	Brassica napus	MATTFASVSMQATSLATTTRISF QKPVLVSNHGRTNLSFNLSRTRLISI SC	30	Eur. J. Bio- chem. 174, 287 (1988)
15	Chlamydomo- nas reinhardtii	MQALSSRVNIAAKPQRAQRLVVRA EEVKAAPKKEVGPKRGSLVK	31	Plant Mol. Biol. 12, 463 (1989)
16	Cucurbita moschata	MAELIQDKESAQSAATAAAASSGY ERRNEPAHSRKFLVRSEEELL- SCIKK	32	FEBS Lett. 238, 424 (1988)
17	Spinacea oleracea	MSTINGCLTSISPSRTQLKNTSTL RPTFIANSRVNPSSSVPPSLIRNQ PVFAAPAPIITPTL	33	J. Biol. Chem. 265, (10) 5414 (1990)
18	Spinacea oleracea	MTTAVTAAVSFPSTKTTSLSARCS SVISPDKISYKKVPLYRNVSATG KMGPIRAQIASDVEAPPPAPAK- VEKMS	34	Curr. Genet. 13, 517 (1988)
19	Spinacea oleracea	MTTAVTAAVSFPSTKTTSLSARSS SVISPDKISYKKVPLYRNVSATG KMGPIRA	35	

[0061.1.1.1] Alternatively to the targeting of the sequences shown in table II, ap-
plication no. 1, columns 5 and 7, preferably of sequences in general encoded in the
nucleus with the aid of the targeting sequences mentioned for example in table V alone
or in combination with other targeting sequences preferably into the plastids, the nu-
cleic acids of the invention can directly be introduced into the plastidal genome. There-
fore in a preferred embodiment the nucleic acid sequences shown in table I, application
no. 1, columns 5 and 7 are directly introduced and expressed in plastids.

- 10 The term "introduced" in the context of this specification shall mean the insertion of a
nucleic acid sequence into the organism by means of a "transfection", "transduction" or
preferably by "transformation".

- 15 A plastid, such as a chloroplast, has been "transformed" by an exogenous (preferably
foreign) nucleic acid sequence if nucleic acid sequence has been introduced into the
plastid that means that this sequence has crossed the membrane or the membranes of
the plastid. The foreign DNA may be integrated (covalently linked) into plastid DNA

making up the genome of the plastid, or it may remain unintegrated (e.g., by including a chloroplast origin of replication). "Stably" integrated DNA sequences are those, which are inherited through plastid replication, thereby transferring new plastids, with the features of the integrated DNA sequence to the progeny.

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[0062.1.1.1] For expression a person skilled in the art is familiar with different methods to introduce the nucleic acid sequences into different organelles such as the preferred plastids. Such methods are for example disclosed by Maiga P.(Annu. Rev. Plant Biol. 55, 289 (2004)), Evans T. (WO 2004/040973), McBride K.E.et al. (US 5,455,818), Daniell H. et al. (US 5,932,479 and US 5,693,507) and Straub J.M. et al. (US 6,781,033). A preferred method is the transformation of microspore-derived hypocotyl or cotyledonary tissue (which are green and thus contain numerous plastids) leaf tissue and afterwards the regeneration of shoots from said transformed plant material on selective medium. As methods for the transformation bombarding of the plant material or the use of independently replicating shuttle vectors are well known by the skilled worker. But also a PEG-mediated transformation of the plastids or Agrobacterium transformation with binary vectors is possible. Useful markers for the transformation of plastids are positive selection markers for example the chloramphenicol-, streptomycin-, kanamycin-, neomycin-, amikamycin-, spectinomycin-, triazine- and/or lincomycin-resistance genes. As additional markers named in the literature often as secondary markers, genes coding for the resistance against herbicides such as phosphinothricin (= glufosinate, BASTA™, Liberty™, encoded by the bar gene), glyphosate (= N-(phosphonomethyl)glycine, Roundup™, encoded by the 5-enolpyruvylshikimate-3-phosphate synthase gene = epsps), sulfonyleureas (like Staple™, encoded by the acetolactate synthase (ALS) gene), imidazolinones [= IMI, like imazethapyr, imazamox, Clearfield™, encoded by the acetohydroxyacid synthase (AHAS) gene, also known as acetolactate synthase (ALS) gene] or bromoxynil (= Buctril™, encoded by the oxy gene) or genes coding for antibiotics such as hygromycin or G418 are useful for further selection. Such secondary markers are useful in the case when most genome copies are transformed. In addition negative selection markers such as the bacterial cytosine deaminase (encoded by the codA gene) are also useful for the transformation of plastids.

[0063.1.1.1] To increase the possibility of identification of transformants it is also desirable to use reporter genes other than the aforementioned resistance genes or in addition to said genes. Reporter genes are for example β -galactosidase-, β -glucuronidase-(GUS), alkaline phosphatase- and/or green-fluorescent protein-genes (GFP).

[0064.1.1.1] For the inventive process it is of great advantage that by transforming the plastids the intraspecies specific transgene flow is blocked, because a lot of species such as corn, cotton and rice have a strict maternal inheritance of plastids. By placing the genes specified in table I, application no. 1, columns 5 and 7 or active

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fragments thereof in the plastids of plants, these genes will not be present in the pollen of said plants.

5 A further preferred embodiment of the invention relates to the use of so called "chloroplast localization sequences", in which a first RNA sequence or molecule is capable of transporting or "chaperoning" a second RNA sequence, such as a RNA sequence transcribed from the sequences depicted in table 1, application no. 1, columns 5 and 7 or a sequence encoding a protein, as depicted in table II, application no. 1, columns 5 and 7, from an external environment inside a cell or outside a plastid into a chloroplast. In
10 one embodiment the chloroplast localization signal is substantially similar or complementary to a complete or intact viroid sequence. The chloroplast localization signal may be encoded by a DNA sequence, which is transcribed into the chloroplast localization RNA. The term "viroid" refers to a naturally occurring single stranded RNA molecule (Flores, C. R. Acad Sci III. 324 (10), 943 (2001)). Viroids usually contain about
15 200-500 nucleotides and generally exist as circular molecules. Examples of viroids that contain chloroplast localization signals include but are not limited to ASBVd, PLMVd, CChMVd and ELVd. The viroid sequence or a functional part of it can be fused to the sequences depicted in table I, application no. 1, columns 5 and 7 or a sequence encoding a protein, as depicted in table II, application no. 1, columns 5 and 7 in such a
20 manner that the viroid sequence transports a sequence transcribed from a sequence as depicted in table 1, application no. 1, columns 5 and 7 or a sequence encoding a protein as depicted in table II, application no. 1, columns 5 and 7 into the chloroplasts. A preferred embodiment uses a modified ASBVd (Navarro et al., Virology. 268 (1), 218 (2000)).

25 In a further specific embodiment the protein to be expressed in the plastids such as the proteins depicted in table II, application no. 1, columns 5 and 7 are encoded by different nucleic acids. Such a method is disclosed in WO 2004/040973, which shall be incorporated by reference. WO 2004/040973 teaches a method, which relates to the
30 translocation of an RNA corresponding to a gene or gene fragment into the chloroplast by means of a chloroplast localization sequence. The genes, which should be expressed in the plant or plants cells, are split into nucleic acid fragments, which are introduced into different compartments in the plant e.g. the nucleus, the plastids and/or mitochondria. Additionally plant cells are described in which the chloroplast contains a
35 ribozyme fused at one end to an RNA encoding a fragment of a protein used in the inventive process such that the ribozyme can trans-splice the translocated fusion RNA to the RNA encoding the gene fragment to form and as the case may be reunite the nucleic acid fragments to an intact mRNA encoding a functional protein for example as disclosed in table II, columns 5 and 7.

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[0065.1.1.1] In a preferred embodiment of the invention the nucleic acid sequences as shown in table I, application no. 1, columns 5 and 7 used in the inventive

process are transformed into plastids, which are metabolically active. Those plastids should preferably maintain at a high copy number in the plant or plant tissue of interest, most preferably the chloroplasts found in green plant tissues, such as leaves or cotyledons or in seeds.

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[0066.1.1.1] For a good expression in the plastids the nucleic acid sequences as shown in table I, application no. 1, columns 5 and 7 are introduced into an expression cassette using a preferably a promoter and terminator, which are active in plastids preferably a chloroplast promoter. Examples of such promoters include the psbA promoter from the gene from spinach or pea, the rbcL promoter, and the atpB promoter from corn.

10

For the purposes of the description of the present invention, the terms "cytoplasmic" shall indicate, that the nucleic acid of the invention is expressed without the addition of an non-natural transit peptide encoding sequence. A non-natural transit peptide encoding sequence is a sequence which is not a natural part of a nucleic acid of the invention, e.g. of the nucleic acids depicted in table I column 5 or 7, but is rather added by molecular manipulation steps as for example described in the example under "plastid targeted expression". Therefore the terms "cytoplasmic" shall not exclude a targeted localisation to any cell compartment for the products of the inventive nucleic acid sequences by their naturally occurring sequence properties within the background of the transgenic organism. The subcellular location of the mature polypeptide derived from the enclosed sequences can be predicted by a skilled person for the organism (plant) by using software tools like TargetP (Emanuelsson et al., (2000), Predicting subcellular localization of proteins based on their N-terminal amino acid sequence., J.Mol. Biol. 300, 1005-1016.), ChloroP (Emanuelsson et al. (1999), ChloroP, a neural network-based method for predicting chloroplast transit peptides and their cleavage sites., Protein Science, 8: 978-984.) or other predictive software tools (Emanuelsson et al. (2007), Locating proteins in the cell using TargetP, SignalP, and related tools., Nature Protocols 2, 953-971).

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[0067.1.1.1] Comprises/comprising and grammatical variations thereof when used in this specification are to be taken to specify the presence of stated features, integers, steps or components or groups thereof, but not to preclude the presence or addition of one or more other features, integers, steps, components or groups thereof.

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[0068.1.1.1] In accordance with the invention, the term "plant cell" or the term "organism" as understood herein relates always to a plant cell or an organelle thereof, preferably a plastid, more preferably chloroplast.

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As used herein, "plant" is meant to include not only a whole plant but also a part thereof i.e., one or more cells, and tissues, including for example, leaves, stems, shoots, roots, flowers, fruits and seeds.

5 [0069.1.1.1] Surprisingly it was found, that the transgenic expression of a protein as shown in table II, application no. 1, column 3, especially from the *Saccharomyces cerevisiae* and/or the transgenic expression of a protein as shown in table II, applica-
 10 tion no. 1, column 3, especially from the *E. coli*, in a plant, such as *Arabidopsis thaliana* for example, conferred a yield increase, especially an enhanced NUE and/or increased biomass production, to the transgenic plant cell, plant or a part thereof as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof. In addi-
 15 tion the yield increase may be generated by an increased tolerance to stress, espe- cially abiotic stress, particularly low temperature stress and/or enhanced water use efficiency and/or enhanced intrinsic yield in the absence of nutrient deficiencies as well as stress conditions.

[0070.1.1.1] Accordingly, in one embodiment, in case the *Escherichia coli* nucleic acid molecule SEQ ID NO. 38, or a nucleic acid which differs from nucleic acid SEQ ID NO. 38 by exchanging the stop codon *taa* by *tga*, or the activity of a polypeptide en-
 20 coded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 38 (or a nu- cleic acid which differs from nucleic acid SEQ ID NO. 38 by exchanging the stop codon *taa* by *tga*) or a polypeptide SEQ ID NO. 39, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nu-
 25 cleic acid or polypeptide or the consensus sequence or the polypeptide motif, as de- picted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 38 or polypeptide SEQ ID NO. 39, respectively, is increased or generated, or if the activity "b0017-protein" is increased or generated in an
 30 plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an in- creased stress tolerance and/or an increased yield, in the absence of a nutrient defi-
 35 ciency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.19-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

40 Accordingly, in one embodiment, in case the *Escherichia coli* nucleic acid molecule SEQ ID NO. 42, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 42 or a polypeptide SEQ ID NO. 43, respec-

tively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 42 or polypeptide SEQ ID NO. 43, respectively, is increased or generated, or if the activity "transport protein" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.15-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* nucleic acid molecule SEQ ID NO. 123, or a nucleic acid which differs from nucleic acid SEQ ID NO. 123 by exchanging the stop codon taa by tga, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 123 (or a nucleic acid which differs from nucleic acid SEQ ID NO. 123 by exchanging the stop codon taa by tga) or a polypeptide SEQ ID NO. 124, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 123 or polypeptide SEQ ID NO. 124, respectively, is increased or generated, or if the activity "hydroxymyristol acyl carrier protein dehydratase" is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.41-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.33-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* K12 nucleic acid molecule SEQ ID NO. 380, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 380 or a polypeptide SEQ ID NO. 381, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 380 or polypeptide SEQ ID NO. 381, respectively, is increased or generated, or if the activity “gamma-glutamyl kinase” is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.16-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* nucleic acid molecule SEQ ID NO. 679, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 679 or a polypeptide SEQ ID NO. 680, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 679 or polypeptide SEQ ID NO. 680, respectively, is increased or generated, or if the activity “alpha-glucosidase” is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.10-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* nucleic acid molecule SEQ ID NO. 812, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 812 or a polypeptide SEQ ID NO. 813, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 812 or polypeptide SEQ ID NO. 813, respectively, is increased or generated, or if the activity "adenylate kinase" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.24-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.09-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* nucleic acid molecule SEQ ID NO. 1055, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 1055 or a polypeptide SEQ ID NO. 1056, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 1055 or polypeptide SEQ ID NO. 1056, respectively, is increased or generated, or if the activity "2-dehydro-3-deoxy-phosphoheptonate aldolase" is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.15-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-

fold to 1.23-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* nucleic acid molecule
 5 SEQ ID NO. 1563, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 1563 or a polypeptide SEQ ID NO. 1564, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in
 10 the respective same line as the nucleic acid molecule SEQ ID NO. 1563 or polypeptide SEQ ID NO. 1564, respectively, is increased or generated, or if the activity “molybdopterin biosynthesis protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred,
 15 especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an in-
 20 crease of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.20-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* nucleic acid molecule
 25 SEQ ID NO. 1705, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 1705 or a polypeptide SEQ ID NO. 1706, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in
 30 the respective same line as the nucleic acid molecule SEQ ID NO. 1705 or polypeptide SEQ ID NO. 1706, respectively, is increased or generated, or if the activity “hydroxylamine reductase” is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding
 35 non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof
 40 is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.17-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* nucleic acid molecule
5 SEQ ID NO. 1844, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 1844 or a polypeptide SEQ ID NO. 1845, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in
10 the respective same line as the nucleic acid molecule SEQ ID NO. 1844 or polypeptide SEQ ID NO. 1845, respectively, is increased or generated, or if the activity "proline dehydrogenase" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially
15 an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of
20 biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.19-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* nucleic acid molecule
25 SEQ ID NO. 1950, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 1950 or a polypeptide SEQ ID NO. 1951, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in
30 the respective same line as the nucleic acid molecule SEQ ID NO. 1950 or polypeptide SEQ ID NO. 1951, respectively, is increased or generated, or if the activity "PhoH-like protein" is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof
35 is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.
40

Particularly, an increase from 1.1-fold to 1.10-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.17-fold plus at least 100% thereof under low temperature conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

5 Accordingly, in one embodiment, in case the *Escherichia coli* nucleic acid molecule SEQ ID NO. 1975, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 1975 or a polypeptide SEQ ID NO. 1976, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence
10 or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 1975 or polypeptide SEQ ID NO. 1976, respectively, is increased or generated, or if the activity "isomerase" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-
15 transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof
20 is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.23-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-
25 fold to 1.18-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* nucleic acid molecule SEQ ID NO. 2127, or a nucleic acid which differs from nucleic acid SEQ ID NO. 2127
30 by exchanging the stop codon taa by tga, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 2127 (or a nucleic acid which differs from nucleic acid SEQ ID NO. 2127 by exchanging the stop codon taa by tga) or a polypeptide SEQ ID NO. 2128, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid
35 or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 2127 or polypeptide SEQ ID NO. 2128, respectively, is increased or generated, or if the activity "b1933-protein" is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield
40 as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient defi-

ciency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.55-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.12-fold plus at least 100% thereof under low temperature conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* nucleic acid molecule SEQ ID NO. 2135, or a nucleic acid which differs from nucleic acid SEQ ID NO. 2135 by exchanging the stop codon taa by tga, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 2135 (or a nucleic acid which differs from nucleic acid SEQ ID NO. 2135 by exchanging the stop codon taa by tga) or a polypeptide SEQ ID NO. 2136, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 2135 or polypeptide SEQ ID NO. 2136, respectively, is increased or generated, or if the activity "glycosyltransferase" is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.24-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.14-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* K12 nucleic acid molecule SEQ ID NO. 2171, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 2171 or a polypeptide SEQ ID NO. 2172, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 2171 or polypeptide SEQ ID NO. 2172, respectively, is increased or generated, or if the activity

“b2165-protein” is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.24-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.24-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* K12 nucleic acid molecule SEQ ID NO. 2297, or a nucleic acid which differs from nucleic acid SEQ ID NO. 2297 by exchanging the stop codon taa by tga, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 2297 (or a nucleic acid which differs from nucleic acid SEQ ID NO. 2297 by exchanging the stop codon taa by tga) or a polypeptide SEQ ID NO. 2298, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 2297 or polypeptide SEQ ID NO. 2298, respectively, is increased or generated, or if the activity “short chain fatty acid transporter” is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.36-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* nucleic acid molecule SEQ ID NO. 2426, or a nucleic acid which differs from nucleic acid SEQ ID NO. 2426 by exchanging the stop codon taa by tga, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 2426 (or a nucleic acid

which differs from nucleic acid SEQ ID NO. 2426 by exchanging the stop codon taa by tga) or a polypeptide SEQ ID NO. 2427, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 2426 or polypeptide SEQ ID NO. 2427, respectively, is increased or generated, or if the activity "b2238-protein" is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance, especially an increased tolerance to low temperatures, and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.26-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.19-fold plus at least 100% thereof under low temperature conditions; also particularly, an increase from 1.05-fold to 1.18-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the Escherichia coli nucleic acid molecule SEQ ID NO. 2426, or a nucleic acid which differs from nucleic acid SEQ ID NO. 2426 by exchanging the stop codon taa by tga, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 2426 (or a nucleic acid which differs from nucleic acid SEQ ID NO. 2426 by exchanging the stop codon taa by tga) or a polypeptide SEQ ID NO. 2427, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 2426 or polypeptide SEQ ID NO. 2427, respectively, is increased or generated, or if the activity "b2238-protein" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance, especially an increased tolerance to drought conditions, and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions.

Particularly, an increase from 1.05-fold to 1.11-fold plus at least 100% thereof under drought conditions is conferred; also particularly, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* K12 nucleic acid molecule SEQ ID NO. 2452, or a nucleic acid which differs from nucleic acid SEQ ID NO. 2452 by exchanging the stop codon taa by tga, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 2452 (or a nucleic acid which differs from nucleic acid SEQ ID NO. 2452 by exchanging the stop codon taa by tga) or a polypeptide SEQ ID NO. 2453, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 2452 or polypeptide SEQ ID NO. 2453, respectively, is increased or generated, or if the activity "lysine/arginine/ornithine transporter subunit" is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.18-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.25-fold plus at least 100% thereof under low temperature conditions; also particularly, an increase from 1.05-fold to 1.20-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* nucleic acid molecule SEQ ID NO. 2551, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 2551 or a polypeptide SEQ ID NO. 2552, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 2551 or polypeptide SEQ ID NO. 2552, respectively, is increased or generated, or if the activity "b2431-protein" is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in

particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.47-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.34-fold plus at least 100% thereof under low temperature conditions; also particularly, an increase from 1.05-fold to 1.17-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* K12 nucleic acid molecule SEQ ID NO. 2600, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 2600 or a polypeptide SEQ ID NO. 2601, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 2600 or polypeptide SEQ ID NO. 2601, respectively, is increased or generated, or if the activity “chorismate mutase T / prephenate dehydrogenase (bifunctional)” is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.12-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.16-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* nucleic acid molecule SEQ ID NO. 2668, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 2668 or a polypeptide SEQ ID NO. 2669, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 2668 or polypeptide SEQ ID NO. 2669, respectively, is increased or generated, or if the activity “b2766-

protein" is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.10-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.26-fold plus at least 100% thereof under low temperature conditions; also particularly, an increase from 1.05-fold to 1.20-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the Escherichia coli nucleic acid molecule SEQ ID NO. 2772, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 2772 or a polypeptide SEQ ID NO. 2773, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 2772 or polypeptide SEQ ID NO. 2773, respectively, is increased or generated, or if the activity "glycine decarboxylase" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.65-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the Escherichia coli nucleic acid molecule SEQ ID NO. 3117, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 3117 or a polypeptide SEQ ID NO. 3118, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence

or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 3117 or polypeptide SEQ ID NO. 3118, respectively, is increased or generated, or if the activity "threonine ammonia-lyase" is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.42-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.16-fold plus at least 100% thereof under low temperature conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof. Accordingly, in one embodiment, in case the Escherichia coli nucleic acid molecule SEQ ID NO. 3390, or a nucleic acid which differs from nucleic acid SEQ ID NO. 3390 by exchanging the stop codon taa by tga, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 3390 (or a nucleic acid which differs from nucleic acid SEQ ID NO. 3390 by exchanging the stop codon taa by tga) or a polypeptide SEQ ID NO. 3391, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 3390 or polypeptide SEQ ID NO. 3391, respectively, is increased or generated, or if the activity "b3120-protein" is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.28-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.15-fold plus at least 100% thereof under low temperature conditions; also particularly, an increase from 1.05-fold to 1.39-fold plus at least 100% thereof of yield in

the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* nucleic acid molecule SEQ ID NO. 3396, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 3396 or a polypeptide SEQ ID NO. 3397, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 3396 or polypeptide SEQ ID NO. 3397, respectively, is increased or generated, or if the activity “outer membrane usher protein” is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.19-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* K12 nucleic acid molecule SEQ ID NO. 3470, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 3470 or a polypeptide SEQ ID NO. 3471, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 3470 or polypeptide SEQ ID NO. 3471, respectively, is increased or generated, or if the activity “glycerol-3-phosphate transporter subunit” is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.21-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.10-fold plus at least 100% thereof under low temperature conditions; also particularly, an increase from 1.05-fold to 1.23-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* nucleic acid molecule SEQ ID NO. 3563, or a nucleic acid which differs from nucleic acid SEQ ID NO. 3563 by exchanging the stop codon taa by tga, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 3563 (or a nucleic acid which differs from nucleic acid SEQ ID NO. 3563 by exchanging the stop codon taa by tga) or a polypeptide SEQ ID NO. 3564, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 3563 or polypeptide SEQ ID NO. 3564, respectively, is increased or generated, or if the activity "hydro-lyase" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.25-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Escherichia coli* nucleic acid molecule SEQ ID NO. 3770, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 3770 or a polypeptide SEQ ID NO. 3771, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 3770 or polypeptide SEQ ID NO. 3771, respectively, is increased or generated, or if the activity "lysophospholipase" is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in

particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.42-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 3868, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 3868 or a polypeptide SEQ ID NO. 3869, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 3868 or polypeptide SEQ ID NO. 3869, respectively, is increased or generated, or if the activity "yal019w-protein" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.42-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.14-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 3895, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 3895 or a polypeptide SEQ ID NO. 3896, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 3895 or polypeptide SEQ ID NO. 3896, respectively, is increased or generated, or if the activity "carnitine acetyltransferase" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred,

especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.38-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.43-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 3953, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 3953 or a polypeptide SEQ ID NO. 3954, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 3953 or polypeptide SEQ ID NO. 3954, respectively, is increased or generated, or if the activity "Transcriptional activator" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.15-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 4111, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 4111 or a polypeptide SEQ ID NO. 4112, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4111 or polypeptide SEQ ID NO. 4112, respectively, is increased or generated, or if the activity "splicing factor" is increased or generated in an plant cell, plant or part thereof, espe-

- cially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.
- 5 Particularly, an increase from 1.1-fold to 1.10-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.
- Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 4149, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 4149 or a polypeptide SEQ ID NO. 15 4150, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4149 or polypeptide SEQ ID NO. 4150, respectively, is increased or generated, or if the activity 20 "autophagy-specific phosphatidylinositol 3-kinase complex protein subunit" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence 25 of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.
- 30 Particularly, an increase from 1.1-fold to 1.19-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.
- Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 4162, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 4162 or a polypeptide SEQ ID NO. 35 4163, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4162 or polypeptide SEQ ID NO. 4163, respectively, is increased or generated, or if the activity 40 "microsomal beta-keto-reductase" is increased or generated in an plant cell, plant or

- part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress
- 5 conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.
- 10 Particularly, an increase from 1.1-fold to 1.23-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.07-fold plus at least 100% thereof under low temperature conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof. Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid
- 15 molecule SEQ ID NO. 4235, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 4235 or a polypeptide SEQ ID NO. 4236, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, col-
- 20 umn 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4235 or polypeptide SEQ ID NO. 4236, respectively, is increased or generated, or if the activity "UDP-N-acetyl-glucosamine-1-P transferase" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part
- 25 thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of
- 30 NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.
- Particularly, an increase from 1.1-fold to 1.16-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.
- 35 Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 4235, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 4235 or a polypeptide SEQ ID NO. 4236, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus
- 40 sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4235 or polypeptide SEQ ID NO. 4236, respectively, is increased or generated, or if the activity

“UDP-N-acetyl-glucosamine-1-P transferase” is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions.

Particularly, an increase from 1.05-fold to 1.26-fold plus at least 100% thereof under low temperature conditions; also particularly, an increase from 1.05-fold to 1.29 -fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 4280, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 4280 or a polypeptide SEQ ID NO. 4281, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4280 or polypeptide SEQ ID NO. 4281, respectively, is increased or generated, or if the activity “ybr262c-protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.31-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 4288, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 4288 or a polypeptide SEQ ID NO. 4289, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4288 or polypeptide SEQ ID NO. 4289, respectively, is increased or generated, or if the activity “protein necessary for structural stability of L-A double-stranded RNA-containing particles” is increased or generated in an plant cell, plant or part thereof, especially with

- cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.
- 5 Particularly, an increase from 1.1-fold to 1.31-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.24-fold plus at least 100% thereof under low temperature conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof. Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 4315, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 4315 or a polypeptide SEQ ID NO. 15 4316, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4315 or polypeptide SEQ ID NO. 4316, respectively, is increased or generated, or if the activity "YDR070C-protein" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.
- 20 Particularly, an increase from 1.1-fold to 1.20-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.47-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.
- 25 Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 4325, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 4325 or a polypeptide SEQ ID NO. 4326, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, col-
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umn 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4325 or polypeptide SEQ ID NO. 4326, respectively, is increased or generated, or if the activity “chaperone” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.29-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.09-fold plus at least 100% thereof under low temperature conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof. Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 4335, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 4335 or a polypeptide SEQ ID NO. 4336, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4335 or polypeptide SEQ ID NO. 4336, respectively, is increased or generated, or if the activity “helix-loop-helix transcription activator that binds inositol/choline-responsive elements” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.19-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 4346, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 4346 or a polypeptide SEQ ID NO. 4347, respectively, is increased or generated, e.g. if the activity of such a nucleic acid

- molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4346 or polypeptide SEQ ID NO. 4347, respectively, is increased or generated, or if the activity
- 5 “golgi membrane exchange factor subunit” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an
- 10 increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.
- 15 Particularly, an increase from 1.1-fold to 1.22-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.14-fold plus at least 100% thereof under low temperature conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof. Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid
- 20 molecule SEQ ID NO. 4361, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 4361 or a polypeptide SEQ ID NO. 4362, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4361 or
- 25 polypeptide SEQ ID NO. 4362, respectively, is increased or generated, or if the activity “dihydrosphingosine phosphate lyase” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase
- 30 of biomass production.
- Particularly, an increase from 1.1-fold to 1.13-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.
- 40 Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 4361, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 4361 or a polypeptide SEQ ID NO.

4362, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4361 or
 5 polypeptide SEQ ID NO. 4362, respectively, is increased or generated, or if the activity “dihydrosphingosine phosphate lyase” is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress
 10 conditions.

Particularly, an increase from 1.05-fold to 1.35 -fold plus at least 100% thereof under drought conditions is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

15 Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 4402, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 4402 or a polypeptide SEQ ID NO. 4403, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus
 20 sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4402 or polypeptide SEQ ID NO. 4403, respectively, is increased or generated, or if the activity “ubiquitin regulatory protein ” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a
 25 corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part
 30 thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.38-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-
 35 fold to 1.24-fold plus at least 100% thereof under low temperature conditions; also particularly, an increase from 1.05-fold to 1.14-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid
 40 molecule SEQ ID NO. 4431, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 4431 or a polypeptide SEQ ID NO. 4432, respectively, is increased or generated, e.g. if the activity of such a nucleic acid

molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4431 or polypeptide SEQ ID NO. 4432, respectively, is increased or generated, or if the activity
5 “ydr355c-protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in
10 particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

15 Particularly, an increase from 1.1-fold to 1.34-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 4435, or the activity of a polypeptide encoded by a nucleic acid
20 molecule comprising the nucleic acid SEQ ID NO. 4435 or a polypeptide SEQ ID NO. 4436, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4435 or
25 polypeptide SEQ ID NO. 4436, respectively, is increased or generated, or if the activity “lysine-specific metalloprotease” is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance
30 and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass
35 production.

Particularly, an increase from 1.1-fold to 1.16-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.10-fold plus at least 100% thereof under low temperature conditions; also particularly, an increase from 1.05-fold to 1.61-fold plus at least 100% thereof of yield in
40 the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 4485, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 4485 or a polypeptide SEQ ID NO. 4486, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4485 or polypeptide SEQ ID NO. 4486, respectively, is increased or generated, or if the activity “subunit of the transport protein particle (TRAPP) complex of the cis-Golgi ” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.20-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 4506, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 4506 or a polypeptide SEQ ID NO. 4507, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4506 or polypeptide SEQ ID NO. 4507, respectively, is increased or generated, or if the activity “myo-inositol transporter” is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.16-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.23-fold plus at least 100% thereof under low temperature conditions; also par-

particularly, an increase from 1.05-fold to 1.10-fold plus at least 100% thereof under drought conditions; also particularly, an increase from 1.05-fold to 1.14-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 4790, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 4790 or a polypeptide SEQ ID NO. 4791, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4790 or polypeptide SEQ ID NO. 4791, respectively, is increased or generated, or if the activity “SM complex B protein for mRNA splicing” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.23-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.13-fold plus at least 100% thereof under low temperature conditions; also particularly, an increase from 1.05-fold to 1.10-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 4806, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 4806 or a polypeptide SEQ ID NO. 4807, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4806 or polypeptide SEQ ID NO. 4807, respectively, is increased or generated, or if the activity “YFR007W-protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress con-

ditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.36-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 4836, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 4836 or a polypeptide SEQ ID NO. 4837, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 4836 or polypeptide SEQ ID NO. 4837, respectively, is increased or generated, or if the activity "oxidoreductase" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.22-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.32-fold plus at least 100% thereof under low temperature conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof. Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 5311, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 5311 or a polypeptide SEQ ID NO. 5312, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 5311 or polypeptide SEQ ID NO. 5312, respectively, is increased or generated, or if the activity "transcription elongation factor" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance

and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.26-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 5346, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 5346 or a polypeptide SEQ ID NO. 5347, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 5346 or polypeptide SEQ ID NO. 5347, respectively, is increased or generated, or if the activity "cytosolic catalase" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.13-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 5533, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 5533 or a polypeptide SEQ ID NO. 5534, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 5533 or polypeptide SEQ ID NO. 5534, respectively, is increased or generated, or if the activity "ygr122c-a-protein" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance

and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.30-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 5551, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 5551 or a polypeptide SEQ ID NO. 5552, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 5551 or polypeptide SEQ ID NO. 5552, respectively, is increased or generated, or if the activity “v-SNARE binding protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.21-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 5559, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 5559 or a polypeptide SEQ ID NO. 5560, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 5559 or polypeptide SEQ ID NO. 5560, respectively, is increased or generated, or if the activity “protein involved in sphingolipid biosynthesis” is increased or generated in an plant cell, plant or part thereof, especially with Cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an in-

creased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of
5 NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.19-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

10 Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 5602, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 5602 or a polypeptide SEQ ID NO. 5603, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus
15 sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 5602 or polypeptide SEQ ID NO. 5603, respectively, is increased or generated, or if the activity “mitochondrial ribosomal protein of the small subunit” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of
20 yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild
25 type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.23-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.
30

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 5608, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 5608 or a polypeptide SEQ ID NO. 5609, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus
35 sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 5608 or polypeptide SEQ ID NO. 5609, respectively, is increased or generated, or if the activity “phosphatidylserine decarboxylase” is increased or generated in an plant cell, plant or
40 part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress toler-

ance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.12-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 5614, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 5614 or a polypeptide SEQ ID NO. 5615, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 5614 or polypeptide SEQ ID NO. 5615, respectively, is increased or generated, or if the activity "cholinephosphate cytidyltransferase" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.55-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 5666, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 5666 or a polypeptide SEQ ID NO. 5667, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 5666 or polypeptide SEQ ID NO. 5667, respectively, is increased or generated, or if the activity "ygr266w-protein" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an

increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.34-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 5701, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 5701 or a polypeptide SEQ ID NO. 5702, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 5701 or polypeptide SEQ ID NO. 5702, respectively, is increased or generated, or if the activity “cell wall endo-beta-1,3-glucanase” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.21-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 5750, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 5750 or a polypeptide SEQ ID NO. 5751, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 5750 or polypeptide SEQ ID NO. 5751, respectively, is increased or generated, or if the activity “ygr290w-protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an

increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.19-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 5754, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 5754 or a polypeptide SEQ ID NO. 5755, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 5754 or polypeptide SEQ ID NO. 5755, respectively, is increased or generated, or if the activity “yhl021c-protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.19-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.12-fold plus at least 100% thereof under low temperature conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof. Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 5778, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 5778 or a polypeptide SEQ ID NO. 5779, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 5778 or polypeptide SEQ ID NO. 5779, respectively, is increased or generated, or if the activity “v-SNARE protein involved in Golgi transport” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part

thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of

5 NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.21-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-

10 transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 5812, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 5812 or a polypeptide SEQ ID NO. 5813, respectively, is increased or generated, e.g. if the activity of such a nucleic acid

15 molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 5812 or polypeptide SEQ ID NO. 5813, respectively, is increased or generated, or if the activity “mitochondrial seryl-tRNA synthetase” is increased or generated in an plant cell, plant

20 or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass

25 production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.21-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-

30 transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 5967, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 5967 or a polypeptide SEQ ID NO. 5968, respectively, is increased or generated, e.g. if the activity of such a nucleic acid

35 molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 5967 or polypeptide SEQ ID NO. 5968, respectively, is increased or generated, or if the activity “yhr127w-protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding

40 non-transformed wild type plant cell, plant or a part thereof is conferred, especially

an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.36-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 5973, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 5973 or a polypeptide SEQ ID NO. 5974, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 5973 or polypeptide SEQ ID NO. 5974, respectively, is increased or generated, or if the activity “aromatic amino acid aminotransferase II” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.39-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 5973, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 5973 or a polypeptide SEQ ID NO. 5974, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 5973 or polypeptide SEQ ID NO. 5974, respectively, is increased or generated, or if the activity “aromatic amino acid aminotransferase II” is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is

conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.05-fold to 1.13-fold plus at least 100% thereof under low temperature conditions is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 6027, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 6027 or a polypeptide SEQ ID NO. 6028, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 6027 or polypeptide SEQ ID NO. 6028, respectively, is increased or generated, or if the activity “glucoamylase” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 3.09-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 6027, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 6027 or a polypeptide SEQ ID NO. 6028, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 6027 or polypeptide SEQ ID NO. 6028, respectively, is increased or generated, or if the activity “glucoamylase” is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an

enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.05-fold to 1.20-fold plus at least 100% thereof under low temperature conditions is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 6107, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 6107 or a polypeptide SEQ ID NO. 6108, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 6107 or polypeptide SEQ ID NO. 6108, respectively, is increased or generated, or if the activity “histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.21-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 6150, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 6150 or a polypeptide SEQ ID NO. 6151, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 6150 or polypeptide SEQ ID NO. 6151, respectively, is increased or generated, or if the activity “saccharopine dehydrogenase” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred,

especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 2.42-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 6198, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 6198 or a polypeptide SEQ ID NO. 6199, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 6198 or polypeptide SEQ ID NO. 6199, respectively, is increased or generated, or if the activity “spindle checkpoint complex subunit” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.42-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 6208, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 6208 or a polypeptide SEQ ID NO. 6209, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 6208 or polypeptide SEQ ID NO. 6209, respectively, is increased or generated, or if the activity “nuclear pore complex subunit” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred,

especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.41-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 6242, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 6242 or a polypeptide SEQ ID NO. 6243, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 6242 or polypeptide SEQ ID NO. 6243, respectively, is increased or generated, or if the activity “yjl064w-protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.30-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 6246, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 6246 or a polypeptide SEQ ID NO. 6247, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 6246 or polypeptide SEQ ID NO. 6247, respectively, is increased or generated, or if the activity “yjl067w-protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially

an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.29-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 6250, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 6250 or a polypeptide SEQ ID NO. 6251, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 6250 or polypeptide SEQ ID NO. 6251, respectively, is increased or generated, or if the activity “potassium:hydrogen antiporter” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.23-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 6297, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 6297 or a polypeptide SEQ ID NO. 6298, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 6297 or polypeptide SEQ ID NO. 6298, respectively, is increased or generated, or if the activity “GPI-anchored cell wall protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred,

especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.19-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 6326, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 6326 or a polypeptide SEQ ID NO. 6327, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 6326 or polypeptide SEQ ID NO. 6327, respectively, is increased or generated, or if the activity “yjl213w-protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.62-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.12-fold plus at least 100% thereof under low temperature conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof. Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 6488, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 6488 or a polypeptide SEQ ID NO. 6489, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 6488 or polypeptide SEQ ID NO. 6489, respectively, is increased or generated, or if the activity “peptidyl-prolyl cis-trans isomerase” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared

to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.50-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 6550, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 6550 or a polypeptide SEQ ID NO. 6551, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 6550 or polypeptide SEQ ID NO. 6551, respectively, is increased or generated, or if the activity “clathrin associated protein complex small subunit” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.28-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.36-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 6700, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 6700 or a polypeptide SEQ ID NO. 6701, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 6700 or polypeptide SEQ ID NO. 6701, respectively, is increased or generated, or if the activity

“zinc metalloprotease” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance
5 and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass
10 production.

Particularly, an increase from 1.1-fold to 1.81-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.22-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild
15 type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 6816, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 6816 or a polypeptide SEQ ID NO. 6817, respectively, is increased or generated, e.g. if the activity of such a nucleic acid
20 molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 6816 or polypeptide SEQ ID NO. 6817, respectively, is increased or generated, or if the activity “F1F0 ATP synthase beta subunit” is increased or generated in an plant cell, plant or
25 part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or
30 a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.52-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.37-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild
35 type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 7366, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 7366 or a polypeptide SEQ ID NO. 7367, respectively, is increased or generated, e.g. if the activity of such a nucleic acid
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molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 7366 or polypeptide SEQ ID NO. 7367, respectively, is increased or generated, or if the activity
 5 “alpha-mannosidase” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress con-
 10 ditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

15 Particularly, an increase from 1.1-fold to 1.52-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 7475, or the activity of a polypeptide encoded by a nucleic acid
 20 molecule comprising the nucleic acid SEQ ID NO. 7475 or a polypeptide SEQ ID NO. 7476, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 7475 or
 25 polypeptide SEQ ID NO. 7476, respectively, is increased or generated, or if the activity “ribosomal protein of the small subunit” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress
 30 tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase
 35 of biomass production.

Particularly, an increase from 1.1-fold to 1.41-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 7602, or the activity of a polypeptide encoded by a nucleic acid
 40 molecule comprising the nucleic acid SEQ ID NO. 7602 or a polypeptide SEQ ID NO. 7603, respectively, is increased or generated, e.g. if the activity of such a nucleic acid

- molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 7602 or polypeptide SEQ ID NO. 7603, respectively, is increased or generated, or if the activity
- 5 “mitochondrial intermembrane space protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an
- 10 increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.
- 15 Particularly, an increase from 1.1-fold to 1.20-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.10-fold plus at least 100% thereof under low temperature conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof. Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid
- 20 molecule SEQ ID NO. 7651, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 7651 or a polypeptide SEQ ID NO. 7652, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 7651 or
- 25 polypeptide SEQ ID NO. 7652, respectively, is increased or generated, or if the activity “phosphopantothenoylcysteine decarboxylase” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an
- 30 increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.
- Particularly, an increase from 1.1-fold to 1.23-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.
- 40 Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 7661, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 7661 or a polypeptide SEQ ID NO.

7662, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 7661 or polypeptide SEQ ID NO. 7662, respectively, is increased or generated, or if the activity “ykl100c-protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.25-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 7675, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 7675 or a polypeptide SEQ ID NO. 7676, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 7675 or polypeptide SEQ ID NO. 7676, respectively, is increased or generated, or if the activity “ykl131w-protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.22-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 7679, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 7679 or a polypeptide SEQ ID NO.

7680, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 7679 or
5 polypeptide SEQ ID NO. 7680, respectively, is increased or generated, or if the activity “mitochondrial ribosomal protein of the large subunit” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an
10 increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE
15 and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.24-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 7710, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 7710 or a polypeptide SEQ ID NO. 7711, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 7710 or
20 polypeptide SEQ ID NO. 7711, respectively, is increased or generated, or if the activity “G protein coupled pheromone receptor receptor” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of
25 NUE, or in particular an increase of biomass production, or an enhancement of NUE
30 and an increase of biomass production.

Particularly, an increase from 1.1-fold to 2.69-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.57-fold plus at least 100% thereof of yield in the absence of nutrient deficiency
40 as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 7735, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 7735 or a polypeptide SEQ ID NO. 7736, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 7735 or polypeptide SEQ ID NO. 7736, respectively, is increased or generated, or if the activity “golgi membrane protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.58-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.22-fold plus at least 100% thereof under low temperature conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof. Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 7778, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 7778 or a polypeptide SEQ ID NO. 7779, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 7778 or polypeptide SEQ ID NO. 7779, respectively, is increased or generated, or if the activity “regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.77-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 7829, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 7829 or a polypeptide SEQ ID NO. 7830, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 7829 or polypeptide SEQ ID NO. 7830, respectively, is increased or generated, or if the activity “dihydroorotate dehydrogenase” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 2.09-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 8017, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 8017 or a polypeptide SEQ ID NO. 8018, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 8017 or polypeptide SEQ ID NO. 8018, respectively, is increased or generated, or if the activity “ykr016w-protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 2.00-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 8045, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 8045 or a polypeptide SEQ ID NO. 8046, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 8045 or polypeptide SEQ ID NO. 8046, respectively, is increased or generated, or if the activity “ykr021w-protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 2.14-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 8073, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 8073 or a polypeptide SEQ ID NO. 8074, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 8073 or polypeptide SEQ ID NO. 8074, respectively, is increased or generated, or if the activity “non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.57-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.09-fold plus at least 100% thereof under low temperature conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

5 Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 8263, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 8263 or a polypeptide SEQ ID NO. 8264, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus
10 sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 8263 or polypeptide SEQ ID NO. 8264, respectively, is increased or generated, or if the activity “integral membrane protein localized to late Golgi vesicles” is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of
15 yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild
20 type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.29-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-
25 fold to 1.20-fold plus at least 100% thereof under low temperature conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof. Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 8287, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 8287 or a polypeptide SEQ ID NO.
30 8288, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 8287 or polypeptide SEQ ID NO. 8288, respectively, is increased or generated, or if the activity
35 “peptide transporter” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress con-
40 ditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an in-

crease of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 3.98-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 8468, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 8468 or a polypeptide SEQ ID NO. 8469, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 8468 or polypeptide SEQ ID NO. 8469, respectively, is increased or generated, or if the activity “transcription factor” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.15-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.50-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 8484, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 8484 or a polypeptide SEQ ID NO. 8485, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 8484 or polypeptide SEQ ID NO. 8485, respectively, is increased or generated, or if the activity “transmembrane protein with a role in cell wall polymer composition” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE

and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

- 5 Particularly, an increase from 1.1-fold to 4.43-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.12-fold plus at least 100% thereof under low temperature conditions; also particularly, an increase from 1.05-fold to 1.30-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 8492, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 8492 or a polypeptide SEQ ID NO. 8493, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 8492 or polypeptide SEQ ID NO. 8493, respectively, is increased or generated, or if the activity “yll014w-protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

- 30 Particularly, an increase from 1.1-fold to 1.61-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 8514, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 8514 or a polypeptide SEQ ID NO. 8515, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 8514 or polypeptide SEQ ID NO. 8515, respectively, is increased or generated, or if the activity “non-essential Ras guanine nucleotide exchange factor” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a

part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of

5 NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.24-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-

10 transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 8539, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 8539 or a polypeptide SEQ ID NO. 8540, respectively, is increased or generated, e.g. if the activity of such a nucleic acid

15 molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 8539 or polypeptide SEQ ID NO. 8540, respectively, is increased or generated, or if the activity “yll023c-protein” is increased or generated in an plant cell, plant or part thereof, espe-

20 cially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof

25 is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.17-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-

30 transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 8571, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 8571 or a polypeptide SEQ ID NO. 8572, respectively, is increased or generated, e.g. if the activity of such a nucleic acid

35 molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 8571 or polypeptide SEQ ID NO. 8572, respectively, is increased or generated, or if the activity “yll037w-protein” is increased or generated in an plant cell, plant or part thereof, espe-

40 cially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially

an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.32-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 8575, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 8575 or a polypeptide SEQ ID NO. 8576, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 8575 or polypeptide SEQ ID NO. 8576, respectively, is increased or generated, or if the activity “yll049w-protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.75-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 8579, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 8579 or a polypeptide SEQ ID NO. 8580, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 8579 or polypeptide SEQ ID NO. 8580, respectively, is increased or generated, or if the activity “cysteine transporter ” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, es-

pecially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 5.25-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 8661, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 8661 or a polypeptide SEQ ID NO. 8662, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 8661 or polypeptide SEQ ID NO. 8662, respectively, is increased or generated, or if the activity “metal ion transporter” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 4.38-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 8991, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 8991 or a polypeptide SEQ ID NO. 8992, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 8991 or polypeptide SEQ ID NO. 8992, respectively, is increased or generated, or if the activity “ylr042c-protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially

an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.40-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 8995, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 8995 or a polypeptide SEQ ID NO. 8996, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 8995 or polypeptide SEQ ID NO. 8996, respectively, is increased or generated, or if the activity “YLR053C-protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.55-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.17-fold plus at least 100% thereof of yield in the absence of nutrient deficiency as well as stress conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 8999, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 8999 or a polypeptide SEQ ID NO. 9000, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 8999 or polypeptide SEQ ID NO. 9000, respectively, is increased or generated, or if the activity “cytosolic serine hydroxymethyltransferase” is increased or generated in an plant cell,

- plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.
- 5 Particularly, an increase from 1.1-fold to 1.19-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.
- Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 9551, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 9551 or a polypeptide SEQ ID NO. 15 9552, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 9551 or polypeptide SEQ ID NO. 9552, respectively, is increased or generated, or if the activity 20 “subunit of cytoplasmic phenylalanyl-tRNA synthetase” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of 25 NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.
- Particularly, an increase from 1.1-fold to 3.72-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.
- Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 9637, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 9637 or a polypeptide SEQ ID NO. 35 9638, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 9637 or polypeptide SEQ ID NO. 9638, respectively, is increased or generated, or if the activity 40 “ylr065c-protein” is increased or generated in an plant cell, plant or part thereof, espe-

- cially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.
- 5 Particularly, an increase from 1.1-fold to 1.88-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; also particularly, an increase from 1.05-fold to 1.24-fold plus at least 100% thereof under drought conditions; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.
- 10 Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 9672, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 9672 or a polypeptide SEQ ID NO. 9673, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 9672 or polypeptide SEQ ID NO. 9673, respectively, is increased or generated, or if the activity “xylitol dehydrogenase” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.
- 20 Particularly, an increase from 1.1-fold to 2.66-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.
- 25 Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 10182, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 10182 or a polypeptide SEQ ID NO. 10183, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 10182 or polypeptide SEQ ID NO. 10183, respectively, is increased or generated, or if the activ-
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ity "3-keto sterol reductase" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance
5 and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass
10 production.

Particularly, an increase from 1.1-fold to 1.57-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 10214, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 10214 or a polypeptide SEQ ID NO. 10215, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 10214 or polypeptide SEQ ID NO. 10215, respectively, is increased or generated, or if the activity "alkyl hydroperoxide reductase" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.
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Particularly, an increase from 1.1-fold to 1.55-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 10447, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 10447 or a polypeptide SEQ ID NO. 10448, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 10447 or polypeptide SEQ ID NO. 10448, respectively, is increased or generated, or if the activ-
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ity “ylr125w-protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance
5 and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass
10 production.

Particularly, an increase from 1.1-fold to 1.28-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred; as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid
15 molecule SEQ ID NO. 10451, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 10451 or a polypeptide SEQ ID NO. 10452, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus
20 sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 10451 or polypeptide SEQ ID NO. 10452, respectively, is increased or generated, or if the activity “anaphase promoting complex (APC) subunit” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield
25 as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild
30 type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.22-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid
35 molecule SEQ ID NO. 10463, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 10463 or a polypeptide SEQ ID NO. 10464, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus
40 sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 10463 or polypeptide SEQ ID NO. 10464, respectively, is increased or generated, or if the activ-

ity "protein component of the large ribosomal subunit" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.14-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 10533, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 10533 or a polypeptide SEQ ID NO. 10534, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 10533 or polypeptide SEQ ID NO. 10534, respectively, is increased or generated, or if the activity "mitochondrial protein" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.38-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 10533, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 10533 or a polypeptide SEQ ID NO. 10534, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 10533 or polypeptide SEQ ID NO. 10534, respectively, is increased or generated, or if the activ-

ity "mitochondrial protein" is increased or generated in an plant cell, plant or part thereof, especially with plastidic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.05-fold to 1.22 -fold plus at least 100% thereof under low temperature conditions is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 10541, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 10541 or a polypeptide SEQ ID NO. 10542, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 10541 or polypeptide SEQ ID NO. 10542, respectively, is increased or generated, or if the activity "ARV1 protein " is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.61-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 10562, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 10562 or a polypeptide SEQ ID NO. 10563, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 10562 or polypeptide SEQ ID NO. 10563, respectively, is increased or generated, or if the activ-

ity "GTP-binding protein" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance
5 and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass
10 production.

Particularly, an increase from 1.1-fold to 2.75-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 10990, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 10990 or a polypeptide SEQ ID NO. 10991, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 10990 or polypeptide SEQ ID NO. 10991, respectively, is increased or generated, or if the activity "protein involved in shmoo formation and bipolar bud site selection" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.
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Particularly, an increase from 1.1-fold to 1.25-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 10998, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 10998 or a polypeptide SEQ ID NO. 10999, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 10998 or polypeptide SEQ ID NO. 10999, respectively, is increased or generated, or if the activ-
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ity "non-essential kinetochore protein" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.54-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 11004, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 11004 or a polypeptide SEQ ID NO. 11005, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 11004 or polypeptide SEQ ID NO. 11005, respectively, is increased or generated, or if the activity "Meiotic recombination protein" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.27-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 11012, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 11012 or a polypeptide SEQ ID NO. 11013, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 11012 or polypeptide SEQ ID NO. 11013, respectively, is increased or generated, or if the activ-

ity "signal transducing MEK kinase" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 3.40-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 11054, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 11054 or a polypeptide SEQ ID NO. 11055, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 11054 or polypeptide SEQ ID NO. 11055, respectively, is increased or generated, or if the activity "cytochrome c oxidase subunit VIII" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.56-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 11066, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 11066 or a polypeptide SEQ ID NO. 11067, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 11066 or polypeptide SEQ ID NO. 11067, respectively, is increased or generated, or if the activ-

ity "ylr404w-protein" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance
5 and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass
10 production.

Particularly, an increase from 1.1-fold to 1.33-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid
15 molecule SEQ ID NO. 11074, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 11074 or a polypeptide SEQ ID NO. 11075, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus
20 sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 11074 or polypeptide SEQ ID NO. 11075, respectively, is increased or generated, or if the activity "ylr463c-protein" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance
25 and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass
30 production.

Particularly, an increase from 1.1-fold to 1.33-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid
35 molecule SEQ ID NO. 11080, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 11080 or a polypeptide SEQ ID NO. 11081, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus
40 sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 11080 or polypeptide SEQ ID NO. 11081, respectively, is increased or generated, or if the activ-

ity "adenine phosphoribosyltransferase" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.27-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 11552, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 11552 or a polypeptide SEQ ID NO. 11553, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 11552 or polypeptide SEQ ID NO. 11553, respectively, is increased or generated, or if the activity "Mcm1p binding transcriptional repressor" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.42-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 11569, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 11569 or a polypeptide SEQ ID NO. 11570, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 11569 or polypeptide SEQ ID NO. 11570, respectively, is increased or generated, or if the activ-

ity "origin recognition complex subunit" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.14-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 11596, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 11596 or a polypeptide SEQ ID NO. 11597, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 11596 or polypeptide SEQ ID NO. 11597, respectively, is increased or generated, or if the activity "yml089c-protein" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 1.17-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 11600, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 11600 or a polypeptide SEQ ID NO. 11601, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 11600 or polypeptide SEQ ID NO. 11601, respectively, is increased or generated, or if the activ-

ity “yml128c-protein” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance
5 and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass
10 production.

Particularly, an increase from 1.1-fold to 1.12-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 11612, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 11612 or a polypeptide SEQ ID NO. 11613, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus
15 sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 11612 or polypeptide SEQ ID NO. 11613, respectively, is increased or generated, or if the activity “hexose transporter” is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance
20 and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass
25 production.

Particularly, an increase from 1.1-fold to 1.52-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 12246, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 12246 or a polypeptide SEQ ID NO. 12247, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus
35 sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 12246 or polypeptide SEQ ID NO. 12247, respectively, is increased or generated, or if the activ-
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ity "Zinc finger protein" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance
5 and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass
10 production.

Particularly, an increase from 1.1-fold to 1.41-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid
15 molecule SEQ ID NO. 12263, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 12263 or a polypeptide SEQ ID NO. 12264, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus
20 sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 12263 or polypeptide SEQ ID NO. 12264, respectively, is increased or generated, or if the activity "protein required for maturation of ribosomal RNAs" is increased or generated in an
25 plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an
30 increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass production.

Particularly, an increase from 1.1-fold to 3.71-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid
35 molecule SEQ ID NO. 12316, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 12316 or a polypeptide SEQ ID NO. 12317, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus
40 sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 12316 or polypeptide SEQ ID NO. 12317, respectively, is increased or generated, or if the activ-

ity "Factor arrest protein " is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance
5 and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass
10 production.

Particularly, an increase from 1.1-fold to 1.28-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 12327, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 12327 or a polypeptide SEQ ID NO. 12328, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus
15 sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 12327 or polypeptide SEQ ID NO. 12328, respectively, is increased or generated, or if the activity "YMR082C-protein" is increased or generated in an plant cell, plant or part thereof, especially with cytoplasmic localization, an increase of yield as compared to a corresponding non-transformed wild type plant cell, plant or a part thereof is conferred, especially an enhanced nutrient use efficiency and/or an increased stress tolerance
20 and/or an increased yield, in the absence of a nutrient deficiency as well as stress conditions, in particular an enhancement of NUE and/or an increase of biomass production as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof is conferred, or in particular an enhancement of NUE, or in particular an increase of biomass production, or an enhancement of NUE and an increase of biomass
25 production.

Particularly, an increase from 1.1-fold to 1.26-fold plus at least 100% thereof under conditions of nitrogen deficiency is conferred as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.

Accordingly, in one embodiment, in case the *Saccharomyces cerevisiae* nucleic acid molecule SEQ ID NO. 12331, or the activity of a polypeptide encoded by a nucleic acid molecule comprising the nucleic acid SEQ ID NO. 12331 or a polypeptide SEQ ID NO. 12332, respectively, is increased or generated, e.g. if the activity of such a nucleic acid molecule or a polypeptide comprising the nucleic acid or polypeptide or the consensus
35 sequence or the polypeptide motif, as depicted in table I, II or IV, application no. 1, column 7 in the respective same line as the nucleic acid molecule SEQ ID NO. 12331 or polypeptide SEQ ID NO. 12332, respectively, is increased or generated, or if the activ-
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CLAIMS

1. A method for producing a transgenic plant cell, a plant or a part thereof with increased yield, especially enhanced nitrogen use efficiency (NUE) and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof by increasing or generating one or more activities selected from the group consisting of 2-dehydro-3-deoxy-phosphoheptonate aldolase, 3-keto sterol reductase, 60S ribosomal protein, adenine phosphoribosyltransferase, adenylate kinase, alkyl hydroperoxide reductase, Alkyl/aryl-sulfatase, alpha-glucosidase, alpha-mannosidase, anaphase promoting complex (APC) subunit, antiviral adaptor protein, aromatic amino acid aminotransferase II, ARV1 protein, autophagy-specific phosphatidylinositol 3-kinase complex protein subunit, b0017-protein, B0165-protein, B1258-protein, B1267-protein, B1381-protein, b1933-protein, b2165-protein, b2238-protein, b2431-protein, B2646-protein, b2766-protein, b3120-protein, carnitine acetyltransferase, cell wall endo-beta-1,3-glucanase, chaperone, Chitin synthase 3 complex protein, cholinephosphate cytidyltransferase, chorismate mutase T / prephenate dehydrogenase (bifunctional), clathrin associated protein complex small subunit, component of the RAM signaling network, cysteine transporter, cytochrome c oxidase subunit VIII, cytosolic catalase, cytosolic serine hydroxymethyltransferase, dihydroorotate dehydrogenase, dihydrosphingosine phosphate lyase, exoribonuclease, F1F0 ATP synthase beta subunit, Factor arrest protein, G protein coupled pheromone receptor, gamma-glutamyl kinase, glucoamylase, glycerol-3-phosphate transporter subunit, glycine decarboxylase, glycosyltransferase, golgi membrane exchange factor subunit, golgi membrane protein, GPI-anchored cell wall protein, GTP-binding protein, helix-loop-helix transcription activator that binds inositol/choline-responsive elements, hexose transporter, histidine kinase osmosensor that regulates an osmosensing MAP kinase cascade, hydro-lyase, hydroxylamine reductase, hydroxymyristol acyl carrier protein dehydratase, inheritance of peroxisomes protein, integral membrane protein localized to late Golgi vesicles, iron sulfur cluster assembly protein, isomerase, lysine/arginine/ornithine transporter subunit, lysine-specific metalloprotease, lysophospholipase, Mcm1p binding transcriptional repressor, Meiotic recombination protein, membrane protein, metal ion transporter, microsomal beta-ketoreductase, mitochondrial intermembrane space protein, mitochondrial protein, mitochondrial ribosomal protein of the large subunit, mitochondrial ribosomal protein of the small subunit, mitochondrial seryl-tRNA synthetase, molybdopterin biosynthesis protein, myo-inositol transporter, non-essential kinetochore protein, non-essential Ras guanine nucleotide exchange factor, non-essential small GTPase of the Rho/Rac subfamily of Ras-like proteins, Nuclear cap-binding protein complex subunit, nuclear fusion protein precursor, nuclear pore complex subunit, origin recognition complex subunit, outer membrane usher protein, oxi-

- doreductase, peptide transporter, peptidyl-prolyl cis-trans isomerase, PhoH-like protein, phosphatidylserine decarboxylase, phosphoglucomutase/phosphomannomutase, phosphopantothenoylcysteine decarboxylase, Phosphoribosylaminoimidazole carboxylase, potassium:hydrogen antiporter, proline dehydrogenase, protein component of the large ribosomal subunit, protein involved in shmoo formation and bipolar bud site selection, protein involved in sphingolipid biosynthesis, protein kinase, protein necessary for structural stability of L-A double-stranded RNA-containing particles, protein required for maturation of ribosomal RNAs, protein translocase protein, Regulatory CAT8 protein, regulatory subunit of Glc7p type 1 protein serine- threonine phosphatase, regulatory subunit of the 26S proteasome, repressor of G1 transcription, Rho GDP-dissociation inhibitor, ribonucleoprotein, ribosomal protein of the small subunit, RNA polymerase III subunit, saccharopine dehydrogenase, short chain fatty acid transporter, signal recognition particle subunit (SRP54), signal transducing MEK kinase, SM complex B protein for mRNA splicing, spindle checkpoint complex subunit, splicing factor, Stationary phase protein , subunit of cytoplasmic phenylalanyl-tRNA synthetase, subunit of the transport protein particle (TRAPP) complex of the cis-Golgi , threonine ammonia-lyase, transcription elongation factor, transcription factor, Transcriptional activator , translational elongation factor EF-3 (HEF3), transmembrane protein with a role in cell wall polymer composition, transport protein, ubiquitin regulatory protein , UDP-N-acetyl-glucosamine-1-P transferase, v-SNARE binding protein, v-SNARE protein involved in Golgi transport, xylitol dehydrogenase, yal019w-protein, ybr262c-protein, YDR070C-protein, ydr355c-protein, YFR007W-protein, ygr122c-a-protein, ygr266w-protein, ygr290w-protein, YHL005C-protein, yhl021c-protein, yhr127w-protein, YJL010C-protein, yjl064w-protein, yjl067w-protein, yjl213w-protein, ykl100c-protein, YKL111C-protein, ykl131w-protein, ykr016w-protein, ykr021w-protein, yll014w-protein, yll023c-protein, yll037w-protein, yll049w-protein, ylr042c-protein, YLR053C-protein, ylr065c-protein, ylr125w-protein, ylr404w-protein, ylr463c-protein, yml089c-protein, YML101C-protein, yml128c-protein, YMR082C-protein, YMR126C membrane protein, YMR144W-protein, YMR160W-protein, YMR209C-protein, YMR233W-protein, YNL320W-protein, YOR097C-protein, YOR203W-protein, YPL068C-protein, Zinc finger protein, and zinc metalloprotease.
2. A method for producing a transgenic plant cell, a plant or a part thereof with increased yield, especially with enhanced nitrogen use efficiency (NUE) and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof by increasing or generating the activity of at least one polypeptide comprising a polypeptide selected from the group consisting of:

- (i) a polypeptide comprising a polypeptide, a consensus sequence or at least one polypeptide motif as depicted in column 5 or 7 of table II or of table IV, respectively; or
- (ii) an expression product of a nucleic acid molecule comprising a polynucleotide as depicted in column 5 or 7 of table I; or
- (iii) a functional equivalent of (i) or (ii).
- 5
3. A method for producing a transgenic plant cell, a plant or a part thereof with increased yield, especially enhanced nitrogen use efficiency (NUE) and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof by increasing or generating
- 10
- (i) the expression of; and/or
- (ii) the expression of an expression product of; and/or
- (iii) the activity of an expression product encoded by;
- 15
- at least one nucleic acid molecule comprising a nucleic acid molecule selected from the group consisting of:
- (a) a nucleic acid molecule encoding the polypeptide shown in column 5 or 7 of table II;
- (b) a nucleic acid molecule shown in column 5 or 7 of table I;
- 20
- (c) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence depicted in column 5 or 7 of table II and confers an increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof;
- 25
- (d) a nucleic acid molecule having at least 30 % identity with the nucleic acid molecule sequence of a polynucleotide comprising the nucleic acid molecule shown in column 5 or 7 of table I and confers an increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof ;
- 30
- (e) a nucleic acid molecule encoding a polypeptide having at least 30 % identity with the amino acid sequence of the polypeptide encoded by the nucleic acid molecule of (a) to (c) and having the activity represented by a nucleic acid molecule comprising a polynucleotide as depicted in column 5 of table I and confers an increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof;
- 35
- (f) nucleic acid molecule which hybridizes with a nucleic acid molecule of (a) to (c) under stringent hybridization conditions and confers an increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof;
- 40

- 5 (g) a nucleic acid molecule encoding a polypeptide which can be isolated with the aid of monoclonal or polyclonal antibodies made against a polypeptide encoded by one of the nucleic acid molecules of (a) to (e) and having the activity represented by the nucleic acid molecule comprising a polynucleotide as depicted in column 5 of table I;
- (h) a nucleic acid molecule encoding a polypeptide comprising the consensus sequence or one or more polypeptide motifs as shown in column 7 of table IV and preferably having the activity represented by a nucleic acid molecule comprising a polynucleotide as depicted in column 5 of table II or IV;
- 10 (i) a nucleic acid molecule encoding a polypeptide having the activity represented by a protein as depicted in column 5 of table II and confers an increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof;
- 15 (j) nucleic acid molecule which comprises a polynucleotide, which is obtained by amplifying a cDNA library or a genomic library using the primers in column 7 of table III and preferably having the activity represented by a nucleic acid molecule comprising a polynucleotide as depicted in column 5 of table II or IV;
- 20 and
- k) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of (a) or (b) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 25 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in (a) to (e) and encoding a polypeptide having the activity represented by a protein comprising a polypeptide as depicted in column 5 of table II.
- 30 4. A method according to claim 1, wherein the increased yield, especially the enhanced nitrogen use efficiency (NUE) and/or increased biomass production, is conferred by increasing or generating the activity of at least one polypeptide comprising a polypeptide as defined in claim 2, and/or is conferred by increasing or generating the activity of at least one nucleic acid molecule comprising a nucleic acid molecule as defined in claim 3.
- 35
5. A method according to claim 2, wherein the increased yield, especially the enhanced nitrogen use efficiency (NUE) and/or increased biomass production, is conferred by increasing or generating the activity of at least one nucleic acid molecule comprising a nucleic acid molecule as defined in claim 3.
- 40

6. A method for producing a transgenic plant cell, a plant or a part thereof with increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, plant or part thereof, by transforming a plant cell or a plant cell nucleus or a plant tissue with a nucleic acid molecule comprising a nucleic acid molecule selected from the group consisting of:
- 5 (a) a nucleic acid molecule encoding the polypeptide shown in column 5 or 7 of table II;
- (b) a nucleic acid molecule shown in column 5 or 7 of table I;
- 10 (c) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence depicted in column 5 or 7 of table II and confers an increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof;
- 15 (d) a nucleic acid molecule having at least 30 % identity with the nucleic acid molecule sequence of a polynucleotide comprising the nucleic acid molecule shown in column 5 or 7 of table I and confers an increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof;
- 20 (e) a nucleic acid molecule encoding a polypeptide having at least 30 % identity with the amino acid sequence of the polypeptide encoded by the nucleic acid molecule of (a) to (c) and having the activity represented by a nucleic acid molecule comprising a polynucleotide as depicted in column 5 of table I and confers an increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof;
- 25 (f) nucleic acid molecule which hybridizes with a nucleic acid molecule of (a) to (c) under stringent hybridization conditions and confers an increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof;
- 30 (g) a nucleic acid molecule encoding a polypeptide which can be isolated with the aid of monoclonal or polyclonal antibodies made against a polypeptide encoded by one of the nucleic acid molecules of (a) to (e) and having the activity represented by the nucleic acid molecule comprising a polynucleotide as depicted in column 5 of table I;
- 35 (h) a nucleic acid molecule encoding a polypeptide comprising the consensus sequence or one or more polypeptide motifs as shown in column 7 of table IV and preferably having the activity represented by a nucleic acid molecule comprising a polynucleotide as depicted in column 5 of table II or IV;
- 40

- 5 (i) a nucleic acid molecule encoding a polypeptide having the activity represented by a protein as depicted in column 5 of table II and confers an increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof;
- 10 (j) nucleic acid molecule which comprises a polynucleotide, which is obtained by amplifying a cDNA library or a genomic library using the primers in column 7 of table III and preferably having the activity represented by a nucleic acid molecule comprising a polynucleotide as depicted in column 5 of table II or IV;
- and
- 15 (k) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of (a) or (b) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in (a) to (e) and encoding a polypeptide having the activity represented by a protein comprising a polypeptide as depicted in column 5 of table II;
- 20 and regenerating a transgenic plant from that transformed plant cell nucleus, plant cell or plant tissue with increased yield.
- 25 7. The method of any one of claims 1 to 5 resulting in increased yield compared to a corresponding non-transformed wild type plant cell, plant or part thereof, under standard growth conditions.
- 30 8. An isolated nucleic acid molecule comprising a nucleic acid molecule selected from the group consisting of:
- (a) a nucleic acid molecule encoding the polypeptide shown in column 5 or 7 of table II B;
- (b) a nucleic acid molecule shown in column 5 or 7 of table I B;
- (c) a nucleic acid molecule, which, as a result of the degeneracy of the genetic code, can be derived from a polypeptide sequence depicted in column 5 or 7 of table II and confers an increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof;
- 35 (d) a nucleic acid molecule having at least 30 % identity with the nucleic acid molecule sequence of a polynucleotide comprising the nucleic acid molecule shown in column 5 or 7 of table I and confers an increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof;
- 40

pared to a corresponding non-transformed wild type plant cell, a plant or a part thereof;

- 5 (e) a nucleic acid molecule encoding a polypeptide having at least 30 % identity with the amino acid sequence of the polypeptide encoded by the nucleic acid molecule of (a) to (c) and having the activity represented by a nucleic acid molecule comprising a polynucleotide as depicted in column 5 of table I and confers an increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof;
- 10 (f) nucleic acid molecule which hybridizes with a nucleic acid molecule of (a) to (c) under stringent hybridization conditions and confers increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof;
- 15 (g) a nucleic acid molecule encoding a polypeptide which can be isolated with the aid of monoclonal or polyclonal antibodies made against a polypeptide encoded by one of the nucleic acid molecules of (a) to (e) and having the activity represented by the nucleic acid molecule comprising a polynucleotide as depicted in column 5 of table I;
- 20 (h) a nucleic acid molecule encoding a polypeptide comprising the consensus sequence or one or more polypeptide motifs as shown in column 7 of table IV and preferably having the activity represented by a nucleic acid molecule comprising a polynucleotide as depicted in column 5 of table II or IV;
- 25 (i) a nucleic acid molecule encoding a polypeptide having the activity represented by a protein as depicted in column 5 of table II and confers increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof;
- 30 (j) nucleic acid molecule which comprises a polynucleotide, which is obtained by amplifying a cDNA library or a genomic library using the primers in column 7 of table III and preferably having the activity represented by a nucleic acid molecule comprising a polynucleotide as depicted in column 5 of table II or IV;
- and
- 35 (k) a nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising a complementary sequence of a nucleic acid molecule of (a) or (b) or with a fragment thereof, having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of a nucleic acid molecule complementary to a nucleic acid molecule sequence characterized in (a) to (e) and encoding a polypeptide having the activity represented by a protein comprising a polypeptide as depicted in column 5 of table II.
- 40

- 5 9. A nucleic acid molecule which distinguishes over a nucleic acid molecule as defined in claim 8 at least in one or more nucleotides of the sequences depicted in column 5 or 7 of table IA and preferably which encodes a protein which differs at least in one or more amino acids from the protein sequences depicted in column 5 or 7 of table IIA.
- 10 10. A nucleic acid construct which confers the expression of said nucleic acid molecule of claim 8 or 9, or of said nucleic acid molecule as described in claim 6, comprising one or more regulatory elements, especially whereby expression of the nucleic acid in a host cell results in increased yield, especially in enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.
- 15 11. A vector comprising the nucleic acid molecule as claimed in claim 8 or 9, or the nucleic acid molecule as described in claim 6, or the nucleic acid construct of claim 10, especially whereby expression of said coding nucleic acid in a host cell results in increased yield, especially in enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.
- 20 12. A host cell, which has been transformed stably or transiently with the vector as claimed in claim 11 or the nucleic acid molecule as claimed in claim 8 or 9, or the nucleic acid molecule as described in claim 6, or the nucleic acid construct of claim 10, especially which shows due to the transformation an increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof.
- 25 13. A process for producing a polypeptide, wherein the polypeptide is expressed in a host cell as claimed in claim 12.
- 30 14. A polypeptide produced by the process as claimed in claim 13 or encoded by the nucleic acid molecule as claimed in claim 8 or 9, or encoded by the nucleic acid molecule as described in claim 6, whereby the polypeptide distinguishes over the sequence as shown in table II A by one or more amino acids, or especially as depicted in table IIB.
- 35 15. An antibody, which binds specifically to the polypeptide as claimed in claim 14.
- 40 16. A transgenic plant cell nucleus, plant cell, plant tissue, propagation material, harvested material, a plant or a part thereof comprising the nucleic acid molecule as

claimed in claim 8 or 9, or a nucleic acid molecule as described in claim 6 or the host cell as claimed in claim 12.

- 5 17. A transgenic plant cell nucleus, plant cell, plant tissue, propagation material, harvested material or a part of a plant resulting after regeneration in a plant with increased yield, especially enhanced NUE and/or increased biomass production, or a transgenic plant with increased yield, especially enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type, produced by a method according to claim 1 to 7 or being transformed
10 with the nucleic acid molecule as claimed in claim 8 or 9 or the nucleic acid molecule as described in claim 6, or the nucleic acid construct of claim 10.
18. The transgenic plant cell, a plant or a part thereof of claim 17 derived from a
15 monocotyledonous plant.
19. The transgenic plant cell, a plant or a part thereof of claim 17 derived from a dicotyledonous plant.
20. The transgenic plant cell, a plant or a part thereof of claim 17, wherein the plant
20 is selected from the group consisting of maize, wheat, rye, oat, triticale, rice, barley, soybean, peanut, cotton, oil seed rape, including canola and winter oil seed rape, corn, manihot, pepper, sunflower, flax, borage, safflower, linseed, primrose, rapeseed, turnip rape, tagetes, solanaceous plants, potato, tobacco, eggplant, tomato, Vicia species, pea, alfalfa, coffee, cacao, tea, Salix species, oil palm, coconut, perennial grass, forage crops and Arabidopsis thaliana.
25
21. The transgenic plant cell, a plant or a part thereof of claim 17, wherein the plant
is selected from the group consisting of corn, soy, oil seed rape (including canola and winter oil seed rape), cotton, wheat and rice.
30
22. A seed produced by a transgenic plant of any of claims 16 to 21, wherein the
seed is genetically homozygous for a transgene conferring an increased yield, especially an enhanced NUE and/or increased biomass production, as compared
35 to a corresponding non-transformed wild type.
23. A process for the identification of a compound conferring increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a
corresponding non-transformed wild type plant cell, a plant or a part thereof in a transgenic plant cell, a plant or a part thereof, comprising the steps:
40 (a) culturing a transgenic plant cell, a plant or a part thereof or maintaining a transgenic plant expressing the polypeptide encoded by the nucleic acid molecule of claim 8 or 9, or encoded by the nucleic acid molecule as de-

- scribed in claim 6, conferring an increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof; optionally a non-transformed wild type plant or a part thereof; and a readout system capable of interacting with the polypeptide under suitable conditions which permit the interaction of the polypeptide with said readout system in the presence of a compound or a sample comprising a plurality of compounds and capable of providing a detectable signal in response to the binding of a compound to said polypeptide under conditions which permit the expression of said readout system and of the polypeptide encoded by the nucleic acid molecule of claim 8 or 9, or encoded by the nucleic acid molecule as described in claim 6, conferring an increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof; a non-transformed wild type plant or a part thereof;
- (b) identifying if the compound is an effective agonist by detecting the presence or absence or increase of a signal produced by said readout system.
24. A method for the production of an agricultural composition comprising the steps of the method of claim 23 and formulating the compound identified in claim 23 in a form acceptable for an application in agriculture.
25. A composition comprising the nucleic acid molecule of any of the claims 8 or 9, or the nucleic acid molecule as described in claim 6, the polypeptide of claim 14, the polypeptide as described in claim 2, the nucleic acid construct of claim 10, the vector of claim 11, the compound of claim 24 and/or the antibody of claim 15, and optionally an agricultural acceptable carrier.
26. An isolated polypeptide as claimed in claim 14, especially which is depicted in table II, preferably table II B; and which is selected from yeast, preferably *Saccharomyces cerevisiae*, or *E.coli*.
27. A method of producing a transgenic plant cell, a plant or a part thereof with increased yield, especially enhanced NUE and/or increased biomass production, compared to a corresponding non transformed wild type plant cell, a plant or a part thereof, wherein the increased yield, especially the enhanced NUE and/or increased biomass production, is increased by expression of a polypeptide encoded by a nucleic acid according to claim 14 or by expression of a polypeptide as described in claim 2, and results in increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or a part thereof, comprising

- (a) transforming a plant cell, or a part of a plant with an expression vector according to claim 11, or an expression vector comprising the nucleic acid molecule as described in claim 6, and
- (b) generating from the plant cell or the part of a plant a transgenic plant with increased yield, especially enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant.
28. Use of a NUERP encoding nucleic acid molecule selected from the group comprising the nucleic acid of claim 8 or 9, or a nucleic acid as described in claim 6, for preparing a transgenic plant cell, plant or part thereof with increased yield, especially with enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell, a plant or part of a plant.
29. Use of a NUERP encoding nucleic acid molecule selected from the group comprising the nucleic acid according to claim 8 or 9, or parts thereof, or a nucleic acid as described in claim 6, or parts thereof, as markers for identification and/or selection of plants, parts thereof or plant cells with an increased yield, especially an enhanced NUE and/or increased biomass production, as compared to a corresponding non-transformed wild type plant cell; a non-transformed wild type plant or a part thereof.
30. Use of a NUERP encoding nucleic acid molecule selected from the group comprising the nucleic acid according to claim 8 or 9, or parts thereof, or a nucleic acid as described in claim 6, or a part thereof, as markers for detection of increased yield and/or stress in plants or plant cells.
31. The method of any one of claims 1 to 6 or the plant according to any one of claims 16 to 21, wherein said plant shows an improved nutrient use efficiency and/or abiotic stress tolerance.
32. The method of any one of claims 1 to 6 or 31 or the plant according to any one of claims 16 to 21, wherein said plant shows an improved nutrient use efficiency, especially an enhanced NUE.
33. The method of any one of claims 1 to 6, or 31 to 32, or the plant according to any one of claims 16 to 21, wherein said plant shows an improved abiotic stress tolerance.
34. The method of any one of claims 1 to 6, or 31 to 33, or the plant according to any one of claims 16 to 21, wherein said plant shows an improved stress tolerance,

especially an increased low temperature tolerance and/or an increase tolerance to drought conditions.

- 5 35. The method of any one of claims 1 to 6, or 31 to 34, or the plant according to any one of claims 16 or 21, wherein said plant shows an improved yield in the absence of stress as well as nutrient deficiency.

Fig. 1a Vector VC-MME220-1 SEQ ID NO: 1 used for cloning gene of interest for non-targeted expression.

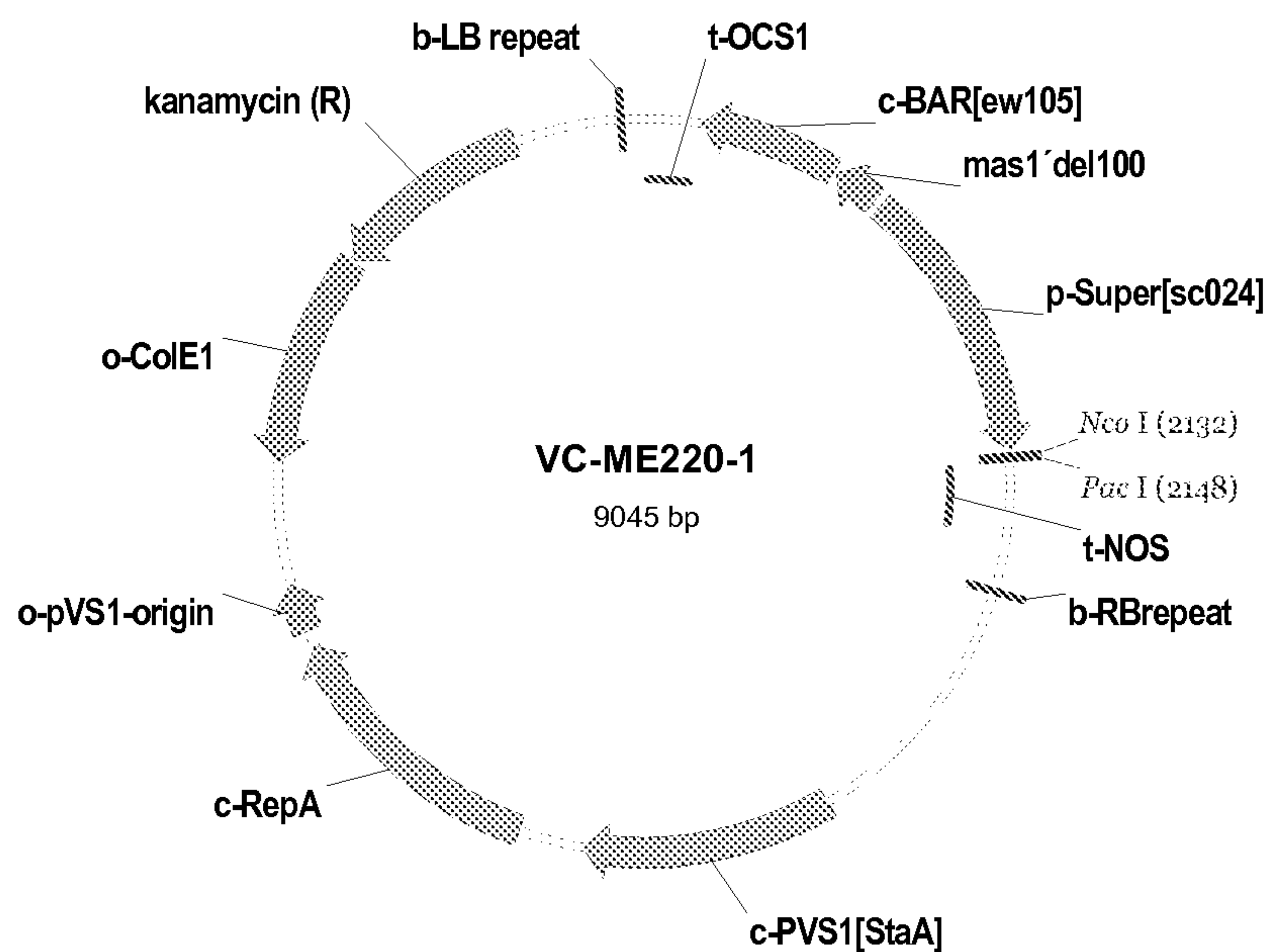
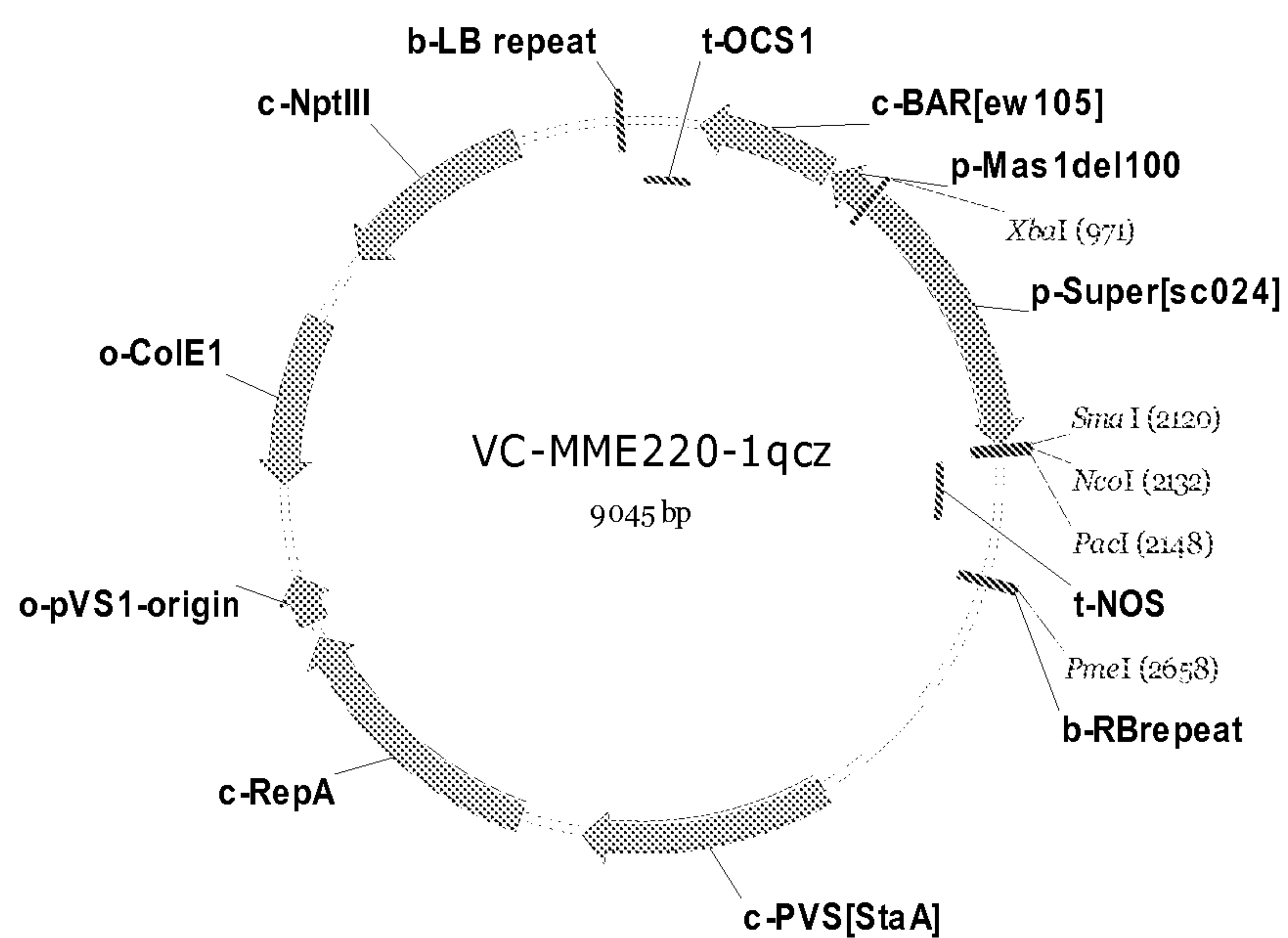


Fig. 1b Vector VC-MME220-1qcz SEQ ID NO: 14389 used for cloning gene of interest for non-targeted expression.



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Fig. 2a Vector VC-MME221-1 SEQ ID NO: 2 used for cloning gene of interest for non-targeted expression.

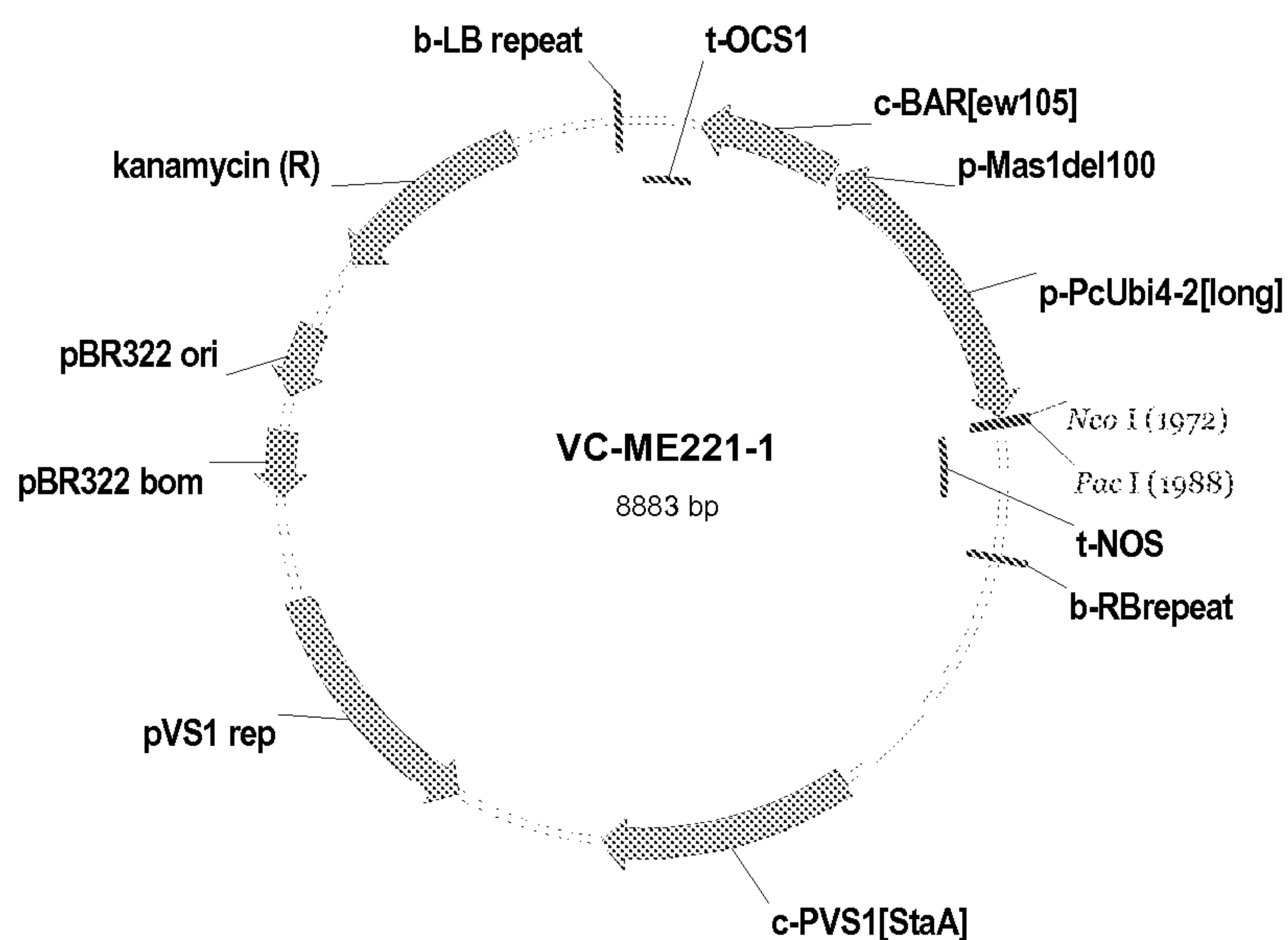
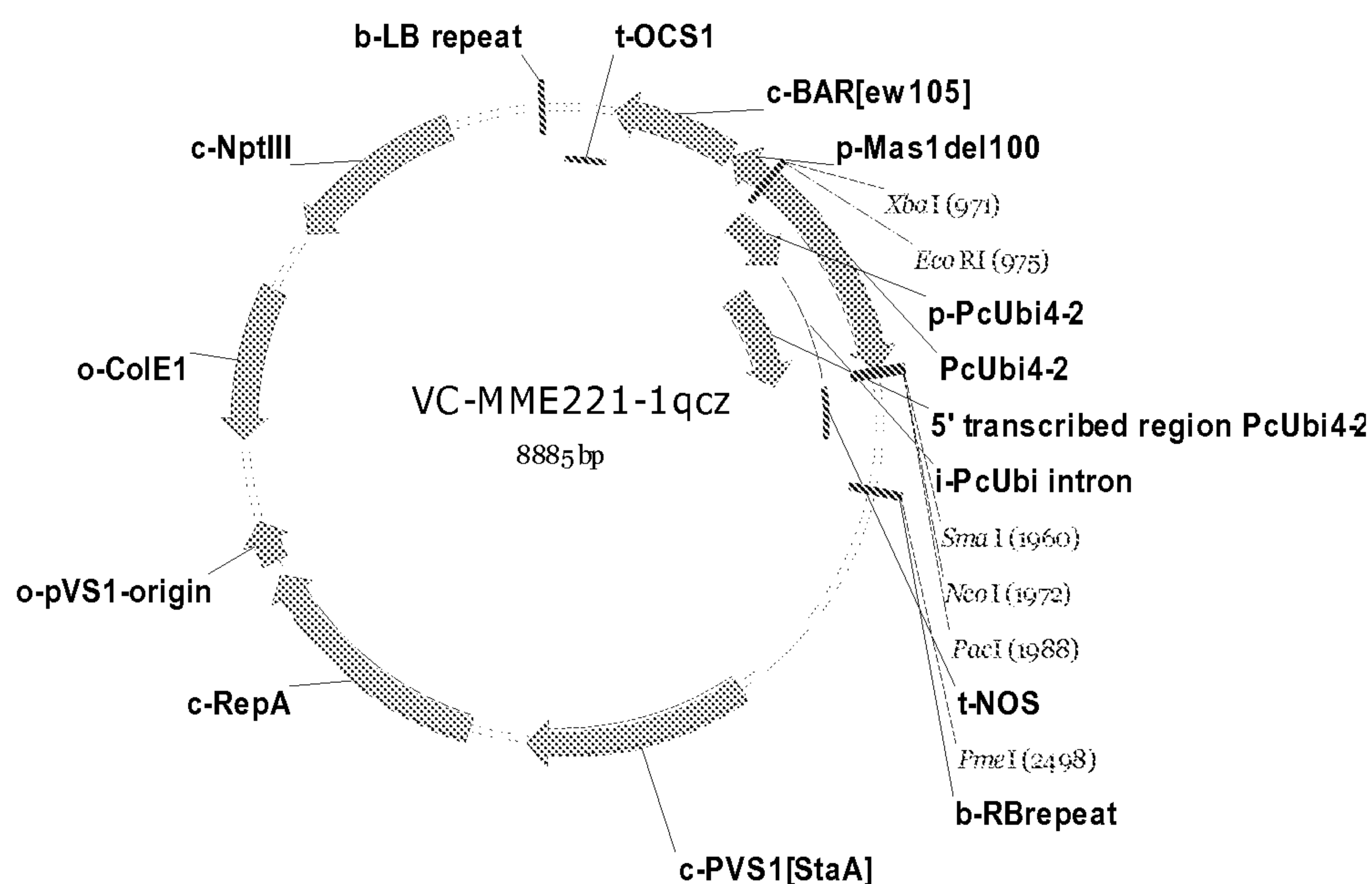


Fig. 2b Vector VC-MME221-1qcz (SEQ ID NO: 14390) used for cloning gene of interest for non-targeted expression.



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Fig. 3a Vector VC-MME354-1 SEQ ID NO: 3 used for cloning gene of interest for targeted expression.

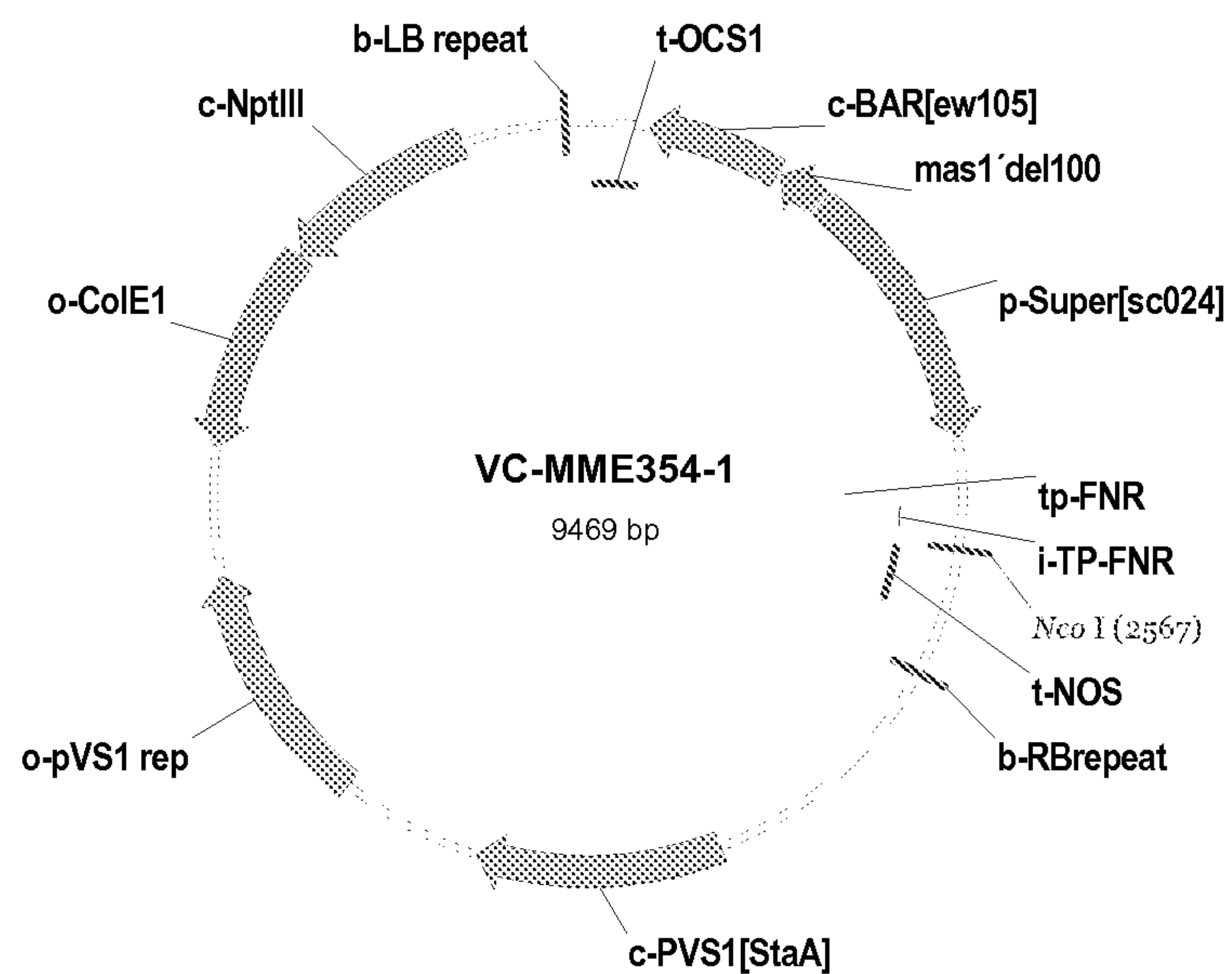
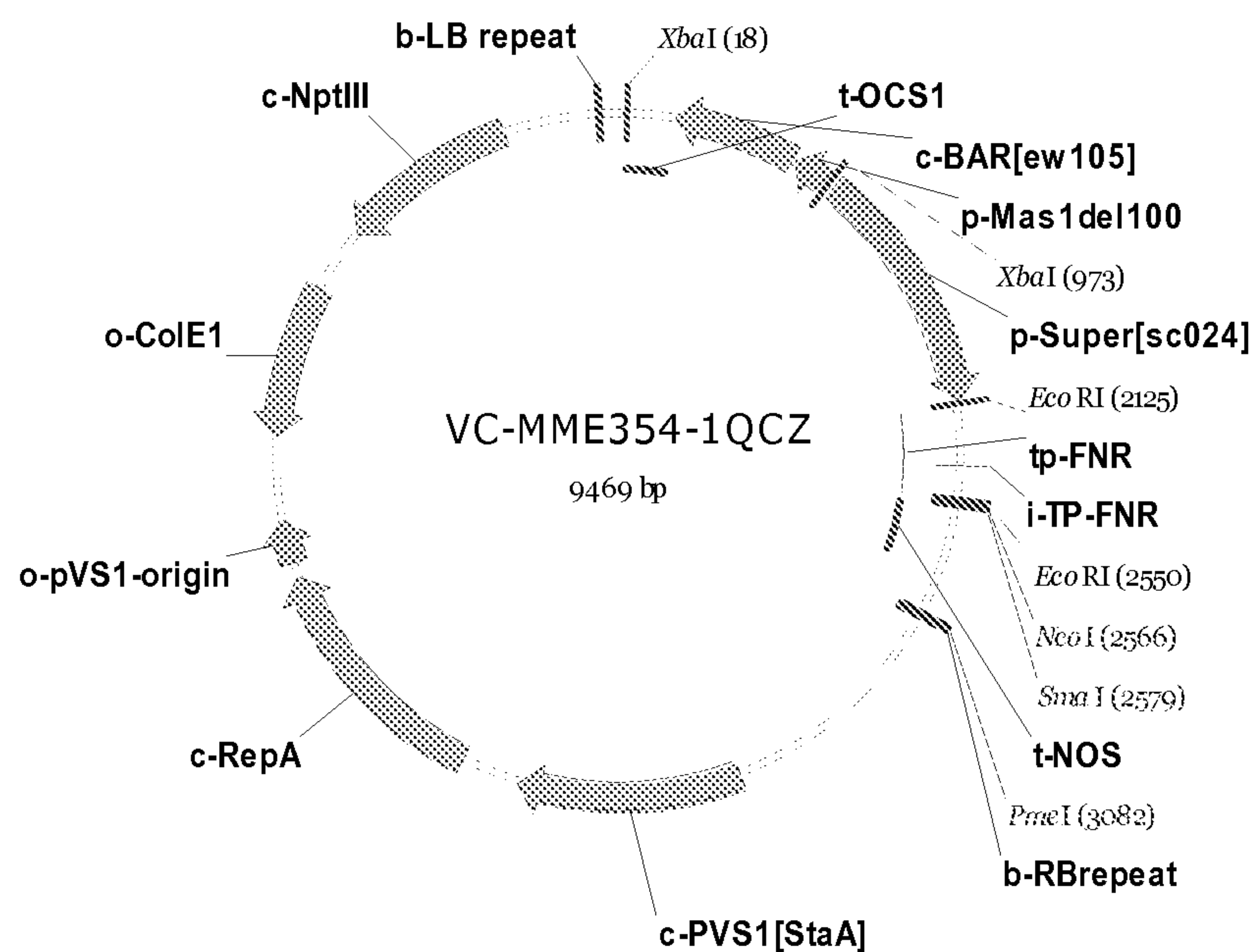


Fig. 3b Vector VC-MME354-1QCZ SEQ ID NO: 14391 used for cloning gene of interest for targeted expression.



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Fig. 4a Vector VC-MME432-1 SEQ ID NO: 5 used for cloning gene of interest for targeted expression.

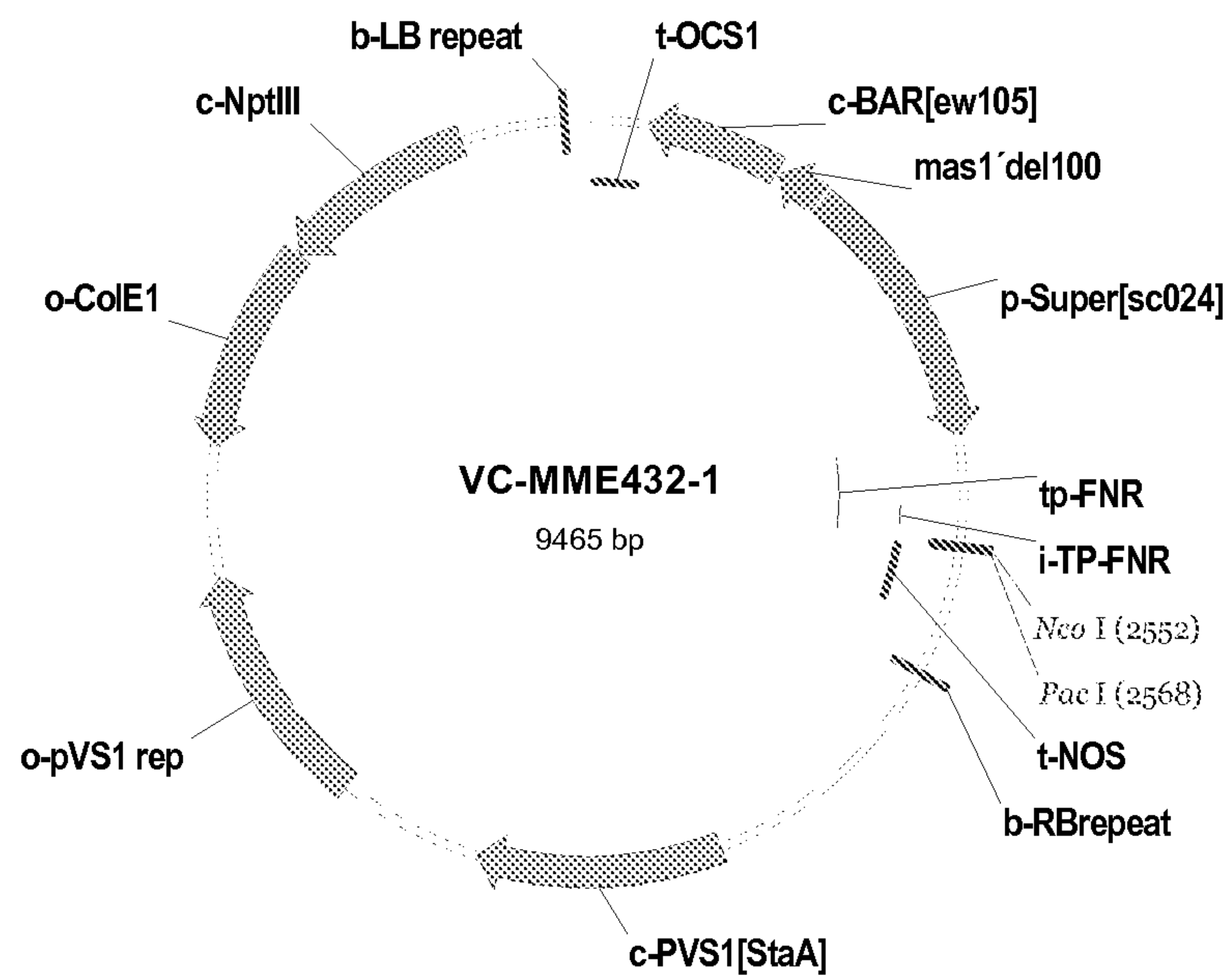
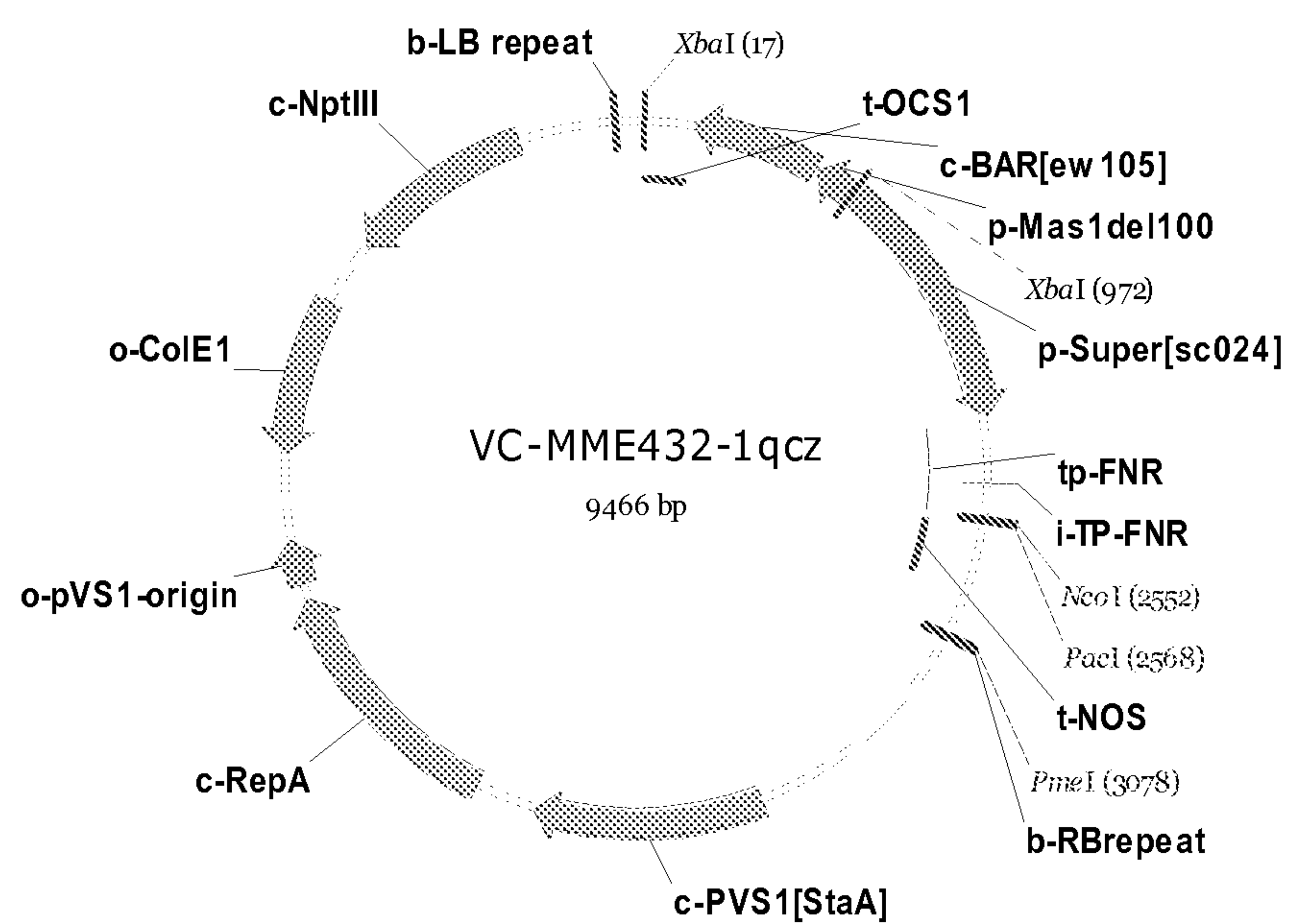


Fig. 4b Vector VC-MME432-1qcz SEQ ID NO: 14393 used for cloning gene of interest for targeted expression.



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Fig. 5a Vector VC-MME489-1 SEQ ID NO: 15 used for cloning gene of interest for non-targeted expression and cloning of a targeting sequence.

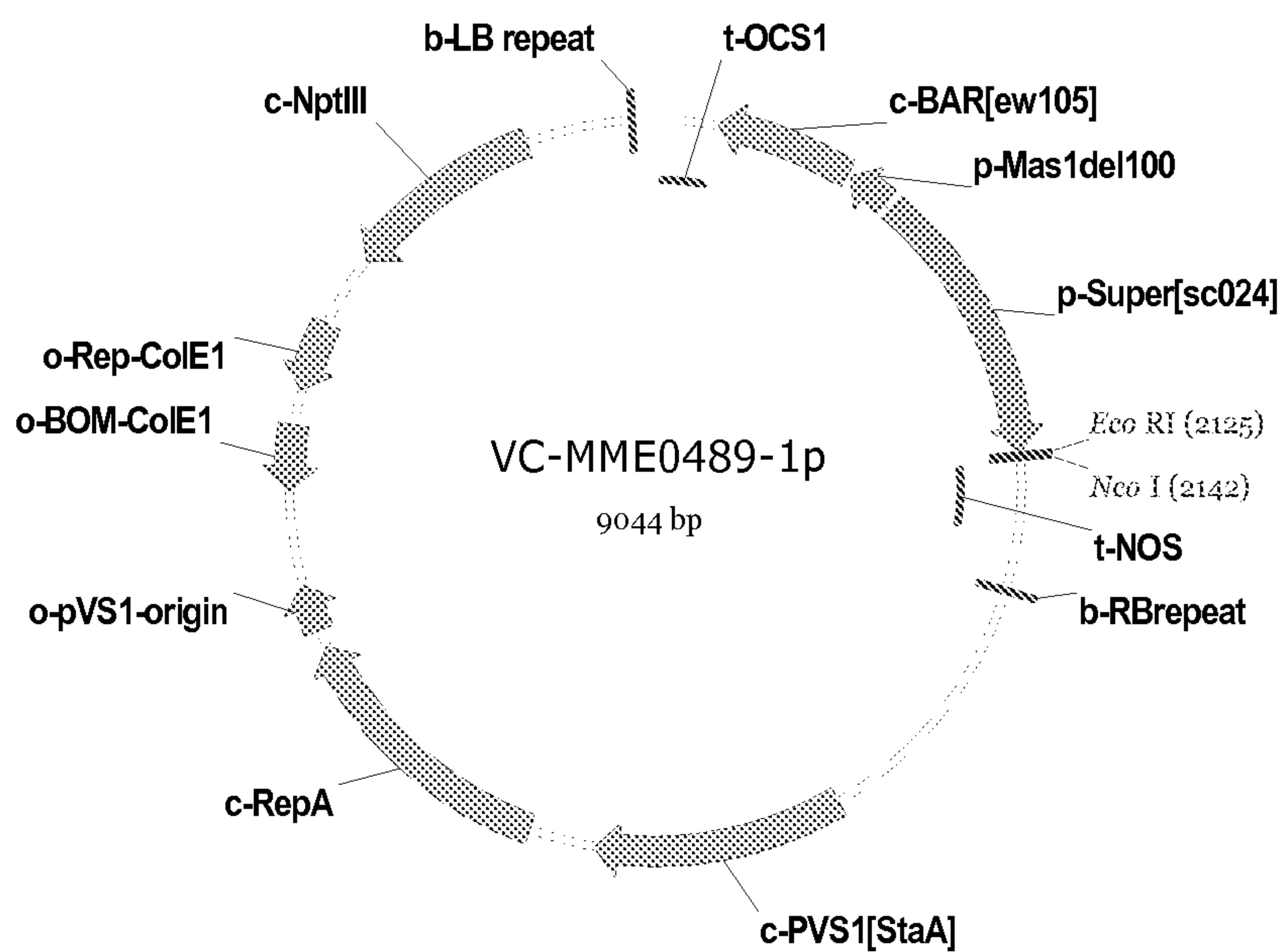
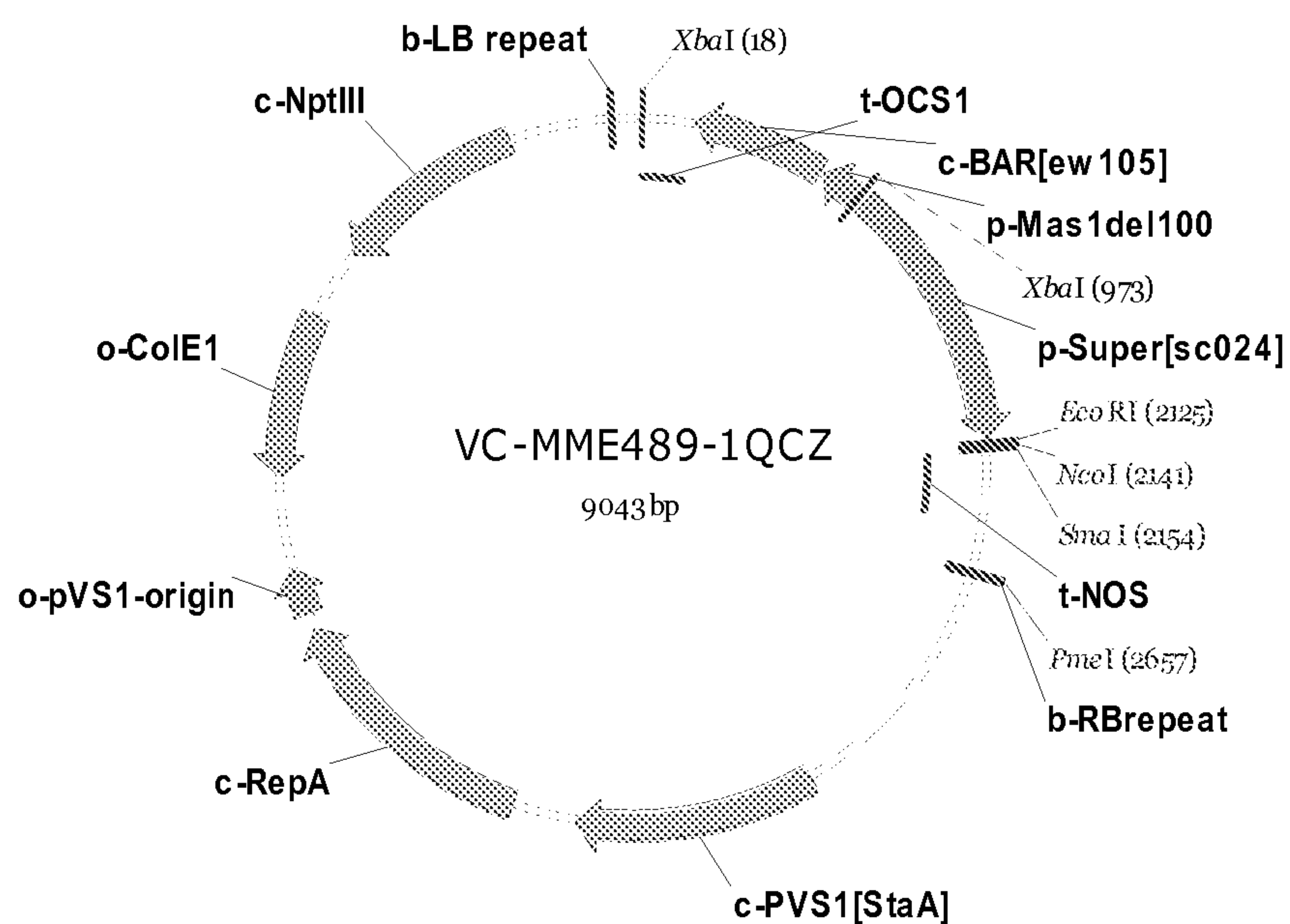


Fig. 5b Vector VC-MME489-1QCZ SEQ ID NO: 14395 used for cloning gene of interest for non-targeted expression and cloning of a targeting sequence.



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Fig. 6 Vector pMTX02270p SEQ ID NO: 16 used for cloning of a targeting sequence.

