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(54) **NUCLEIC ACID AGENTS FOR OVEREXPRESSING OR DOWNREGULATING RNA INTERFERENCE TARGETS AND USES OF SAME IN IMPROVING NITROGEN USE EFFICIENCY, ABIOTIC STRESS TOLERANCE, BIOMASS, VIGOR OR YIELD OF A PLANT**

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C12N 15/113 (2010.01)
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CPC ***C12N 15/113*** (2013.01); ***C07K 14/415*** (2013.01); ***C12N 15/8261*** (2013.01); ***C12N 15/8271*** (2013.01)

(58) **Field of Classification Search**
None
See application file for complete search history.

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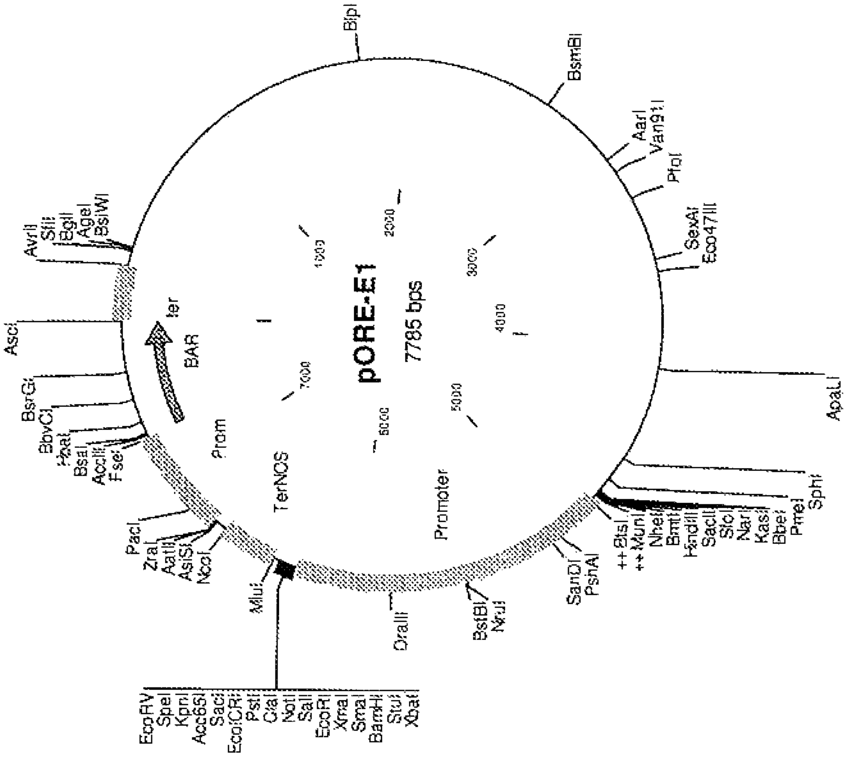
(57) **ABSTRACT**

A method of improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant is provided by expressing within the plant an exogenous polynucleotide encoding a polypeptide having an amino acid sequence at least 80% homologous to SEQ ID NOs: 687-981, 992-1248, 1281-1310, 1389-1391, and 2806-3081. Also provided is a method of improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plan by expressing within the plant an exogenous polynucleotide which downregulates an activity or expression of a polypeptide having an amino acid sequence at least 80% homologous to SEQ ID NOs: 311-514, 2007-2436, 1311-1320, 982-991, 1249-1280, 1321-1388. Transgenic plants and constructs are provided as well.

12 Claims, 1 Drawing Sheet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Eco47III
ApaLI
SphI
PmeI
BbeI
KasI
NarI
SfoI
SacII
HindIII
BmtI
NheI
++MunI
++BtsI
PshAI
SanDI
NruI
BstBI
DraIII
MluI
NcoI
AsiSI
AatII
ZraI
PacI
FseI
AccIII
BsaI
HpaI
BbvCI
BsrGI
AscI
AvrII
SfiI
BglI
AgeI
BsiWI
EcoRV
SpeI
KpnI
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NotI
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NUCLEIC ACID AGENTS FOR OVEREXPRESSING OR DOWNREGULATING RNA INTERFERENCE TARGETS AND USES OF SAME IN IMPROVING NITROGEN USE EFFICIENCY, ABIOTIC STRESS TOLERANCE, BIOMASS, VIGOR OR YIELD OF A PLANT

RELATED APPLICATIONS

This application is a National Phase of PCT Patent Application No. PCT/IB2012/054149 having International filing date of Aug. 14, 2012, which claims the benefit of priority under 35 USC § 119(e) of U.S. Provisional Patent Application No. 61/523,355 filed on Aug. 14, 2011. The contents of the above applications are all incorporated by reference as if fully set forth herein in their entirety.

SEQUENCE LISTING STATEMENT

The ASCII file, entitled 58604SequenceListing.txt, created on Feb. 13, 2014, comprising 9,493,532 bytes, submitted concurrently with the filing of this application is incorporated herein by reference.

FIELD AND BACKGROUND OF THE INVENTION

The present invention, in some embodiments thereof, relates to nucleic acid agents for overexpressing or downregulating RNA interference targets and uses of same in improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant.

Plant growth is reliant on a number of basic factors: light, air, water, nutrients, and physical support. All these factors, with the exception of light, are controlled by soil to some extent, which integrates non-living substances (minerals, organic matter, gases and liquids) and living organisms (bacteria, fungi, insects, worms, etc.). The soil's volume is almost equally divided between solids and water/gases. An adequate nutrition in the form of natural as well as synthetic fertilizers, may affect crop yield and quality, and its response to stress factors such as disease and adverse weather. The great importance of fertilizers can best be appreciated when considering the direct increase in crop yields over the last 40 years, and the fact that they account for most of the overhead expense in agriculture. Sixteen natural nutrients are essential for plant growth, three of which, carbon, hydrogen and oxygen, are retrieved from air and water. The soil provides the remaining 13 nutrients.

Nutrients are naturally recycled within a self-sufficient environment, such as a rainforest. However, when grown in a commercial situation, plants consume nutrients for their growth and these nutrients need to be replenished in the system. Several nutrients are consumed by plants in large quantities and are referred to as macronutrients. Three macronutrients are considered the basic building blocks of plant growth, and are provided as main fertilizers; Nitrogen (N), Phosphate (P) and Potassium (K). Yet, only nitrogen needs to be replenished every year since plants only absorb approximately half of the nitrogen fertilizer applied. A proper balance of nutrients is crucial; when too much of an essential nutrient is available, it may become toxic to plant growth. Utilization efficiencies of macronutrients directly correlate with yield and general plant tolerance, and increasing them will benefit the plants themselves and the environment by decreasing seepage to ground water.

Nitrogen is responsible for biosynthesis of amino and nucleic acids, prosthetic groups, plant hormones, plant chemical defenses, etc, and thus is utterly essential for the plant. For this reason, plants store nitrogen throughout their developmental stages, in the specific case of corn during the period of grain germination, mostly in the leaves and stalk. However, due to the low nitrogen use efficiency (NUE) of the main crops (e.g., in the range of only 30-70%), nitrogen supply needs to be replenished at least twice during the growing season. This requirement for fertilizer refill may become the rate-limiting element in plant growth and increase fertilizer expenses for the farmer. Limited land resources combined with rapid population growth will inevitably lead to added increase in fertilizer use. In light of this prediction, advanced, biotechnology-based solutions to allow stable high yields with an added potential to reduce fertilizer costs are highly desirable. Subsequently, developing plants with increased NUE will lower fertilizer input in crop cultivation, and allow growth on lower-quality soils.

The major agricultural crops (corn, rice, wheat, canola and soybean) account for over half of total human caloric intake, giving their yield and quality vast importance. They can be consumed either directly (eating their seeds which are also used as a source of sugars, oils and metabolites), or indirectly (eating meat products raised on processed seeds or forage). Various factors may influence a crop's yield, including but not limited to, quantity and size of the plant organs, plant architecture, vigor (e.g. seedling), growth rate, root development, utilization of water and nutrients (e.g., nitrogen), and stress tolerance. Plant yield may be amplified through multiple approaches; (1) enhancement of innate traits (e.g., dry matter accumulation rate, cellulose/lignin composition), (2) improvement of structural features (e.g., stalk strength, meristem size, plant branching pattern), and (3) amplification of seed yield and quality (e.g., fertilization efficiency, seed development, seed filling or content of oil, starch or protein). Increasing plant yield through any of the above methods would ultimately have many applications in agriculture and additional fields such as in the biotechnology industry.

Two main adverse environmental conditions, malnutrition (nutrient deficiency) and drought, elicit a response in the plant that mainly affects root architecture (Jiang and Huang (2001), *Crop Sci* 41:1168-1173; Lopez-Bucio et al. (2003), *Curr Opin Plant Biol,* 6:280-287; Morgan and Condon (1986), *Aust J Plant Physiol* 13:523-532), causing activation of plant metabolic pathways to maximize water assimilation. Improvement of root architecture, i.e. making branched and longer roots, allows the plant to reach water and nutrient/fertilizer deposits located deeper in the soil by an increase in soil coverage. Root morphogenesis has already shown to increase tolerance to low phosphorus availability in soybean (Miller et al., (2003), *Funct Plant Biol* 30:973-985) and maize (Zhu and Lynch (2004), *Funct Plant Biol* 31:949-958). Thus, genes governing enhancement of root architecture may be used to improve NUE and drought tolerance. An example for a gene associated with root developmental changes is ANR1, a putative transcription factor with a role in nitrate ($NO3^-$) signaling. When expression of ANR1 is down-regulated, the resulting transgenic lines are defective in their root response to localized supplies of nitrate (Zhang and Forde (1998), *Science* 270:407). Enhanced root system and/or increased storage capabilities, which are seen in responses to different environmental stresses, are strongly favorable at normal or optimal growing conditions as well.

Abiotic stress refers to a range of suboptimal conditions as water deficit or drought, extreme temperatures and salt levels, and high or low light levels. High or low nutrient level also falls into the category of abiotic stress. The response to any stress may involve both stress specific and common stress pathways (Pastori and Foyer (2002), *Plant Physiol,* 129: 460-468), and drains energy from the plant, eventually resulting in lowered yield. Thus, distinguishing between the genes activated in each pathway and subsequent manipulation of only specific relevant genes could lead to a partial stress response without the parallel loss in yield. Contrary to the complex polygenic nature of plant traits responsible for adaptations to adverse environmental stresses, information on miRNAs involved in these responses is very limited. The most common approach for crop and horticultural improvements is through cross breeding, which is relatively slow, inefficient, and limited in the degree of variability achieved because it can only manipulate the naturally existing genetic diversity. Taken together with the limited genetic resources (i.e., compatible plant species) for crop improvement, conventional breeding is evidently unfavorable. By creating a pool of genetically modified plants, one broadens the possibilities for producing crops with improved economic or horticultural traits.

SUMMARY OF THE INVENTION

According to an aspect of some embodiments of the present invention there is provided a method of improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant, the method comprising expressing within the plant an exogenous polynucleotide encoding a polypeptide having an amino acid sequence at least 80% homologous to the polypeptide selected from the group consisting of SEQ ID NOs: 687-981, 992-1248, 1281-1310, 1389-1391, and 2806-3081, wherein the polypeptide is capable of regulating nitrogen use efficiency of the plant, thereby improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of the plant.

According to an aspect of some embodiments of the present invention there is provided a transgenic plant exogenously expressing a polynucleotide encoding a polypeptide having an amino acid sequence at least 80% homologous to the polypeptide selected from the group consisting of SEQ ID NOs: 687-981, 992-1248, 1281-1310, 1389-1391, and 2806-3081, wherein the polypeptide is capable of regulating nitrogen use efficiency of the plant.

According to an aspect of some embodiments of the present invention there is provided a nucleic acid construct comprising a polynucleotide encoding a polypeptide having an amino acid sequence at least 80% homologous to SEQ ID NOs:687-981, 992-1248, 1281-1310, 1389-1391, and 2806-3081, wherein the polypeptide is capable of regulating nitrogen use efficiency of the plant, and wherein the polynucleotide is under a transcriptional control of a cis-acting regulatory element.

According to an aspect of some embodiments of the present invention there is provided a method of improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant, the method comprising expressing within the plant an exogenous polynucleotide which downregulates an activity or expression of a polypeptide having an amino acid sequence at least 80% homologous to SEQ ID NOs: 311-514, 2007-2436, 1311-1320, 982-991, 1249-1280, 1321-1388, wherein the polypeptide is capable of regulating nitrogen use efficiency of the plant, thereby improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of the plant.

According to an aspect of some embodiments of the present invention there is provided a transgenic plant exogenously expressing a polynucleotide which downregulates an activity or expression of a polypeptide having an amino acid sequence at least 80% homologous to SEQ ID NOs: 311-514, 2007-2436, 1311-1320, 982-991, 1249-1280, 1321-1388, wherein the polypeptide is capable of regulating nitrogen use efficiency of the plant.

According to an aspect of some embodiments of the present invention there is provided a nucleic acid construct comprising a polynucleotide which downregulates an activity or expression of a polypeptide having an amino acid sequence at least 80% homologous to SEQ ID NOs: 311-514, 2007-2436, 1311-1320, 982-991, 1249-1280, 1321-1388, wherein the polypeptide is capable of regulating nitrogen use efficiency of a plant, the nucleic acid sequence being under the regulation of a cis-acting regulatory element.

According to some embodiments of the invention, the polynucleotide is selected from the group consisting of SEQ ID NO: 1392-1646, 1655-1888, 1911-1938, 3082-3316.

According to some embodiments of the invention, the polypeptide is selected from the group consisting of SEQ ID NO: 687-981, 992-1248, 1281-1310, 1389-1391, and 2806-3081.

According to some embodiments of the invention, the cis-acting regulatory element comprises a promoter.

According to some embodiments of the invention, the promoter comprises a tissue-specific promoter.

According to some embodiments of the invention, the tissue-specific promoter comprises a root specific promoter.

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

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

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

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

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

According to some embodiments of the invention, the polynucleotide acts by a mechanism selected from the group consisting of sense suppression, antisense suppression, ribozyme inhibition, and gene disruption.

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

BRIEF DESCRIPTION OF THE DRAWINGS

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

In the drawings:

FIG. **1** is a scheme of a binary vector that can be used according to some embodiments of the invention.

DESCRIPTION OF SPECIFIC EMBODIMENTS OF THE INVENTION

The present invention, in some embodiments thereof, relates to nucleic acid agents for overexpressing or downregulating RNA interference targets and uses of same in improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant.

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

The doubling of agricultural food production worldwide over the past four decades has been associated with a 7-fold increase in the use of nitrogen (N) fertilizers. As a consequence, both the recent and future intensification of the use of nitrogen fertilizers in agriculture already has and will continue to have major detrimental impacts on the diversity and functioning of the non-agricultural neighbouring bacterial, animal, and plant ecosystems. The most typical examples of such an impact are the eutrophication of freshwater and marine ecosystems as a result of leaching when high rates of nitrogen fertilizers are applied to agricultural fields. In addition, there can be gaseous emission of nitrogen oxides reacting with the stratospheric ozone and the emission of toxic ammonia into the atmosphere. Furthermore, farmers are facing increasing economic pressures with the rising fossil fuels costs required for production of nitrogen fertilizers.

It is therefore of major importance to identify the critical steps controlling plant nitrogen use efficiency (NUE). Such studies can be harnessed towards generating new energy crop species that have a larger capacity to produce biomass with the minimal amount of nitrogen fertilizer.

While reducing the present invention to practice, the present inventors have uncovered dsRNA sequences that are differentially expressed in maize plants grown under nitrogen limiting conditions versus corn plants grown under conditions wherein nitrogen is a non-limiting factor. Following further screening the present inventors were able to identify the target genes of these dsRNA sequences and suggest using same or sequences modulating expression of same in the generation of transgenic plants having improved nitrogen use efficiency.

According to some embodiments, the target genes or nucleic acid sequences controlling expression of same relay their effect by affecting at least one of:

root architecture so as to increase nutrient uptake;

activation of plant metabolic pathways so as to maximize nitrogen absorption or localization; or alternatively or additionally

modulating plant surface permeability.

Each of the above mechanisms may affect water uptake as well as salt absorption and therefore embodiments of the invention further relate to enhancement of abiotic stress tolerance, biomass, vigor or yield of the plant.

Thus, according to an aspect of the invention there is provided a method of improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant, the method comprising expressing within the plant an exogenous polynucleotide encoding a polypeptide having an amino acid sequence at least 80% homologous to SEQ ID NOs: 687-981, 992-1248, 1281-1310, 1389-1391, and 2806-3081—wherein the polypeptide is capable of regulating nitrogen use efficiency of the plant, thereby improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of the plant.

As used herein the phrase "nitrogen use efficiency (NUE)" refers to a measure of crop production per unit of nitrogen fertilizer input. Fertilizer use efficiency (FUE) is a measure of NUE. Crop production can be measured by biomass, vigor or yield. The plant's nitrogen use efficiency is typically a result of an alteration in at least one of the uptake, spread, absorbance, accumulation, relocation (within the plant) and use of nitrogen absorbed by the plant. Improved NUE is with respect to that of a non-transgenic plant (i.e., lacking the transgene of the transgenic plant) of the same species and of the same developmental stage and grown under the same conditions.

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

The phrase "abiotic stress" as used herein refers to any adverse effect on metabolism, growth, viability and/or reproduction of a plant. Abiotic stress can be induced by any of suboptimal environmental growth conditions such as, for example, water deficit or drought, flooding, freezing, low or high temperature, strong winds, heavy metal toxicity, anaerobiosis, high or low nutrient levels (e.g. nutrient deficiency), high or low salt levels (e.g. salinity), atmospheric pollution, high or low light intensities (e.g. insufficient light) or UV irradiation. Abiotic stress may be a short term effect (e.g. acute effect, e.g. lasting for about a week) or alternatively may be persistent (e.g. chronic effect, e.g. lasting for example 10 days or more). The present invention contemplates situations in which there is a single abiotic stress condition or alternatively situations in which two or more abiotic stresses occur.

According to an exemplary embodiment the abiotic stress refers to salinity.

According to another exemplary embodiment the abiotic stress refers to drought.

As used herein the phrase "abiotic stress tolerance" refers to the ability of a plant to endure an abiotic stress without exhibiting substantial physiological or physical damage (e.g. alteration in metabolism, growth, viability and/or reproductivity of the plant).

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

As used herein the term/phrase "vigor", "vigor of a plant" or "plant vigor" refers to the amount (e.g., measured by weight) of tissue produced by the plant in a given time.

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

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

According to an exemplary embodiment the yield is measured by cellulose content.

According to another exemplary embodiment the yield is measured by oil content.

According to another exemplary embodiment the yield is measured by protein content.

According to another exemplary embodiment, the yield is measured by seed number per plant or part thereof (e.g., kernel).

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

As used herein the term "improving" or "increasing" refers to at least about 2%, at least about 3%, at least about 4%, at least about 5%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90% or greater increase in NUE, in tolerance to abiotic stress, in yield, in biomass or in vigor of a plant, as compared to a native or wild-type plants [i.e., plants not genetically modified to express the biomolecules (polynucleotides or polypeptides) of the invention, e.g., a non-transformed plant of the same species and of the same developmental stage which is grown under the same growth conditions as the transformed plant].

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

The term "plant" as used herein encompasses whole plants, ancestors and progeny of the plants and plant parts, including seeds, shoots, stems, roots (including tubers), and isolated plant cells, tissues and organs. The plant may be in any form including suspension cultures, embryos, meristematic regions, callus tissue, leaves, gametophytes, sporophytes, pollen, and microspores.

As used herein the phrase "plant cell" refers to plant cells which are derived and isolated from disintegrated plant cell tissue or plant cell cultures.

As used herein the phrase "plant cell culture" refers to any type of native (naturally occurring) plant cells, plant cell lines and genetically modified plant cells, which are not assembled to form a complete plant, such that at least one biological structure of a plant is not present. Optionally, the plant cell culture of this aspect of the present invention may comprise a particular type of a plant cell or a plurality of different types of plant cells. It should be noted that optionally plant cultures featuring a particular type of plant cell may be originally derived from a plurality of different types of such plant cells.

Any commercially or scientifically valuable plant is envisaged in accordance with these embodiments of the invention. Plants that are particularly useful in the methods of the invention include all plants which belong to the super family Viridiplantae, in particular monocotyledonous and dicotyledonous plants including a fodder or forage legume, ornamental plant, food crop, tree, or shrub selected from the list comprising *Acacia* spp., *Acer* spp., *Actinidia* spp., *Aesculus* spp., *Agathis australis, Albizia amara, Alsophila tricolor, Andropogon* spp., *Arachis* spp, *Areca catechu, Astelia fragrans, Astragalus cicer, Baikiaea plurijuga, Betula* spp., *Brassica* spp., *Bruguiera gymnorrhiza, Burkea africana, Butea frondosa, Cadaba farinosa, Calliandra* spp, *Camellia sinensis, Canna indica, Capsicum* spp., *Cassia* spp., *Centroema pubescens, Chacoomeles* spp., *Cinnamomum cassia, Coffea arabica, Colophospermum mopane, Coronillia varia, Cotoneaster serotina, Crataegus* spp., *Cucumis* spp., *Cupressus* spp., *Cyathea dealbata, Cydonia oblonga, Cryptomeria japonica, Cymbopogon* spp., *Cynthea dealbata, Cydonia oblonga, Dalbergia monetaria, Davallia divaricata, Desmodium* spp., *Dicksonia squarosa, Dibeteropogon amplectens, Dioclea* spp, *Dolichos* spp., *Dorycnium* rectum, *Echinochloa pyramidalis, Ehraffia* spp., *Eleusine coracana, Eragrestis* spp., *Erythrina* spp., *Eucalyptus* spp., *Euclea schimperi, Eulalia vi/losa, Pagopyrum* spp., *Feijoa sellowlana, Fragaria* spp., *Flemingia* spp, *Freycinetia banksli, Geranium thunbergii, GinAgo biloba, Glycine javanica, Gliricidia* spp, *Gossypium hirsutum, Grevillea* spp., *Guibourtia coleosperma, Hedysarum* spp., *Hemaffhia altissima, Heteropogon contoffus, Hordeum vulgare, Hyparrhenia rufa, Hypericum erectum, Hypeffhelia dissolute, Indigo incamata, Iris* spp., *Leptarrhena pyrolifolia, Lespediza* spp., *Lettuca* spp., *Leucaena leucocephala, Loudetia simplex, Lotonus bainesli, Lotus* spp., *Macrotyloma axillare, Malus* spp., *Manihot esculenta, Medicago saliva, Metasequoia glyptostroboides, Musa sapientum, Nicotianum* spp., *Onobrychis* spp., *Ornithopus* spp., *Oryza* spp., *Peltophorum africanum, Pennisetum* spp., *Persea gratissima, Petunia* spp., *Phaseolus* spp., *Phoenix canariensis, Phormium cookianum, Photinia* spp., *Picea glauca, Pinus* spp., *Pisum sativam, Podocarpus totara, Pogonarthria fleckii, Pogonaffhria squarrosa, Populus* spp., *Prosopis cineraria, Pseudotsuga menziesii, Pterolobium stellatum, Pyrus communis, Quercus* spp., *Rhaphiolepsis umbellata, Rhopalostylis sapida, Rhus natalensis, Ribes grossularia, Ribes* spp., *Robinia pseudoacacia, Rosa* spp., *Rubus* spp., *Salix* spp., *Schyzachyrium sanguineum, Sciadopitys vefficillata, Sequoia sempervirens, Sequoiadendron giganteum, Sorghum bicolor, Spinacia* spp., *Sporobolus fimbriatus, Stiburus alopecuroides, Stylosanthos humilis, Tadehagi* spp, *Taxodium distichum, Themeda triandra, Trifolium* spp., *Triticum* spp., *Tsuga heterophylla, Vaccinium* spp., *Vicia* spp., *Vitis vinifera, Watsonia pyramidata, Zantedeschia aethiopica, Zea mays*, amaranth, artichoke, asparagus, broccoli, Brussels sprouts, cabbage, canola, carrot, cauliflower, celery, collard greens, flax, kale, lentil, oilseed rape, okra, onion, potato, rice, soybean, straw, sugar beet, sugar cane, sunflower, tomato, squash tea, maize, wheat, barely, rye, oat, peanut, pea, lentil and alfalfa, cotton, rapeseed, canola, pepper, sunflower, tobacco, eggplant, *eucalyptus*, a tree, an ornamental plant, a perennial grass and a forage crop. Alternatively algae and other non-Viridiplantae can be used for the methods of the present invention.

According to some embodiments of the invention, the plant used by the method of the invention is a crop plant including, but not limited to, cotton, *Brassica* vegetables, oilseed rape, sesame, olive tree, palm oil, banana, wheat, corn or maize, barley, alfalfa, peanuts, sunflowers, rice, oats, sugarcane, soybean, turf grasses, barley, rye, *sorghum*, sugar cane, chicory, lettuce, tomato, zucchini, bell pepper, eggplant, cucumber, melon, watermelon, beans, hibiscus, okra, apple, rose, strawberry, chile, garlic, pea, lentil, canola, mums, *arabidopsis*, broccoli, cabbage, beet, *quinoa*, spinach, squash, onion, leek, tobacco, potato, sugarbeet, *papaya*, pineapple, mango, *Arabidopsis thaliana*, and also plants used in horticulture, floriculture or forestry, such as, but not limited to, poplar, fir, *eucalyptus*, pine, an ornamental plant, a perennial grass and a forage crop, coniferous plants, moss, algae, as well as other plants listed in World Wide Web (dot) nationmaster (dot) com/encyclopedia/Plantae.

According to a specific embodiment of the present invention, the plant comprises corn.

According to a specific embodiment of the present invention, the plant comprises *sorghum*.

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

A "transgenic plant" refers to a plant that has incorporated a nucleic acid sequence (i.e., polynucleotides encoding target genes or a silencing polynucleotide), including but not limited to genes that are not normally present in a host plant genome, nucleic acid sequences not normally transcribed into RNA, or any other genes or nucleic acid sequences that one desires to exogenously introduce into the wild-type plant, such as genes that normally may be present in the wild-type plant (control) but that one desires either to genetically engineer or to have altered expression.

Also contemplated are hybrids of the above described transgenic plants. A "hybrid plant" refers to a plant or a part thereof resulting from a cross between two parent plants, wherein one parent is a genetically engineered plant of the invention (transgenic plant expressing the polypeptides of the present invention). Such a cross can occur naturally by, for example, sexual reproduction, or artificially by, for example, in vitro nuclear fusion. Methods of plant breeding are well-known and within the level of one of ordinary skill in the art of plant biology.

The terms siRNA and miRNA are collectively referred to herein as RNA interfering molecules (RNAi).

As used herein, the phrase "siRNA" (also referred to herein interchangeably as "small interfering RNA" or "silencing RNA", is a class of double-stranded RNA molecules, 20-25 nucleotides in length. The most notable role of siRNA is its involvement in the RNA interference (RNAi) pathway, where it interferes with the expression of a specific gene.

The siRNA precursor relates to a long dsRNA structure (at least 90% complementarity) of at least 30 bp.

As used herein, the phrase "microRNA (also referred to herein interchangeably as "miRNA" or "miR") or a precursor thereof" refers to a microRNA (miRNA) molecule acting as a post-transcriptional regulator. Typically, the miRNA molecules are RNA molecules of about 20 to 22 nucleotides in length which can be loaded into a RISC complex and which direct the cleavage of another RNA molecule, wherein the other RNA molecule comprises a nucleotide sequence essentially complementary to the nucleotide sequence of the miRNA molecule.

Typically, a miRNA molecule is processed from a "pre-miRNA" or as used herein a precursor of a pre-miRNA molecule by proteins, such as DCL proteins, present in any plant cell and loaded onto a RISC complex where it can guide the cleavage of the target RNA molecules.

Pre-microRNA molecules are typically processed from pri-microRNA molecules (primary transcripts). The single stranded RNA segments flanking the pre-microRNA are important for processing of the pri-miRNA into the pre-miRNA. The cleavage site appears to be determined by the distance from the stem-ssRNA junction (Han et al. 2006, Cell 125, 887-901, 887-901).

As used herein, a "pre-miRNA" molecule is an RNA molecule of about 100 to about 200 nucleotides, preferably about 100 to about 130 nucleotides which can adopt a secondary structure comprising a double stranded RNA stem and a single stranded RNA loop (also referred to as "hairpin") and further comprising the nucleotide sequence of the miRNA (and its complement sequence) in the double stranded RNA stem. According to a specific embodiment, the miRNA and its complement are located about 10 to about 20 nucleotides from the free ends of the miRNA double stranded RNA stem. The length and sequence of the single stranded loop region are not critical and may vary considerably, e.g. between 30 and 50 nt in length. The complementarity between the miRNA and its complement need not be perfect and about 1 to 3 bulges of unpaired nucleotides can be tolerated. The secondary structure adopted by an RNA molecule can be predicted by computer algorithms conventional in the art such as mFOLD. The particular strand of the double stranded RNA stem from the pre-miRNA which is released by DCL activity and loaded onto the RISC complex is determined by the degree of complementarity at the 5' end, whereby the strand which at its 5' end is the least involved in hydrogen bounding between the nucleotides of the different strands of the cleaved dsRNA stem is loaded onto the RISC complex and will determine the sequence specificity of the target RNA molecule degradation. However, if empirically the miRNA molecule from a particular synthetic pre-miRNA molecule is not functional (because the "wrong" strand is loaded on the RISC complex), it will be immediately evident that this problem can be solved by exchanging the position of the miRNA molecule and its complement on the respective strands of the dsRNA stem of the pre-miRNA molecule. As is known in the art, binding between A and U involving two hydrogen bounds, or G and U involving two hydrogen bounds is less strong that between G and C involving three hydrogen bounds. Exemplary siRNA sequences or precursors thereof as well as hairpin sequences and miRNA sequences are provided in Tables 1-4, below.

The tables provided in the Examples section are to be considered an integral part of the specification.

As used herein a "target gene" refers to a gene that is processed by microRNA activity. Typically the gene encodes a polypeptide which expression is downregulated due to microRNA processing.

Target genes are typically identified using the WMD3 website (http://wmd3dotweigelworlddotorg/).

As mentioned, the method of the present invention is effected by expressing within a plant an exogenous polynucleotide encoding a target gene of the RNA interfering molecules uncovered by the present inventors, as explained below.

As used herein, the phrase "expressing within the plant an exogenous polynucleotide" refers to upregulating the expression level of an exogenous polynucleotide within the plant e.g., by introducing the exogenous polynucleotide into a plant or plant cell and expressing by recombinant means, as described in detail hereinbelow.

As used herein "expressing" refers to expression at the mRNA level (e.g., in case the target gene expresses an mRNA product but no protein) or at the polypeptide level of the desired exogenous polynucleotide.

As used herein, the phrase "exogenous polynucleotide" refers to a heterologous nucleic acid sequence which may not be naturally expressed within the plant or which overexpression in the plant is desired (i.e., overexpression of an endogenous gene). The exogenous polynucleotide may be introduced into the plant in a stable or transient manner, so as to produce a ribonucleic acid (RNA) molecule and/or a polypeptide molecule. The exogenous polynucleotide may comprise a nucleic acid sequence which is identical or partially homologous to an endogenous nucleic acid sequence expressed within the plant.

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

As used herein the term "polynucleotide" refers to a single or double stranded nucleic acid sequence which is isolated and provided in the form of an RNA sequence, a complementary polynucleotide sequence (cDNA), a genomic polynucleotide sequence (e.g. sequence isolated from a chromosome) and/or a composite polynucleotide sequences (e.g., a combination of the above). This term includes polynucleotides and/or oligonucleotides derived from naturally occurring nucleic acid molecules (e.g., RNA or DNA), synthetic polynucleotide and/or oligonucleotide molecules composed of naturally occurring bases, sugars, and covalent internucleoside linkages (e.g., backbone), as well as synthetic polynucleotides and/or oligonucleotides having non-naturally occurring portions, which function similarly to the respective naturally occurring portions.

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

Nucleic acid sequences of the polypeptides of some embodiments of the invention may be optimized for expression in a specific plant host. Examples of such sequence modifications include, but are not limited to, an altered G/C content to more closely approach that typically found in the plant species of interest, and the removal of codons atypically found in the plant species commonly referred to as codon optimization.

The phrase "codon optimization" refers to the selection of appropriate DNA nucleotides for use within a structural gene or fragment thereof that approaches codon usage within the plant of interest. Therefore, an optimized gene or nucleic acid sequence refers to a gene in which the nucleotide sequence of a native or naturally occurring gene has been modified in order to utilize statistically-preferred or statistically-favored codons within the plant. The nucleotide sequence typically is examined at the DNA level and the coding region optimized for expression in the plant species determined using any suitable procedure, for example as described in Sardana et al. (1996, Plant Cell Reports 15:677-681). In this method, the standard deviation of codon usage, a measure of codon usage bias, may be calculated by first finding the squared proportional deviation of usage of each codon of the native gene relative to that of highly expressed plant genes, followed by a calculation of the average squared deviation. The formula used is: 1 SDCU=n=1 N [(Xn−Yn)/Yn]2/N, where Xn refers to the frequency of usage of codon n in highly expressed plant genes, where Yn to the frequency of usage of codon n in the gene of interest and N refers to the total number of codons in the gene of interest. A table of codon usage from highly expressed genes of dicotyledonous plants is compiled using the data of Murray et al. (1989, Nuc Acids Res. 17:477-498).

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

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

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

Target genes which are contemplated according to the present teachings are provided in the polynucleotide sequences which comprise nucleic acid sequences as set forth in SEQ ID NO: 1392-1646, 1655-1888, 1911-1938, 3082-3316. However the present teachings also relate to orthologs or homologs at least about 60%, at least about

65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, or at least about 95% or more identical or similar to SEQ ID NO: 1392-1646, 1655-1888, 1911-1938, 3082-3316. Parameters for determining the level of identity are provided hereinbelow.

Alternatively or additionally, target genes which are contemplated according to the present teachings are provided in the polypeptide sequences which comprise amino acid sequences as set forth in SEQ ID NO: 687-981, 992-1248, 1281-1310, 1389-1391, and 2806-3081 (Tables 6 and 8). However the present teachings also relate to of orthologs or homologs at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, or at least about 95% or more identical or similar to SEQ ID NO: 687-981, 992-1248, 1281-1310, 1389-1391, and 2806-3081 (Tables 6 and 8).

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

According to some embodiments of the invention, the term "homology" or "homologous" refers to identity of two or more nucleic acid sequences; or identity of two or more amino acid sequences.

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

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

As mentioned the present inventors have also identified genes which down-regulation thereof may be done in order to improve their NUE, biomass, vigor, yield and abiotic stress tolerance.

Thus, according to an aspect of the invention there is provided a method of improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant, the method comprising expressing within the plant an exogenous polynucleotide which downregulates an activity or expression of a polypeptide having an amino acid sequence at least 80%, 85%, 90%, 95%, or 100% homologous or identical to SEQ ID NOs: 311-514, 2007-2436, 1311-1320, 982-991, 1249-1280, 1321-1388 (Tables 5, 7 and 9), wherein the polypeptide is capable of regulating nitrogen use efficiency of the plant, thereby improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of the plant.

Down regulation of activity or expression is by at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or even complete (100%) loss of activity or expression. Assays for measuring gene expression can be effected at the protein level (e.g., Western blot, ELISA) or at the mRNA level such as by RT-PCR.

According to a specific embodiment the amino acid sequence of the target gene is as set forth in SEQ ID NOs: 311-514, 2007-2436, 1311-1320, 982-991, 1249-1280, 1321-1388 of Tables 5, 7 and 9.

Alternatively or additionally, the amino acid sequence of the target gene is encoded by a polynucleotide sequence as set forth in SEQ ID NOs: 515-686, 2437-2805, 1939-1948, 1647-1654, 1889-1910, 1949-2004 of Tables 5, 7 and 9.

Examples of polynucleotide downregulating agents that inhibit (also referred to herein as inhibitors or nucleic acid agents) the expression of a target gene are given below.

1. Polynucleotide-Based Inhibition of Gene Expression.

It will be appreciated, that any of these methods when specifically referring to downregulating expression/activity of the target genes can be used, at least in part, to downregulate expression or activity of endogenous RNA molecules.

i. Sense Suppression/Cosuppression

In some embodiments of the invention, inhibition of the expression of target gene may be obtained by sense suppression or cosuppression. For cosuppression, an expression cassette is designed to express an RNA molecule corresponding to all or part of a messenger RNA encoding a target gene in the "sense" orientation. Over-expression of the RNA molecule can result in reduced expression of the native gene. Accordingly, multiple plant lines transformed with the cosuppression expression cassette are screened to identify those that show the greatest inhibition of target gene expression.

The polynucleotide used for cosuppression may correspond to all or part of the sequence encoding the target gene, all or part of the 5' and/or 3' untranslated region of a target transcript, or all or part of both the coding sequence and the untranslated regions of a transcript encoding the target gene. In some embodiments where the polynucleotide comprises all or part of the coding region for the target gene, the expression cassette is designed to eliminate the start codon of the polynucleotide so that no protein product will be transcribed.

Cosuppression may be used to inhibit the expression of plant genes to produce plants having undetectable protein levels for the proteins encoded by these genes. See, for example, Broin, et al., (2002) Plant Cell 15:1517-1532. Cosuppression may also be used to inhibit the expression of multiple proteins in the same plant. Methods for using cosuppression to inhibit the expression of endogenous genes in plants are described in Flavell, et al., (1995) Proc. Natl. Acad. Sci. USA 91:3590-3596; Jorgensen, et al., (1996) Plant Mol. Biol. 31:957-973; Johansen and Carrington, (2001) Plant Physiol. 126:930-938; Broin, et al., (2002) Plant Cell 15:1517-1532; Stoutjesdijk, et al., (2002) Plant Physiol. 129:1723-1731; Yu, et al., (2003) Phytochemistry

63:753-763; and U.S. Pat. Nos. 5,035,323, 5,283,185 and 5,952,657; each of which is herein incorporated by reference. The efficiency of cosuppression may be increased by including a poly-dt region in the expression cassette at a position 3' to the sense sequence and 5' of the polyadenylation signal. See, US Patent Publication Number 20020058815, herein incorporated by reference. Typically, such a nucleotide sequence has substantial sequence identity to the sequence of the transcript of the endogenous gene, optimally greater than about 65% sequence identity, more optimally greater than about 85% sequence identity, most optimally greater than about 95% sequence identity. See, U.S. Pat. Nos. 5,283,185 and 5,035,323; herein incorporated by reference.

Transcriptional gene silencing (TGS) may be accomplished through use of hpRNA constructs wherein the inverted repeat of the hairpin shares sequence identity with the promoter region of a gene to be silenced. Processing of the hpRNA into short RNAs which can interact with the homologous promoter region may trigger degradation or methylation to result in silencing. (Aufsatz, et al., (2002) PNAS 99(4):16499-16506; Mette, et al., (2000) EMBO J. 19(19):5194-5201),

ii. Antisense Suppression

In some embodiments of the invention, inhibition of the expression of the target gene may be obtained by antisense suppression. For antisense suppression, the expression cassette is designed to express an RNA molecule complementary to all or part of a messenger RNA encoding the target gene. Over-expression of the antisense RNA molecule can result in reduced expression of the native gene. Accordingly, multiple plant lines transformed with the antisense suppression expression cassette are screened to identify those that show the greatest inhibition of target gene expression.

The polynucleotide for use in antisense suppression may correspond to all or part of the complement of the sequence encoding the target gene, all or part of the complement of the 5' and/or 3' untranslated region of the target gene transcript, or all or part of the complement of both the coding sequence and the untranslated regions of a transcript encoding the target gene. In addition, the antisense polynucleotide may be fully complementary (i.e., 100% identical to the complement of the target sequence) or partially complementary (i.e., less than 100% identical to the complement of the target sequence) to the target sequence. Antisense suppression may be used to inhibit the expression of multiple proteins in the same plant. Furthermore, portions of the antisense nucleotides may be used to disrupt the expression of the target gene. Generally, sequences of at least 50 nucleotides, 100 nucleotides, 200 nucleotides, 300, 500, 550, 500, 550 or greater may be used. Methods for using antisense suppression to inhibit the expression of endogenous genes in plants are described, for example, in Liu, et al., (2002) Plant Physiol. 129:1732-1753 and U.S. Pat. No. 5,759,829, which is herein incorporated by reference. Efficiency of antisense suppression may be increased by including a poly-dt region in the expression cassette at a position 3' to the antisense sequence and 5' of the polyadenylation signal. See, US Patent Publication Number 20020058815.

iii. Double-Stranded RNA Interference

In some embodiments of the invention, inhibition of the expression of a target gene may be obtained by double-stranded RNA (dsRNA) interference. For dsRNA interference, a sense RNA molecule like that described above for cosuppression and an antisense RNA molecule that is fully or partially complementary to the sense RNA molecule are expressed in the same cell, resulting in inhibition of the expression of the corresponding endogenous messenger RNA.

Expression of the sense and antisense molecules can be accomplished by designing the expression cassette to comprise both a sense sequence and an antisense sequence. Alternatively, separate expression cassettes may be used for the sense and antisense sequences. Multiple plant lines transformed with the dsRNA interference expression cassette or expression cassettes are then screened to identify plant lines that show the greatest inhibition of target gene expression. Methods for using dsRNA interference to inhibit the expression of endogenous plant genes are described in Waterhouse, et al., (1998) Proc. Natl. Acad. Sci. USA 95:13959-13965, Liu, et al., (2002) Plant Physiol. 129:1732-1753, and WO 99/59029, WO 99/53050, WO 99/61631, and WO 00/59035,

iv. Hairpin RNA Interference and Intron-Containing Hairpin RNA Interference

In some embodiments of the invention, inhibition of the expression of one or more target gene may be obtained by hairpin RNA (hpRNA) interference or intron-containing hairpin RNA (ihpRNA) interference. These methods are highly efficient at downregulating the expression of endogenous genes. See, Waterhouse and Helliwell, (2003) Nat. Rev. Genet. 5:29-38 and the references cited therein.

For hpRNA interference, the expression cassette is designed to express an RNA molecule that hybridizes with itself to form a hairpin structure that comprises a single-stranded loop region and a base-paired stem. The base-paired stem region comprises a sense sequence corresponding to all or part of the endogenous messenger RNA encoding the gene whose expression is to be inhibited, and an antisense sequence that is fully or partially complementary to the sense sequence. Thus, the base-paired stem region of the molecule generally determines the specificity of the RNA interference. hpRNA molecules are highly efficient at inhibiting the expression of endogenous genes, and the RNA interference they induce is inherited by subsequent generations of plants. See, for example, Chuang and Meyerowitz, (2000) Proc. Natl. Acad. Sci. USA 97:5985-5990; Stoutjesdijk, et al., (2002) Plant Physiol. 129:1723-1731; and Waterhouse and Helliwell, (2003) Nat. Rev. Genet. 5:29-38. Methods for using hpRNA interference to inhibit or silence the expression of genes are described, for example, in Chuang and Meyerowitz, (2000) Proc. Natl. Acad. Sci. USA 97:5985-5990; Stoutjesdijk, et al., (2002) Plant Physiol. 129:1723-1731; Waterhouse and Helliwell, (2003) Nat. Rev. Genet. 5:29-38; Pandolfini, et al., BMC Biotechnology 3:7, and US Patent Publication Number 20030175965; each of which is herein incorporated by reference. A transient assay for the efficiency of hpRNA constructs to silence gene expression in vivo has been described by Panstruga, et al., (2003) Mol. Biol. Rep. 30:135-150, herein incorporated by reference.

ForihpRNA, the interfering molecules have the same general structure as for hpRNA, but the RNA molecule additionally comprises an intron that is capable of being spliced in the cell in which the ihpRNA is expressed. The use of an intron minimizes the size of the loop in the hairpin RNA molecule following splicing, and this increases the efficiency of interference. See, for example, Smith, et al., (2000) Nature 507:319-320. In fact, Smith, et al., show 100% suppression of endogenous gene expression using ihpRNA-mediated interference. Methods for using ihpRNA interference to inhibit the expression of endogenous plant genes are described, for example, in Smith, et al., (2000) Nature 507:319-320; Wesley, et al., (2001) Plant J. 27:581-590; Wang and Waterhouse, (2001) Curr. Opin. Plant Biol. 5:156-150; Waterhouse and Helliwell, (2003) Nat. Rev. Genet. 5:29-38; Helliwell and Waterhouse, (2003) Methods 30:289-295, and US Patent Publication Number 20030180955, each of which is herein incorporated by reference.

The expression cassette for hpRNA interference may also be designed such that the sense sequence and the antisense sequence do not correspond to an endogenous RNA. In this embodiment, the sense and antisense sequence flank a loop sequence that comprises a nucleotide sequence corresponding to all or part of the endogenous messenger RNA of the target gene. Thus, it is the loop region that determines the specificity of the RNA interference. See, for example, WO 02/00905, herein incorporated by reference.

v. Amplicon-Mediated Interference

Amplicon expression cassettes comprise a plant virus-derived sequence that contains all or part of the target gene but generally not all of the genes of the native virus. The viral sequences present in the transcription product of the expression cassette allow the transcription product to direct its own replication. The transcripts produced by the amplicon may be either sense or antisense relative to the target sequence (i.e., the messenger RNA for target gene). Methods of using amplicons to inhibit the expression of endogenous plant genes are described, for example, in Angell and Baulcombe, (1997) EMBO J. 16:3675-3685, Angell and Baulcombe, (1999) Plant J. 20:357-362, and U.S. Pat. No. 6,656,805, each of which is herein incorporated by reference.

vi. Ribozymes

In some embodiments, the polynucleotide expressed by the expression cassette of the invention is catalytic RNA or has ribozyme activity specific for the messenger RNA of target gene. Thus, the polynucleotide causes the degradation of the endogenous messenger RNA, resulting in reduced expression of the target gene. This method is described, for example, in U.S. Pat. No. 5,987,071, herein incorporated by reference.

2. Gene Disruption

In some embodiments of the present invention, the activity of a miRNA or a target gene is reduced or eliminated by disrupting the gene encoding the target polypeptide. The gene encoding the target polypeptide may be disrupted by any method known in the art. For example, in one embodiment, the gene is disrupted by transposon tagging. In another embodiment, the gene is disrupted by mutagenizing plants using random or targeted mutagenesis, and selecting for plants that have reduced response regulator activity.

Any of the nucleic acid agents described herein (for overexpression or downregulation) can be provided to the plant as naked RNA or expressed from a nucleic acid expression construct, where it is operaly linked to a regulatory sequence.

According to a specific embodiment of the invention, there is provided a nucleic acid construct comprising a nucleic acid sequence (a polynucleotide) encoding the RNAi target polypeptide or the nucleic acid agent for downregulating the expression of the target gene, the nucleic acid sequence being under a transcriptional control a cis-acting regulatory element.

Exemplary nucleic acid constructs which can be used for plant transformation include, but are not limited to, pORE156, pORE164, pORE167 and pORE169, which are all constructed by ligating the appropriate DNA fragments into the pORE E2 binary vector (Accession number: AY562535, FIG. **1**) under the transcriptional control of a promoter.

A coding nucleic acid sequence is "operably linked" or "transcriptionally linked to a regulatory sequence (e.g., promoter)" if the regulatory sequence is capable of exerting a regulatory effect on the coding sequence linked thereto. Thus the regulatory sequence controls the transcription of the target polynucleotide.

The term "regulatory sequence", as used herein, means any DNA, that is involved in driving transcription and controlling (i.e., regulating) the timing and level of transcription of a given DNA sequence, such as a DNA coding for the target polypeptide, as described above. For example, a 5' regulatory region (or "promoter region") is a DNA sequence located upstream (i.e., 5') of a coding sequence and which comprises the promoter and the 5'-untranslated leader sequence. A 3' regulatory region is a DNA sequence located downstream (i.e., 3') of the coding sequence and which comprises suitable transcription termination (and/or regulation) signals, including one or more polyadenylation signals.

For the purpose of the invention, the promoter is a plant-expressible promoter. As used herein, the term "plant-expressible promoter" means a DNA sequence which is capable of controlling (initiating) transcription in a plant cell. This includes any promoter of plant origin, but also any promoter of non-plant origin which is capable of directing transcription in a plant cell, i.e., certain promoters of viral or bacterial origin Thus, any suitable promoter sequence can be used by the nucleic acid construct of the present invention. According to some embodiments of the invention, the promoter is a constitutive promoter, a tissue-specific promoter or an inducible promoter (e.g. an abiotic stress-inducible promoter).

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

Suitable tissue-specific promoters include, but not limited to, leaf-specific promoters [such as described, for example, by Yamamoto et al., Plant J. 12:255-265, 1997; Kwon et al., Plant Physiol. 105:357-67, 1994; Yamamoto et al., Plant Cell Physiol. 35:773-778, 1994; Gotor et al., Plant J. 3:509-18, 1993; Orozco et al., Plant Mol. Biol. 23:1129-1138, 1993; and Matsuoka et al., Proc. Natl. Acad. Sci. USA 90:9586-9590, 1993], seed-preferred promoters [e.g., from seed specific genes (Simon, et al., Plant Mol. Biol. 5. 191, 1985; Scofield, et al., J. Biol. Chem. 262: 12202, 1987; Baszczynski, et al., Plant Mol. Biol. 14: 633, 1990), Brazil Nut albumin (Pearson' et al., Plant Mol. Biol. 18: 235-245, 1992), legumin (Ellis, et al. Plant Mol. Biol. 10: 203-214, 1988), Glutelin (rice) (Takaiwa, et al., Mol. Gen. Genet.

208: 15-22, 1986; Takaiwa, et al., FEBS Letts. 221: 43-47, 1987), Zein (Matzke et al., Plant MoI Biol, 143)323-32 1990), napA (Stalberg, et al., Planta 199: 515-519, 1996), Wheat SPA (Albani et al, Plant Cell, 9: 171-184, 1997), sunflower oleosin (Cummins, et al, Plant MoI. Biol. 19: 873-876, 1992)], endosperm specific promoters [e.g., wheat LMW and HMW, glutenin-1 (MoI Gen Genet 216:81-90, 1989; NAR 17:461-2), wheat a, b and g gliadins (EMBO3: 1409-15, 1984), Barley ltrl promoter, barley Bl, C, D hordein (Theor Appl Gen 98:1253-62, 1999; Plant J 4:343-55, 1993; MoI Gen Genet 250:750-60, 1996), Barley DOF (Mena et al., The Plant Journal, 116(1): 53-62, 1998), Biz2 (EP99106056.7), Synthetic promoter (Vicente-Carbajosa et al., Plant J. 13: 629-640, 1998), rice prolamin NRP33, rice-globulin GIb-I (Wu et al., Plant Cell Physiology 39(8) 885-889, 1998), rice alpha-globulin REB/OHP-1 (Nakase et al. Plant MoI. Biol. 33: 513-S22, 1997), rice ADP-glucose PP (Trans Res 6:157-68, 1997), maize ESR gene family (Plant J 12:235-46, 1997), *sorghum* gamma-kafirin (PMB 32:1029-35, 1996); e.g., the Napin promoter], embryo specific promoters [e.g., rice OSH1 (Sato et al, Proc. Natl. Acad. Sci. USA, 93: 8117-8122), KNOX (Postma-Haarsma et al, Plant MoI. Biol. 39:257-71, 1999), rice oleosin (Wu et at, J. Biochem., 123:386, 1998)], and flower-specific promoters [e.g., AtPRP4, chalene synthase (chsA) (Van der Meer, et al., Plant MoI. Biol. 15, 95-109, 1990), LAT52 (Twell et al., MoI. Gen Genet. 217:240-245; 1989), apetala-3]. Also contemplated are root-specific promoters such as the ROOTP promoter described in Vissenberg K, et al. Plant Cell Physiol. 2005 January; 46(1):192-200.

The nucleic acid construct of some embodiments of the invention can further include an appropriate selectable marker and/or an origin of replication.

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

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

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

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

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

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

According to a specific embodiment of the present invention, the exogenous polynucleotide is introduced into the plant by infecting the plant with a bacteria, such as using a floral dip transformation method (as described in further detail in Example 5, of the Examples section which follows).

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

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

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

Micropropagation is a multi-stage procedure that requires alteration of culture medium or growth conditions between stages. Thus, the micropropagation process involves four basic stages: Stage one, initial tissue culturing; stage two, tissue culture multiplication; stage three, differentiation and plant formation; and stage four, greenhouse culturing and hardening. During stage one, initial tissue culturing, the tissue culture is established and certified contaminant-free. During stage two, the initial tissue culture is multiplied until a sufficient number of tissue samples are produced to meet production goals. During stage three, the tissue samples grown in stage two are divided and grown into individual plantlets. At stage four, the transformed plantlets are transferred to a greenhouse for hardening where the plants' tolerance to light is gradually increased so that it can be grown in the natural environment.

Although stable transformation is presently preferred, transient transformation of leaf cells, meristematic cells or the whole plant is also envisaged by the present invention.

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

Viruses that have been shown to be useful for the transformation of plant hosts include CaMV, Tobacco mosaic virus (TMV), brome mosaic virus (BMV) and Bean Common Mosaic Virus (BV or BCMV). Transformation of plants using plant viruses is described in U.S. Pat. No. 4,855,237 (bean golden mosaic virus; BGV), EP-A 67,553 (TMV), Japanese Published Application No. 63-14693 (TMV), EPA 194,809 (BV), EPA 278,667 (BV); and Gluzman, Y. et al., Communications in Molecular Biology: Viral Vectors, Cold Spring Harbor Laboratory, New York, pp. 172-189 (1988). Pseudovirus particles for use in expressing foreign DNA in many hosts, including plants are described in WO 87/06261. According to some embodiments of the invention, the virus used for transient transformations is avirulent and thus is incapable of causing severe symptoms such as reduced growth rate, mosaic, ring spots, leaf roll, yellowing, streaking, pox formation, tumor formation and pitting. A suitable avirulent virus may be a naturally occurring avirulent virus or an artificially attenuated virus. Virus attenuation may be effected by using methods well known in the art including, but not limited to, sub-lethal heating, chemical treatment or by directed mutagenesis techniques such as described, for example, by Kurihara and Watanabe (Molecular Plant Pathology 4:259-269, 2003), Galon et al. (1992), Atreya et al. (1992) and Huet et al. (1994).

Suitable virus strains can be obtained from available sources such as, for example, the American Type culture Collection (ATCC) or by isolation from infected plants. Isolation of viruses from infected plant tissues can be effected by techniques well known in the art such as described, for example by Foster and Tatlor, Eds. "Plant Virology Protocols: From Virus Isolation to Transgenic Resistance (Methods in Molecular Biology (Humana Pr), Vol 81)", Humana Press, 1998. Briefly, tissues of an infected plant believed to contain a high concentration of a suitable virus, preferably young leaves and flower petals, are ground in a buffer solution (e.g., phosphate buffer solution) to produce a virus infected sap which can be used in subsequent inoculations.

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

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

In one embodiment, a plant viral nucleic acid is provided in which the native coat protein coding sequence has been deleted from a viral nucleic acid, a non-native plant viral coat protein coding sequence and a non-native promoter, preferably the subgenomic promoter of the non-native coat protein coding sequence, capable of expression in the plant host, packaging of the recombinant plant viral nucleic acid, and ensuring a systemic infection of the host by the recombinant plant viral nucleic acid, has been inserted. Alternatively, the coat protein gene may be inactivated by insertion of the non-native nucleic acid sequence within it, such that a protein is produced. The recombinant plant viral nucleic acid may contain one or more additional non-native subgenomic promoters. Each non-native subgenomic promoter is capable of transcribing or expressing adjacent genes or nucleic acid sequences in the plant host and incapable of recombination with each other and with native subgenomic promoters. Non-native (foreign) nucleic acid sequences may be inserted adjacent the native plant viral subgenomic promoter or the native and a non-native plant viral subgenomic promoters if more than one nucleic acid sequence is included. The non-native nucleic acid sequences are transcribed or expressed in the host plant under control of the subgenomic promoter to produce the desired products.

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

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

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

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

In addition to the above, the nucleic acid molecule of the present invention can also be introduced into a chloroplast genome thereby enabling chloroplast expression.

A technique for introducing exogenous nucleic acid sequences to the genome of the chloroplasts is known. This technique involves the following procedures. First, plant cells are chemically treated so as to reduce the number of chloroplasts per cell to about one. Then, the exogenous nucleic acid is introduced via particle bombardment into the cells with the aim of introducing at least one exogenous nucleic acid molecule into the chloroplasts. The exogenous nucleic acid is selected such that it is integratable into the chloroplast's genome via homologous recombination which is readily effected by enzymes inherent to the chloroplast. To this end, the exogenous nucleic acid includes, in addition to a gene of interest, at least one nucleic acid stretch which is derived from the chloroplast's genome. In addition, the exogenous nucleic acid includes a selectable marker, which serves by sequential selection procedures to ascertain that all or substantially all of the copies of the chloroplast genomes following such selection will include the exogenous nucleic acid. Further details relating to this technique are found in U.S. Pat. Nos. 4,945,050; and 5,693,507 which are incorporated herein by reference. A polypeptide can thus be produced by the protein expression system of the chloroplast and become integrated into the chloroplast's inner membrane.

Since NUE, abiotic stress tolerance as well as yield, vigor or biomass of the plant can involve multiple genes acting additively or in synergy (see, for example, in Quesda et al., Plant Physiol. 130:951-063, 2002), the invention also envisages expressing a plurality of exogenous polynucleotides in a single host plant to thereby achieve superior effect on NUE, abiotic stress tolerance, yield, vigor and biomass of the plant.

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

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

Alternatively, expressing a plurality of exogenous polynucleotides can be effected by introducing different nucleic acid constructs, including different exogenous polynucleotides, into a plurality of plants. The regenerated transformed plants can then be cross-bred and resultant progeny selected for superior NUE, abiotic stress tolerance, yield as described above, using conventional plant breeding techniques.

As mentioned, expression (or reduction in a level of expression) of the target polynucleotides/polypeptides of the present invention can be qualified using methods which are well known in the art such as those involving gene amplification Western blotting, ELISA, or at the mRNA level involving e.g., PCR or RT-PCR or Northern blot or in-situ hybridization (in which one monitors the level of target gene expression).

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

According to some embodiments of the invention, the method further comprises growing the plant expressing the exogenous polynucleotide(s) under abiotic stress or nitrogen limiting conditions. Non-limiting examples of abiotic stress conditions include, water deprivation, drought, excess of water (e.g., flood, waterlogging), freezing, low temperature, high temperature, strong winds, heavy metal toxicity, anaerobiosis, nutrient deficiency, nutrient excess, salinity, atmospheric pollution, intense light, insufficient light, or UV irradiation, etiolation and atmospheric pollution.

Thus, the invention encompasses plants exogenously expressing the polynucleotide(s), the nucleic acid constructs of the invention.

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

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

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

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

Thus, according to an additional embodiment of the present invention, there is provided a method of evaluating a trait of a plant, the method comprising: (a) expressing in a plant or a portion thereof the nucleic acid construct; and (b) evaluating a trait of a plant as compared to a wild type plant of the same type; thereby evaluating the trait of the plant.

Thus, the effect of the transgene (the exogenous polynucleotide) on different plant characteristics may be determined any method known to one of ordinary skill in the art.

Thus, for example, tolerance to limiting nitrogen conditions may be compared in transformed plants {i.e., expressing the transgene) compared to non-transformed (wild type) plants exposed to the same stress conditions (other stress conditions are contemplated as well, e.g. water deprivation, salt stress e.g. salinity, suboptimal temperature, osmotic stress, and the like), using the following assays.

Methods of qualifying plants as being tolerant or having improved tolerance to abiotic stress or limiting nitrogen levels are well known in the art and are further described hereinbelow.

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

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

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

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

Tolerance to abiotic stress (e.g. tolerance to drought or salinity) can be evaluated by determining the differences in physiological and/or physical condition, including but not limited to, vigor, growth, size, or root length, or specifically, leaf color or leaf area size of the transgenic plant compared to a non-modified plant of the same species grown under the same conditions. Other techniques for evaluating tolerance to abiotic stress include, but are not limited to, measuring chlorophyll fluorescence, photosynthetic rates and gas exchange rates. Further assays for evaluating tolerance to abiotic stress are provided hereinbelow and in the Examples section which follows.

Drought tolerance assay—Soil-based drought screens are performed with plants overexpressing the polynucleotides detailed above. Seeds from control *Arabidopsis* plants, or other transgenic plants overexpressing nucleic acid of the invention are germinated and transferred to pots. Drought stress is obtained after irrigation is ceased. Transgenic and control plants are compared to each other when the majority of the control plants develop severe wilting. Plants are re-watered after obtaining a significant fraction of the control plants displaying a severe wilting. Plants are ranked comparing to controls for each of two criteria: tolerance to the drought conditions and recovery (survival) following re-watering.

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

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

For example, a salinity tolerance test can be performed by irrigating plants at different developmental stages with increasing concentrations of sodium chloride (for example 50 mM, 150 mM, 300 mM NaCl) applied from the bottom and from above to ensure even dispersal of salt. Following exposure to the stress condition the plants are frequently monitored until substantial physiological and/or morphological effects appear in wild type plants. Thus, the external phenotypic appearance, degree of chlorosis and overall success to reach maturity and yield progeny are compared between control and transgenic plants. Quantitative parameters of tolerance measured include, but are not limited to, the average wet and dry weight, growth rate, leaf size, leaf coverage (overall leaf area), the weight of the seeds yielded, the average seed size and the number of seeds produced per plant. Transformed plants not exhibiting substantial physiological and/or morphological effects, or exhibiting higher biomass than wild-type plants, are identified as abiotic stress tolerant plants.

Osmotic tolerance test—Osmotic stress assays (including sodium chloride and PEG assays) are conducted to determine if an osmotic stress phenotype was sodium chloride-specific or if it was a general osmotic stress related phenotype. Plants which are tolerant to osmotic stress may have more tolerance to drought and/or freezing. For salt and osmotic stress experiments, the medium is supplemented for example with 50 mM, 100 mM, 200 mM NaCl or 15%, 20% or 25% PEG.

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

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

The biomass, vigor and yield of the plant can also be evaluated using any method known to one of ordinary skill in the art. Thus, for example, plant vigor can be calculated by the increase in growth parameters such as leaf area, fiber length, rosette diameter, plant fresh weight and the like per time.

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

Thus, the present invention is of high agricultural value for increasing tolerance of plants to nitrogen deficiency or abiotic stress as well as promoting the yield, biomass and vigor of commercially desired crops.

According to another embodiment of the present invention, there is provided a food or feed comprising the plants or a portion thereof of the present invention.

In a further aspect the invention, the transgenic plants of the present invention or parts thereof are comprised in a food or feed product (e.g., dry, liquid, paste). A food or feed product is any ingestible preparation containing the transgenic plants, or parts thereof, of the present invention, or preparations made from these plants. Thus, the plants or preparations are suitable for human (or animal) consumption, i.e. the transgenic plants or parts thereof are more readily digested. Feed products of the present invention further include a oil or a beverage adapted for animal consumption.

It will be appreciated that the transgenic plants, or parts thereof, of the present invention may be used directly as feed products or alternatively may be incorporated or mixed with feed products for consumption. Furthermore, the food or feed products may be processed or used as is. Exemplary feed products comprising the transgenic plants, or parts thereof, include, but are not limited to, grains, cereals, such as oats, e.g. black oats, barley, wheat, rye, *sorghum*, corn, vegetables, leguminous plants, especially soybeans, root vegetables and cabbage, or green forage, such as grass or hay.

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

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

The term "consisting of" means "including and limited to".

The term "consisting essentially of" means that the composition, method or structure may include additional ingredients, steps and/or parts, but only if the additional ingredients, steps and/or parts do not materially alter the basic and novel characteristics of the claimed composition, method or structure.

As used herein, the singular form "a", "an" and "the" include plural references unless the context clearly dictates otherwise. For example, the term "a compound" or "at least one compound" may include a plurality of compounds, including mixtures thereof.

Throughout this application, various embodiments of this invention may be presented in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of the invention. Accordingly, the description of a range should be considered to have specifically disclosed all the possible subranges as well as individual numerical values within that range. For example, description of a range such as from 1 to 6 should be considered to have specifically disclosed subranges such as from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual numbers within that range, for example, 1, 2, 3, 4, 5, and 6. This applies regardless of the breadth of the range.

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

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

As used herein, the term "treating" includes abrogating, substantially inhibiting, slowing or reversing the progression of a condition, substantially ameliorating clinical or aesthetical symptoms of a condition or substantially preventing the appearance of clinical or aesthetical symptoms of a condition.

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

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

EXAMPLES

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

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

Example 1

Differential Expression of dsRNAs in Maize Plant Under Optimal Versus Deficient Nitrogen Conditions

Experimental Procedures

Plant Material

Corn seeds were obtained from Galil seeds (Israel). Corn variety 5605 was used in all experiments. Plants were grown at 24° C. under a 16 hr light:8 hr dark regime.

Stress Induction

Corn seeds were germinated and grown on agar with defined growth media containing either optimal (100% N_2, 20.61 mM) or suboptimal nitrogen levels (1% or 10% N_2, 0.2 mM or 2.06 mM, respectively). Seedlings aged one or two weeks were used for tissue samples for RNA analysis, as described below.

Total RNA Extraction

Total RNA of leaf or root samples from four to eight biological repeats were extracted using the mirVana™ kit (Ambion, Austin, Tex.) by pooling 3-4 plants to one biological repeat.

Microarray Design

Custom microarrays were manufactured by Agilent Technologies by in situ synthesis. The first generation microarray consisted of a total of 13619 non-redundant DNA probes, the majority of which arose from deep sequencing data and includes different small RNA molecules (i.e. miRNAs, siRNA and predicted small RNA sequences), with each probe being printed once. An in-depth analysis of the first generation microarray, which included hybridization experiments as well as structure and orientation verifications on all its small RNAs, resulted in the formation of an improved, second generation, microarray. The second generation microarray consists of a total 4721 non-redundant DNA 45-nucleotide long probes for all known plant small RNAs, with 912 sequences (19.32%) from Sanger version 15 and the rest (3809), encompassing miRNAs (968=20.5%), siRNAs (1626=34.44%) and predicted small RNA sequences (1215=25.74%), from deep sequencing data accumulated by the inventors, with each probe being printed in triplicate.

Results

Wild type maize plants were allowed to grow at standard, optimal conditions or nitrogen deficient conditions for one or two weeks, at the end of which they were evaluated for NUE. Three to four plants from each group were used for reproducibility. Four to eight repeats were obtained for each group and RNA was extracted from leaf or root tissue. The expression level of the maize miRNAs was analyzed by high throughput microarray to identify miRNAs that were differentially expressed between the experimental groups.

Tables 1-4 below present dsRNA sequences that were found to be differentially expressed (upregulated=up; downregulated=down) in corn grown under low nitrogen conditions (nitrogen limiting conditions, as described above).

TABLE 1

miRNAs found upregulated in Plants Growing under Nitrogen Deficient Conditions versus Optimal conditions

Mir Name	SEQ ID NO:	Stem Loop SEQ ID NO:	Direction	Fold Change Leaf	Fold Change Root
osa-miR1430	TGGTGAGCCTTCCTGGCTAAG/1	196	Up		3.99
osa-miR1868	TCACGGAAAACGAGGGAGCAGCCA/2	197	Up		2.63
osa-miR2096-3p	CCTGAGGGGAAATCGGCGGGA/3	198	Up	3.48	2.71
zma-miR399f*	GGGCAACTTCTCCTTTGGCAGA/4	199	Up		2.13
Predicted folded 24-nts-long seq 50935	AACTAAAACGAAACGGAAGGAGTA/5	200	Up	2.1	
Predicted folded 24-nts-long seq 51052	AAGGTGCTTTTAGGAGTAGGACGG/6	201	Up	2.08	
Predicted folded 24-nts-long seq 51215	ACAAAGGAATTAGAACGGAATGGC/7	202	Up	3.23	2.49
Predicted folded 24-nts-long seq 51468	AGAATCAGGAATGGAACGGCTCCG/8	203	Up		1.54
Predicted folded 24-nts-long seq 51469	AGAATCAGGGATGGAACGGCTCTA/9	204	Up		1.9
Predicted folded 24-nts-long seq 51577	AGAGTCACGGGCGAGAAGAGGACG/10	205	Up		2.34
Predicted folded 24-nts-long seq 51691	AGGACCTAGATGAGCGGGCGGTTT/11	206	Up		1.72
Predicted folded 24-nts-long seq 51695	AGGACGCTGCTGGAGACGGAGAAT/12	207	Up		2.4

TABLE 1-continued

miRNAs found upregulated in Plants Growing under Nitrogen Deficient Conditions versus Optimal conditions

Mir Name	SEQ ID NO:	Stem Loop SEQ ID NO:	Direction	Fold Change Leaf	Fold Change Root
Predicted folded 24-nts-long seq 51814	AGGGCTTGTTCGGTTTG AAGGGGT/13	208	Up	2.52	
Predicted folded 24-nts-long seq 52057	ATCTTTCAACGGCTGCG AAGAAGG/14	209	Up		2.11
Predicted folded 24-nts-long seq 52327	CTAGAATTAGGGATGG AACGGCTC/15	210	Up		1.57
Predicted folded 24-nts-long seq 52499	GAGGGATAACTGGGGA CAACACGG/16	211	Up	2.97	
Predicted folded 24-nts-long seq 52633	GCGGAGTGGGATGGGG AGTGTTGC/17	212	Up		1.51
Predicted folded 24-nts-long seq 52688	GGAGACGGATGCGGAG ACTGCTGG/18	213	Up		1.51
Predicted folded 24-nts-long seq 52805	GGTTAGGAGTGGATTG AGGGGGAT/19	214	Up	3.77	
Predicted folded 24-nts-long seq 52850	GTCAAGTGACTAAGAG CATGTGGT/20	215	Up	4.93	10.17
Predicted folded 24-nts-long seq 52882	GTGGAATGGAGGAGAT TGAGGGGA/21	216	Up	2.01	
Predicted folded 24-nts-long seq 53118	TGGCTGAAGGCAGAAC CAGGGGAG/22	217	Up		4.45
Predicted folded 24-nts-long seq 53149	TGTGGTAGAGAGGAAG AACAGGAC/23	218	Up	3.25	
Predicted folded 24-nts-long seq 53594	AGGGACTCTCTTTATTT CCGACGG/24	219	Up		1.83
Predicted folded 24-nts-long seq 53604	AGGGTTCGTTTCCTGGG AGCGCGG/25	220	Up		1.66
Predicted folded 24-nts-long seq 54081	TCCTAGAATCAGGGAT GGAACGGC/26	221	Up		1.6
Predicted folded 24-nts-long seq 54132	TGGGAGCTCTCTGTTCG ATGGCGC/27	222	Up		3.47
Predicted zma mir 48061	AACGTCGTGTCGTGCTT GGGCT/28	223	Up		1.62
Predicted zma mir 48295	ACCTGGACCAATACAT GAGATT/29	224	Up	2.58	
Predicted zma mir 48350	AGAAGCGACAATGGGA CGGAGT/30	225	Up	4.65	
Predicted zma mir 48457	AGGAAGGAACAAACGA GGATAAG/31	226	Up		2.08

TABLE 1-continued

miRNAs found upregulated in Plants Growing under Nitrogen Deficient Conditions versus Optimal conditions

Mir Name	SEQ ID NO:	Stem Loop SEQ ID NO:	Direction	Fold Change Leaf	Fold Change Root
Predicted zma mir 48877	CCAAGAGATGGAAGGG CAGAGC/32	227	Up	2	
Predicted zma mir 48922	CGACAACGGGACGGAG TTCAA/33	228	Up		1.58
Predicted zma mir 49123	GAGGATGGAGAGGTAC GTCAGA/34	229	Up	2.02	
Predicted zma mir 49161	GATGGGTAGGAGAGCG TCGTGTG/35	230	Up	1.51	1.55
Predicted zma mir 49162	GATGGTTCATAGGTGA CGGTAG/36	231	Up		4.2
Predicted zma mir 49262	GGGAGCCGAGACATAG AGATGT/37	232	Up		2.64
Predicted zma mir 49323	GTGAGGAGTGATAATG AGACGG/38	233	Up		2.17
Predicted zma mir 49369	GTTTGGGGCTTTAGCAG GTTTAT/39	234	Up	1.58	
Predicted zma mir 49609	TCCATAGCTGGGCGGA AGAGAT/40	235	Up		5.52
Predicted zma mir 49638	TCGGCATGTGTAGGAT AGGTG/41	236	Up	3.24 ± 1.00	3.235 ± 0.205
Predicted zma mir 49761	TGATAGGCTGGGTGTG GAAGCG/42	237	Up	2.01	1.73
Predicted zma mir 49787	TGCAAACAGACTGGGG AGGCGA/43	238	Up		3
Predicted zma mir 50077	TTTGGCTGACAGGATA AGGGAG/44	239	Up	2.44	
Predicted zma mir 50095	TTTTCATAGCTGGGCGG AAGAG/45	240	Up	19.94	
Predicted zma mir 50110	AACTTTAAATAGGTAG GACGGCGC/46	241	Up		1.51
Predicted zma mir 50204	GGAATGTTGTCTGGTTC AAGG/47	242	Up	14.34	
Predicted zma mir 50261	TGTAATGTTCGCGGAA GGCCAC/48	243	Up		1.7
Predicted zma mir 50267	TGTTGGCATGGCTCAAT CAAC/49	244	Up		1.82
Predicted zma mir 50460	CGCTGACGCCGTGCCA CCTCAT/50	245	Up		2.33
Predicted zma mir 50545	GCCTGGGCCTCTTTAGA CCT/51	246	Up		1.5
Predicted zma mir 50578	GTAGGATGGATGGAGA GGGTTC/52	247	Up		2.07
Predicted zma mir 50611	TCAACGGGCTGGCGGA TGTG/53	248	Up		1.55

Table 1. provided are miRNAs that were found upregulated in Plants Growing under Nitrogen Deficient Conditions versus Optimal conditions.

TABLE 2

miRNAs found downregulated in Plants Growing under Nitrogen Deficient Conditions versus Optimal conditions

Mir Name	Mature Sequence/seq id no:	Stem Loop Sequence/ seq id no:	Direction	Fold Change Leaf	Fold Change Root
aqc-miR529	AGAAGAGAGAG AGCACAACCC/54	249	Down	1.53	
ath-miR2936	CTTGAGAGAGAG AACACAGACG/55	250	Down	1.54	
mtr-miR169q	TGAGCCAGGATG ACTTGCCGG/56	251	Down	3.04	
peu-miR2911	GGCCGGGGGACG GGCTGGGA/59	254	Down	1.66	
Predicted folded 24-nts-long seq 50703	AAAAAAGACTGA GCCGAATTGAAA/ 60	255	Down		2.66
Predicted folded 24-nts-long seq 51022	AAGGAGTTTAAT GAAGAAAGAGA G/61	256	Down	1.62	
Predicted folded 24-nts-long seq 51381	ACTGATGACGAC ACTGAGGAGGCT/ 62	257	Down	7.7	
Predicted folded 24-nts-long seq 51542	AGAGGAACCAGA GCCGAAGCCGTT/ 63	258	Down	1.52	
Predicted folded 24-nts-long seq 51757	AGGCAAGGTGGA GGACGTTGATGA/ 64	259	Down	2.07	
Predicted folded 24-nts-long seq 51802	AGGGCTGATTTG GTGACAAGGGGA/ 65	260	Down	3.7	2.04
Predicted folded 24-nts-long seq 51966	ATATAAAGGGAG GAGGTATGGACC/ 66	261	Down	2.1	
Predicted folded 24-nts-long seq 52041	ATCGGTCAGCTG GAGGAGACAGGT/ 67	262	Down	1.7	
Predicted folded 24-nts-long seq 52109	ATGGTAAGAGAC TATGATCCAACT/ 68	263	Down		1.62
Predicted folded 24-nts-long seq 52212	CAATTTTGTACT GGATCGGGGCAT/ 69	264	Down		1.53
Predicted folded 24-nts-long seq 52218	CAGAGGAACCAG AGCCGAAGCCGT/ 70	265	Down	1.58	
Predicted folded 24-nts-long seq 52299	CGGCTGGACAGG GAAGAAGAGCAC/ 71	266	Down	1.63	

TABLE 2-continued

miRNAs found downregulated in Plants Growing under Nitrogen Deficient Conditions versus Optimal conditions

Mir Name	Mature Sequence/seq id no:	Stem Loop Sequence/ seq id no:	Direction	Fold Change Leaf	Fold Change Root
Predicted folded 24-nts-long seq 52347	GAAACTTGGAGA GATGGAGGCTTT/ 72	267	Down		1.7
Predicted folded 24-nts-long seq 52452	GAGAGAGAAGG GAGCGGATCTGG T/73	268	Down	3.25	2.52
Predicted folded 24-nts-long seq 52648	GCTGCACGGGAT TGGTGGAGAGGT/ 74	269	Down	2.34	
Predicted folded 24-nts-long seq 52739	GGCTGCTGGAGA GCGTAGAGGACC/ 75	270	Down	2.13	
Predicted folded 24-nts-long seq 52792	GGGTTTTGAGAG CGAGTGAAGGGG/ 76	271	Down		2.9
Predicted folded 24-nts-long seq 52795	GGTATTGGGGTG GATTGAGGTGGA/ 77	272	Down	1.59	
Predicted folded 24-nts-long seq 52801	GGTGGCGATGCA AGAGGAGCTCAA/ 78	273	Down	2.52	3.87
Predicted folded 24-nts-long seq 52955	GTTGCTGGAGAG AGTAGAGGACGT/ 79	274	Down		2.35
Predicted zma mir 47944	AAAAGAGAAACC GAAGACACAT/80	275	Down		1.78
Predicted zma mir 47976	AAAGAGGATGAG GAGTAGCATG/81	276	Down	4.09	
Predicted zma mir 48185	AATACACATGGG TTGAGGAGG/82	277	Down	1.85	
Predicted zma mir 48351	AGAAGCGGACTG CCAAGGAGGC/83	278	Down	3.18	
Predicted zma mir 48397	AGAGGGTTTGGG GATAGAGGGAC/84	279	Down		8.95
Predicted zma mir 48588	TAAGGGATGAGG CAGAGCATG/85	280	Down		2.1
Predicted zma mir 48669	ATGCTATTTGTA CCCGTCACCG/86	281	Down		1.67
Predicted zma mir 48708	ATGTGGATAAAA GGAGGGATGA/87	282	Down		1.61

TABLE 2-continued

miRNAs found downregulated in Plants Growing under Nitrogen Deficient Conditions versus Optimal conditions

Mir Name	Mature Sequence/seq id no:	Stem Loop Sequence/ seq id no:	Direction	Fold Change Leaf	Fold Change Root
Predicted zma mir 48771	CAACAGGAACAA GGAGGACCAT/88	283	Down	1.52	
Predicted zma mir 49002	CTCGAGTTGAGAA AGAGATGCT/89	284	Down		1.51
Predicted zma mir 49003	CTCGATGGGAGGT GGAGTTGCAT/90	285	Down	1.61	
Predicted zma mir 49011	CTGGGAAGATGG AACATTTTGGT/91	286	Down		1.64
Predicted zma mir 49053	GAAGATATACGA TGATGAGGAG/92	287	Down	1.55	
Predicted zma mir 49070	GAATCTATCGTT TGGGCTCAT/93	288	Down	1.65	2.01
Predicted zma mir 49082	GAGCGAGCTACAA AAGGATTCG/94	289	Down	1.6	
Predicted zma mir 49155	GAGTGACGAGGAG TGAGAGTAGG/95	290	Down		3.64
Predicted zma mir 49269	GGGCATCTTCTG GCAGGAGGACA/ 96	291	Down	1.64	
Predicted zma mir 49435	TACGGAAGAAGA GCAAGTTTT/97	292	Down	1.64	
Predicted zma mir 49445	TAGAAAGAGCGA GAGAACAAAG/98	293	Down		1.55
Predicted zma mir 49762	TGATATTATGGA CGACTGGTT/99	294	Down	1.54	1.57
Predicted zma mir 49816	TGGAAGGGCCAT GCCGAGGAG/100	295	Down		2.45
Predicted zma mir 49985	TTGAGCGCAGCG TTGATGAGC/101	296	Down		2.93
Predicted zma mir 50021	TTGGATAACGGG TAGTTTGGAGT/ 102	297	Down		1.79
Predicted zma mir 50144	AGCTGCCGACTC ATTCACCCA/103	298	Down		1.54
Predicted zma mir 50263	TGTACGATGATC AGGAGGAGGT/ 104	299	Down	1.53	
Predicted zma mir 50266	TGTGTTCTCAGG TCGCCCCCG/105	300	Down		2.51

TABLE 2-continued

miRNAs found downregulated in Plants Growing under Nitrogen Deficient Conditions versus Optimal conditions

Mir Name	Mature Sequence/seq id no:	Stem Loop Sequence/ seq id no:	Direction	Fold Change Leaf	Fold Change Root
Predicted zma mir 50318	ACTAAAAAGAAACAGAGGGAG/106	301	Down	1.5	
Predicted zma mir 50517	GACCGGCTCGACCCTTCTGC/107	302	Down	1.55	
Predicted zma mir 50670	TGGTAGGATGGATGGAGAGGGT/108	303	Down	1.55	
zma-miR166d*	GGAATGTTGTCTGGTTCAAGG/109	304	Down	1.73	
zma-miR169c*	GGCAAGTCTGTCCTTGGCTACA/110	305	Down	2.41	
zma-miR399g	TGCCAAAGGGGATTTGCCCGG/113	309	Down		1.55

Table 2. provided are miRNAs that were found downregulated in Plants Growing under Nitrogen Deficient Conditions versus Optimal conditions.

TABLE 3

siRNAs found upregulated in Plants Growing under Nitrogen Deficient Conditions versus Optimal conditions

Mir Name	Mature Sequence/SEQ ID NO:	Direction	Fold Change Leaf	Fold Change Root
Predicted siRNA 54339	AAGAAACGGGGCAGTGAGATGGAC/114	Up		1.51
Predicted siRNA 54631	AGAAAAGATTGAGCCGAATTGAATT/115	Up	2.02	
Predicted siRNA 54991	AGAGCCTGTAGCTAATGGTGGG/116	Up	1.95	
Predicted siRNA 55111	AGGTAGCGGCCTAAGAACGACACA/117	Up	2.36	1.67
Predicted siRNA 55423	CCTATATACTGGAACGGAACGGCT/118	Up		1.57
Predicted siRNA 55806	CTATATACTGGAACGGAACGGCTT/119	Up		2.23
Predicted siRNA 56052	GACGAGATCGAGTCTGGAGCGAGC/120	Up	1.86	
Predicted siRNA 56106	GAGTATGGGGAGGGACTAGGGA/121	Up		2.3
Predicted siRNA 56353	GACGAAATAGAGGCTCAGGAGAGG/122	Up	2.08	
Predicted siRNA 56388	GGATTCGTGATTGGCGATGGGG/123	Up		1.51
Predicted siRNA 56406	GGTGAGAAACGGAAAGGCAGGACA/124	Up	4.04	
Predicted siRNA 56443	GTGTCTGAGCAGGGTGAGAAGGCT/125	Up	1.53	1.58
Predicted siRNA 56450	GTTTTGGAGGCGTAGGCGAGGGAT/126	Up	3.04	

TABLE 3-continued

siRNAs found upregulated in Plants Growing under Nitrogen Deficient Conditions versus Optimal conditions

Mir Name	Mature Sequence/SEQ ID NO:	Direction	Fold Change Leaf	Fold Change Root
Predicted siRNA 56542	TGGGACGCTGCATCTGTTGAT/127	Up	2.96	
Predicted siRNA 56706	TCTATATACTGGAACGGAACGGCT/128	Up		1.76
Predicted siRNA 56856	GTTGTTGGAGGGGTAGAGGACGTC/129	Up	1.55	
Predicted siRNA 57034	AATGACAGGACGGGATGGGACGGG/130	Up		2.87
Predicted siRNA 57054	ACGGAACGGCTTCATACCACAATA/131	Up		2.43
Predicted siRNA 57193	GACGGGCCGACATTTAGAGCACGG/132	Up		1.69
Predicted siRNA 57884	ACGGATAAAAGGTACTCT/133	Up		2.82
Predicted siRNA 58292	AGTATGTCGAAAACTGGAGGGC/134	Up	4.54	
Predicted siRNA 58362	ATAAGCACCGGCTAACTCT/135	Up		2.87
Predicted siRNA 58665	ATTCAGCGGGCGTGGTTATTGGCA/136	Up		1.55
Predicted siRNA 58872	CAGCGGGTGCCATAGTCGAT/137	Up		1.92
Predicted siRNA 58940	CATTGCGACGGTCCTCAA/138	Up		1.57
Predicted siRNA 59380	CTCAACGGATAAAAGGTAC/139	Up		2.21
Predicted siRNA 59626	GACAGTCAGGATGTTGGCT/140	Up	2.68	2.12
Predicted siRNA 59659	GACTGATCCTTCGGTGTCGGCG/141	Up		1.67
Predicted siRNA 59846	GCCGAAGATTAAAAGACGAGACGA/142	Up	1.64	
Predicted siRNA 59867	GCCTTTGCCGACCATCCTGA/143	Up		1.6
Predicted siRNA 59952	GGAATCGCTAGTAATCGTGGAT/144	Up	1.87	1.76
Predicted siRNA 59961	GGAGCAGCTCTGGTCGTGGG/145	Up		1.85 ± 0.007
Predicted siRNA 59965	GGAGGCTCGACTATGTTCAAA/146	Up		2.97
Predicted siRNA 59966	GGAGGGATGTGAGAACATGGGC/147	Up		1.62
Predicted siRNA 60081	GTCCCCTTCGTCTAGAGGC/148	Up		2.82
Predicted siRNA 60095	GTCTGAGTGGTGTAGTTGGT/149	Up	2.12	
Predicted siRNA 60188	GTTGGTAGAGCAGTTGGC/150	Up		4.11
Predicted siRNA 60285	TACGTTCCCGGGTCTTGTACA/151	Up		1.95

TABLE 3-continued

siRNAs found upregulated in Plants Growing under Nitrogen Deficient Conditions versus Optimal conditions

Mir Name	Mature Sequence/SEQ ID NO:	Direction	Fold Change Leaf	Fold Change Root
Predicted siRNA 60387	TATGGATGAAGATGGGGTG/152	Up	3.68	
Predicted siRNA 60434	TCAACGGATAAAAGGTACTCCG/153	Up		2.23
Predicted siRNA 60837	TGCCCAGTGCTTTGAATG/154	Up		3.37
Predicted siRNA 60850	TGCGAGACCGACAAGTCGAGC/155	Up	1.64	1.86
Predicted siRNA 61382	TTTGCGACACGGGCTGCTCT/156	Up		1.52

Table 3. Provided are siRNAs that were found upregulated in Plants Growing under Nitrogen Deficient Conditions versus Optimal conditions.

TABLE 4

siRNAs found downregulated in Plants Growing under Nitrogen Deficient Conditions versus Optimal conditions

Mir Name	Mature Sequence/SEQ ID No:	Direction	Fold Change Leaf	Fold Change Root
Predicted siRNA 58924	CATCGCTCAACGGACAAAAGGT/157	Down		1.55
Predicted siRNA 54240	AAGACGAAGGTAGCAGCGCGATAT/158	Down	2.79	
Predicted siRNA 54957	AGCCAGACTGATGAGAGAAGGAGG/159	Down	1.51	
Predicted siRNA 55081	ACGTTGTTGGAAGGGTAGAGGACG/160	Down	1.56	
Predicted siRNA 55393	CAAGTTATGCAGTTGCTGCCT/161	Down		5.98
Predicted siRNA 55404	CAGAATGGAGGAAGAGATGGTG/162	Down	3.49	
Predicted siRNA 55472	ATCTGTGGAGAGAGAAGGTTGCCC/163	Down	1.58	
Predicted siRNA 55720	ATGTCAGGGGGCCATGCAGTAT/164	Down	2.41	
Predicted siRNA 55732	ATCCTGACTGTGCCGGGCCGGCCC/165	Down	1.96	
Predicted siRNA 56034	CGAGTTCGCCGTAGAGAAAGCT/166	Down		2.24
Predicted siRNA 56162	GACTGATTCGGACGAAGGAGGGTT/167	Down		3.23
Predicted siRNA 56205	GTCTGAACACTAAACGAAGCACA/168	Down	1.87	
Predicted siRNA 56277	GACGTTGTTGGAAGGGTAGAGGAC/169	Down	3.94	
Predicted siRNA 56307	GCTACTGTAGTTCACGGGCCGGCC/170	Down	1.71	
Predicted siRNA 56425	GGTATTCGTGAGCCTGTTTCTGGTT/171	Down	1.67	

TABLE 4-continued

siRNAs found downregulated in Plants Growing under Nitrogen Deficient Conditions versus Optimal conditions

Mir Name	Mature Sequence/SEQ ID No:	Direction	Fold Change Leaf	Fold Change Root
Predicted siRNA 56837	TGGAAGGAGCATGCATCTTGAG/172	Down		2.68
Predicted siRNA 56965	TTCTTGACCTTGTAAGACCCA/173	Down		3.66
Predicted siRNA 57088	AGCAGAATGGAGGAAGAGATGG/174	Down	1.53	
Predicted siRNA 57179	CTGGACACTGTTGCAGAAGGAGGA/175	Down	1.58	
Predicted siRNA 57181	GAAATAGGATAGGAGGAGGGATGA/176	Down	3.34	2.91
Predicted siRNA 57228	GGCACGACTAACAGACTCACGGGC/177	Down		2.45
Predicted siRNA 57685	AATCCCGGTGGAACCTCCA/178	Down	3.6	2.7
Predicted siRNA 57772	ACACGACAAGACGAATGAGAGAGA/179	Down		1.57
Predicted siRNA 57863	ACGACGAGGACTTCGAGACG/180	Down	1.53	
Predicted siRNA 58721	CAAAGTGGTCGTGCCGGAG/181	Down	1.61	
Predicted siRNA 58877	CAGCTTGAGAATCGGGCCGC/182	Down	3.8	
Predicted siRNA 59032	CCCTGTGACAAGAGGAGGA/183	Down	1.6	
Predicted siRNA 59102	CCTGCTAACTAGTTATGCGGAGC/184	Down	1.74	
Predicted siRNA 59123	CGAACTCAGAAGTGAAACC/185	Down	2.11	2.62
Predicted siRNA 59235	CGCTTCGTCAAGGAGAAGGGC/186	Down	1.59	
Predicted siRNA 59485	CTTAACTGGGCGTTAAGTTGCAGGGT/187	Down		2.17
Predicted siRNA 59954	GGACGAACCTCTGGTGTACC/188	Down		1.76
Predicted siRNA 59993	GGCGCTGGAGAACTGAGGG/189	Down		2.58
Predicted siRNA 60012	GGGGGCCTAAATAAAGACT/190	Down	2.48	
Predicted siRNA 60123	GTGCTAACGTCCGTCGTGAA/191	Down		3.15
Predicted siRNA 60334	TAGCTTAACCTTCGGGAGGG/192	Down		1.9
Predicted siRNA 60750	TGAGAAAGAAAGAGAAGGCTCA/193	Down	1.64	
Predicted siRNA 60803	TGATGTCCTTAGATGTTCTGGGC/194	Down		1.99

TABLE 4-continued

siRNAs found downregulated in Plants Growing under Nitrogen Deficient Conditions versus Optimal conditions

Mir Name	Mature Sequence/SEQ ID No:	Direction	Fold Change Leaf	Fold Change Root
Predicted siRNA 55413	CATGTGTTCTCAGGTCGCCC C/195	Down		2.55

Table 4. Provided are siRNAs that were found downregulated in Plants Growing under Nitrogen Deficient Conditions versus Optimal conditions.

Example 2

Target Prediction Using Bioinformatics Tools

A high throughput screening was performed on microarrays loaded with miRNAs/siRNAs that were found to be differentially expressed under multiple stress and optimal environmental conditions and in different plant tissues. The initial trait-associated miRNAs are later validated by quantitative Real Time PCR (qRT-PCR).

Target prediction—orthologous genes to the genes of interest in maize and/or *Arabidopsis* are found through a proprietary tool that analyzes publicly available genomic as well as expression and gene annotation databases from multiple plant species. Homologous as well as orthologous protein and nucleotide sequences of target genes of the small RNA sequences of the invention, were found using BLAST having at least 70% identity on at least 60% of the entire master gene length, and are summarized in Tables 5-8 below. BLAST version used was Version 2.2.25+, Released March 2011, at default parameters as follows: For step 1 using BlastX to find the master homolog: Word size 3, Gap open 11, gap extend 1. For step 2 using BlastN to find orthologs from other organisms: Word size 28, Gap open 0, Gap extend 0, Reward (match score) 1, Penalty (mismatch score)−2.

TABLE 5

Target Genes of miRNAs Associated with Increased NUE (Table 1)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
osa-miR2096-3p	95-115	XP_002468137	hypothetical protein SORBIDRAFT_01g040220 [*Sorghum bicolor*] > gi|241921991|gb|EER95135.1| hypothetical protein SORBIDRAFT_01g040220 [*Sorghum bicolor*]	1.00	311	515
		ACN26598	unknown [*Zea mays*]	0.95	312	516
		NP_001148956	LOC100282576 [*Zea mays*] > gi|195623616|gb|ACG33638.1| CONSTANS interacting protein 4 [*Zea mays*]	0.95	313	517
		ACG37488	CONSTANS interacting protein 4 [*Zea mays*]	0.96	314	518
		NP_001148721	CONSTANS interacting protein 4 [*Zea mays*] > gi|195621640|gb|ACG32650.1| CONSTANS interacting protein 4 [*Zea mays*]	0.96	315	519
		NP_001049637	Os03g0263800 [*Oryza sativa Japonica* Group] > gi|29893607|gb|AAP06861.1| unknown protein [*Oryza sativa Japonica* Group] > gi|108707320|gb|ABF95115.1| S-ribonuclease binding protein SBP1, putative, expressed [*Oryza sativa Japonica* Group] > gi|113548108|dbj|BAF11551.1| Os03g0263800 [*Oryza sativa Japonica* Group] > gi|215692696|dbj|BAG88116.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.89	316	520

TABLE 5-continued

Target Genes of miRNAs Associated with Increased NUE (Table 1)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			> gi|215704492|dbj|BAG93926.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222624614|gb|EEE58746.1| hypothetical protein OsJ_10235 [*Oryza sativa Japonica* Group]			
		EEC74912	hypothetical protein OsI_10851 [*Oryza sativa Indica* Group]	0.88	317	
		BAJ94154	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326493392|dbj|BAJ85157.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.85	318	521
Predicted zma mir 49161	292-314	NP_001169860	hypothetical protein LOC100383754 [*Zea mays*] > gi|224032063|gb|ACN35107.1| unknown [*Zea mays*]	1.00	319	522
		XP_002458357	hypothetical protein SORBIDRAFT_03g031980 [*Sorghum bicolor*] > gi|241930332|gb|EES03477.1| hypothetical protein SORBIDRAFT_03g031980 [*Sorghum bicolor*]	0.88	320	523
	282-304	ACN34890	unknown [*Zea mays*]	1.00	321	524
		EEC71328	hypothetical protein OsI_03374 [*Oryza sativa Indica* Group] > gi|222619103|gb|EEE55235.1| hypothetical protein OsJ_03112 [*Oryza sativa Japonica* Group]	0.74	322	
		BAD81811	hypothetical protein [*Oryza sativa Japonica* Group]	0.74	323	525
		BAJ90295	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.74	324	526
	353-375	XP_002458357	hypothetical protein SORBIDRAFT_03g031980 [*Sorghum bicolor*] > gi|241930332|gb|EES03477.1| hypothetical protein SORBIDRAFT_03g031980 [*Sorghum bicolor*]	1.00	325	527
		NP_001169860	hypothetical protein LOC100383754 [*Zea mays*] > gi|224032063|gb|ACN35107.1| unknown [*Zea mays*]	0.88	326	528
Predicted zma mir 50460	982-1003	XP_002446326	hypothetical protein SORBIDRAFT_06g014320 [*Sorghum bicolor*] > gi|241937509|gb|EES10654.1| hypothetical protein SORBIDRAFT_06g014320 [*Sorghum bicolor*]	1.00	327	529
		NP_001169348	hypothetical protein LOC100383215 [*Zea mays*] > gi|224028855|gb|ACN33503.1| unknown [*Zea mays*]	0.84	328	530
		ACN25775	unknown [*Zea mays*]	0.75	329	531
	426-447	NP_001136483	hypothetical protein LOC100216597 [*Zea mays*] > gi|194695886|gb|ACF82027.1| unknown [*Zea mays*]	1.00	330	532
	295-316	ACG40990	RING-H2 finger protein ATL5I [*Zea mays*]	1.00	331	533
		NP_001159129	hypothetical protein LOC100304207 [*Zea mays*] > gi|223942155|gb|ACN25161.1| unknown [*Zea mays*]	0.85	332	534

TABLE 5-continued

Target Genes of miRNAs Associated with Increased NUE (Table 1)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		NP_001130949	hypothetical protein LOC100192054 [*Zea mays*] > gi|194690534|gb|ACF79351.1| unknown [*Zea mays*]	0.77	333	535
		BAJ92353	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.76	334	536
		NP_001057231	Os06g0233200 [*Oryza sativa Japonica* Group] > gi|51535192|dbj|BAD38165.1| putative RING finger 1 [*Oryza sativa Japonica* Group] > gi|113595271|dbj|BAF19145.1| Os06g0233200 [*Oryza sativa Japonica* Group] > gi|125554660|gb|EAZ00266.1| hypothetical protein OsI_22277 [*Oryza sativa Indica* Group] > gi|215766038|dbj|BAG98266.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222635260|gb|EEE65392.1| hypothetical protein OsJ_20714 [*Oryza sativa Japonica* Group]	0.76	335	537
	154-175	NP_001183617	hypothetical protein LOC100502211 [*Zea mays*] > gi|238013474|gb|ACR37772.1| unknown [*Zea mays*]	1.00	336	538
		XP_002465702	hypothetical protein SORBIDRAFT_01g044080 [*Sorghum bicolor*] > gi|241919556|gb|EER92700.1| hypothetical protein SORBIDRAFT_01g044080 [*Sorghum bicolor*]	0.73	337	539
	93-114	NP_001152266	BHLH transcription factor [*Zea mays*] > gi|195654447|gb|ACG46691.1| BHLH transcription factor [*Zea mays*]	1.00	338	540
	1159-1180	ACN25775	unknown [*Zea mays*]	1.00	339	541
		NP_001169348	hypothetical protein LOC100383215 [*Zea mays*] > gi|224028855|gb|ACN33503.1| unknown [*Zea mays*]	1.00	340	542
		XP_002446326	hypothetical protein SORBIDRAFT_06g014320 [*Sorghum bicolor*] > gi|241937509|gb|EES10654.1| hypothetical protein SORBIDRAFT_06g014320 [*Sorghum bicolor*]	0.80	341	543
Predicted folded 24-nts-long seq 51695	1984-2007	XP_002444807	hypothetical protein SORBIDRAFT_07g028330 [*Sorghum bicolor*] > gi|241941157|gb|EES14302.1| hypothetical protein SORBIDRAFT_07g028330 [*Sorghum bicolor*]	1.00	342	544
		NP_001169681	hypothetical protein LOC100383562 [*Zea mays*] > gi|224030801|gb|ACN34476.1| unknown [*Zea mays*] > gi|224030845|gb|ACN34498.1| unknown [*Zea mays*]	0.90	343	545
Predicted zma mir 48457	584-606	NP_001161741	hypothetical protein LOC100192929 isoform 3 [*Zea mays*] > gi|226713359|sp|B6UGG4.1| NNJA4_MAIZE	1.00	344	546

TABLE 5-continued

Target Genes of miRNAs Associated with Increased NUE (Table 1)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			RecName: Full = Ninja-family protein 4 > gi|195657959|gb|ACG48447.1| hypothetical protein [*Zea mays*]			
		NP_001161740	hypothetical protein LOC100192929 isoform 2 [*Zea mays*] > gi|226713259|sp|B4FM28.1| NNJA2_MAIZE RecName: Full = Ninja-family protein 2 > gi|194698174|gb|ACF83171.1| unknown [*Zea mays*]	1.00	345	547
		B6SLJ0	RecName: Full = Ninja-family protein 3 > gi|195607786|gb|ACG25723.1| hypothetical protein [*Zea mays*]	0.98	346	
		ACN33721	unknown [*Zea mays*]	0.97	347	548
	62-84	B6SLJ0	RecName: Full = Ninja-family protein 3 > gi|195607786|gb|ACG25723.1| hypothetical protein [*Zea mays*]	1.00	348	
		NP_001161740	hypothetical protein LOC100192929 isoform 2 [*Zea mays*] > gi|226713259|sp|B4FM28.1| NNJA2_MAIZE RecName: Full = Ninja-family protein 2 > gi|194698174|gb|ACF83171.1| unknown [*Zea mays*]	0.98	349	549
		ACN33721	unknown [*Zea mays*]	0.95	350	550
		NP_001161741	hypothetical protein LOC100192929 isoform 3 [*Zea mays*] > gi|226713359|sp|B6UGG4.1| NNJA4_MAIZE RecName: Full = Ninja-family protein 4 > gi|195657959|gb|ACG48447.1| hypothetical protein [*Zea mays*]	0.97	351	551
	543-565	NP_001161740	hypothetical protein LOC100192929 isoform 2 [*Zea mays*] > gi|226713259|sp|B4FM28.1| NNJA2_MAIZE RecName: Full = Ninja-family protein 2 > gi|194698174|gb|ACF83171.1| unknown [*Zea mays*]	1.00	352	552
		ACN33721	unknown [*Zea mays*]	0.97	353	553
		NP_001161741	hypothetical protein LOC100192929 isoform 3 [*Zea mays*] > gi|226713359|sp|B6UGG4.1| NNJA4_MAIZE RecName: Full = Ninja-family protein 4 > gi|195657959|gb|ACG48447.1| hypothetical protein [*Zea mays*]	0.99	354	554
		B6SLJ0	RecName: Full = Ninja-family protein 3 > gi|195607786|gb|ACG25723.1| hypothetical protein [*Zea mays*]	0.98	355	

TABLE 5-continued

Target Genes of miRNAs Associated with Increased NUE (Table 1)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
	450-472	NP_001131584	hypothetical protein LOC100192929 isoform 1 [*Zea mays*] > gi|226713190|sp|B4FAF3.1| NNJA1_MAIZE RecName: Full = Ninja-family protein 1 > gi|194690024|gb|ACF79096.1| unknown [*Zea mays*] > gi|194691932|gb|ACF80050.1| unknown [*Zea mays*] > gi|195638284|gb|ACG38610.1| hypothetical protein [*Zea mays*]	1.00	356	555
		XP_002465644	hypothetical protein SORBIDRAFT_01g042880 [*Sorghum bicolor*] > gi|241919498|gb|EER92642.1| hypothetical protein SORBIDRAFT_01g042880 [*Sorghum bicolor*]	0.83	357	556
Predicted zma mir 50261	1313-1334	NP_001182893	hypothetical protein LOC100501172 [*Zea mays*] > gi|238008020|gb|ACR35045.1| unknown [*Zea mays*]	1.00	358	557
Predicted folded 24-nts-long seq 52805	86-109	XP_002447337	hypothetical protein SORBIDRAFT_06g033160 [*Sorghum bicolor*] > gi|241938520|gb|EES11665.1| hypothetical protein SORBIDRAFT_06g033160 [*Sorghum bicolor*]	1.00	359	558
		NP_001142056	hypothetical protein LOC100274212 [*Zea mays*] > gi|194706940|gb|ACF87554.1| unknown [*Zea mays*] > gi|223947485|gb|ACN27826.1| unknown [*Zea mays*]	0.96	360	559
		ACG45259	hypothetical protein [*Zea mays*]	0.96	361	560
		EEC78262	hypothetical protein OsI_17948 [*Oryza sativa Indica* Group]	0.86	362	
		EEE61915	hypothetical protein OsJ_16648 [*Oryza sativa Japonica* Group]	0.86	363	
		BAJ96591	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.86	364	561
		CAJ86266	H0901F07.3 [*Oryza sativa Indica* Group]	0.76	365	562
	596-619	AAY57857	cysteine proteinase inhibitor [*Zea mays* subsp. *parviglumis*] > gi|66866419|gb|AAY57858.1| cysteine proteinase inhibitor [*Zea mays* subsp. *parviglumis*] > gi|66866423|gb|AAY57860.1| cysteine proteinase inhibitor [*Zea mays* subsp. *parviglumis*] > gi|66866425|gb|AAY57861.1| cysteine proteinase inhibitor [*Zea mays* subsp. *parviglumis*] > gi|66866427|gb|AAY57862.1| cysteine proteinase inhibitor [*Zea mays* subsp. *parviglumis*] > gi|66866429|gb|AAY57863.1| cysteine proteinase inhibitor [*Zea mays* subsp. *parviglumis*]	1.00	366	563

TABLE 5-continued

Target Genes of miRNAs Associated with Increased NUE (Table 1)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			> gi|66866435|gb|AAY57866.1| cysteine proteinase inhibitor [*Zea mays* subsp. *parviglumis*]			
		AAY57867	cysteine proteinase inhibitor [*Zea mays* subsp. *parviglumis*]	0.99	367	564
		ABQ32295	cysteine protease inhibitor [*Zea mays*]	0.99	368	565
		AAY57864	cysteine proteinase inhibitor [*Zea mays* subsp. *parviglumis*] > gi|66866439|gb|AAY57868.1| cysteine proteinase inhibitor [*Zea mays* subsp. *parviglumis*]	0.96	369	566
		AAY57859	cysteine proteinase inhibitor [*Zea mays* subsp. *parviglumis*]	0.98	370	567
		BAA09666	cysteine proteinase inhibitor [*Zea mays*] > gi|66866433|gb|AAY57865.1| cysteine proteinase inhibitor [*Zea mays* subsp. *parviglumis*] > gi|71794635|emb|CAJ20024.1| putative cystatin [*Zea mays*]	0.95	371	568
		CAA60610	cysteine proteinase inhibitor [*Zea mays*]	0.94	372	569
		NP_001106013	cystatin2 [*Zea mays*] > gi|1008922|dbj|BAA07327.1| cystatin II [*Zea mays*]	0.94	373	570
		BAB21558	cystatin [Coix lacryma-jobi]	0.86	374	571
		NP_001105295	cystatin-1 precursor [*Zea mays*] > gi|399334|sp|P31726.1|CYT1_MAIZE RecName: Full = Cystatin-1; AltName: Full = Corn kernel cysteine proteinase inhibitor; AltName: Full = Cystatin I; Flags: Precursor > gi|217962|dbj|BAA01472.1| corn cystatin I [*Zea mays*]	0.84	375	572
	2324-2347	BAJ85758	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	1.00	376	573
		NP_001044791	Os01g0846600 [*Oryza sativa Japonica* Group] > gi|15408875|dbj|BAB64266.1| ankyrin-like protein [*Oryza sativa Japonica* Group] > gi|20160625|dbj|BAB89571.1| ankyrin-like protein [*Oryza sativa Japonica* Group] > gi|113534322|dbj|BAF06705.1| Os01g0846600 [*Oryza sativa Japonica* Group] > gi|215687255|dbj|BAG91820.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222619533|gb|EEE55665.1| hypothetical protein OsJ_04065 [*Oryza sativa Japonica* Group]	0.81	377	574
		XP_002458754	hypothetical protein SORBIDRAFT_03g039680 [*Sorghum bicolor*] > gi|241930729|gb|EES03874.1| hypothetical protein	0.81	378	575

TABLE 5-continued

Target Genes of miRNAs Associated with Increased NUE (Table 1)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			SORBIDRAFT__03g039680 [*Sorghum bicolor*]			
		ACR35053	unknown [*Zea mays*]	0.81	379	576
		NP__001147927	LOC100281537 [*Zea mays*] > gi|195614640|gb|ACG29150.1| ankyrin-like protein [*Zea mays*]	0.79	380	577
Predicted folded 24-nts-long seq 51469	1320-1343	XP__002457719	hypothetical protein SORBIDRAFT__03g012350 [*Sorghum bicolor*] > gi|241929694|gb|EES02839.1| hypothetical protein SORBIDRAFT__03g012350 [*Sorghum bicolor*]	1.00	381	578
		NP__001183022	hypothetical protein LOC100501344 [*Zea mays*] > gi|238008824|gb|ACR35447.1| unknown [*Zea mays*]	0.85	382	579
		XP__002457721	hypothetical protein SORBIDRAFT__03g012360 [*Sorghum bicolor*] > gi|241929696|gb|EES02841.1| hypothetical protein SORBIDRAFT__03g012360 [*Sorghum bicolor*]	0.77	383	580
		XP__002457722	hypothetical protein SORBIDRAFT__03g012370 [*Sorghum bicolor*] > gi|241929697|gb|EES02842.1| hypothetical protein SORBIDRAFT__03g012370 [*Sorghum bicolor*]	0.73	384	581
zma-miR399f*	158-179	NP__001147885	LOC100281495 [*Zea mays*] > gi|195611982|gb|ACG27821.1| citrate transporter family protein [*Zea mays*] > gi|195614372|gb|ACG29016.1| citrate transporter family protein [*Zea mays*]	1.00	385	582
		ACF86945	unknown [*Zea mays*]	0.93	386	583
		ACG28034	citrate transporter family protein [*Zea mays*]	0.98	387	584
		NP__001048962	Os03g0147400 [*Oryza sativa Japonica* Group] > gi|15451603|gb|AAK98727.1| AC090485__6 Putative anion transporter [*Oryza sativa Japonica* Group] > gi|108706182|gb|ABF93977.1| transmembrane protein, putative, expressed [*Oryza sativa Japonica* Group] > gi|108706183|gb|ABF93978.1| transmembrane protein, putative, expressed [*Oryza sativa Japonica* Group] > gi|108706184|gb|ABF93979.1| transmembrane protein, putative, expressed [*Oryza sativa Japonica* Group] > gi|108706185|gb|ABF93980.1| transmembrane protein, putative, expressed [*Oryza sativa Japonica* Group] > gi|13547433|dbj|BAF10876.1| Os03g0147400 [*Oryza sativa Japonica* Group] > gi|125542408|gb|EAY88547.1| hypothetical protein	0.80	388	585

TABLE 5-continued

Target Genes of miRNAs Associated with Increased NUE (Table 1)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			OsI_10021 [*Oryza sativa Indica* Group] > gi|125584918|gb|EAZ25582.1| hypothetical protein OsJ_09409 [*Oryza sativa Japonica* Group]			
		EAY78724	hypothetical protein OsI_33828 [*Oryza sativa Indica* Group] > gi|125574971|gb|EAZ16255.1| hypothetical protein OsJ_31712 [*Oryza sativa Japonica* Group]	0.83	389	
		NP_001151517	LOC100285151 [*Zea mays*] > gi|195647360|gb|ACG43148.1| citrate transporter family protein [*Zea mays*] > gi|223948219|gb|ACN28193.1| unknown [*Zea mays*] > gi|223974939|gb|ACN31657.1| unknown [*Zea mays*] > gi|238009364|gb|ACR35717.1| unknown [*Zea mays*]	0.80	390	586
		ACG43196	citrate transporter family protein [*Zea mays*]	0.80	391	587
		ACL54556	unknown [*Zea mays*]	0.77	392	588
		BAK05230	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.78	393	589
		BAK06146	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.78	394	590
	650-671	XP_002460963	hypothetical protein SORBIDRAFT_02g038300 [*Sorghum bicolor*] > gi|241924340|gb|EER97484.1| hypothetical protein SORBIDRAFT_02g038300 [*Sorghum bicolor*]	1.00	395	591
		NP_001148467	LOC100282082 [*Zea mays*] > gi|195619570|gb|ACG31615.1| saccharopine dehydrogenase [*Zea mays*]	0.92	396	592
		EAZ04584	hypothetical protein OsI_26734 [*Oryza sativa Indica* Group]	0.79	397	
		BAJ97022	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.79	398	593
		EAZ40532	hypothetical protein OsJ_24988 [*Oryza sativa Japonica* Group]	0.73	399	
Predicted folded 24-nts-long seq 52499	2327-2350	NP_001169325	hypothetical protein LOC100383191 [*Zea mays*] > gi|224028683|gb|ACN33417.1| unknown [*Zea mays*]	1.00	400	594
		XP_002447125	hypothetical protein SORBIDRAFT_06g029090 [*Sorghum bicolor*] > gi|241938308|gb|EES11453.1| hypothetical protein SORBIDRAFT_06g029090 [*Sorghum bicolor*]	0.98	401	595
Predicted zma mir 50545	287-306	XP_002447878	hypothetical protein SORBIDRAFT_06g017360 [*Sorghum bicolor*] > gi|241939061|gb|EES12206.1| hypothetical protein SORBIDRAFT_06g017360 [*Sorghum bicolor*]	1.00	402	596
		NP_001151469	translocon Tic40 [*Zea mays*] > gi|219887501|gb|ACL54125.1| unknown [*Zea mays*]	0.90	403	597

TABLE 5-continued

Target Genes of miRNAs Associated with Increased NUE (Table 1)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		ACG42966	translocon Tic40 [*Zea mays*]	0.90	404	598
		NP_001149949	translocon Tic40 [*Zea mays*] > gi|195635683|gb|ACG37310.1| translocon Tic40 [*Zea mays*]	0.90	405	599
		NP_001052871	Os04g0439900 [*Oryza sativa Japonica* Group] > gi|113564442|dbj|BAF14785.1| Os04g0439900 [*Oryza sativa Japonica* Group] > gi|116309806|emb|CAH66845.1| H0525C06.8 [*Oryza* sativa *Indica* Group] > gi|215704350|dbj|BAG93784.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218194904|gb|EEC77331.1| hypothetical protein OsI_16005 [*Oryza sativa Indica* Group] > gi|222628923|gb|EEE61055.1| hypothetical protein OsJ_14912 [*Oryza sativa Japonica* Group]	0.81	406	600
		BAJ97578	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.78	407	601
	46-65	NP_001182915	hypothetical protein LOC100501201 [*Zea mays*] > gi|238008164|gb|ACR35117.1| unknown [*Zea mays*]	1.00	408	602
		ACN33347	unknown [*Zea mays*]	0.84	409	603
		NP_001150079	CID11 [*Zea mays*] > gi|195636508|gb|ACG37722.1| CID11 [*Zea mays*]	0.83	410	604
		XP_002444926	hypothetical protein SORBIDRAFT_07g001560 [*Sorghum bicolor*] > gi|241941276|gb|EES14421.1| hypothetical protein SORBIDRAFT_07g001560 [*Sorghum bicolor*]	0.78	411	605
		BAD33089	putative RNA-binding protein RBP37 [*Oryza sativa Japonica* Group] > gi|182375457|dbj|BAG24017.1| RNA-binding protein [*Oryza sativa Japonica* Group] > gi|215736921|dbj|BAG95850.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222639804|gb|EEE67936.1| hypothetical protein OsJ_25822 [*Oryza sativa Japonica* Group]	0.74	412	
		EEC82815	hypothetical protein OsI_27601 [*Oryza sativa Indica* Group]	0.72	413	
		BAJ96189	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.75	414	606
		XP_002518926	RNA-binding protein, putative [*Ricinus communis*] > gi|223541913|gb|EEF43459.1| RNA-binding protein, putative [*Ricinus communis*]	0.75	415	607
		XP_002272223	PREDICTED: hypothetical protein [*Vitis vinifera*] > gi|302143972|emb|CBI23077.3| unnamed protein product [*Vitis vinifera*]	0.75	416	608

TABLE 5-continued

Target Genes of miRNAs Associated with Increased NUE (Table 1)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
	605-624	NP_001142867	hypothetical protein LOC100275266 [*Zea mays*] > gi|195610696|gb|ACG27178.1| hypothetical protein [*Zea mays*]	1.00	417	609
		XP_002448750	hypothetical protein SORBIDRAFT_06g032540 [*Sorghum bicolor*] > gi|241939933|gb|EES13078.1| hypothetical protein SORBIDRAFT_06g032540 [*Sorghum bicolor*]	0.83	418	610
		NP_001143447	hypothetical protein LOC100276102 [*Zea mays*] > gi|195620654|gb|ACG32157.1| hypothetical protein [*Zea mays*]	0.78	419	611
		NP_001054225	Os04g0672300 [*Oryza sativa Japonica* Group] > gi|90265231|emb|CAH67766.1| H0322F07.3 [*Oryza* sativa *Indica* Group] > gi|113565796|dbj|BAF16139.1| Os04g0672300 [*Oryza sativa Japonica* Group] > gi|215715224|dbj|BAG94975.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.72	420	612
	360-379	NP_001043014	Os01g0358300 [*Oryza sativa Japonica* Group] > gi|53791615|dbj|BAD52962.1| unknown protein [*Oryza sativa Japonica* Group] > gi|113532545|dbj|BAF04928.1| Os01g0358300 [*Oryza sativa Japonica* Group] > gi|215765732|dbj|BAG87429.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218188197|gb|EEC70624.1| hypothetical protein OsI_01883 [*Oryza sativa Indica* Group] > gi|222618419|gb|EEE54551.1| hypothetical protein OsJ_01736 [*Oryza sativa Japonica* Group]	1.00	421	613
		ACF87799	unknown [*Zea mays*]	0.86	422	614
		ACN30638	unknown [*Zea mays*]	0.85	423	615
		BAJ94646	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.84	424	616
	557-576	XP_002455496	hypothetical protein SORBIDRAFT_03g011990 [*Sorghum bicolor*] > gi|241927471|gb|EES00616.1| hypothetical protein SORBIDRAFT_03g011990 [*Sorghum bicolor*]	1.00	425	617
		XP_002457709	hypothetical protein SORBIDRAFT_03g011980 [*Sorghum bicolor*] > gi|241929684|gb|EES02829.1| hypothetical protein SORBIDRAFT_03g011980 [*Sorghum bicolor*]	0.98	426	618
		ACN26409	unknown [*Zea mays*]	0.93	427	619
		ACN27987	unknown [*Zea mays*]	0.93	428	620
		NP_001152255	peroxidase 1 [*Zea mays*] > gi|195654333|gb|ACG46634.1| peroxidase 1 precursor [*Zea mays*]	0.93	429	621

TABLE 5-continued

Target Genes of miRNAs Associated with Increased NUE (Table 1)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		EAY73614	hypothetical protein OsI_01501 [*Oryza sativa Indica* Group]	0.81	430	
		NP_001042800	Os01g0294700 [*Oryza sativa Japonica* Group] > gi|9909174|dbj|BAB12033.1| putative peroxidase [*Oryza sativa Japonica* Group] > gi|55700889|tpe|CAH69254.1| TPA: class III peroxidase 11 precursor [*Oryza sativa Japonica* Group] > gi|113532331|dbj|BAF04714.1| Os01g0294700 [*Oryza sativa Japonica* Group] > gi|215697074|dbj|BAG91068.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215737508|dbj|BAG96638.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215740794|dbj|BAG96950.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.81	431	622
		EEE54389	hypothetical protein OsJ_01407 [*Oryza sativa Japonica* Group]	0.76	432	
	517-536	ACN27987	unknown [*Zea mays*]	1.00	433	623
		NP_001152255	peroxidase 1 [*Zea mays*] > gi|195654333|gb|ACG46634.1| peroxidase 1 precursor [*Zea mays*]	1.00	434	624
		ACN26409	unknown [*Zea mays*]	0.94	435	625
		XP_002457709	hypothetical protein SORBIDRAFT_03g011980 [*Sorghum bicolor*] > gi|241929684|gb|EES02829.1| hypothetical protein SORBIDRAFT_03g011980 [*Sorghum bicolor*]	0.93	436	626
		XP_002455496	hypothetical protein SORBIDRAFT_03g011990 [*Sorghum bicolor*] > gi|241927471|gb|EES00616.1| hypothetical protein SORBIDRAFT_03g011990 [*Sorghum bicolor*]	0.93	437	627
		EAY73614	hypothetical protein OsI_01501 [*Oryza sativa Indica* Group]	0.81	438	
		NP_001042800	Os01g0294700 [*Oryza sativa Japonica* Group] > gi|9909174|dbj|BAB12033.1| putative peroxidase [*Oryza sativa Japonica* Group] > gi|55700889|tpe|CAH69254.1| TPA: class III peroxidase 11 precursor [*Oryza sativa Japonica* Group] > gi|113532331|dbj|BAF04714.1| Os01g0294700 [*Oryza sativa Japonica* Group] > gi|215697074|dbj|BAG91068.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.81	439	628

TABLE 5-continued

Target Genes of miRNAs Associated with Increased NUE (Table 1)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			> gi|215737508|dbj|BAG96638.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215740794|dbj|BAG96950.1| unnamed protein product [*Oryza sativa Japonica* Group]			
		EEE54389	hypothetical protein OsJ_01407 [*Oryza sativa Japonica* Group]	0.76	440	
	286-305	ACG31680	pepsin A [*Zea mays*]	1.00	441	629
		NP_001141522	hypothetical protein LOC100273634 [*Zea mays*] > gi|194704920|gb|ACF86544.1| unknown [*Zea mays*] > gi|223949445|gb|ACN28806.1| unknown [*Zea mays*]	0.99	442	630
		ACL54367	unknown [*Zea mays*]	0.99	443	631
		NP_001132197	hypothetical protein LOC100193625 [*Zea mays*] > gi|194693730|gb|ACF80949.1| unknown [*Zea mays*] > gi|195605492|gb|ACG24576.1| pepsin A [*Zea mays*]	0.89	444	632
		NP_001048134	Os02g0751100 [*Oryza sativa Japonica* Group] > gi|46390211|dbj|BAD15642.1| aspartyl protease-like [*Oryza sativa Japonica* Group] > gi|113537665|dbj|BAF10048.1| Os02g0751100 [*Oryza sativa Japonica* Group] > gi|222623681|gb|EEE57813.1| hypothetical protein OsJ_08401 [*Oryza sativa Japonica* Group]	0.80	445	633
		EEC74016	hypothetical protein OsI_08957 [*Oryza sativa Indica* Group]	0.79	446	
		ACN27411	unknown [*Zea mays*]	0.77	447	634
		BAK05106	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.75	448	635
	309-328	NP_001143133	hypothetical protein LOC100275611 [*Zea mays*] > gi|195614826|gb|ACG29243.1| hypothetical protein [*Zea mays*]	1.00	449	636
		ACF83002	unknown [*Zea mays*]	0.99	450	637
		BAJ87435	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.72	451	638
	46-65	XP_002444926	hypothetical protein SORBIDRAFT_07g001560 [*Sorghum bicolor*] > gi|241941276|gb|EES14421.1| hypothetical protein SORBIDRAFT_07g001560 [*Sorghum bicolor*]	1.00	452	639
		ACN33347	unknown [*Zea mays*]	0.85	453	640
		NP_001182915	hypothetical protein LOC100501201 [*Zea mays*] > gi|238008164|gb|ACR35117.1| unknown [*Zea mays*]	0.87	454	641
		NP_001150079	CID11 [*Zea mays*] > gi|195636508|gb|ACG37722.1| CID11 [*Zea mays*]	0.86	455	642
		BAD33089	putative RNA-binding protein RBP37 [*Oryza sativa Japonica* Group] > gi|182375457|dbj|BAG24017.1|	0.75	456	

TABLE 5-continued

Target Genes of miRNAs Associated with Increased NUE (Table 1)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			RNA-binding protein [*Oryza sativa Japonica* Group] > gi|215736921|dbj|BAG95850.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222639804|gb|EEE67936.1| hypothetical protein OsJ_25822 [*Oryza sativa Japonica* Group]			
		EEC82815	hypothetical protein OsI_27601 [*Oryza sativa Indica* Group]	0.72	457	
	40563	NP_001059821	Os07g0524100 [*Oryza sativa Japonica* Group] > gi|75118816|sp|Q69SA9.1| PDI54_ORYSJ RecName: Full = Protein disulfide isomerase-like 5-4; Short = OsPDIL5-4; AltName: Full = Protein disulfide isomerase-like 8-1; Short = OsPDIL8-1; Flags: Precursor > gi|50508559|dbj|BAD30858.1| thioredoxin family-like protein [*Oryza sativa Japonica* Group] > gi|113611357|dbj|BAF21735.1| Os07g0524100 [*Oryza sativa Japonica* Group] > gi|215704615|dbj|BAG94243.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218199742|gb|EEC82169.1| hypothetical protein OsI_26259 [*Oryza sativa Indica* Group] > gi|222637167|gb|EEE67299.1| hypothetical protein OsJ_24505 [*Oryza sativa Japonica* Group]	1.00	458	643
		BAJ86285	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.93	459	644
		CBG91903	putative PDI-like protein [*Triticum aestivum*] > gi|299469398|emb|CBG91917.1| putative PDI-like protein [*Triticum aestivum*]	0.93	460	
		ACG39185	PDIL5-4-*Zea mays* protein disulfide isomerase	0.91	461	645
		NP_001105762	protein disulfide isomerase12 [*Zea mays*] > gi|59861281|gb|AAX09970.1| protein disulfide isomerase [*Zea mays*]	0.91	462	646
		ACN34146	unknown [*Zea mays*]	0.91	463	647
		XP_002522864	thioredoxin domain-containing protein, putative [*Ricinus communis*] > gi|223537948|gb|EEF39562.1| thioredoxin domain-containing protein, putative [*Ricinus communis*]	0.76	464	648
		XP_002281649	PREDICTED: hypothetical protein [*Vitis vinifera*] > gi|297735969|emb|CBI23943.3| unnamed protein product [*Vitis vinifera*]	0.74	465	649

TABLE 5-continued

Target Genes of miRNAs Associated with Increased NUE (Table 1)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		XP_002319814	predicted protein [*Populus trichocarpa*] > gi|222858190|gb|EEE95737.1| predicted protein [*Populus trichocarpa*]	0.74	466	650
		XP_002317580	predicted protein [*Populus trichocarpa*] > gi|222860645|gb|EEE98192.1| predicted protein [*Populus trichocarpa*]	0.74	467	651
	301-320	ACF87799	unknown [*Zea mays*]	1.00	468	652
		ACN30638	unknown [*Zea mays*]	0.97	469	653
		NP_001043014	Os01g0358300 [*Oryza sativa Japonica* Group] > gi|53791615|dbj|BAD52962.1| unknown protein [*Oryza sativa Japonica* Group] > gi|113532545|dbj|BAF04928.1| Os01g0358300 [*Oryza sativa Japonica* Group] > gi|215765732|dbj|BAG87429.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218188197|gb|EEC70624.1| hypothetical protein OsI_01883 [*Oryza sativa Indica* Group] > gi|222618419|gb|EEE54551.1| hypothetical protein OsJ_01736 [*Oryza sativa Japonica* Group]	0.87	470	654
		BAJ94646	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.83	471	655
Predicted zma mir 48350	40752	ACF86440	unknown [*Zea mays*]	1.00	472	656
	22-43	ABF67946	putative Opie4 pol protein [*Zea mays*]	1.00	473	
		AAC49502	Pol [*Zea mays*]	0.97	474	657
		ABF67947	Opie2 pol protein [*Zea mays*]	0.96	475	
		ABF67934	Opie3 pol polyprotein [*Zea mays*]	0.96	476	
		AAL35396	Opie2a pol [*Zea mays*] > gi|168251075|gb|ACA21858.1| Opie2a pol protein [*Zea mays*]	0.92	477	
		ABF67921	Ji1 putative pol protein [*Zea mays*]	0.79	478	
		AAD20307	copia-type pol polyprotein [*Zea mays*]	0.79	479	
Predicted zma mir 49162	810-831	XP_002455047	hypothetical protein SORBIDRAFT_03g003530 [*Sorghum bicolor*] > gi|241927022|gb|EES00167.1| hypothetical protein SORBIDRAFT_03g003530 [*Sorghum bicolor*]	1.00	480	658
		AAK51797	small heat shock protein HSP17.8 [*Triticum aestivum*]	0.83	481	659
		BAJ86365	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.82	482	660
		NP_001105954	17.8 kDa class II heat shock protein [*Zea mays*] > gi|123553|sp|P24632.1|HSP22_MAIZE RecName: Full = 17.8 kDa class II heat shock protein > gi|22337|emb|CAA38012.1| 18 kDa heat shock protein [*Zea mays*]	0.87	483	661

TABLE 5-continued

Target Genes of miRNAs Associated with Increased NUE (Table 1)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			> gi|238009918|gb|ACR35994.1| unknown [*Zea mays*] > gi|238015198|gb|ACR38634.1| unknown [*Zea mays*]			
		CAI96500	17.6 kDa heat-shock protein [*Triticum turgidum* subsp. *dicoccon*]	0.83	484	662
		BAK07165	predicted protein [*Hordeum* *vulgare* subsp. *vulgare*]	0.81	485	663
		CAI96499	17.5 kDa heat-shock protein [*Triticum turgidum* subsp. *dicoccoides*]	0.81	486	664
		CAI96501	17.6 kDa heat-shock protein [*Triticum turgidum* subsp. *durum*]	0.82	487	665
		NP_001148454	17.5 kDa class II heat shock protein [*Zea mays*] > gi|195619384|gb|ACG31522.1| 17.5 kDa class II heat shock protein [*Zea mays*]	0.87	488	666
		BAK05681	predicted protein [*Hordeum* *vulgare* subsp. *vulgare*]	0.80	489	667
Predicted zma mir 48877	597-618	XP_002456299	hypothetical protein SORBIDRAFT_03g033710 [*Sorghum bicolor*] > gi|241928274|gb|EES01419.1| hypothetical protein SORBIDRAFT_03g033710 [*Sorghum bicolor*]	1.00	490	668
		ACF79056	unknown [*Zea mays*] > gi|194693496|gb|ACF80832.1| unknown [*Zea mays*] > gi|195626284|gb|ACG34972.1| GTP-binding protein [*Zea mays*] > gi|223946703|gb|ACN27435.1| unknown [*Zea mays*]	0.92	491	669
		NP_001140242	hypothetical protein LOC100272283 [*Zea mays*] > gi|194698666|gb|ACF8417.1| unknown [*Zea mays*]	0.92	492	670
		NP_001044154	Os01g0732200 [*Oryza sativa* *Japonica* Group] > gi|57899709|dbj|BAD87429.1| putative GTP-binding protein [*Oryza sativa* *Japonica* Group] > gi|113533685|dbj|BAF06068.1| Os01g0732200 [*Oryza* *sativa Japonica* Group] > gi|215695283|dbj|BAG90474.1| unnamed protein product [*Oryza sativa* *Japonica* Group]	0.84	493	671
		EEC71435	hypothetical protein OsI_03633 [*Oryza sativa* *Indica* Group] > gi|222619209|gb|EEE5541.1| hypothetical protein OsJ_03357 [*Oryza sativa* *Japonica* Group]	0.84	494	
	218-239	XP_002463058	hypothetical protein SORBIDRAFT_02g036900 [*Sorghum bicolor*] > gi|241926435|gb|EER99579.1| hypothetical protein SORBIDRAFT_02g036900 [*Sorghum bicolor*]	1.00	495	672
		NP_001142066	hypothetical protein LOC100274223 [*Zea mays*] > gi|194706978|gb|ACF87573.1| unknown [*Zea mays*]	0.90	496	673

TABLE 5-continued

Target Genes of miRNAs Associated with Increased NUE (Table 1)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		BAJ95349	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326526013|dbj|BAJ93183.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.75	497	674
		EAZ40364	hypothetical protein OsJ_24810 [*Oryza sativa Japonica* Group]	0.73	498	
		EAZ04406	hypothetical protein OsI_26550 [*Oryza sativa Indica* Group]	0.73	499	
Predicted folded 24-nts-long seq 52057	63-86	AAD11615	prpol [*Zea mays*]	1.00	500	675
		AAL76007	prpol [*Zea mays*]	0.97	501	
	907-930	AAD11616	prpol [*Zea mays*]	1.00	502	676
Predicted folded 24-nts-long seq 52633	387-410	XP_002445682	hypothetical protein SORBIDRAFT_07g024170 [*Sorghum bicolor*] > gi|241942032|gb|EES15177.1| hypothetical protein SORBIDRAFT_07g024170 [*Sorghum bicolor*]	1.00	503	677
		ACF83553	unknown [*Zea mays*] > gi|195646380|gb|ACG42658.1| glutathione S-transferase, N-terminal domain containing protein [*Zea mays*]	0.90	504	678
		ACN26529	unknown [*Zea mays*]	0.89	505	679
Predicted zma mir 48922	450-470	NP_001141971	hypothetical protein LOC100274121 [*Zea mays*] > gi|194706630|gb|ACF87399.1| unknown [*Zea mays*]	1.00	506	680
		XP_002455881	hypothetical protein SORBIDRAFT_03g026750 [*Sorghum bicolor*] > gi|241927856|gb|EES01001.1| hypothetical protein SORBIDRAFT_03g026750 [*Sorghum bicolor*]	0.79	507	681
Predicted zma mir 50077	1046-1067	XP_002465053	hypothetical protein SORBIDRAFT_01g031330 [*Sorghum bicolor*] > gi|241918907|gb|EER92051.1| hypothetical protein SORBIDRAFT_01g031330 [*Sorghum bicolor*]	1.00	508	682
		NP_001137129	hypothetical protein LOC100217311 [*Zea mays*] > gi|194698486|gb|ACF83327.1| unknown [*Zea mays*]	0.90	509	683
		NP_001149312	fas-associated factor 1-like protein [*Zea mays*] > gi|195626306|gb|ACG34983.1| fas-associated factor 1-like protein [*Zea mays*] > gi|223975789|gb|ACN32082.1| unknown [*Zea mays*]	0.93	510	684
		BAJ89712	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326495414|dbj|BAJ85803.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.83	511	685
		AAG13433	unknown protein [*Oryza sativa Japonica* Group] > gi|31433109|gb|AAP54662.1|	0.85	512	686

TABLE 5-continued

Target Genes of miRNAs Associated with Increased NUE (Table 1)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			UBX domain containing protein, expressed [*Oryza sativa Japonica* Group] > gi|215678662|dbj|BAG92317.1| unnamed protein product [*Oryza sativa Japonica* Group]			
		EAY79232	hypothetical protein OsI_34349 [*Oryza sativa Indica* Group]	0.85	513	
		EAZ16707	hypothetical protein OsJ_32183 [*Oryza sativa Japonica* Group]	0.81	514	

Table 5: Provided are the target Genes of miRNAs Associated with Increased NUE (Table 1) along with their GenBank Accession numbers and sequence identifiers (SEQ ID NO:).
"bind" = binding;
"pos" = position;
"hom" = homologue;
"p.p." = polypeptide;
"p.n." = polynucleotide.

TABLE 6

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
Predicted zma mir 50318	743-763	NP_001148146	terpene synthase 7 [*Zea mays*] > gi|195616112|gb|ACG29886.1| terpene synthase 7 [*Zea mays*]	1.00	687	1392
		ACL54589	unknown [*Zea mays*]	0.99	688	1393
		XP_002447434	hypothetical protein SORBIDRAFT_06g001020 [*Sorghum bicolor*] > gi|241938617|gb|EES11762.1| hypothetical protein SORBIDRAFT_06g001020 [*Sorghum bicolor*]	0.71	689	1394
	776-796	XP_002455470	hypothetical protein SORBIDRAFT_03g011420 [*Sorghum bicolor*] > gi|241927445|gb|EES00590.1| hypothetical protein SORBIDRAFT_03g011420 [*Sorghum bicolor*]	1.00	690	1395
		NP_001151624	cyclin-like F-box [*Zea mays*] > gi|195648178|gb|ACG43557.1| cyclin-like F-box [*Zea mays*]	0.90	691	1396
		BAJ88045	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326521874|dbj|BAK04065.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.79	692	1397
		NP_001042756	Os01g0281000 [*Oryza sativa Japonica* Group] > gi|6498442|dbj|BAA87845.1| unknown protein [*Oryza sativa Japonica* Group] > gi|11041564|dbj|BAB00648.2| unnamed protein product [*Oryza sativa Japonica* Group] > gi|11138071|dbj|BAB17744.1| OSJNBa0036E02.18 [*Oryza sativa Japonica* Group] > gi|13873014|dbj|BAB44118.1|	0.81	693	1398

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			unknown protein [*Oryza sativa Japonica* Group] > gi|113532287|dbj|BAF04670.1| Os01g0281000 [*Oryza sativa Japonica* Group] > gi|215694300|dbj|BAG89293.1| unnamed protein product [*Oryza sativa Japonica* Group]			
		EEE54342	hypothetical protein OsJ_01321 [*Oryza sativa Japonica* Group]	0.75	694	
		EEC70414	hypothetical protein OsI_01411 [*Oryza sativa Indica* Group]	0.75	695	
	2058-2078	XP_002468633	hypothetical protein SORBIDRAFT_01g049370 [*Sorghum bicolor*] > gi|241922487|gb|EER95631.1| hypothetical protein SORBIDRAFT_01g049370 [*Sorghum bicolor*]	1.00	696	1399
		NP_001130361	hypothetical protein LOC100191456 [*Zea mays*] > gi|194688936|gb|ACF78552.1| unknown [*Zea mays*] > gi|194707734|gb|ACF87951.1| unknown [*Zea mays*]	0.98	697	1400
		NP_001167830	hypothetical protein LOC100381530 [*Zea mays*] > gi|223944309|gb|ACN26238.1| unknown [*Zea mays*]	0.96	698	1401
		NP_001046725	Os02g0332200 [*Oryza sativa Japonica* Group] > gi|46390985|dbj|BAD16520.1| putative cytosolic chaperonin delta-subunit [*Oryza sativa Japonica* Group] > gi|113536256|dbj|BAF08639.1| Os02g0332200 [*Oryza sativa Japonica* Group] > gi|215695341|dbj|BAG90532.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222636848|gb|EEE66980.1| hypothetical protein OsJ_23870 [*Oryza sativa Japonica* Group]	0.95	699	1402
		EAZ06856	hypothetical protein OsI_29091 [*Oryza sativa Indica* Group]	0.95	700	
		BAJ97289	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.92	701	1403
		NP_001065054	Os10g0514600 [*Oryza sativa Japonica* Group] > gi|10140686|gb|AAG13521.1| AC068924_26 putative cytosolic chaperonin, delta-subunit [*Oryza sativa Japonica* Group] > gi|31433047|gb|AAP54607.1| T-complex protein 1, delta subunit, putative, expressed [*Oryza sativa Japonica* Group] > gi|113639663|dbj|BAF26968.1| Os10g0514600 [*Oryza sativa Japonica* Group] > gi|215687328|dbj|BAG91872.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.88	702	1404

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		XP_002322076	predicted protein [*Populus trichocarpa*] > gi|222869072|gb|EEF06203.1| predicted protein [*Populus trichocarpa*]	0.81	703	1405
		XP_002317895	predicted protein [*Populus trichocarpa*] > gi|222858568|gb|EEE96115.1| predicted protein [*Populus trichocarpa*]	0.80	704	1406
		CAN70636	hypothetical protein VITISV_008621 [*Vitis vinifera*]	0.82	705	1407
	554-574	XP_002465983	hypothetical protein SORBIDRAFT_01g049510 [*Sorghum bicolor*] > gi|241919837|gb|EER92981.1| hypothetical protein SORBIDRAFT_01g049510 [*Sorghum bicolor*]	1.00	706	1408
		NP_001149716	fusca homolog [*Zea mays*] > gi|195629716|gb|ACG36499.1| COP9 signalosome complex subunit 1 [*Zea mays*]	0.95	707	1409
		NP_00148760	Os03g0116500 [*Oryza sativa Japonica* Group] > gi|108705858|gb|ABF93653.1| COP9 signalosome complex subunit 1, putative, expressed [*Oryza sativa Japonica* Group] > gi|113547231|dbj|BAF10674.1| Os03g0116500 [*Oryza sativa Japonica* Group] > gi|125542143|gb|EAY88282.1| hypothetical protein OsI_09737 [*Oryza sativa Indica* Group] > gi|125584695|gb|EAZ25359.1| hypothetical protein OsJ_09174 [*Oryza sativa Japonica* Group] > gi|215678827|dbj|BAG95264.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.89	708	1410
		AAF40112	constitutive photomorphogenic 11 [*Oryza sativa Indica* Group]	0.88	709	1411
		AAG17476	rCOP11 protein [*Oryza sativa Indica* Group]	0.88	710	1412
		BAJ99160	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.84	711	1413
		BAK01545	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.78	712	1414
		XP_002275895	PREDICTED: hypothetical protein [*Vitis vinifera*] > gi|296089065|emb|CBI38768.3| unnamed protein product [*Vitis vinifera*]	0.72	713	1415
		CAN74681	hypothetical protein VITISV_025856 [*Vitis vinifera*]	0.72	714	
	372-392	XP_002448372	hypothetical protein SORBIDRAFT_06g026160 [*Sorghum bicolor*] > gi|241939555|gb|EES12700.1| hypothetical protein SORBIDRAFT_06g026160 [*Sorghum bicolor*]	1.00	715	1416
		ADZ96243	ACC synthase 1 [*Saccharum* hybrid cultivar SP80-3280]	0.92	716	1417
		AAR25558	acc synthase [*Zea mays*]	0.92	717	1418
		AAR25559	acc synthase [*Zea mays*]	0.91	718	1419

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		NP_001146401	1-aminocyclopropane-1-carboxylate synthase7 [*Zea mays*] > gi|219886697|gb|ACL53723.1| unknown [*Zea mays*]	0.91	719	1420
		ACN31344	unknown [*Zea mays*]	0.90	720	1421
		BAJ95898	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.81	721	1422
		NP_001053637	Os04g0578000 [*Oryza sativa Japonica* Group] > gi|32488497|emb|CAE03249.1| OSJNBa0011J08.4 [*Oryza sativa Japonica* Group] > gi|113565208|dbj|BAF15551.1| Os04g0578000 [*Oryza sativa Japonica* Group] > gi|215693849|dbj|BAG89048.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.80	722	1423
		CAH66732	H0404F02.8 [*Oryza sativa Indica* Group] > gi|125549433|gb|EAY95255.1| hypothetical protein OsI_17075 [*Oryza sativa Indica* Group]	0.80	723	1424
		AAB18416	ACC synthase [*Triticum aestivum*]	0.80	724	1425
	1204-1224	ACN26771	unknown [*Zea mays*]	1.00	725	1426
		ACG31388	F-box domain containing protein [*Zea mays*]	1.00	726	1427
		ACG45892	F-box domain containing protein [*Zea mays*]	1.00	727	1428
		ACG25717	F-box domain containing protein [*Zea mays*]	0.99	728	1429
		NP_001152119	F-box domain containing protein [*Zea mays*] > gi|195652827|gb|ACG45881.1| F-box domain containing protein [*Zea mays*]	0.96	729	1430
		XP_002467684	hypothetical protein SORBIDRAFT_01g032310 [*Sorghum bicolor*] > gi|241921538|gb|EER94682.1| hypothetical protein SORBIDRAFT_01g032310 [*Sorghum bicolor*]	0.89	730	1431
		EAY90508	hypothetical protein OsI_12108 [*Oryza sativa Indica* Group]	0.82	731	
		NP_001050391	Os03g0423000 [*Oryza sativa Japonica* Group] > gi|30089733|gb|AAP20837.1| expressed protein [*Oryza sativa Japonica* Group] > gi|108708889|gb|ABF96684.1| F-box domain containing protein, expressed [*Oryza sativa Japonica* Group] > gi|113548862|dbj|BAF12305.1| Os03g0423000 [*Oryza sativa Japonica* Group] > gi|125586708|gb|EAZ27372.1| hypothetical protein OsJ_11320 [*Oryza sativa Japonica* Group] > gi|215697584|dbj|BAG91578.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.82	732	1432

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
	1019-1039	XP_002464111	hypothetical protein SORBIDRAFT_01g012470 [*Sorghum bicolor*] > gi|241917965|gb|EER91109.1| hypothetical protein SORBIDRAFT_01g012470 [*Sorghum bicolor*]	1.00	733	1433
		NP_001140844	hypothetical protein LOC100272920 [*Zea mays*] > gi|194701412|gb|ACF84790.1| unknown [*Zea mays*] > gi|223943945|gb|ACN26056.1| unknown [*Zea mays*]	0.97	734	1434
		NP_001149791	transmembrane protein 56 [*Zea mays*] > gi|195634693|gb|ACG36815.1| transmembrane protein 56 [*Zea mays*]	0.94	735	1435
		NP_001050848	Os03g0666700 [*Oryza sativa Japonica* Group] > gi|40538924|gb|AAR87181.1| expressed protein [*Oryza sativa Japonica* Group] > gi|108710279|gb|ABF98074.1| expressed protein [*Oryza sativa Japonica* Group] > gi|113549319|dbj|BAF12762.1| Os03g0666700 [*Oryza sativa Japonica* Group] > gi|215692429|dbj|BAG87849.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215692647|dbj|BAG88067.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215716974|dbj|BAG95337.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.90	736	1436
		BAJ94278	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326505624|dbj|BAJ95483.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326513826|dbj|BAJ87931.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326518414|dbj|BAJ88236.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.91	737	1437
		ACF84098	unknown [*Zea mays*]	0.93	738	1438
		EEE53990	hypothetical protein OsJ_00621 [*Oryza sativa Japonica* Group]	0.90	739	
	1917-1937	XP_002453927	hypothetical protein SORBIDRAFT_04g021570 [*Sorghum bicolor*] > gi|241933758|gb|EES06903.1| hypothetical protein SORBIDRAFT_04g021570 [*Sorghum bicolor*]	1.00	740	1439
		NP_001105849	putative glycosyltransferase [*Zea mays*] > gi|84794314|emb|CAJ57382.1| putative glycosyltransferase [*Zea mays*]	0.96	741	1440
		BAK03947	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.86	742	1441

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		NP_001047014	Os02g0529600 [*Oryza sativa Japonica* Group] > gi|49388322|dbj|BAD25434.1| putative galactomannan galactosyltransferase [*Oryza sativa Japonica* Group] > gi|113536545|dbj|BAF08928.1| Os02g0529600 [*Oryza sativa Japonica* Group] > gi|215704838|dbj|BAG94866.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218190881|gb|EEC73308.1| hypothetical protein OsI_07488 [*Oryza sativa Indica* Group] > gi|222622984|gb|EEE57116.1| hypothetical protein OsJ_06989 [*Oryza sativa Japonica* Group]	0.86	743	1442
	1590-1610	NP_001131407	hypothetical protein LOC100192736 [*Zea mays*] > gi|194691442|gb|ACF79805.1 unknown [*Zea mays*]	1.00	744	1443
		NP_001141840	hypothetical protein LOC100273982 [*Zea mays*] > gi|194706136|gb|ACF87152.1| unknown [*Zea mays*]	0.78	745	1444
	510-530	XP_002460574	hypothetical protein SORBIDRAFT_02g031070 [*Sorghum bicolor*] > gi|241923951|gb|EER97095.1| hypothetical protein SORBIDRAFT_02g031070 [*Sorghum bicolor*]	1.00	746	1445
		NP_001151754	collagen, type IV, alpha 5 [*Zea mays*] > gi|195649521|gb|ACG44228.1 collagen, type IV, alpha 5 [*Zea mays*]	0.87	747	1446
	876-896	XP_002437709	hypothetical protein SORBIDRAFT_10g001120 [*Sorghum bicolor*] > gi|241915932|gb|EER89076.1| hypothetical protein SORBIDRAFT_10g001120 [*Sorghum bicolor*]	1.00	748	1447
		ACN34709	unknown [*Zea mays*]	0.99	749	1448
		ACN28096	unknown [*Zea mays*] > gi|223948483|gb|ACN28325.1| unknown [*Zea mays*]	0.99	750	1449
		NP_001056601	Os06g0114000 [*Oryza sativa Japonica* Group] > gi|7248401|dbj|BAA92724.1| putative chaperonin 60 beta precursor [*Oryza sativa Japonica* Group] > gi|113594641|dbj|BAF18515.1| Os06g0114000 [*Oryza sativa Japonica* Group] > gi|164375533|gb|ABY52934.1| RuBisCo subunit binding-protein beta subunit [*Oryza sativa Japonica* Group] > gi|215715264|dbj|BAG95015.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.97	751	1450
		EEE64974	hypothetical protein OsJ_19883 [*Oryza sativa Japonica* Group]	0.93	752	

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		NP_001045601	Os02g0102900 [*Oryza sativa Japonica* Group] > gi|41052909|dbj|BAD07821.1| putative RuBisCO subunit binding-protein beta subunit, chloroplast precursor [*Oryza sativa Japonica* Group] > gi|113535132|dbj|BAF07515.1| Os02g0102900 [*Oryza sativa Japonica* Group] > gi|218189867|gb|EEC72294.1| hypothetical protein OsI_05469 [*Oryza sativa Indica* Group] > gi|222621999|gb|EEE56131.1| hypothetical protein OsJ_05004 [*Oryza sativa Japonica* Group] > gi|313575775|gb|ADR66967.1| 60 kDa chaperonin beta subunit [*Oryza sativa Japonica* Group]	0.87	753	1451
		XP_002285746	PREDICTED: hypothetical protein [*Vitis vinifera*] > gi|297746501|emb|CBI16557.3| unnamed protein product [*Vitis vinifera*]	0.88	754	1452
		XP_002303983	predicted protein [*Populus trichocarpa*] > gi|222841415|gb|EEE78962.1| predicted protein [*Populus trichocarpa*]	0.87	755	1453
		XP_002523404	rubisco subunit binding-protein beta subunit, rubb, putative [*Ricinus communis*] > gi|223537354|gb|EEF38983.1| rubisco subunit binding-protein beta subunit, rubb, putative [*Ricinus communis*]	0.87	756	1454
		XP_002894506	CPN60B [*Arabidopsis lyrata* subsp. *lyrata*] > gi|297340348|gb|EFH70765.1| CPN60B [*Arabidopsis lyrata* subsp. *lyrata*]	0.87	757	1455
	640-660	XP_002456142	hypothetical protein SORBIDRAFT_03g031180 [*Sorghum bicolor*] > gi|241928117|gb|EES01262.1| hypothetical protein SORBIDRAFT_03g031180 [*Sorghum bicolor*]	1.00	758	1456
		NP_001148838	LOC100282456 [*Zea mays*] > gi|195622536|gb|ACG33098.1| THAP domain-containing protein 4 [*Zea mays*]	0.94	759	1457
		EEC71270	hypothetical protein OsI_03268 [*Oryza sativa Indica* Group]	0.87	760	
		CBH32601	conserved hypothetical protein, expressed [*Triticum aestivum*]	0.83	761	1458
		NP_001043867	Os01g0679600 [*Oryza sativa Japonica* Group] > gi|56202146|dbj|BAD73479.1| unknown protein [*Oryza sativa Japonica* Group] > gi|255673554|dbj|BAF05781.2| Os01g0679600 [*Oryza sativa Japonica* Group]	0.80	762	1459
		BAJ94714	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.78	763	1460

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)						
Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		BAD73478	unknown protein [*Oryza sativa Japonica* Group] > gi|215693000|dbj|BAG88420.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222619045|gb|EEE55177.1| hypothetical protein OsJ_03010 [*Oryza sativa Japonica* Group]	0.78	764	1461
	1204-1224	ACR38511	unknown [*Zea mays*]	1.00	765	1462
		ACG45146	hypothetical protein [*Zea mays*]	1.00	766	1463
		XP_002440220	hypothetical protein SORBIDRAFT_09g027950 [*Sorghum bicolor*] > gi|241945505|gb|EES18650.1| hypothetical protein SORBIDRAFT_09g027950 [*Sorghum bicolor*]	0.71	767	1464
		NP_001144829	hypothetical protein LOC100277913 [*Zea mays*] > gi|195647628|gb|ACG43282.1| hypothetical protein [*Zea mays*]	0.71	768	1465
	916-936	NP_001143951	hypothetical protein LOC100276764 [*Zea mays*] > gi|195631554|gb|ACG36672.1| hypothetical protein [*Zea mays*]	1.00	769	1466
		NP_001169519	hypothetical protein LOC100383393 [*Zea mays*] > gi|224029837|gb|ACN33994.1| unknown [*Zea mays*]	0.81	770	1467
	1178-1198	XP_002468109	hypothetical protein SORBIDRAFT_01g039740 [*Sorghum bicolor*] > gi|241921963|gb|EER95107.1| hypothetical protein SORBIDRAFT_01g039740 [*Sorghum bicolor*]	1.00	771	1468
		NP_001131833	hypothetical protein LOC100193208 [*Zea mays*] > gi|194688576|gb|ACF78372.1| unknown [*Zea mays*] > gi|195627610|gb|ACG35635.1| protein binding protein [*Zea mays*]	0.95	772	1469
		ACL53375	unknown [*Zea mays*]	0.94	773	1470
		NP_001147045	protein binding protein [*Zea mays*] > gi|195606842|gb|ACG25251.1| protein binding protein [*Zea mays*]	0.93	774	1471
		ABF95226	zinc finger family protein, putative, expressed [*Oryza sativa Japonica* Group] > gi|108707432|gb|ABF95227.1| zinc finger family protein, putative, expressed [*Oryza sativa Japonica* Group] > gi|218192524|gb|EEC74951.1| hypothetical protein OsI_10935 [*Oryza sativa Indica* Group] > gi|222624650|gb|EEE58782.1| hypothetical protein OsJ_10309 [*Oryza sativa Japonica* Group]	0.86	775	
		BAJ90599	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.81	776	1472

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		ADX86798	zinc-finger transcription factor [*Triticum aestivum*]	0.79	777	1473
		ACN35095	unknown [*Zea mays*]	0.70	778	1474
		NP_001049696	Os03g0272300 [*Oryza sativa Japonica* Group] > gi|108707430|gb|ABF95225.1| zinc finger family protein, putative, expressed [*Oryza sativa Japonica* Group] > gi|215765669|dbj|BAG87366.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|255674397|dbj|BAF11610.2| Os03g0272300 [*Oryza sativa Japonica* Group]	0.70	779	1475
	1068-1088	NP_001144727	hypothetical protein LOC100277769 [*Zea mays*] > gi|195646260|gb|ACG42598.1| hypothetical protein [*Zea mays*]	1.00	780	1476
		NP_001141817	hypothetical protein LOC100273956 [*Zea mays*] > gi|194706038|gb|ACF87103.1| unknown [*Zea mays*]	0.99	781	1477
		NP_001170260	hypothetical protein LOC100384217 [*Zea mays*] > gi|224034675|gb|ACN36413.1| unknown [*Zea mays*]	0.96	782	1478
		NP_001170241	hypothetical protein LOC100384195 [*Zea mays*] > gi|224034547|gb|ACN36349.1| unknown [*Zea mays*]	0.71	783	1479
	573-593	XP_002454448	hypothetical protein SORBIDRAFT_04g031260 [*Sorghum bicolor*] > gi|241934279|gb|EES07424.1| hypothetical protein SORBIDRAFT_04g031260 [*Sorghum bicolor*]	1.00	784	1480
		NP_001149829	LOC100283456 [*Zea mays*] > gi|195634913|gb|ACG36925.1| acetylornithine deacetylase [*Zea mays*]	0.97	785	1481
		EEC73818	hypothetical protein OsI_08537 [*Oryza sativa Indica* Group]	0.85	786	
		NP_001047794	Os02g0690800 [*Oryza sativa Japonica* Group] > gi|41053258|dbj|BAD07684.1| putative silverleaf whitefly-induced protein 1 [*Oryza sativa Japonica* Group] > gi|113537325|dbj|BAF09708.1| Os02g0690800 [*Oryza sativa Japonica* Group] > gi|215715374|dbj|BAG95125.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215740943|dbj|BAG97438.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222623478|gb|EEE57610.1| hypothetical protein OsJ_07995 [*Oryza sativa Japonica* Group]	0.85	787	1482
	1820-1840	XP_002456060	hypothetical protein SORBIDRAFT_03g029660 [*Sorghum bicolor*] > gi|241928035|gb|EES01180.1| hypothetical protein	1.00	788	1483

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			SORBIDRAFT_03g029660 [*Sorghum bicolor*]			
		ACG31412	wax synthase isoform 3 [*Zea mays*]	0.86	789	1484
		NP_001150127	wax synthase [*Zea mays*] > gi|195636988|gb|ACG37962.1| wax synthase isoform 3 [*Zea mays*]	0.86	790	1485
		NP_001043733	Os01g0651500 [*Oryza sativa Japonica* Group] > gi|20146429|dbj|BAB89209.1| wax synthase-like [*Oryza sativa Japonica* Group] > gi|113533264|dbj|BAF05647.1| Os01g0651500 [*Oryza sativa Japonica* Group] > gi|125571401|gb|EAZ12916.1| hypothetical protein OsJ_02839 [*Oryza sativa Japonica* Group]	0.73	791	1486
		EAY75194	hypothetical protein OsI_03086 [*Oryza sativa Indica* Group]	0.72	792	
		BAK07830	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.70	793	1487
	1709-1729	XP_002448959	hypothetical protein SORBIDRAFT_05g002450 [*Sorghum bicolor*] > gi|241934802|gb|EES07947.1| hypothetical protein SORBIDRAFT_05g002450 [*Sorghum bicolor*]	1.00	794	1488
		ACF84627	unknown [*Zea mays*] > gi|223942887|gb|ACN25527.1| unknown [*Zea mays*]	0.95	795	1489
		NP_001150994	PP2A regulatory subunit TAP46 [*Zea mays*] > gi|195643460|gb|ACG41198.1| PP2A regulatory subunit TAP46 [*Zea mays*]	0.95	796	1490
		ACF84366	unknown [*Zea mays*]	0.94	797	1491
		EAY79895	hypothetical protein OsI_35058 [*Oryza sativa Indica* Group]	0.89	798	
		NP_001066109	Os12g0137500 [*Oryza sativa Japonica* Group] > gi|77552970|gb|ABA95766.1| TAP42-like family protein, expressed [*Oryza sativa Japonica* Group] > gi|113648616|dbj|BAF29128.1| Os12g0137500 [*Oryza sativa Japonica* Group] > gi|2157690835|dbj|BAH01312.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.89	799	1492
		EAZ19586	hypothetical protein OsJ_35163 [*Oryza sativa Japonica* Group]	0.89	800	
		AAO72555	PP2A regulatory subunit-like protein [*Oryza sativa Japonica* Group]	0.89	801	1493
		ABA91420	TAP42-like family protein, expressed [*Oryza sativa Japonica* Group] > gi|222615497|gb|EEE51629.1| hypothetical protein OsJ_32912 [*Oryza sativa Japonica* Group]	0.88	802	1494
		NP_001148561	PP2A regulatory subunit TAP46 [*Zea mays*] > gi|195620440|gb|ACG32050.1|	0.86	803	1495

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			PP2A regulatory subunit TAP46 [*Zea mays*]			
	1417-1437	XP_002465624	hypothetical protein SORBIDRAFT_01g042450 [*Sorghum bicolor*] > gi|194326198|emb|CAQ86599.1| glutamine synthetase [*Sorghum bicolor*] > gi|241919478|gb|EER92622.1| hypothetical protein SORBIDRAFT_01g042450 [*Sorghum bicolor*]	1.00	804	1496
		AAW21274	glutamine synthetase [*Saccharum officinarum*]	0.98	805	1497
		NP_001105538	glutamine synthetase root isozyme 1 [*Zea mays*] > gi|6996235|dbj|BAA03433.1| glutamine synthetase [*Zea mays*] > gi|194701040|gb|ACF84604.1| unknown [*Zea mays*]	0.97	806	1498
		P38559	RecName: Full = Glutamine synthetase root isozyme 1; AltName: Full = GS122; AltName: Full = Glutamate--ammonia ligase > gi|434324|emb|CAA46719.1| glutamine synthetase [*Zea mays*]	0.97	807	
		P38563	RecName: Full = Glutamine synthetase root isozyme 5; AltName: Full = GS117; AltName: Full = Glutamate--ammonia ligase	0.96	808	
		NP_001105297	glutamine synthetase root isozyme 5 [*Zea mays*] > gi|699621|dbj|BAA03432.1| glutamine synthetase [*Zea mays*]	0.96	809	1499
		ACG47508	glutamine synthetase root isozyme 5 [*Zea mays*]	0.95	810	1500
		NP_001049424	Os03g0223400 [*Oryza sativa Japonica* Group] > gi|121332|sp|P14654.1|GLN12_ORYSJ RecName: Full = Glutamine synthetase cytosolic isozyme 1-2; AltName: Full = Glutamate--ammonia ligase GLN1; 2; Short = OsGLN1; 2; AltName: Full = Glutamine synthetase root isozyme; AltName: Full = OsGS1; 2 > gi|20358|emb|CAA32460.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|565414215|dbj|BAD77931.1| cytosolic glutamine synthetase 1; 2 [*Oryza sativa Japonica* Group] > gi|108706922|gb|ABF94717.1| Glutamine synthetase root isozyme 5, putative, expressed [*Oryza sativa Japonica* Group] > gi|1135478955|dbj|BAF11338.1| Os03g0223400 [*Oryza sativa Japonica* Group] > gi|215769188|dbj|BAH01417.1| unnamed protein	0.91	811	1501

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			product [*Oryza sativa Japonica* Group] > gi|218192361|gb|EEC74788.1| hypothetical protein OsI_10575 [*Oryza sativa Indica* Group] > gi|222624488|gb|EEE58620.1| hypothetical protein OsJ_09974 [*Oryza sativa Japonica* Group]			
		AAR84347	glutamine synthetase isoform GSr1 [*Triticum aestivum*]	0.89	812	1502
		AAR84348	glutamine synthetase isoform GSr2 [*Triticum aestivum*]	0.89	813	1503
	1527-1547	XP_002454761	hypothetical protein SORBIDRAFT_04g036890 [*Sorghum bicolor*] > gi|241934592|gb|EES07737.1| hypothetical protein SORBIDRAFT_04g036890 [*Sorghum bicolor*]	1.00	814	1504
		NP_001130621	hypothetical protein LOC100191720 [*Zea mays*] > gi|194689664|gb|ACF78916.1| unknown [*Zea mays*]	0.87	815	1505
		XP_002454762	hypothetical protein SORBIDRAFT_04g036900 [*Sorghum bicolor*] > gi|241934593|gb|EES07738.1| hypothetical protein SORBIDRAFT_04g036900 [*Sorghum bicolor*]	0.78	816	1506
		XP_002437453	hypothetical protein SORBIDRAFT_10g027360 [*Sorghum bicolor*] > gi|241915676|gb|EER88820.1| hypothetical protein SORBIDRAFT_10g027360 [*Sorghum bicolor*]	0.70	817	1507
		XP_002438878	hypothetical protein SORBIDRAFT_10g027650 [*Sorghum bicolor*] > gi|241917101|gb|EER90245.1| hypothetical protein SORBIDRAFT_10g027650 [*Sorghum bicolor*]	0.69	818	1508
		XP_002438877	hypothetical protein SORBIDRAFT_10g027640 [*Sorghum bicolor*] > gi|241917100|gb|EER90244.1| hypothetical protein SORBIDRAFT_10g027640 [*Sorghum bicolor*]	0.70	819	1509
	2363-2383	XP_002436826	hypothetical protein SORBIDRAFT_10g009530 [*Sorghum bicolor*] > gi|241915049|gb|EER88193.1| hypothetical protein SORBIDRAFT_10g009530 [*Sorghum bicolor*]	1.00	820	1510
		ACN31818	unknown [*Zea mays*]	0.94	821	1511
		BAJ98035	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.81	822	1512
		NP_001057335	Os06g0264500 [*Oryza sativa Japonica* Group] > gi|53793159|dbj|BAD54367.1| putative nitrite transporter [*Oryza sativa Japonica* Group] > gi|53793165|dbj|BAD54372.1| putative nitrite transporter [*Oryza sativa*	0.79	823	1513

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			Japonica Group] > gi|113595375|dbj|BAF19249.1| Os06g0264500 [*Oryza sativa Japonica* Group] > gi|215767857|dbj|BAH00086.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218197932|gb|EEC80359.1| hypothetical protein OsI_22454 [*Oryza sativa Indica* Group] > gi|222635351|gb|EEE65483.1| hypothetical protein OsJ_20894 [*Oryza sativa Japonica* Group]			
	2309-2329	XP_002446671	hypothetical protein SORBIDRAFT_06g020190 [*Sorghum bicolor*] > gi|241937854|gb|EES10999.1| hypothetical protein SORBIDRAFT_06g020190 [*Sorghum bicolor*]	1.00	824	1514
		NP_001151527	ATSWI3A [*Zea mays*] > gi|195647424|gb|ACG43180.1| ATSWI3A [*Zea mays*]	0.92	825	1515
		NP_001053100	Os04g0480300 [*Oryza sativa Japonica* Group] > gi|113564671|dbj|BAF15014.1| Os04g0480300 [*Oryza sativa Japonica* Group] > gi|215734840|dbj|BAG95562.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.76	826	1516
		CAH66875	OSIGBa0158F13.6 [*Oryza sativa Indica* Group]	0.76	827	1517
		EEC77490	hypothetical protein OsI_16334 [*Oryza sativa Indica* Group]	0.73	828	
	1469-1489	NP_001148712	plant-specific domain TIGR01589 family protein [*Zea mays*] > gi|195621580|gb|ACG32620.1| plant-specific domain TIGR01589 family protein [*Zea mays*]	1.00	829	1518
	2030-2050	NP_001105116	SBP-domain protein3 [*Zea mays*] > gi|5931782|emb|CAB56629.1| SBP-domain protein 3 [*Zea mays*]	1.00	830	1519
		XP_002437398	hypothetical protein SORBIDRAFT_10g026200 [*Sorghum bicolor*] > gi|241915621|gb|EER88765.1| hypothetical protein SORBIDRAFT_10g026200 [*Sorghum bicolor*]	0.78	831	1520
		ACF78942	unknown [*Zea mays*] > gi|194690438|gb|ACF79303.1| unknown [*Zea mays*] > gi|223974801|gb|ACN31588.1| unknown [*Zea mays*]	0.70	832	1521
		NP_001105656	SBP-domain protein4 [*Zea mays*] > gi|5931784|emb|CAB56630.1| SBP-domain protein 4 [*Zea mays*]	0.69	833	1522
	1925-1945	NP_001142263	hypothetical protein LOC100274432 [*Zea mays*] > gi|194707898|gb|ACF88033.1| unknown [*Zea mays*]	1.00	834	1523

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		XP_002468497	hypothetical protein SORBIDRAFT_01g046950 [*Sorghum bicolor*] > gi|241922351|gb|EER95495.1| hypothetical protein SORBIDRAFT_01g046950 [*Sorghum bicolor*]	0.81	835	1524
	88-108	XP_002448249	hypothetical protein SORBIDRAFT_06g023950 [*Sorghum bicolor*] > gi|241939432|gb|EES12577.1| hypothetical protein SORBIDRAFT_06g023950 [*Sorghum bicolor*]	1.00	836	1525
		NP_001141834	hypothetical protein LOC100273976 [*Zea mays*] > gi|194706118|gb|ACF87143.1| unknown [*Zea mays*]	0.92	837	1526
		BAJ88132	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.86	838	1527
		CAE02784	OSJNBa0011L07.8 [*Oryza sativa Japonica* Group] > gi|116310379|emb|CAH67390.1| H0115B09.2 [*Oryza sativa Indica* Group] > gi|215768681|dbj|BAH00910.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218195296|gb|EEC77723.1| hypothetical protein OsI_16815 [*Oryza sativa Indica* Group] > gi|222629289|gb|EEE61421.1| hypothetical protein OsJ_15623 [*Oryza sativa Japonica* Group]	0.87	839	1528
		ACF88110	unknown [*Zea mays*]	0.76	840	1529
		NP_001065045	Os10g0512700 [*Oryza sativa Japonica* Group] > gi|78708906|gb|ABB47881.1| SH3 domain-containing protein 3, putative, expressed [*Oryza sativa Japonica* Group] > gi|113639654|dbj|BAF26959.1| Os10g0512700 [*Oryza sativa Japonica* Group] > gi|218184876|gb|EEC67303.1| hypothetical protein OsI_34298 [*Oryza sativa Indica* Group] > gi|222613131|gb|EEE51263.1| hypothetical protein OsJ_32141 [*Oryza sativa Japonica* Group]	0.73	841	1530
		BAJ89635	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.72	842	1531
		ACG28140	clathrin binding protein [*Zea mays*]	0.72	843	1532
		NP_001130175	hypothetical protein LOC100191269 [*Zea mays*] > gi|194688470|gb|ACF78319.1| unknown [*Zea mays*]	0.72	844	1533
		XP_002464381	hypothetical protein SORBIDRAFT_01g017250 [*Sorghum bicolor*] > gi|241918235|gb|EER91379.1| hypothetical protein SORBIDRAFT_01g017250 [*Sorghum bicolor*]	0.71	845	1534

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
	2810-2830	XP_002458234	hypothetical protein SORBIDRAFT_03g029520 [*Sorghum bicolor*] > gi|241930209|gb|EES03354.1| hypothetical protein SORBIDRAFT_03g029520 [*Sorghum bicolor*]	1.00	846	1535
		CAI77627	potassium uptake channel [*Zea mays*]	0.93	847	
		NP_001105480	potassium channel5 [*Zea mays*] > gi|2104908|emb|CAA68912.1| potassium channel [*Zea mays*]	0.91	848	1536
		NP_001043713	Os01g0648000 [*Oryza sativa Japonica* Group] > gi|122241153|sp|Q0JKV1.1| AKT1_ORYSJ RecName: Full = Potassium channel AKT1; Short = OsAKT1 > gi|113533244|dbj|BAF05627.1| Os01g0648000 [*Oryza sativa Japonica* Group]	0.82	849	1537
		P0C550	RecName: Full = Potassium channel AKT1; Short = OsAKT1	0.82	850	
		ABE99810	inwardly rectifying potassium channel AKT1 [*Hordeum vulgare*] > gi|326519172|dbj|BAJ96585.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.81	851	1538
		AAF36832	AKT1-like potassium channel [*Triticum aestivum*]	0.81	852	1539
		AAL40894	AKT1-like potassium channel [*Oryza sativa*]	0.78	853	1540
		ADK93728	inward-rectifying potassium channel [*Puccinellia tenuiflora*]	0.79	854	1541
		EEE55080	hypothetical protein OsJ_02815 [*Oryza sativa Japonica* Group]	0.78	855	
	1465-1485	NP_001151754	collagen, type IV, alpha 5 [*Zea mays*] > gi|195649521|gb|ACG44228.1| collagen, type IV, alpha 5 [*Zea mays*]	1.00	856	1542
		XP_002460574	hypothetical protein SORBIDRAFT_02g031070 [*Sorghum bicolor*] > gi|241923951|gb|EER97095.1| hypothetical protein SORBIDRAFT_02g031070 [*Sorghum bicolor*]	0.87	857	1543
	1702-1722	XP_002460183	hypothetical protein SORBIDRAFT_02g024090 [*Sorghum bicolor*] > gi|241923560|gb|EER96704.1| hypothetical protein SORBIDRAFT_02g024090 [*Sorghum bicolor*]	1.00	858	1544
		NP_001149599	LOC100283225 [*Zea mays*] > gi|194705944|gb|ACF87056.1| unknown [*Zea mays*] > gi|195628360|gb|ACG36010.1| annexin A4 [*Zea mays*]	0.96	859	1545
		ACG40326	annexin A4 [*Zea mays*]	0.95	860	1546
		NP_001063096	Os09g0394900 [*Oryza sativa Japonica* Group] > gi|49389155|dbj|BAD26449.1| putative annexin [*Oryza sativa Japonica* Group]	0.89	861	1547

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			> gi|49389211|dbj|BAD26499.1| putative annexin [*Oryza sativa Japonica* Group] > gi|113631329|dbj|BAF25010.1| Os09g0394900 [*Oryza sativa Japonica* Group] > gi|215692709|dbj|BAG88129.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215704491|dbj|BAG93925.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222641513|gb|EEE69645.1| hypothetical protein OsJ_29255 [*Oryza sativa Japonica* Group]			
		EEC84533	hypothetical protein OsI_31267 [*Oryza sativa Indica* Group]	0.89	862	
		NP_001132118	hypothetical protein LOC100193535 [*Zea mays*] > gi|238908661|gb|ACF80822.2| unknown [*Zea mays*]	0.86	863	1548
		BAJ85227	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326510845|dbj|BAJ91770.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.73	864	1549
		NP_001147343	annexin A4 [*Zea mays*] > gi|195610314|gb|ACG26987.1| annexin A4 [*Zea mays*] > gi|219887403|gb|ACL54076.1| unknown [*Zea mays*]	0.72	865	1550
		AAR25142	annexin [*Triticum aestivum*]	0.73	866	1551
		ACF06448	annexin [*Elaeis guineensis*]	0.74	867	1552
Predicted folded 24-nts-long seq 51802	891-914	ACG34432	L-allo-threonine aldolase [*Zea mays*]	1.00	868	1553
		ACG33933	L-allo-threonine aldolase [*Zea mays*]	0.99	869	1554
		NP_001149239	L-allo-threonine aldolase [*Zea mays*] > gi|195625716|gb|ACG34688.1| L-allo-threonine aldolase [*Zea mays*]	0.98	870	1555
		NP_001053314	Os04g0516600 [*Oryza sativa Japonica* Group] > gi|38344656|emb|CAD4182.21| OSJNBb0072M01.18 [*Oryza sativa Japonica* Group] > gi|113564885|dbj|BAF15228.1| Os04g0516600 [*Oryza sativa Japonica* Group] > gi|116310209|emb|CAH67219.1| OSIGBa0145M07.1 [*Oryza sativa Indica* Group] > gi|215708770|dbj|BAG94039.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215765369|dbj|BAG87066.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218195217|gb|EEC77644.1| hypothetical protein	0.79	871	1556

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			OsI_16646 [*Oryza sativa Indica* Group] > gi|222629209|gb|EEE61341.1| hypothetical protein OsJ_15466 [*Oryza sativa Japonica* Group]			
		CAE05443	OSJNBa0073E02.3 [*Oryza sativa Japonica* Group]	0.75	872	1557
		XP_002448187	hypothetical protein SORBIDRAFT_06g022630 [*Sorghum bicolor*] > gi|241939370|gb|EES12515.1| hypothetical protein SORBIDRAFT_06g022630 [*Sorghum bicolor*]	0.79	873	1558
		ACG36649	L-allo-threonine aldolase [*Zea mays*]	0.80	874	1559
		BAK03835	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.79	875	1560
		BAJ93201	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.76	876	1561
		NP_001140767	hypothetical protein LOC100272842 [*Zea mays*] > gi|194700996|gb|ACF84582.1| unknown [*Zea mays*]	0.72	877	1562
	700-723	AAS47590	phospholipid-hydroperoxide glutathione peroxidase [*Setaria italica*]	1.00	878	1563
		XP_002446921	hypothetical protein SORBIDRAFT_06g024920 [*Sorghum bicolor*] > gi|48374968|gb|AAT42166.1| putative glutathione peroxidase [*Sorghum bicolor*] > gi|241938104|gb|EES11249.1| hypothetical protein SORBIDRAFT_06g024920 [*Sorghum bicolor*]	0.99	879	1564
		NP_001141210	hypothetical protein LOC100273297 [*Zea mays*] > gi|48374955|gb|AAT42154.1| putative glutathione peroxidase [*Zea mays*] > gi|194703274|gb|ACF85721.1| unknown [*Zea mays*] > gi|195622840|gb|ACG33250.1| phospholipid hydroperoxide glutathione peroxidase [*Zea mays*] > gi|223975959|gb|ACN32167.1| unknown [*Zea mays*]	0.96	880	1565
		ACG39625	phospholipid hydroperoxide glutathione peroxidase [*Zea mays*]	0.96	881	1566
		EEC77777	hypothetical protein OsI_16938 [*Oryza sativa Indica* Group]	0.95	882	
		NP_001146472	hypothetical protein LOC100280060 [*Zea mays*] > gi|219887431|gb|ACL54090.1| unknown [*Zea mays*]	0.94	883	1567
		NP_001147681	phospholipid hydroperoxide glutathione peroxidase [*Zea mays*] > gi|195613068|gb|ACG28364.1| phospholipid hydroperoxide glutathione peroxidase [*Zea mays*]	0.94	884	1568

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		NP_001053524	Os04g0556300 [*Oryza sativa Japonica* Group] > gi|21360380|gb|AAM47493.1| glutathione peroxidase 1 [*Oryza sativa*] > gi|113565095|dbj|BAF15438.1| Os04g0556300 [*Oryza sativa Japonica* Group] > gi|215693018|dbj|BAG88438.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222629338|gb|EEE61470.1| hypothetical protein OsJ_15735 [*Oryza sativa Japonica* Group]	0.94	885	1569
		NP_001105091	GP protein [*Zea mays*] > gi|22268405|gb|AAM88847.2| AF520911_1 putative glutathione peroxidase [*Zea mays*]	0.94	886	1570
		AAQ64633	cytosolic glutathione peroxidase [*Triticum monococcum*]	0.93	887	1571
	714-737	XP_002446921	hypothetical protein SORBIDRAFT_06g024920 [*Sorghum bicolor*] > gi|48374968|gb|AAT42166.1| putative glutathione peroxidase [*Sorghum bicolor*] > gi|241938104|gb|EES11249.1| hypothetical protein SORBIDRAFT_06g024920 [*Sorghum bicolor*]	1.00	888	1572
		AAS47590	phospholipid-hydroperoxide glutathione peroxidase [*Setaria italica*]	0.99	889	1573
		NP_001141210	hypothetical protein LOC100273297 [*Zea mays*] > gi|48374955|gb|AAT42154.1| putative glutathione peroxidase [*Zea mays*] > gi|194703274|gb|ACF85721.1| unknown [*Zea mays*] > gi|195622840|gb|ACG33250.1| phospholipid hydroperoxide glutathione peroxidase [*Zea mays*] > gi|223975959|gb|ACN32167.1| unknown [*Zea mays*]	0.98	890	1574
		ACG39625	phospholipid hydroperoxide glutathione peroxidase [*Zea mays*]	0.97	891	1575
		EEC77777	hypothetical protein OsI_16938 [*Oryza sativa Indica* Group]	0.96	892	
		NP_001146472	hypothetical protein LOC100280060 [*Zea mays*] > gi|219887431|gb|ACL54090.1| unknown [*Zea mays*]	0.95	893	1576
		NP_001147681	phospholipid hydroperoxide glutathione peroxidase [*Zea mays*] > gi|195613068|gb|ACG28364.1| phospholipid hydroperoxide glutathione peroxidase [*Zea mays*]	0.95	894	1577
		NP_001053524	Os04g0556300 [*Oryza sativa Japonica* Group] > gi|21360380|gb|AAM47493.1| glutathione peroxidase 1	0.95	895	1578

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			[*Oryza sativa*] > gi|113565095|dbj|BAF15438.1| Os04g0556300 [*Oryza sativa Japonica* Group] > gi|215693018|dbj|BAG88438.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222629338|gb|EEE61470.1| hypothetical protein OsJ_15735 [*Oryza sativa Japonica* Group]			
		NP_001105091	GP protein [*Zea mays*] > gi|22268405|gb|AAM88847.2| AF520911_1 putative glutathione peroxidase [*Zea mays*]	0.95	896	1579
		AAQ64633	cytosolic glutathione peroxidase [*Triticum monococcum*]	0.95	897	1580
	160-183	NP_001159179	hypothetical protein LOC100304264 [*Zea mays*] > gi|223942501|gb|ACN25334.1| unknown [*Zea mays*]	1.00	898	1581
		NP_001105290	LOC542207 [*Zea mays*] > gi|57791232|gb|AAW56446.1| methyl-binding domain protein MBD113 [*Zea mays*]	0.74	899	1582
	1054-1077	XP_002450144	hypothetical protein SORBIDRAFT_05g001160 [*Sorghum bicolor*] > gi|241935987|gb|EES09132.1| hypothetical protein SORBIDRAFT_05g001160 [*Sorghum bicolor*]	1.00	900	1583
		NP_001065992	Os12g0116000 [*Oryza sativa Japonica* Group] > gi|108862099|gb|ABA96293.2| Vacuolar sorting receptor 1 precursor, putative, expressed [*Oryza sativa Japonica* Group] > gi|113648499|dbj|BAF29011.1| Os12g0116000 [*Oryza sativa Japonica* Group] > gi|215694863|dbj|BAG90054.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.89	901	1584
		EEC68730	hypothetical protein OsI_37233 [*Oryza sativa Indica* Group]	0.89	902	
		EEE51529	hypothetical protein OsJ_32728 [*Oryza sativa Japonica* Group]	0.89	903	
		EEC67546	hypothetical protein OsI_34875 [*Oryza sativa Indica* Group]	0.89	904	
		BAK03786	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.87	905	1585
		BAK00302	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.87	906	1586
		CBI18031	unnamed protein product [*Vitis vinifera*]	0.78	907	
		XP_002267833	PREDICTED: hypothetical protein [*Vitis vinifera*]	0.78	908	1587
		XP_002309184	predicted protein [*Populus trichocarpa*] > gi|222855160|gb|EEE92707.1| predicted protein [*Populus trichocarpa*]	0.78	909	1588

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
	1792-1815	NP_001140790	hypothetical protein LOC100272865 [*Zea mays*] > gi|194701088|gb|ACF84628.1| unknown [*Zea mays*]	1.00	910	1589
		XP_002464219	hypothetical protein SORBIDRAFT_01g014350 [*Sorghum bicolor*] > gi|241918073|gb|EER91217.1| hypothetical protein SORBIDRAFT_01g014350 [*Sorghum bicolor*]	0.85	911	1590
		XP_002464218	hypothetical protein SORBIDRAFT_01g014340 [*Sorghum bicolor*] > gi|241918072|gb|EER91216.1| hypothetical protein SORBIDRAFT_01g014340 [*Sorghum bicolor*]	0.84	912	1591
		AAL73972	putative cytochrome P450-like protein [*Sorghum bicolor*]	0.73	913	1592
	2477-2500	XP_002454227	hypothetical protein SORBIDRAFT_04g027100 [*Sorghum bicolor*] > gi|241934058|gb|EES07203.1| hypothetical protein SORBIDRAFT_04g027100 [*Sorghum bicolor*]	1.00	914	1593
		NP_001169751	hypothetical protein LOC100383632 [*Zea mays*] > gi|224031415|gb|ACN34783.1| unknown [*Zea mays*]	0.93	915	1594
		BAJ95386	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.78	916	1595
		EEC73665	hypothetical protein OsI_08209 [*Oryza sativa Indica* Group]	0.77	917	
		NP_001047529	Os02g0637800 [*Oryza sativa Japonica* Group] > gi|49387984|dbj|BAD25092.1| unknown protein [*Oryza sativa Japonica* Group] > gi|49388709|dbj|BAD25890.1| unknown protein [*Oryza sativa Japonica* Group] > gi|113537060|dbj|BAF09443.1| Os02g0637800 [*Oryza sativa Japonica* Group] > gi|215704166|dbj|BAG93006.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222623311|gb|EEE57443.1| hypothetical protein OsJ_07658 [*Oryza sativa Japonica* Group]	0.77	918	1596
	3108-3131	NP_001169691	hypothetical protein LOC100383572 [*Zea mays*] > gi|224030935|gb|ACN34543.1| unknown [*Zea mays*]	1.00	919	1597
		ACN33688	unknown [*Zea mays*]	0.96	920	1598
		NP_001131248	hypothetical protein LOC100192560 [*Zea mays*] > gi|195656461|gb|ACG47698.1| nucleic acid binding protein [*Zea mays*]	0.81	921	1599
		XP_002441761	hypothetical protein SORBIDRAFT_08g001980 [*Sorghum bicolor*] > gi|241942454|gb|EES15599.1| hypothetical protein SORBIDRAFT_08g001980 [*Sorghum bicolor*]	0.80	922	1600

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
	2192-2215	NP_001150353	LOC100283983 [*Zea mays*] > gi|195638608|gb|ACG38772.1| ubiquilin-1 [*Zea mays*] > gi|195644430|gb|ACG41683.1| ubiquilin-1 [*Zea mays*] > gi|224029247|gb|ACN33699.1| unknown [*Zea mays*]	1.00	923	1601
		XP_002465921	hypothetical protein SORBIDRAFT_01g048260 [*Sorghum bicolor*] > gi|241919775|gb|EER92919.1| hypothetical protein SORBIDRAFT_01g048260 [*Sorghum bicolor*]	0.92	924	1602
		NP_001048862	Os03g0131300 [*Oryza sativa Japonica* Group] > gi|108706017|gb|ABF93812.1| Ubiquitin family protein, expressed [*Oryza sativa Japonica* Group] > gi|113547333|dbj|BAF10776.1| Os03g0131300 [*Oryza sativa Japonica* Group] > gi|215713564|dbj|BAG94701.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222624144|gb|EEE58276.1| hypothetical protein OsJ_09294 [*Oryza sativa Japonica* Group]	0.78	925	1603
		EEC74450	hypothetical protein OsI_09858 [*Oryza sativa Indica* Group]	0.78	926	
		NP_001169509	hypothetical protein LOC100383383 [*Zea mays*] > gi|224029753|gb|ACN33952.1| unknown [*Zea mays*]	0.78	927	1604
		EAY79386	hypothetical protein OsI_34513 [*Oryza sativa Indica* Group]	0.71	928	
		N_001065193	Os10g0542200 [*Oryza sativa Japonica* Group] > gi|10140758|gb|AAG13589.1| AC051633_5 putative ubiquitin protein [*Oryza sativa Japonica* Group] > gi|31433330|gb|AAP54859.1| Ubiquitin family protein, expressed [*Oryza sativa Japonica* Group] > gi|113639802|dbj|BAF27107.1| Os10g0542200 [*Oryza sativa Japonica* Group]	0.71	929	1605
		EEE51337	hypothetical protein OsJ_32327 [*Oryza sativa Japonica* Group]	0.71	930	
		BAJ87273	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.73	931	1606
		BAK06552	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.74	932	1607
	1289-1312	NP_001046031	Os02g0171100 [*Oryza sativa Japonica* Group] > gi|49387565|dbj|BAD25496.1| putative glyceraldehyde-3-phosphate dehydrogenase [*Oryza sativa Japonica* Group] > gi|49388082|dbj|BAD25194.1| putative glyceraldehyde-3-phosphate dehydrogenase	1.00	933	1608

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			[*Oryza sativa Japonica* Group] > gi|113535562|dbj|BAF07945.1| Os02g0171100 [*Oryza sativa Japonica* Group] > gi|215697739|dbj|BAG91733.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218190154|gb|EEC72581.1| hypothetical protein OsI_06028 [*Oryza sativa Indica* Group] > gi|222622270|gb|EEE56402.1| hypothetical protein OsJ_05558 [*Oryza sativa Japonica* Group]			
		NP_001149357	LOC100282981 [*Zea mays*] > gi|195626622|gb|ACG35141.1| glyceraldehyde-3-phosphate dehydrogenase, cytosolic [*Zea mays*] > gi|195641440|gb|ACG40188.1| glyceraldehyde-3-phosphate dehydrogenase, cytosolic [*Zea mays*]	0.92	934	1609
		ACL54292	unknown [*Zea mays*]	0.92	935	1610
		XP_002451619	hypothetical protein SORBIDRAFT_04g004750 [*Sorghum bicolor*] > gi|241931450|gb|EES04595.1| hypothetical protein SORBIDRAFT_04g004750 [*Sorghum bicolor*]	0.90	936	1611
		NP_001130796	hypothetical protein LOC100191900 [*Zea mays*] > gi|194690136|gb|ACF79152.1| unknown [*Zea mays*] > gi|195622606|gb|ACG33133.1| glyceraldehyde-3-phosphate dehydrogenase, cytosolic [*Zea mays*] > gi|195625996|gb|ACG34828.1| glyceraldehyde-3-phosphate dehydrogenase, cytosolic [*Zea mays*]	0.88	937	1612
		NP_001058309	Os06g0666600 [*Oryza sativa Japonica* Group] > gi|52076528|dbj|BAD45405.1| putative glyceraldehyde-3-phosphate dehydrogenase [*Oryza sativa Japonica* Group] > gi|113596349|dbj|BAF20223.1| Os06g0666600 [*Oryza sativa Japonica* Group] > gi|125556399|gb|EAZ02005.1| hypothetical protein OsI_24036 [*Oryza sativa Indica* Group] > gi|215741351|dbj|BAG97846.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.85	938	1613
		BAJ86344	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326520716|dbj|BAJ92721.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.82	939	1614
		ADJ96634	glyceraldehyde-3-phosphate dehydrogenase [*Guzmania wittmackii* x *Guzmania lingulata*]	0.82	940	1615

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		CAC80377	glyceraldehyde-3-phosphate dehydrogenase [*Capsicum annuum*] > gi|26986729|emb|CAC88118.1| glyceraldehyde-3-phosphate dehydrogenase [*Capsicum annuum*]	0.77	941	1616
		XP_002263263	PREDICTED: hypothetical protein [*Vitis vinifera*] > gi|297736130|emb|CBI24168.3| unnamed protein product [*Vitis vinifera*]	0.75	942	1617
Predicted folded 24-nts-long seq 52801	173-196	AAL76004	putative gag-pol polyprotein [*Zea mays*]	1.00	943	
		AAN40035	putative gag-pol polyprotein [*Zea mays*]	0.90	944	
		AAN40025	putative gag-pol polyprotein [*Zea mays*]	0.85	945	
		AAL66753	putative copia-type pol polyprotein [*Zea mays*]	0.81	946	
		AAP94599	putative copia-type pol polyprotein [*Zea mays*]	0.81	947	
Predicted folded 24-nts-long seq 52452	14-37	XP_002458660	hypothetical protein SORBIDRAFT_03g037610 [*Sorghum bicolor*] > gi|241930635|gb|EES03780.1| hypothetical protein SORBIDRAFT_03g037610 [*Sorghum bicolor*]	1.00	948	1618
		NP_001106055	ribonuclease III domain protein1 [*Zea mays*] > gi|149980667|gb|ABR53724.1| chloroplast ribonuclease III domain protein [*Zea mays*] > gi|194704042|gb|ACF86105.1| unknown [*Zea mays*] > gi|195647406|gb|ACG43171.1| RNA binding protein [*Zea mays*] > gi|223950477|gb|ACN29322.1| unknown [*Zea mays*]	0.98	949	1619
		BAJ85766	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326503490|dbj|BAJ86251.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326520661|dbj|BAJ92694.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.91	950	1620
		EEE55556	hypothetical protein OsJ_03820 [*Oryza sativa Japonica* Group]	0.89	951	
		NP_001044581	Os01g0810100 [*Oryza sativa Japonica* Group] > gi|20160696|dbj|BAB89639.1| unknown protein [*Oryza sativa Japonica* Group] > gi|113534112|dbj|BAF06495.1| Os01g0810100 [*Oryza sativa Japonica* Group] > gi|215701330|dbj|BAG92754.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215704464|dbj|BAG93898.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.92	952	1621

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		EEC71679	hypothetical protein OsI_04153 [*Oryza sativa Indica* Group]	0.86	953	
		BAJ91324	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.85	954	1622
		XP_002533159	RNA binding protein, putative [*Ricinus communis*] > gi|223527031|gb|EEF29218.1| RNA binding protein, putative [*Ricinus communis*]	0.75	955	1623
		NP_195467	Ribonuclease III family protein [*Arabidopsis thaliana*] > gi|4468817|emb|CAB38218.1| putative protein [*Arabidopsis thaliana*] > gi|7270733|emb|CAB80416.1| putative protein [*Arabidopsis thaliana*] > gi|95147308|gb|ABF57289.1| At4g37510 [*Arabidopsis thaliana*] > gi|332661403|gb|AEE86803.1| Ribonuclease III family protein [*Arabidopsis thaliana*]	0.74	956	1624
		XP_002866942	ribonuclease III family protein [*Arabidopsis lyrata* subsp. *lyrata*] > gi|297312778|gb|EFH43201.1| ribonuclease III family protein [*Arabidopsis lyrata* subsp. *lyrata*]	0.74	957	1625
	86-109	NP_001169273	hypothetical protein LOC100383136 [*Zea mays*] > gi|224028313|gb|ACN33232.1| unknown [*Zea mays*]	1.00	958	1626
		XP_022462951	hypothetical protein SORBIDRAFT_02g035180 [*Sorghum bicolor*] > gi|241926328|gb|EER99472.1| hypothetical protein SORBIDRAFT_02g035180 [*Sorghum bicolor*]	0.94	959	1627
		BAK06716	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.82	960	1628
		EEC82174	hypothetical protein OsI_26284 [*Oryza sativa Indica* Group]	0.81	961	
		NP_001059844	Os07g0530100 [*Oryza sativa Japonica* Group] > gi|33146648|dbj|BAC79984.1| putative tyrosyl-DNA phosphodiesterase [*Oryza sativa Japonica* Group] > gi|113611380|dbj|BAF21758.1| Os07g0530100 [*Oryza sativa Japonica* Group] > gi|215697362|dbj|BAG91356.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222637174|gb|EEE67306.1| hypothetical protein OsJ_24533 [*Oryza sativa Japonica* Group]	0.81	962	1629
Predicted zma mir 48588	69-89	NP_001167972	hypothetical protein LOC100381689 [*Zea mays*] > gi|223945237|gb|ACN26702.1| unknown [*Zea mays*]	1.00		
zma-miR166d*	1395-1415	NP_001151161	riboflavin kinase family protein [*Zea mays*] > gi|195644710|gb|ACG41823.1| riboflavin kinase family protein [*Zea mays*]	1.00	963	1630

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		EEC76352	hypothetical protein OsI__13934 [*Oryza sativa Indica* Group]	0.78	964	
		ABF99395	riboflavin biosynthesis protein, putative, expressed [*Oryza sativa Japonica* Group]	0.77	965	1631
		NP__001051594	Os03g0801700 [*Oryza sativa Japonica* Group] > gi|108711599|gb|ABF99394.1| riboflavin biosynthesis protein, putative, expressed [*Oryza sativa Japonica* Group] > gi|113550065|dbj|BAF13508.1| Os03g0801700 [*Oryza sativa Japonica* Group] > gi|222625981|gb|EEE60113.1| hypothetical protein OsJ__12987 [*Oryza sativa Japonica* Group]	0.77	966	1632
		BAK03408	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.73	967	1633
		BAJ90790	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.72	968	1634
Predicted folded 24-nts-long seq 52795	923-946	XP__002461133	hypothetical protein SORBIDRAFT__02g041270 [*Sorghum bicolor*] > gi|241924510|gb|EER97654.1| hypothetical protein SORBIDRAFT__02g041270 [*Sorghum bicolor*]	1.00	969	1635
		ACR36108	unknown [*Zea mays*]	0.97	970	1636
		NP__001149600	protein SFT2 [*Zea mays*] > gi|195628366|gb|ACG36013.1| protein SFT2 [*Zea mays*]	0.96	971	1637
		BAJ93024	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.90	972	1638
		BAJ93185	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.90	973	1639
		NP__001057449	Os06g0300300 [*Oryza sativa Japonica* Group] > gi|53792521|dbj|BAD53485.1| unknown protein [*Oryza sativa Japonica* Group] > gi|113595489|dbj|BAF19363.1| Os06g0300300 [*Oryza sativa Japonica* Group] > gi|215697111|dbj|BAG91105.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215766579|dbj|BAG98738.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218198021|gb|EEC80448.1| hypothetical protein OsI__22649 [*Oryza sativa Indica* Group] > gi|222635438|gb|EEE65570.1| hypothetical protein OsJ__21068 [*Oryza sativa Japonica* Group]	0.89	974	1640
		XP__002532175	Protein transport protein SFT2, putative [*Ricinus communis*] > gi|223528143|gb|EEF30212.1| Protein transport protein SFT2, putative [*Ricinus communis*]	0.73	975	1641
		XP__002264182	PREDICTED: hypothetical protein [*Vitis vinifera*] > gi|296085064|emb|CBI28479.3| unnamed protein product [*Vitis vinifera*]	0.70	976	1642

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
	149-172	XP_002445951	hypothetical protein SORBIDRAFT_07g028610 [*Sorghum bicolor*] > gi|241942301|gb|EES15446.1| hypothetical protein SORBIDRAFT_07g028610 [*Sorghum bicolor*]	1.00	977	1643
		NP_001131191	hypothetical protein LOC100192499 [*Zea mays*] > gi|194690830|gb|ACF79499.1| unknown [*Zea mays*]	0.92	978	1644
		BAK06465	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326515200|dbj|BAK03513.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.83	979	1645
		EAZ07476	hypothetical protein OsI_29735 [*Oryza sativa Indica* Group] > gi|125603873|gb|EAZ43198.1| hypothetical protein OsJ_27795 [*Oryza sativa Japonica* Group]	0.83	980	
		NP_001062134	Os08g0496000 [*Oryza sativa Japonica* Group] > gi|42408865|dbj|BAD10124.1| putative cytochrome c oxidase subunit 15(COX15) homolog isoform 1 precursor [*Oryza sativa Japonica* Group] > gi|113624103|dbj|BAF24048.1| Os08g0496000 [*Oryza sativa Japonica* Group] > gi|215737013|dbj|BAG95942.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.83	981	1646
zma-miR169c*	107-128	XP_002451684	hypothetical protein SORBIDRAFT_04g005850 [*Sorghum bicolor*] > gi|241931515|gb|EES04660.1| hypothetical protein SORBIDRAFT_04g005850 [*Sorghum bicolor*]	1.00	992	1655
		NP_001169303	hypothetical protein LOC100383167 [*Zea mays*] > gi|195627360|gb|ACG35510.1| cytochrome P450 CYP71K14 [*Zea mays*]	0.85	993	1656
		ACN33338	unknown [*Zea mays*]	0.76	994	1657
	1135-1156	NP_001169303	hypothetical protein LOC100383167 [*Zea mays*] > gi|195627360|gb|ACG35510.1| cytochrome P450 CYP71K14 [*Zea mays*]	1.00	995	1658
		ACN33338	unknown [*Zea mays*]	0.88	996	1659
		XP_002451684	hypothetical protein SORBIDRAFT_04g005850 [*Sorghum bicolor*] > gi|241931515|gb|EES04660.1| hypothetical protein SORBIDRAFT_04g005850 [*Sorghum bicolor*]	0.85	997	1660
Predicted zma mir 50517	606-625	XP_002436376	hypothetical protein SORBIDRAFT_10g001390 [*Sorghum bicolor*] > gi|241914599|gb|EER87743.1| hypothetical protein SORBIDRAFT_10g001390 [*Sorghum bicolor*]	1.00	998	1661

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		NP_001150208	DAG protein [*Zea mays*] > gi|195637572|gb|ACG38254.1| DAG protein [*Zea mays*] > gi|223947219|gb|ACN27693.1| unknown [*Zea mays*]	0.81	999	1662
		BAC22214	putative plastid protein [*Oryza sativa Japonica* Group]	0.81	1000	1663
		BAK01694	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.80	1001	1664
		BAJ87670	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.76	1002	1665
	560-579	NP_001056622	Os06g0116600 [*Oryza sativa Japonica* Group] > gi|55296199|dbj|BAD67917.1| putative DAL1 protein [*Oryza sativa Japonica* Group] > gi|113594662|dbj|BAF18536.1| Os06g0116600 [*Oryza sativa Japonica* Group] > gi|218197457|gb|EEC79884.1| hypothetical protein OsI_21391 [*Oryza sativa Indica* Group] > gi|222634859|gb|EEE64991.1| hypothetical protein OsJ_19911 [*Oryza sativa Japonica* Group]	1.00	1003	1666
	3352-3371	NP_001170545	hypothetical protein LOC100384563 [*Zea mays*] > gi|238005944|gb|ACR34007.1| unknown [*Zea mays*]	1.00	1004	1667
		XP_002436375	hypothetical protein SORBIDRAFT_10g001380 [*Sorghum bicolor*] > gi|241914598|gb|EER87742.1| hypothetical protein SORBIDRAFT_10g001380 [*Sorghum bicolor*]	0.85	1005	1668
		EEC79883	hypothetical protein OsI_21390 [*Oryza sativa Indica* Group]	0.81	1006	
		EEE64990	hypothetical protein OsJ_19910 [*Oryza sativa Japonica* Group]	0.78	1007	
		NP_001045600	Os02g0102800 [*Oryza sativa Japonica* Group] > gi|41052906|dbj|BAD07818.1| unknown protein [*Oryza sativa Japonica* Group] > gi|41053240|dbj|BAD08201.1| unknown protein [*Oryza sativa Japonica* Group] > gi|113535131|dbj|BAF07514.1| Os02g0102800 [*Oryza sativa Japonica* Group]	0.75	1008	1669
Predicted zma mir 49435	965-985	NP_001141527	hypothetical protein LOC100273639 [*Zea mays*] > gi|194704936|gb|ACF86552.1| unknown [*Zea mays*] > gi|195642904|gb|ACG40920.1| hypothetical protein [*Zea mays*]	1.00	1009	1670
		XP_002440488	hypothetical protein SORBIDRAFT_09g001840 [*Sorghum bicolor*] > gi|241945773|gb|EES18918.1| hypothetical protein SORBIDRAFT_09g001840 [*Sorghum bicolor*]	0.85	1010	1671

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
	358-378	ACF85023	unknown [*Zea mays*]	1.00	1011	1672
		NP_001151177	transposon protein [*Zea mays*] > gi|195644822|gb|ACG41879.1| transposon protein [*Zea mays*]	0.99	1012	1673
		XP_002452722	hypothetical protein SORBIDRAFT_04g031370 [*Sorghum bicolor*] > gi|241932553|gb|EES05698.1| hypothetical protein SORBIDRAFT_04g031370 [*Sorghum bicolor*]	0.86	1013	1674
		NP_001047784	Os02g0689500 [*Oryza sativa Japonica* Group] > gi|41052806|dbj|BAD07674.1| unknown protein [*Oryza sativa Japonica* Group] > gi|113537315|dbj|BAF09698.1| Os02g0689500 [*Oryza sativa Japonica* Group] > gi|125540730|gb|EAY87125.1| hypothetical protein OsI_08527 [*Oryza sativa Indica* Group] > gi|215704259|dbj|BAG93099.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.77	1014	1675
mtr-miR169q	174-194	XP_002468544	hypothetical protein SORBIDRAFT_01g047710 [*Sorghum bicolor*] > gi|241922398|gb|EER95542.1| hypothetical protein SORBIDRAFT_01g047710 [*Sorghum bicolor*]	1.00	1015	1676
		NP_001142595	hypothetical protein LOC100274862 [*Zea mays*] > gi|195607096|gb|ACG25378.1| hypothetical protein [*Zea mays*]	0.85	1016	1677
		ACN31627	unknown [*Zea mays*]	0.85	1017	1678
		ACR38267	unknown [*Zea mays*]	0.85	1018	1679
		NP_001144209	hypothetical protein LOC100277070 [*Zea mays*] > gi|195638456|gb|ACG38696.1| hypothetical protein [*Zea mays*]	0.85	1019	1680
		NP_001048909	Os03g0138500 [*Oryza sativa Japonica* Group] > gi|108706085|gb|ABF93880.1| expressed protein [*Oryza sativa Japonica* Group] > gi|113547380|dbj|BAF10823.1| Os03g0138500 [*Oryza sativa Japonica* Group]	0.72	1020	1681
		EAZ25513	hypothetical protein OsJ_09336 [*Oryza sativa Japonica* Group]	0.71	1021	
		EAY88465	hypothetical protein OsI_09934 [*Oryza sativa Indica* Group]	0.71	1022	
	1074-1094	NP_001150090	PIT1 [*Zea mays*] > gi|195636634|gb|ACG37785.1| PIT1 [*Zea mays*]	1.00	1023	1682
		NP_001042834	Os01g0303600 [*Oryza sativa Japonica* Group] > gi|52075677|dbj|BAD44897.1| zinc finger protein-like [*Oryza sativa Japonica* Group] > gi|52077476|dbj|BAD45040.1| zinc finger protein-like [*Oryza sativa Japonica* Group] > gi|218188061|gb|EEC70488.1|	0.76	1024	1683

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			hypothetical protein OsI_01559 [*Oryza sativa Indica* Group] > gi|255673151|dbj|BAF04748.2| Os01g0303600 [*Oryza sativa Japonica* Group]			
Predicted zma mir 49003	71-92	XP_002437560	hypothetical protein SORBIDRAFT_10g029400 [*Sorghum bicolor*] > gi|241915783|gb|EER88927.1| hypothetical protein SORBIDRAFT_10g029400 [*Sorghum bicolor*]	1.00	1025	1684
		ACL53917	unknown [*Zea mays*]	0.97	1026	1685
		NP_001152313	LOC100285952 [*Zea mays*] > gi|195654989|gb|ACG46962.1| MPK17-1-putative MAPK [*Zea mays*]	0.97	1027	1686
		NP_001146196	LOC100279766 [*Zea mays*] > gi|219886151|gb|ACL53450.1| unknown [*Zea mays*] > gi|297595201|gb|ADI48121.1| putative mitogen-activated protein kinase 17-3 [*Zea mays*]	0.95	1028	1687
		EEC81289	hypothetical protein OsI_24409 [*Oryza sativa Indica* Group]	0.91	1029	
		NP_001058530	Os06g0708000 [*Oryza sativa Japonica* Group] > gi|108860803|sp|Q5Z9J0.2| MPK12_ORYSJ RecName: Full = Mitogen-activated protein kinase 12; Short = MAP kinase 12; AltName: Full = Blast- and wound-induced MAP kinase 1; AltName: Full = MAP kinase 1; AltName: Full = OsBWMK1; AltName: Full = OsMAPK1 > gi|53792601|dbj|BAD53616.1| putative MAP kinase [*Oryza sativa Japonica* Group] > gi|113596570|dbj|BAF20444.1| Os06g0708000 [*Oryza sativa Japonica* Group]	0.91	1030	1688
		AAX20165	putative MAPK protein kinase [*Triticum aestivum*] > gi|84795226|gb|ABC65849.1| mitogen-activated protein kinase MAPK1e [*Triticum aestivum*]	0.86	1031	1689
		ABC54587	mitogen-activated protein kinase [*Triticum aestivum*]	0.86	1032	1690
		AAX20166	putative MAPK protein kinase [*Triticum aestivum*]	0.86	1033	1691
		ABD97883	mitogen-activated protein kinase [*Triticum aestivum*]	0.86	1034	1692
	53-74	EAY76957	hypothetical protein OsI_04915 [*Oryza sativa Indica* Group]	1.00	1035	
		NP_001045192	Os01g0916200 [*Oryza sativa Japonica* Group] > gi|19386749|dbj|BAB86130.1| putative adapter-related protein complex 4 epsilon 1 subunit [*Oryza sativa Japonica* Group] > gi|20805003|dbj|BAB92679.1| putative adapter-related protein complex 4 epsilon 1 subunit [*Oryza sativa Japonica* Group]	1.00	1036	1693

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			> gi|113534723|dbj|BAF07106.1| Os01g0916200 [*Oryza sativa Japonica* Group] > gi|215707205|dbj|BAG93665.1| unnamed protein product [*Oryza sativa Japonica* Group]			
		EAZ14613	hypothetical protein OsJ_04538 [*Oryza sativa Japonica* Group]	0.93	1037	
		XP_002458982	hypothetical protein SORBIDRAFT_03g043730 [*Sorghum bicolor*] > gi|241930957|gb|EES04102.1| hypothetical protein SORBIDRAFT_03g043730 [*Sorghum bicolor*]	0.91	1038	1694
		NP_001169710	hypothetical protein LOC100383591 [*Zea mays*] > gi|224031083|gb|ACN34617.1| unknown [*Zea mays*]	0.90	1039	1695
		BAJ89128	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.88	1040	1696
		XP_002328755	predicted protein [*Populus trichocarpa*] > gi|222839053|gb|EEE77404.1| predicted protein [*Populus trichocarpa*]	0.70	1041	1697
		XP_002519936	AP-1 complex subunit gamma-2, putative [*Ricinus communis*] > gi|223540982|gb|EEF42540.1| AP-1 complex subunit gamma-2, putative [*Ricinus communis*]	0.71	1042	1698
zma-miR399g	897-917	NP_001105061	Hageman factor inhibitor [*Zea mays*] > gi|16305146|gb|AAL16995.1| Hageman factor inhibitor [*Zea mays*]	1.00	1043	1699
		NP_001106233	trypsin/factor XIIA inhibitor precursor [*Zea mays*] > gi|266398|sp|P01088.2|ITRF_MAIZE RecName: Full = Trypsin/factor XIIA inhibitor; AltName: Full = CHFI; AltName: Full = Hageman factor inhibitor; Flags: Precursor > gi|22327|emb|CAA37998.1| corn Hageman factor inhibitor [*Zea mays*] > gi|75994173|gb|ABA34122.1| hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|75994177|gb|ABA34124.1| hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|75994189|gb|ABA34130.1| hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|75994193|gb|ABA34132.1| hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|195658559|gb|ACG48747.1| trypsin/factor XIIA inhibitor precursor [*Zea mays*] > gi|195658619|gb|ACG48777.1| trypsin/factor XIIA inhibitor precursor [*Zea mays*] > gi|214014768|gb|ACJ62034.1|	0.84	1044	1700

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014812|gb|ACJ62056.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014814|gb|ACJ62057.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014820|gb|ACJ62060.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014826|gb|ACJ62063.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014828|gb|ACJ62064.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014862|gb|ACJ62081.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014864|gb|ACJ62082.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014870|gb|ACJ62085.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|238014562|gb|ACR38316.1| unknown [*Zea mays*]			
		ABA34135	hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014790|gb|ACJ62045.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014796|gb|ACJ62048.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*]	0.83	1045	1701
		ACJ62011	Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014726|gb|ACJ62013.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014728|gb|ACJ62014.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014730|gb|ACJ62015.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014732|gb|ACJ62016.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014734|gb|ACJ62017.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014744|gb|ACJ62022.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014746|gb|ACJ62023.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014748|gb|ACJ62024.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*]	0.83	1046	1702
		ABA34133	hageman factor inhibitor [*Zea mays* subsp. *parviglumis*]	0.83	1047	1703
		ACJ62080	Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*]	0.83	1048	1704
		ABA34137	hageman factor inhibitor [*Zea diploperennis*] > gi|75994207|gb|ABA34139.1| hageman factor inhibitor [*Zea diploperennis*] > gi|75994211|gb|ABA34141.1| hageman factor inhibitor	0.83	1049	1705

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			[*Zea diploperennis*] > gi|75994213|gb|ABA34142.1| hageman factor inhibitor [*Zea diploperennis*] > gi|75994215|gb|ABA34143.1| hageman factor inhibitor [*Zea diploperennis*] > gi|75994217|gb|ABA34144.1| hageman factor inhibitor [*Zea diploperennis*]			
		ACG48546	trypsin/factor XIIA inhibitor precursor [*Zea mays*]	0.83	1050	1706
		ABA34129	hageman factor inhibitor [*Zea mays* subsp. *parviglumis*]	0.83	1051	1707
		ABA34125	hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|75994185|gb|ABA34128.1| hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014736|gb|ACJ62018.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014752|gb|ACJ62026.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*] > gi|214014822|gb|ACJ62061.1| Hageman factor inhibitor [*Zea mays* subsp. *parviglumis*]	0.83	1052	1708
Predicted zma mir 49985	379-399	XP_002454327	hypothetical protein SORBIDRAFT_04g028730 [*Sorghum bicolor*] > gi|241934158|gb|EES07303.1| hypothetical protein SORBIDRAFT_04g028730 [*Sorghum bicolor*]	1.00	1053	1709
		ACG36841	caleosin related protein [*Zea mays*]	0.81	1054	1710
		ACN31536	unknown [*Zea mays*]	0.78	1055	1711
		NP_001142815	hypothetical protein LOC100275194 [*Zea mays*] > gi|195610158|gb|ACG26909.1| hypothetical protein [*Zea mays*]	0.79	1056	1712
		NP_001148700	caleosin related protein [*Zea mays*] > gi|195621488|gb|ACG32574.1| caleosin related protein [*Zea mays*]	0.77	1057	1713
	632-652	XP_002448765	hypothetical protein SORBIDRAFT_06g032800 [*Sorghum bicolor*] > gi|241939948|gb|EES13093.1| hypothetical protein SORBIDRAFT_06g032800 [*Sorghum bicolor*]	1.00	1058	1714
		NP_001131374	hypothetical protein LOC100192699 [*Zea mays*] > gi|195620734|gb|ACG32197.1| oligosaccharyl transferase STT3 subunit [*Zea mays*]	0.99	1059	1715
		NP_001168720	hypothetical protein LOC100382512 [*Zea mays*] > gi|223950395|gb|ACN29281.1| unknown [*Zea mays*]	0.98	1060	1716
		NP_001054248	Os04g0675500 [*Oryza sativa Japonica* Group] > gi|38344929|emb|CAE03245.2| OSJNBa0018M05.20 [*Oryza sativa Japonica* Group] > gi|90399055|emb|CAJ86104.1| H0103C06.8 [*Oryza sativa Indica* Group]	0.96	1061	1717

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			> gi|113565819|dbj|BAF16162.1| Os04g0675500 [*Oryza sativa Japonica* Group] > gi|125550210|gb|EAY96032.1| hypothetical protein OsI_17905 [*Oryza sativa Indica* Group] > gi|125592048|gb|EAZ32398.1| hypothetical protein OsJ_16609 [*Oryza sativa Japonica* Group] > gi|215708677|dbj|BAG93946.1| unnamed protein product [*Oryza sativa Japonica* Group]			
		BAJ87792	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.95	1062	1718
		CBG76274	OO_Ba0005L10-OO_Ba0081K17.25 [*Oryza officinalis*]	0.93	1063	1719
		XP_002269119	PREDICTED: hypothetical protein [*Vitis vinifera*]	0.86	1064	1720
		XP_002318345	predicted protein [*Populus trichocarpa*] > gi|222859018|gb|EEE96565.1| predicted protein [*Populus trichocarpa*]	0.86	1065	1721
		XP_002891078	hypothetical protein ARALYDRAFT_891007 [*Arabidopsis lyrata* subsp. *lyrata*] > gi|297336920|gb|EFH67337.1| hypothetical protein ARALYDRAFT_891007 [*Arabidopsis lyrata* subsp. *lyrata*]	0.85	1066	1722
		XP_002329687	predicted protein [*Populus trichocarpa*] > gi|222870595|gb|EEF07726.1| predicted protein [*Populus trichocarpa*]	0.85	1067	1723
	795-815	XP_002458747	hypothetical protein SORBIDRAFT_03g039530 [*Sorghum bicolor*] > gi|241930722|gb|EES03867.1| hypothetical protein SORBIDRAFT_03g039530 [*Sorghum bicolor*]	1.00	1068	1724
		NP_001147942	L-ascorbate oxidase [*Zea mays*] > gi|195614732|gb|ACG29196.1| L-ascorbate oxidase precursor [*Zea mays*]	0.96	1069	1725
		ACN34362	unknown [*Zea mays*]	0.96	1070	1726
		EEC71780	hypothetical protein OsI_04394 [*Oryza sativa Indica* Group]	0.86	1071	
		NP_001044773	Os01g0842500 [*Oryza sativa Japonica* Group] > gi|19571025|dbj|BAB86452.1| putative laccase LAC5-6 [*Oryza sativa Japonica* Group] > gi|113534304|dbj|BAF06687.1| Os01g0842500 [*Oryza sativa Japonica* Group] > gi|125572601|gb|EAZ14116.1| hypothetical protein OsJ_04040 [*Oryza sativa Japonica* Group] > gi|215694814|dbj|BAG90005.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.86	1072	1727

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		BAJ84890	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.84	1073	1728
		BAJ96691	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.84	1074	1729
		NP_001105875	putative laccase [*Zea mays*] > gi|84618781|emb|CAJ30500.1| putative laccase [*Zea mays*]	0.79	1075	1730
		ACN28855	unknown [*Zea mays*]	0.79	1076	1731
		XP_002458746	hypothetical protein SORBIDRAFT_03g039520 [*Sorghum bicolor*] > gi|241930721|gb|EES03866.1| hypothetical protein SORBIDRAFT_03g039520 [*Sorghum bicolor*]	0.78	1077	1732
	198-218	XP_002458746	hypothetical protein SORBIDRAFT_03g039520 [*Sorghum bicolor*] > gi|241930721|gb|EES03866.1| hypothetical protein SORBIDRAFT_03g039520 [*Sorghum bicolor*]	1.00	1078	1733
		NP_001105875	putative laccase [*Zea mays*] > gi|84618781|emb|CAJ30500.1| putative laccase [*Zea mays*]	0.94	1079	1734
		NP_001146658	hypothetical protein LOC100280258 [*Zea mays*] > gi|219888209|gb|ACL54479.1| unknown [*Zea mays*]	0.93	1080	1735
		ACN28855	unknown [*Zea mays*]	0.94	1081	1736
		NP_001044772	Os01g0842400 [*Oryza sativa Japonica* Group] > gi|75321217|sp|Q5N9X2.1| LAC4_ORYSJ RecName: Full = Laccase-4; AltName: Full = Benzenediol:oxygen oxidoreductase 4; AltName: Full = Diphenol oxidase 4; AltName: Full = Urishiol oxidase 4; Flags: Precursor > gi|56784239|dbj|BAD81734.1| putative laccase LAC5-6 [*Oryza sativa Japonica* Group] > gi|113534303|dbj|BAF06686.1| Os01g0842400 [*Oryza sativa Japonica* Group] > gi|215697155|dbj|BAG91149.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.80	1082	1737
		EAZ14115	hypothetical protein OsJ_04039 [*Oryza sativa Japonica* Group]	0.80	1083	
		EEC71777	hypothetical protein OsI_04389 [*Oryza sativa Indica* Group]	0.80	1084	
		BAJ99773	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.78	1085	1738
		XP_002458747	hypothetical protein SORBIDRAFT_03g039530 [*Sorghum bicolor*] > gi|241930722|gb|EES03867.1| hypothetical protein SORBIDRAFT_03g039530 [*Sorghum bicolor*]	0.78	1086	1739
		AAC04576	putative high-pI laccase [*Oryza sativa Japonica* Group]	0.79	1087	1740
	751-771	XP_002456566	hypothetical protein SORBIDRAFT_03g038550 [*Sorghum bicolor*] > gi|241928541|gb|EES01686.1|	1.00	1088	1741

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			hypothetical protein SORBIDRAFT_03g038550 [*Sorghum bicolor*]			
		NP_001148479	L-ascorbate oxidase [*Zea mays*] > gi|195619672|gb|ACG31666.1| L-ascorbate oxidase precursor [*Zea mays*]	0.92	1089	1742
		NP_001183899	hypothetical protein LOC100502492 [*Zea mays*] > gi|223948465|gb|ACN28316.1| unknown [*Zea mays*] > gi|238015342|gb|ACR38706.1| unknown [*Zea mays*]	0.90	1090	1743
		NP_001044679	Os01g0827300 [*Oryza sativa Japonica* Group] > gi|75331868|sp|Q941X2.1| LAC3_ORYSJ RecName: Full = Benzenediol: oxygen oxidoreductase 3; AltName: Full = Diphenol oxidase 3; AltName: Full = Urishiol oxidase 3; Flags: Precursor > gi|15624045|dbj|BAB68098.1| putative laccase [*Oryza sativa Japonica* Group] > gi|113534210|dbj|BAF06593.1| Os01g0827300 [*Oryza sativa Japonica* Group] > gi|215701334|dbj|BAG92758.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222619479|gb|EEE55611.1| hypothetical protein OsJ_03932 [*Oryza sativa Japonica* Group]	0.84	1091	1744
		ACN27868	unknown [*Zea mays*]	0.82	1092	1745
		XP_002315131	laccase 90c [*Populus trichocarpa*] > gi|222864171|gb|EEF01302.1| laccase 90c [*Populus trichocarpa*]	0.71	1093	1746
		ABK92474	unknown [*Populus trichocarpa*]	0.70	1094	1747
		XP_002312186	laccase 90a [*Populus trichocarpa*] > gi|222852006|gb|EEE89553.1| laccase 90a [*Populus trichocarpa*]	0.70	1095	1748
	868-888	NP_001141205	hypothetical protein LOC100273292 [*Zea mays*] > gi|223944003|gb|ACN26085.1| unknown [*Zea mays*]	1.00	1096	1749
		ACF85713	unknown [*Zea mays*]	0.91	1097	1750
		XP_002446013	hypothetical protein SORBIDRAFT_06g000500 [*Sorghum bicolor*] > gi|241937196|gb|EES10341.1| hypothetical protein SORBIDRAFT_06g000500 [*Sorghum bicolor*]	0.84	1098	1751
		XP_002446014	hypothetical protein SORBIDRAFT_06g000510 [*Sorghum bicolor*] > gi|241937197|gb|EES10342.1| hypothetical protein SORBIDRAFT_06g000510 [*Sorghum bicolor*]	0.81	1099	1752
		CAH67827	B0616E02-H0507E05.3 [*Oryza sativa Indica* Group] > gi|125546940|gb|EAY92762.1| hypothetical protein	0.80	1100	1753

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			OsI_14564 [*Oryza sativa Indica* Group] > gi|125589087|gb|EAZ29437.1| hypothetical protein OsJ_13511 [*Oryza sativa Japonica* Group]			
		BAJ88131	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.83	1101	1754
	172-192	NP_001148700	caleosin related protein [*Zea mays*] > gi|195621488|gb|ACG32574.1| caleosin related protein [*Zea mays*]	1.00	1102	1755
		ACN31536	unknown [*Zea mays*]	0.99	1103	1756
		ACG36841	caleosin related protein [*Zea mays*]	0.83	1104	1757
		NP_001142815	hypothetical protein LOC100275194 [*Zea mays*] > gi|195610158|gb|ACG26909.1| hypothetical protein [*Zea mays*]	0.82	1105	1758
		XP_002454327	hypothetical protein SORBIDRAFT_04g028730 [*Sorghum bicolor*] > gi|241934158|gb|EES07303.1| hypothetical protein SORBIDRAFT_04g028730 [*Sorghum bicolor*]	0.76	1106	1759
	782-802	XP_002465485	hypothetical protein SORBIDRAFT_01g039690 [*Sorghum bicolor*] > gi|241919339|gb|EER92483.1| hypothetical protein SORBIDRAFT_01g039690 [*Sorghum bicolor*]	1.00	1107	1760
		NP_001131665	hypothetical protein LOC100193025 [*Zea mays*] > gi|194692196|gb|ACF80182.1| unknown [*Zea mays*]	0.92	1108	1761
		NP_001049699	Os03g0273200 [*Oryza sativa Japonica* Group] > gi|122247226|sp|Q10ND7.1| LAC10_ORYSJ RecName: Full = Laccase-10; AltName: Full = Benzenediol:oxygen oxidoreductase 10; AltName: Full = Diphenol oxidase 10; AltName: Full = Urishiol oxidase 10; Flags: Precursor > gi|108707435|gb|ABF95230.1| laccase, putative, expressed [*Oryza sativa Japonica* Group] > gi|113548170|dbj|BAF11613.1| Os03g0273200 [*Oryza sativa Japonica* Group] > gi|215704111|dbj|BAG92951.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215765805|dbj|BAG87502.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222624652|gb|EEE58784.1| hypothetical protein OsJ_10313 [*Oryza sativa Japonica* Group]	0.82	1109	1762
		XP_002531824	laccase, putative [*Ricinus communis*] > gi|223528520|gb|EEF30544.1| laccase, putative [*Ricinus communis*]	0.73	1110	1763

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		XP_002278215	PREDICTED: hypothetical protein [*Vitis vinifera*]	0.73	1111	1764
		CBI16199	unnamed protein product [*Vitis vinifera*]	0.72	1112	
		XP_002278232	PREDICTED: hypothetical protein [*Vitis vinifera*]	0.73	1113	1765
		XP_002282823	PREDICTED: hypothetical protein [*Vitis vinifera*]	0.74	1114	1766
	943-963	NP_001183899	hypothetical protein LOC100502492 [*Zea mays*] > gi|223948465|gb|ACN28316.1| unknown [*Zea mays*] > gi|238015342|gb|ACR38706.1| unknown [*Zea mays*]	1.00	1115	1767
		NP_001148479	L-ascorbate oxidase [*Zea mays*] > gi|195619672|gb|ACG31666.1| L-ascorbate oxidase precursor [*Zea mays*]	0.90	1116	1768
		XP_002456566	hypothetical protein SORBIDRAFT_03g038550 [*Sorghum bicolor*] > gi|241928541|gb|EES01686.1| hypothetical protein SORBIDRAFT_03g038550 [*Sorghum bicolor*]	0.89	1117	1769
		NP_001044679	Os01g0827300 [*Oryza sativa Japonica* Group] > gi|75331868|sp|Q941X2.1| LAC3_ORYSJ RecName: Full = Laccase-3; AltName: Full = Benzenediol:oxygen oxidoreductase 3; AltName: Full = Diphenol oxidase 3; AltName: Full = Urishiol oxidase 3; Flags: Precursor > gi|15624045|dbj|BAB68098.1| putative laccase [*Oryza sativa Japonica* Group] > gi|113534210|dbj|BAF06593.1| Os01g0827300 [*Oryza sativa Japonica* Group] > gi|215701334|dbj|BAG92758.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222619479|gb|EEE55611.1| hypothetical protein OsJ_03932 [*Oryza sativa Japonica* Group]	0.83	1118	1770
		ACN27868	unknown [*Zea mays*]	0.80	1119	1771
		XP_002315131	laccase 90c [*Populus trichocarpa*] > gi|222864171|gb|EEF01302.1| laccase 90c [*Populus trichocarpa*]	0.70	1120	1772
		CBI25418	unnamed protein product [*Vitis vinifera*]	0.71	1121	1773
		XP_002273875	PREDICTED: hypothetical protein [*Vitis vinifera*]	0.71	1122	1774
	852-872	NP_001105875	putative laccase [*Zea mays*] > gi|84618781|emb|CAJ30500.1| putative laccase [*Zea mays*]	1.00	1123	1775
		ACN28855	unknown [*Zea mays*]	0.98	1124	1776
		NP_001146658	hypothetical protein LOC100280258 [*Zea mays*] > gi|219888209|gb|ACL54479.1| unknown [*Zea mays*]	0.94	1125	1777
		XP_002458746	hypothetical protein SORBIDRAFT_03g039520 [*Sorghum bicolor*] > gi|241930721|gb|EES03866.1|	0.91	1126	1778

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			hypothetical protein SORBIDRAFT__03g039520 [*Sorghum bicolor*]			
		NP__001044772	Os01g0842400 [*Oryza sativa Japonica* Group] > gi|75321217|sp|Q5N9X2.1| LAC4__ORYSJ RecName: Full = Laccase-4; AltName: Full = Benzenediol:oxygen oxidoreductase 4; AltName: Full = Diphenol oxidase 4; AltName: Full = Urishiol oxidase 4; Flags: Precursor > gi|56784239|dbj|BAD81734.1| putative laccase LAC5-6 [*Oryza sativa Japonica* Group] > gi|113534303|dbj|BAF06686.1| Os01g0842400 [*Oryza sativa Japonica* Group] > gi|215697155|dbj|BAG91149.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.80	1127	1779
		EAZ14115	hypothetical protein OsJ__04039 [*Oryza sativa Japonica* Group]	0.80	1128	
		EEC71777	hypothetical protein OsI__04389 [*Oryza sativa Indica* Group]	0.80	1129	
		AAC04576	putative high-pI laccase [*Oryza sativa Japonica* Group]	0.79	1130	1780
		BAJ99773	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.77	1131	1781
		XP__002458747	hypothetical protein SORBIDRAFT__03g039530 [*Sorghum bicolor*] > gi|241930722|gb|EES03867.1| hypothetical protein SORBIDRAFT__03g039530 [*Sorghum bicolor*]	0.78	1132	1782
	801-821	XP__002441216	hypothetical protein SORBIDRAFT__09g022460 [*Sorghum bicolor*] > gi|241946501|gb|EES19646.1| hypothetical protein SORBIDRAFT__09g022460 [*Sorghum bicolor*]	1.00	1133	1783
		NP__001105874	putative laccase [*Zea mays*] > gi|84618777|emb|CAJ30498.1| putative laccase [*Zea mays*]	0.89	1134	1784
		Q0DHL5	RecName: Full = Putative laccase-11; AltName: Full = Benzenediol:oxygen oxidoreductase 11; AltName: Full = Diphenol ocidase 11; AltName: Full = Urishiol oxidase 11 > gi|222631843|gb|EEE63975.1| hypothetical protein OsJ__18801 [*Oryza sativa Japonica* Group]	0.88	1135	
		NP__001055744	Os05g0458300 [*Oryza sativa Japonica* Group] > gi|113579295|dbj|BAF17658.1| Os05g0458300 [*Oryza sativa Japonica* Group]	0.81	1136	1785
		XP__002456622	hypothetical protein SORBIDRAFT__03g039570 [*Sorghum bicolor*] > gi|241928597|gb|EES01742.1| hypothetical protein	0.76	1137	1786

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			SORBIDRAFT_03g039570 [*Sorghum bicolor*]			
		ACG47007	L-ascorbate oxidase precursor [*Zea mays*]	0.76	1138	1787
		NP_001105921	putative laccase [*Zea mays*] > gi|84618783|emb|CAJ30497.1| putative laccase [*Zea mays*]	0.74	1139	1788
	673-693	NP_001168720	hypothetical protein LOC100382512 [*Zea mays*] > gi|223950395|gb|ACN29281.1| unknown [*Zea mays*]	1.00	1140	1789
		XP_002448765	hypothetical protein SORBIDRAFT_06g032800 [*Sorghum bicolor*] > gi|241939948|gb|EES13093.1| hypothetical protein SORBIDRAFT_06g032800 [*Sorghum bicolor*]	0.98	1141	1790
		NP_001131374	hypothetical protein LOC100192699 [*Zea mays*] > gi|195620734|gb|ACG32197.1| oligosaccharyl transferase STT3 subunit [*Zea mays*]	0.98	1142	1791
		NP_001054248	Os04g0675500 [*Oryza sativa Japonica* Group] > gi|38344929|emb|CAE03245.2| OSJNBa0018M05.20 [*Oryza sativa Japonica* Group] > gi|90399055|emb|CAJ86104.1| H0103C06.8 [*Oryza sativa Indica* Group] > gi|113565819|dbj|BAF16162.1| Os04g0675500 [*Oryza sativa Japonica* Group] > gi|125550210|gb|EAY96032.1| hypothetical protein OsI_17905 [*Oryza sativa Indica* Group] > gi|125592048|gb|EAZ32398.1| hypothetical protein OsJ_16609 [*Oryza sativa Japonica* Group] > gi|215708677|dbj|BAG93946.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.96	1143	1792
		BAJ87792	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.94	1144	1793
		XP_002269119	PREDICTED: hypothetical protein [*Vitis vinifera*]	0.86	1145	1794
		CBG76274	OO_Ba0005L10-OO_Ba0081K17.25 [*Oryza officinalis*]	0.93	1146	1795
		XP_002318345	predicted protein [*Populus trichocarpa*] > gi|222859018|gb|EEE96565.1| predicted protein [*Populus trichocarpa*]	0.86	1147	1796
		XP_002891078	hypothetical protein ARALYDRAFT_891007 [*Arabidopsis lyrata* subsp. *lyrata*] > gi|297336920|gb|EFH67337.1| hypothetical protein ARALYDRAFT_891007 [*Arabidopsis lyrata* subsp. *lyrata*]	0.86	1148	1797
		XP_002329687	predicted protein [*Populus trichocarpa*]	0.85	1149	1798

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			> gi|222870595|gb|EEF07726.1| predicted protein [*Populus trichocarpa*]			
	1539-1559	XP_002462694	hypothetical protein SORBIDRAFT_02g030360 [*Sorghum bicolor*] > gi|241926071|gb|EER99215.1| hypothetical protein SORBIDRAFT_02g030360 [*Sorghum bicolor*]	1.00	1150	1799
		NP_001168360	hypothetical protein LOC100382128 [*Zea mays*] > gi|223947749|gb|ACN27958.1| unknown [*Zea mays*]	0.92	1151	1800
		NP_001063714	Os09g0524300 [*Oryza sativa Japonica* Group] > gi|52076031|dbj|BAD46484.1| ethionine resistance protein-like [*Oryza sativa Japonica* Group] > gi|255679074|dbj|BAF25628.2| Os09g0524300 [*Oryza sativa Japonica* Group]	0.80	1152	1801
		ABG73448	MATE efflux family protein [*Oryza brachyantha*]	0.80	1153	1802
		EAZ09807	hypothetical protein OsI_32095 [*Oryza sativa Indica* Group]	0.80	1154	
		XP_002444635	hypothetical protein SORBIDRAFT_07g025190 [*Sorghum bicolor*] > gi|241940985|gb|EES14130.1| hypothetical protein SORBIDRAFT_07g025190 [*Sorghum bicolor*]	0.73	1155	1803
		BAD09230	putative ripening regulated protein DDTFR18 [*Oryza sativa Japonica* Group]	0.70	1156	1804
	1198-1218	NP_001146658	hypothetical protein LOC100280258 [*Zea mays*] > gi|219888209|gb|ACL54479.1| unknown [*Zea mays*]	1.00	1157	1805
		NP_001105875	putative laccase [*Zea mays*] > gi|84618781|emb|CAJ30500.1| putative laccase [*Zea mays*]	0.95	1158	1806
		ACN28855	unknown [*Zea mays*]	0.92	1159	1807
		XP_002458746	hypothetical protein SORBIDRAFT_03g039520 [*Sorghum bicolor*] > gi|241930721|gb|EES03866.1| hypothetical protein SORBIDRAFT_03g039520 [*Sorghum bicolor*]	0.91	1160	1808
		NP_001044772	Os01g0842400 [*Oryza sativa Japonica* Group] > gi|75321217|sp|Q5N9X2.1| LAC4_ORYSJ RecName: Full = Laccase-4; AltName: Full = Benzenediol:oxygen oxidoreductase 4; AltName: Full = Diphenol oxidase 4; AltName: Full = Urishiol oxidase 4; Flags: Precursor > gi|56784239|dbj|BAD81734.1| putative laccase LAC5-6 [*Oryza sativa Japonica* Group] > gi|113534303|dbj|BAF06686.1| Os01g0842400 [*Oryza sativa Japonica* Group] > gi|215697155|dbj|BAG91149.1| unnamed protein	0.80	1161	1809

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			product [*Oryza sativa Japonica* Group]			
		EAZ14115	hypothetical protein OsJ_04039 [*Oryza sativa Japonica* Group]	0.80	1162	
		EEC71777	hypothetical protein OsI_04389 [*Oryza sativa Indica* Group]	0.80	1163	
		BAJ99773	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.78	1164	1810
		AAC04576	putative high-pI laccase [*Oryza sativa Japonica* Group]	0.78	1165	1811
		XP_002458747	hypothetical protein SORBIDRAFT_03g039530 [*Sorghum bicolor*] > gi|241930722|gb|EES03867.1| hypothetical protein SORBIDRAFT_03g039530 [*Sorghum bicolor*]	0.77	1166	1812
	934-954	ACN27868	unknown [*Zea mays*]	1.00	1167	1813
		NP_001148479	L-ascorbate oxidase [*Zea mays*] > gi|195619672|gb|ACG31666.1| L-ascorbate oxidase precursor [*Zea mays*]	0.94	1168	1814
		XP_002456566	hypothetical protein SORBIDRAFT_03g038550 [*Sorghum bicolor*] > gi|241928541|gb|EES01686.1| hypothetical protein SORBIDRAFT_03g038550 [*Sorghum bicolor*]	0.90	1169	1815
		NP_001183899	hypothetical protein LOC100502492 [*Zea mays*] > gi|223948465|gb|ACN28316.1| unknown [*Zea mays*] > gi|238015342|gb|ACR38706.1| unknown [*Zea mays*]	0.88	1170	1816
		NP_001044679	Os01g0827300 [*Oryza sativa Japonica* Group] > gi|75331868|sp|Q941X2.1| LAC3_ORYSJ RecName: Full = Laccase-3; AltName: Full = Benzenediol:oxygen oxidoreductase 3; AltName: Full = Diphenol oxidase 3; AltName: Full = Urishiol oxidase 3; Flags: Precursor > gi|15624045|dbj|BAB68098.1| putative laccase [*Oryza sativa Japonica* Group] > gi|113534210|dbj|BAF06593.1| Os01g0827300 [*Oryza sativa Japonica* Group] > gi|215701334|dbj|BAG92758.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222619479|gb|EEE55611.1| hypothetical protein OsJ_03932 [*Oryza sativa Japonica* Group]	0.81	1171	1817
Predicted folded 24-nts-long seq 52739	1620-1643	NP_001137083	hypothetical protein LOC100217256 [*Zea mays*] > gi|194698278|gb|ACF83223.1| unknown [*Zea mays*]	1.00	1172	1818
		XP_002446946	hypothetical protein SORBIDRAFT_06g025600 [*Sorghum bicolor*] > gi|241938129|gb|EES11274.1| hypothetical protein	0.75	1173	1819

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			SORBIDRAFT_06g025600 [*Sorghum bicolor*]			
Predicted zma mir 49816	334-354	XP_002459032	hypothetical protein SORBIDRAFT_03g044830 [*Sorghum bicolor*] > gi|241931007|gb|EES04152.1| hypothetical protein SORBIDRAFT_03g044830 [*Sorghum bicolor*]	1.00	1174	1820
		NP_001131974	hypothetical protein LOC100193372 [*Zea mays*] > gi|194693076|gb|ACF80622.1| unknown [*Zea mays*]	0.90	1175	1821
		BAJ85237	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326511587|dbj|BAJ91938.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.84	1176	1822
		NP_001045294	Os01g0931100 [*Oryza sativa Japonica* Group] > gi|57899654|dbj|BAD87323.1| unknown protein [*Oryza sativa Japonica* Group] > gi|57900117|dbj|BAD88179.1| unknown protein [*Oryza sativa Japonica* Group] > gi|113534825|dbj|BAF07208.1| Os01g0931100 [*Oryza sativa Japonica* Group] > gi|215697092|dbj|BAG91086.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.85	1177	1823
	116-136	CAE04743	OSJNBb0060E08.6 [*Oryza sativa Japonica* Group] > gi|116309791|emb|CAH66831.1| OSIGBa0148A10.8 [*Oryza sativa Indica* Group]	1.00	1178	1824
		NP_001053941	0s04g0625800 [*Oryza sativa Japonica* Group] > gi|113565512|dbj|BAF15855.1| Os04g0625800 [*Oryza sativa Japonica* Group] > gi|215767966|dbj|BAH00195.1| unnamed protein product [*Oryza sativa Japonica* Group]	1.00	1179	1825
		EAY95645	hypothetical protein OsI_17510 [*Oryza sativa Indica* Group]	1.00	1180	
		NP_001131852	hypothetical protein LOC100193230 [*Zea mays*] > gi|194692726|gb|ACF80447.1| unknown [*Zea mays*]	0.79	1181	1826
		BAK03410	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326525779|dbj|BAJ88936.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.81	1182	1827
		XP_002447134	hypothetical protein SORBIDRAFT_06g029180 [*Sorghum bicolor*] > gi|241938317|gb|EES11462.1| hypothetical protein SORBIDRAFT_06g029180 [*Sorghum bicolor*]	0.78	1183	1828
		NP_001168401	hypothetical protein LOC100382170 [*Zea mays*] > gi|223948043|gb|ACN28105.1| unknown [*Zea mays*]	0.77	1184	1829

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		ACF85557	unknown [*Zea mays*]	0.74	1185	1830
		NP_001141359	hypothetical protein LOC100273450 [*Zea mays*] > gi|194704160|gb|ACF86164.1| unknown [*Zea mays*]	0.74	1186	1831
	81-101	XP_002463519	hypothetical protein SORBIDRAFT_01g001270 [*Sorghum bicolor*] > gi|241917373|gb|EER90517.1| hypothetical protein SORBIDRAFT_01g001270 [*Sorghum bicolor*]	1.00	1187	1832
		BAK01513	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.86	1188	1833
		NP_001051898	Os03g0849600 [*Oryza sativa Japonica* Group] > gi|28269403|gb|AAO37946.1| putative conserved oligomeric Golgi complex component [*Oryza sativa Japonica* Group] > gi|108712114|gb|ABF99909.1| brefeldin A-sensitive Golgi protein, putative, expressed [*Oryza sativa Japonica* Group] > gi|113550369|dbj|BAF13812.1| Os03g0849600 [*Oryza sativa Japonica* Group] > gi|125588645|gb|EAZ29309.1| hypothetical protein OsJ_13370 [*Oryza sativa Japonica* Group]	0.85	1189	1834
		EEC76534	hypothetical protein OsI_14326 [*Oryza sativa Indica* Group]	0.85	1190	
	322-342	NP_001168448	hypothetical protein LOC100382221 [*Zea mays*] > gi|223948365|gb|ACN28266.1| unknown [*Zea mays*]	1.00	1191	1835
	98-118	BAD05744	putative RNA Binding Protein 45 [*Oryza sativa Japonica* Group] > gi|40253847|dbj|BAD05783.1| putative RNA Binding Protein 45 [*Oryza sativa Japonica* Group]	1.00	1192	1836
		EEE68172	hypothetical protein OSJ_26296 [*Oryza sativa Japonica* Group]	0.75	1193	
		ACF85557	unknown [*Zea mays*]	0.78	1194	1837
		NP_001141359	hypothetical protein LOC100273450 [*Zea mays*] > gi|194704160|gb|ACF86164.1| unknown [*Zea mays*]	0.78	1195	1838
aqc-miR529	955-975	AAX83875	teosinte glume architecture 1 [*Zea mays* subsp. *mays*]	1.00	1196	1839
		AAX83872	teosinte glume architecture 1 [*Zea mays* subsp. *mays*]	0.99	1197	1840
		AAX83873	teosinte glume architecture 1 [*Zea mays* subsp. *mays*] > gi|62467440|gb|AAX83874.1| teosinte glume architecture 1 [*Zea mays* subsp. *mays*]	0.99	1198	1841
		XP_002445815	hypothetical protein SORBIDRAFT_07g026220 [*Sorghum bicolor*] > gi|241942165|gb|EES15310.1| hypothetical protein SORBIDRAFT_07g026220 [*Sorghum bicolor*]	0.80	1199	1842

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
	831-851	ADX60108	SBP transcription factor [*Zea mays*]	1.00	1200	1843
		XP__002446904	hypothetical protein SORBIDRAFT__06g024630 [*Sorghum bicolor*] > gi|241938087|gb|EES11232.1| hypothetical protein SORBIDRAFT__06g024630 [*Sorghum bicolor*]	0.72	1201	1844
	882-902	ACN30570	unknown [*Zea mays*] > gi|223973927|gb|ACN31151.1| unknown [*Zea mays*] > gi|323388595|gb|ADX60102.1| SBP transcription factor [*Zea mays*]	1.00	1202	1845
		NP__001145445	hypothetical protein LOC100278824 [*Zea mays*] > gi|195656399|gb|ACG47667.1| hypothetical protein [*Zea mays*]	0.98	1203	1846
		XP__002450775	hypothetical protein SORBIDRAFT__05g017510 [*Sorghum bicolor*] > gi|241936618|gb|EES09763.1| hypothetical protein SORBIDRAFT__05g017510 [*Sorghum bicolor*]	0.87	1204	1847
	656-676	NP__001137049	hypothetical protein LOC100217221 [*Zea mays*] > gi|194698154|gb|ACF83161.1| unknown [*Zea mays*]	1.00	1205	1848
	1248-1268	XP__002447211	hypothetical protein SORBIDRAFT__06g030520 [*Sorghum bicolor*] > gi|241938394|gb|EES11539.1| hypothetical protein SORBIDRAFT__06g030520 [*Sorghum bicolor*]	1.00	1206	1849
		NP__001132831	hypothetical protein LOC100194321 [*Zea mays*] > gi|194695516|gb|ACF81842.1| unknown [*Zea mays*]	0.90	1207	1850
		NP__001054060	Os04g0644700 [*Oryza sativa Japonica* Group] > gi|148886836|sp|P0C541.1| COPE2__ORYSJ RecName: Full = Coatomer subunit epsilon-2; AltName: Full = Epsilon-coat protein 2; Short = Epsilon-COP 2 > gi|38344895|emb|CAD41918.2| OSJNBa0033G05.19 [*Oryza sativa Japonica* Group] > gi|113565631|dbj|BAF15974.1| Os04g0644700 [*Oryza sativa Japonica* Group] > gi|125591839|gb|EAZ32189.1| hypothetical protein OsJ__16395 [*Oryza sativa Japonica* Group]	0.80	1208	1851
		A2XY73	RecName: Full = Coatomer subunit epsilon-2; AltName: Full = Epsilon-coat protein 2; Short = Epsilon-COP 2 > gi|90399097|emb|CAJ86157.1| H0413E07.10 [*Oryza sativa Indica* Group]	0.80	1209	
		EAY95783	hypothetical protein OsI__17658 [*Oryza sativa Indica* Group]	0.80	1210	
	82-102	ACR34442	unknown [*Zea mays*]	1.00	1211	1852
	82-102	NP__00145733	hypothetical protein LOC100279240 [*Zea mays*]	1.00	1212	1853

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			> gi|219884215|gb|ACL52482.1| unknown [*Zea mays*]			
		XP_002460490	hypothetical protein SORBIDRAFT_02g029300 [*Sorghum bicolor*] > gi|241923867|gb|EER97011.1| hypothetical protein SORBIDRAFT_02g029300 [*Sorghum bicolor*]	0.87	1213	1854
		NP_001063612	Os09g0507100 [*Oryza sativa Japonica* Group] > gi|122234416|sp|Q0JOK1.1| SPL18_ORYSJ RecName: Full = Squamosa promoter-binding-like protein 18 > gi|113631845|dbj|BAF25526.1| Os09g0507100 [*Oryza sativa Japonica* Group]	0.71	1214	1855
	996-1016	ACF86782	unknown [*Zea mays*] > gi|323388573|gb|ADX60091.1| SBP transcription factor [*Zea mays*]	1.00	1215	1856
		ACG45113	squamosa promoter-binding-like protein 9 [*Zea mays*]	1.00	1216	1857
		XP_002462571	hypothetical protein SORBIDRAFT_02g028420 [*Sorghum bicolor*] > gi|241925948|gb|EER99092.1| hypothetical protein SORBIDRAFT_02g028420 [*Sorghum bicolor*]	0.83	1217	1858
		NP_001136945	hypothetical protein LOC100217104 [*Zea mays*] > gi|194697718|gb|ACF82943.1| unknown [*Zea mays*]	0.76	1218	1859
	1120-1140	ACL52941	unknown [*Zea mays*]	1.00	1219	1860
		XP_002444771	hypothetical protein SORBIDRAFT_07g027740 [*Sorghum bicolor*] > gi|241941121|gb|EES14266.1| hypothetical protein SORBIDRAFT_07g027740 [*Sorghum bicolor*]	0.76	1220	1861
	1348-1368	XP_002438971	hypothetical protein SORBIDRAFT_10g029190 [*Sorghum bicolor*] > gi|241917194|gb|EER90338.1| hypothetical protein SORBIDRAFT_10g029190 [*Sorghum bicolor*]	1.00	1221	1862
		NP_001149534	squamosa promoter-binding-like protein 11 [*Zea mays*] > gi|195627850|gb|ACG35755.1| squamosa promoter-binding-like protein 11 [*Zea mays*] > gi|195644948|gb|ACG41942.1| squamosa promoter-binding-like protein 11 [*Zea mays*]	0.88	1222	1863
	221-241	XP_002447219	hypothetical protein SORBIDRAFT_06g030650 [*Sorghum bicolor*] > gi|241938402|gb|EES11547.1| hypothetical protein SORBIDRAFT_06g030650 [*Sorghum bicolor*]	1.00	1223	1864
		NP_001169344	hypothetical protein LOC100383211 [*Zea mays*] > gi|224028835|gb|ACN33493.1| unknown [*Zea mays*]	0.92	1224	1865

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		NP_001147890	LOC100281500 [*Zea mays*] > gi|195614420|gb|ACG29040.1| zinc finger, C3HC4 type family protein [*Zea mays*]	0.90	1225	1866
		CAD41707	OSJNBa0010D21.9 [*Oryza sativa Japonica* Group] > gi|125549990|gb|EAY95812.1| hypothetical protein OsI_17683 [*Oryza sativa Indica* Group] > gi|125591860|gb|EAZ32210.1| hypothetical protein OsJ_16417 [*Oryza sativa Japonica* Group] > gi|215701084|dbj|BAG92508.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.74	1226	1867
	973-993	NP_001136945	hypothetical protein LOC100217104 [*Zea mays*] > gi|194697718|gb|ACF82943.1| unknown [*Zea mays*]	1.00	1227	1868
		XP_002462571	hypothetical protein SORBIDRAFT_02g028420 [*Sorghum bicolor*] > gi|241925948|gb|EER99092.1| hypothetical protein SORBIDRAFT_02g028420 [*Sorghum bicolor*]	0.82	1228	1869
		ACF86782	unknown [*Zea mays*] > gi|323388573|gb|ADX60091.1| SBP transcription factor [*Zea mays*]	0.76	1229	1870
		ACG45113	squamosa promoter-binding-like protein 9 [*Zea mays*]	0.76	1230	1871
	558-578	CAB56631	SBP-domain protein 5 [*Zea mays*]	1.00	1231	1872
		XP_002444771	hypothetical protein SORBIDRAFT_07g027740 [*Sorghum bicolor*] > gi|241941121|gb|EES14266.1| hypothetical protein SORBIDRAFT_07g027740 [*Sorghum bicolor*]	0.85	1232	1873
		ACL52941	unknown [*Zea mays*]	0.78	1233	1874
	1410-1430	NP_001152658	MTA/SAH nucleosidase [*Zea mays*] > gi|195658647|gb|ACG48791.1| MTA/SAH nucleosidase [*Zea mays*] > gi|223973627|gb|ACN31001.1| unknown [*Zea mays*]	1.00	1234	1875
		ACF83838	unknown [*Zea mays*]	0.88	1235	1876
		ACG39594	MTA/SAH nucleosidase [*Zea mays*]	0.88	1236	1877
		XP_002445813	hypothetical protein SORBIDRAFT_07g026190 [*Sorghum bicolor*] > gi|241942163|gb|EES15308.1| hypothetical protein SORBIDRAFT_07g026190 [*Sorghum bicolor*]	0.88	1237	1878
		ACN31483	unknown [*Zea mays*]	0.90	1238	1879
		NP_001056592	Os06g0112200 [*Oryza sativa Japonica* Group] > gi|7363290|dbj|BAA93034.1| methylthioadenosine/S-adenosyl homocysteine nucleosidase [*Oryza sativa Japonica* Group] > gi|32352128|dbj|BAC78557.1| hypothetical protein [*Oryza sativa Japonica* Group]	0.80	1239	1880

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			> gi|113594632|dbj|BAF18506.1| Os06g0112200 [*Oryza sativa Japonica* Group] > gi|125595804|gb|EAZ35584.1| hypothetical protein OsJ_19870 [*Oryza sativa Japonica* Group] > gi|215694661|dbj|BAG89852.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215740802|dbj|BAG96958.1| unnamed protein product [*Oryza sativa Japonica* Group]			
		AAL58883	methylthioadenosine/S-adenosyl homocysteine nucleosidase [*Oryza sativa*]	0.79	1240	1881
		ABR25495	mta/sah nucleosidase [*Oryza sativa Indica* Group]	0.79	1241	1882
		BAK03317	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326534118|dbj|BAJ89409.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.78	1242	1883
		EAY99382	hypothetical protein OsI_21350 [*Oryza sativa Indica* Group]	0.78	1243	
	1197-1217	AAX83872	teosinte glume architecture 1 [*Zea mays* subsp. *mays*]	1.00	1244	1884
		AAX83875	teosinte glume architecture 1 [*Zea mays* subsp. *mays*]	0.98	1245	1885
		AAX83873	teosinte glume architecture 1 [*Zea mays* subsp. *mays*] > gi|62467440|gb|AAX83874.1| teosinte glume architecture 1 [*Zea mays* subsp. *mays*]	0.99	1246	1886
		XP_002445815	hypothetical protein SORBIDRAFT_07g026220 [*Sorghum bicolor*] > gi|241942165|gb|EES15310.1| hypothetical protein SORBIDRAFT_07g026220 [*Sorghum bicolor*]	0.80	1247	1887
		BAK05794	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.63	1248	1888
Predicted folded 24-nts-long seq 52792	748-771	NP_001143705	hypothetical protein LOC100276442 [*Zea mays*] > gi|195625088|gb|ACG34374.1| hypothetical protein [*Zea mays*]	1.00	1281	1911
		ACF83056	unknown [*Zea mays*]	0.95	1282	1912
	1078-1101	ACF83056	unknown [*Zea mays*]	1.00	1283	1913
		NP_001143705	hypothetical protein LOC100276442 [*Zea mays*] > gi|195625088|gb|ACG34374.1| hypothetical protein [*Zea mays*]	0.88	1284	1914
Predicted folded 24-nts-long seq 51757	278-301	XP_002458944	hypothetical protein SORBIDRAFT_03g043140 [*Sorghum bicolor*] > gi|241930919|gb|EES04064.1| hypothetical protein SORBIDRAFT_03g043140 [*Sorghum bicolor*]	1.00	1285	1915
		ACF79162	unknown [*Zea mays*] > gi|194703646|gb|ACF85907.1| unknown [*Zea mays*]	0.98	1286	1916
		NP_001105336	fructose-bisphosphate aldolase, cytoplasmic isozyme [*Zea mays*]	0.98	1287	1917

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			> gi|113621|sp|P08440.1|ALF_MAIZE RecName: Full = Fructose-bisphosphate aldolase, cytoplasmic isozyme > gi|168420|gb|AAA33435.1| aldolase [*Zea mays*] > gi|295850|emb|CAA31366.1| fructose bisphosphate aldolase [*Zea mays*] > gi|225624|prf||1307278A cytoplasmic aldolase			
		NP_001150049	fructose-bisphosphate aldolase cytoplasmic isozyme [*Zea mays*] > gi|194704898|gb|ACF86533.1| unknown [*Zea mays*] > gi|195636310|gb|ACG37623.1| fructose-bisphosphate aldolase cytoplasmic isozyme [*Zea mays*]	0.98	1288	1918
		XP_002453822	hypothetical protein SORBIDRAFT_04g019020 [*Sorghum bicolor*] > gi|241933653|gb|EES06798.1| hypothetical protein SORBIDRAFT_04g019020 [*Sorghum bicolor*]	0.95	1289	1919
		P17784	RecName: Full = Fructose-bisphosphate aldolase cytoplasmic isozyme; AltName: Full = Gravity-specific protein GSC 233 > gi|41398198|gb|AAS05825.1| fructose 1,6-bisphosphate aldolase [*Oryza sativa Japonica* Group] > gi|50878379|gb|AAT85154.1| putative fructose-bisphosphate aldolase [*Oryza sativa Japonica* Group] > gi|50878433|gb|AAT85207.1| putative fructose-bisphosphate aldolase [*Oryza sativa Japonica* Group] > gi|169244417|gb|ACA50482.1| fructose-bisphosphate aldolase [*Oryza sativa Japonica* Group] > gi|306415953|gb|ADM86851.1| fructose-bisphosphate aldolase [*Oryza sativa Japonica* Group]	0.94	1290	
		BAI59774	aldolase C-1 [Phyllostachys edulis]	0.94	1291	1920
		EAY94426	hypothetical protein OsI_16195 [*Oryza sativa Indica* Group]	0.93	1292	
		CAA37290	unnamed protein product [*Oryza sativa Japonica* Group]	0.93	1293	1921
		ABG65931	Fructose-bisphosphate aldolase, cytoplasmic isozyme, putative, expressed [*Oryza sativa Japonica* Group] > gi|125574121|gb|EAZ15405.1| hypothetical protein OsJ_30817 [*Oryza sativa Japonica* Group] > gi|215701125|dbj|BAG92549.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215708712|dbj|BAG93981.1| unnamed protein	0.92	1294	1922

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			product [*Oryza sativa Japonica* Group]			
	686-709	NP__001145778	hypothetical protein LOC100279285 [*Zea mays*] > gi|219884395|gb|ACL52572.1| unknown [*Zea mays*]	1.00	1295	1923
		ACF87373	unknown [*Zea mays*]	1.00	1296	1924
		ACG25535	ribosomal RNA apurinic site specific lyase [*Zea mays*]	0.99	1297	1925
		XP__002455890	hypothetical protein SORBIDRAFT__03g026880 [*Sorghum bicolor*] > gi|241927865|gb|EES01010.1| hypothetical protein SORBIDRAFT__03g026880 [*Sorghum bicolor*]	0.79	1298	1926
	365-388	ACR36335	unknown [*Zea mays*]	1.00	1299	1927
		ACR35742	unknown [*Zea mays*]	0.75	1300	1928
	512-535	XP__002458102	hypothetical protein SORBIDRAFT__03g026990 [*Sorghum bicolor*] > gi|241930077|gb|EE503222.1| hypothetical protein SORBIDRAFT__03g026990 [*Sorghum bicolor*]	1.00	1301	1929
		NP__001151540	hydrogen-transporting ATP synthase, rotational mechanism [*Zea mays*] > gi|195605790|gb|ACG24725.1| hydrogen-transporting ATP synthase, rotational mechanism [*Zea mays*] > gi|195608344|gb|ACG26002.1| hydrogen-transporting ATP synthase, rotational mechanism [*Zea mays*] > gi|195647528|gb|ACG43232.1| hydrogen-transporting ATP synthase, rotational mechanism [*Zea mays*] > gi|195658703|gb|ACG48819.1| hydrogen-transporting ATP synthase, rotational mechanism [*Zea mays*]	0.93	1302	1930
		ACF82609	unknown [*Zea mays*]	0.93	1303	1931
		NP__001149611	LOC100283237 [*Zea mays*] > gi|194696248|gb|ACF82208.1| unknown [*Zea mays*] > gi|195605550|gb|ACG24605.1| hydrogen-transporting ATP synthase, rotational mechanism [*Zea mays*] > gi|195619622|gb|ACG31641.1| hydrogen-transporting ATP synthase, rotational mechanism [*Zea mays*] > gi|195628500|gb|ACG36080.1| hydrogen-transporting ATP synthase, rotational mechanism [*Zea mays*] > gi|195637444|gb|ACG38190.1| hydrogen-transporting ATP synthase, rotational mechanism [*Zea mays*] > gi|195644406|gb|ACG41671.1| hydrogen-transporting ATP synthase, rotational mechanism [*Zea mays*]	0.93	1304	1932
		BAJ87122	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.89	1305	1933
		NP__001043488	Os01g0600000 [*Oryza sativa Japonica* Group] > gi|113533019|dbj|BAF05402.1|	0.88	1306	1934

TABLE 6-continued

Target Genes of down regulated miRNAs Associated with Increased NUE (Table 2)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			Os01g0600000 [*Oryza sativa Japonica* Group] > gi|125571065|gb|EAZ12580.1| hypothetical protein OsJ_02485 [*Oryza sativa Japonica* Group] > gi|215768142|dbj|BAH00371.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218188591|gb|EEC71018.1| hypothetical protein OsI_02711 [*Oryza sativa Indica* Group]			
		ABF70110	mitochondrial ATP synthase g subunit family protein [*Musabalbisiana*]	0.78	1307	1935
		ABA40451	unknown [*Solanum tuberosum*]	0.72	1308	1936
		NP_001056144	Os05g0533800 [*Oryza sativa Japonica* Group] > gi|48843828|gb|AAT47087.1| unknown protein [*Oryza sativa Japonica* Group] > gi|113579695|dbj|BAF18058.1| Os05g0533800 [*Oryza sativa Japonica* Group] > gi|222632347|gb|EEE64479.1| hypothetical protein OsJ_19329 [*Oryza sativa Japonica* Group]	0.73	1309	1937
		BAJ90534	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.74	1310	1938
ath-miR2936	742-763	ACN26323	unknown [*Zea mays*] > gi|223944533|gb|ACN26350.1| unknown [*Zea mays*]	1.00	1389	2005
		BAC01259	glycosylphosphatidylinositol anchor attachment 1-like [*Oryza sativa Japonica* Group] > gi|125571593|gb|EAZ13108.1| hypothetical protein OsJ_03027 [*Oryza sativa Japonica* Group]	0.78	1390	2006
		EAY75389	hypothetical protein OsI_03287 [*Oryza sativa Indica* Group]	0.78	1391	

Table 6: Provided are the target Genes of miRNAs Associated with Increased NUE (Table 2) along with their GenBank Accession numbers and sequence identifiers (SEQ ID NO:).

"bind" = binding;

"pos" = position;

"hom" = homologue;

"p.p." = polypeptide;

"p.n." = polynucleotide.

TABLE 7

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
Predicted siRNA 59952	1180-1201	XP_002439783	hypothetical protein SORBIDRAFT_09g019980 [*Sorghum bicolor*] > gi|241945068|gb|EES18213.1| hypothetical protein SORBIDRAFT_09g019980 [*Sorghum bicolor*]	1.00	2007	2437

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		NP_001140772	hypothetical protein LOC100272847 [*Zea mays*] > gi|194701020|gb|ACF84594.1| unknown [*Zea mays*]	0.87	2008	2438
		ACG40649	hypothetical protein [*Zea mays*]	0.87	2009	2439
		NP_001140587	hypothetical protein LOC100272657 [*Zea mays*] > gi|194700088|gb|ACF84128.1| unknown [*Zea mays*]	0.85	2010	2440
		ACG28586	hypothetical protein [*Zea mays*]	0.83	2011	2441
		EEC79208	hypothetical protein OsI_19925 [*Oryza sativa Indica* Group]	0.73	2012	
	2775-2796	NP_001146628	hypothetical protein LOC100280226 [*Zea mays*] > gi|219888087|gb|ACL54418.1| unknown [*Zea mays*]	1.00	2013	2442
		EEE65008	hypothetical protein OsJ_19956 [*Oryza sativa Japonica* Group]	0.71	2014	
		BAA90807	putative SEU1 protein [*Oryza sativa Japonica* Group] > gi|215704489|dbj|BAG93923.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.71	2015	2443
Predicted siRNA 59626	220-238	ACR33998	unknown [*Zea mays*]	1.00	2016	2444
		NP_001141472	hypothetical protein LOC100273582 [*Zea mays*] > gi|194704716|gb|ACF86442.1| unknown [*Zea mays*]	1.00	2017	2445
	1435-1453	XP_002446603	hypothetical protein SORBIDRAFT_06g018770 [*Sorghum bicolor*] > gi|241937786|gb|EES10931.1| hypothetical protein SORBIDRAFT_06g018770 [*Sorghum bicolor*]	1.00	2018	2446
		NP_001159223	hypothetical protein LOC100304309 [*Zea mays*] > gi|223942807|gb|ACN25487.1| unknown [*Zea mays*]	0.92	2019	2447
		BAJ94860	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.79	2020	2448
		CAE03375	OSJNBa0036B21.17 [*Oryza sativa Japonica* Group]	0.80	2021	
		EEE61116	hypothetical protein OsJ_15040 [*Oryza sativa Japonica* Group]	0.80	2022	
		CBW45773	ORW1943Ba0077G13.1 [*Oryza rufipogon*]	0.80	2023	
		NP_001052976	Os04g0458200 [*Oryza sativa Japonica* Group] > gi|215715295|dbj|BAG95046.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218194967|gb|EEC77394.1| hypothetical protein OsI_16151 [*Oryza sativa Indica* Group] > gi|255675525|dbj|BAF14890.2| Os04g0458200 [*Oryza sativa Japonica* Group]	0.80	2024	2449
		CAH67071	OSIGBa0097P08.1 [*Oryza sativa Indica* Group]	0.79	2025	2450
	1613-1631	NP_001141472	hypothetical protein LOC100273582 [*Zea mays*] > gi|194704716|gb|ACF86442.1| unknown [*Zea mays*]	1.00	2026	2451
		ACR33998	unknown [*Zea mays*]	0.85	2027	2452
Predicted siRNA 60850	408-428	NP_001131645	hypothetical protein LOC100193004 [*Zea mays*] > gi|194692138|gb|ACF80153.1| unknown [*Zea mays*]	1.00	2028	2453

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
	481-501	ACG31592	hypothetical protein [*Zea mays*]	1.00	2029	2454
		NP_001132267	hypothetical protein LOC100193703 [*Zea mays*] > gi|194693920|gb|ACF81044.1| unknown [*Zea mays*]	1.00	2030	2455
Predicted siRNA 59961	1611-1630	XP_002463038	hypothetical protein SORBIDRAFT_02g036610 [*Sorghum bicolor*] > gi|241926415|gb|EER99559.1| hypothetical protein SORBIDRAFT_02g036610 [*Sorghum bicolor*]	1.00	2031	2456
		NP_001130320	hypothetical protein LOC100191414 [*Zea mays*] > gi|194688838|gb|ACF78503.1| unknown [*Zea mays*]	0.96	2032	2457
		BAJ88611	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.87	2033	2458
		NP_001060016	Os07g0566200 [*Oryza sativa Japonica* Group] > gi|75152457|sp|Q8H4S6.2|P2C64_ORYSJ RecName: Full = Probable protein phosphatase 2C 64; Short = OsPP2C64 > gi|33146759|dbj|BAC79670.1| putative protein phosphatase 2C [*Oryza sativa Japonica* Group] > gi|113611552|dbj|BAF21930.1| Os07g0566200 [*Oryza sativa Japonica* Group] > gi|125600752|gb|EAZ40328.1| hypothetical protein OsJ_24776 [*Oryza sativa Japonica* Group]	0.89	2034	2459
		NP_001150759	LOC100284392 [*Zea mays*] > gi|195641568|gb|ACG40252.1| catalytic/protein phosphatase type 2C [*Zea mays*]	0.92	2035	2460
		ACR38208	unknown [*Zea mays*]	0.92	2036	2461
		EAZ04367	hypothetical protein OsI_26509 [*Oryza sativa Indica* Group]	0.88	2037	
		ACN30598	unknown [*Zea mays*]	0.87	2038	2462
		ACF84784	unknown [*Zea mays*]	0.80	2039	2463
	802-821	XP_002462759	hypothetical protein SORBIDRAFT_02g031500 [*Sorghum bicolor*] > gi|241926136|gb|EER99280.1| hypothetical protein SORBIDRAFT_02g031500 [*Sorghum bicolor*]	1.00	2040	2464
		NP_001151289	RING-H2 finger protein ATL2B [*Zea mays*] > gi|195645562|gb|ACG42249.1| RING-H2 finger protein ATL2B [*Zea mays*] > gi|223946553|gb|ACN27360.1| unknown [*Zea mays*]	0.80	2041	2465
	540-559	XP_002438439	hypothetical protein SORBIDRAFT_10g019640 [*Sorghum bicolor*] > gi|241916662|gb|EER89806.1| hypothetical protein SORBIDRAFT_10g019640 [*Sorghum bicolor*]	1.00	2042	2466
		ACN33733	unknown [*Zea mays*]	0.89	2043	2467
		NP_001150669	amino acid permease [*Zea mays*] > gi|195640964|gb|ACG39950.1| amino acid permease [*Zea mays*]	0.89	2044	2468
		XP_002453115	hypothetical protein SORBIDRAFT_04g000290 [*Sorghum bicolor*]	0.82	2045	2469

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			> gi|241932946|gb|EES06091.1| hypothetical protein SORBIDRAFT_04g000290 [*Sorghum bicolor*]			
		NP_001136459	hypothetical protein LOC100216569 [*Zea mays*] > gi|194695786|gb|ACF81977.1| unknown [*Zea mays*]	0.80	2046	2470
		NP_001045585	Os02g0101000 [*Oryza sativa Japonica* Group] > gi|41053220|dbj|BAD08181.1| putative amino acid transport protein [*Oryza sativa Japonica* Group] > gi|113535116|dbj|BAF07499.1| Os02g0101000 [*Oryza sativa Japonica* Group] > gi|215704334|dbj|BAG93768.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218189857|gb|EEC72284.1| hypothetical protein OsI_05452 [*Oryza sativa Indica* Group] > gi|222621988|gb|EEE56120.1| hypothetical protein OsJ_04987 [*Oryza sativa Japonica* Group]	0.78	2047	2471
		BAJ96557	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326523625|dbj|BAJ92983.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.73	2048	2472
		XP_002446139	hypothetical protein SORBIDRAFT_06g002240 [*Sorghum bicolor*] > gi|241937322|gb|EES10467.1| hypothetical protein SORBIDRAFT_06g002240 [*Sorghum bicolor*]	0.72	2049	2473
		NP_001147785	amino acid permease [*Zea mays*] > gi|195613758|gb|ACG28709.1| amino acid permease [*Zea mays*]	0.71	2050	2474
	987-1006	NP_001132785	hypothetical protein LOC100194274 [*Zea mays*] > gi|194695392|gb|ACF81780.1| unknown [*Zea mays*]	1.00	2051	2475
		NP_001150926	bHLH transcription factor GBOF-1 [*Zea mays*] > gi|195642998|gb|ACG40967.1| bHLH transcription factor GBOF-1 [*Zea mays*]	0.96	2052	2476
		XP_002462650	hypothetical protein SORBIDRAFT_02g029530 [*Sorghum bicolor*] > gi|241926027|gb|EER99171.1| hypothetical protein SORBIDRAFT_02g029530 [*Sorghum bicolor*]	0.79	2053	2477
		NP_001149110	LOC100282732 [*Zea mays*] > gi|195624818|gb|ACG34239.1| bHLH transcription factor GBOF-1 [*Zea mays*]	0.76	2054	2478
		ACR35934	unknown [*Zea mays*]	0.75	2055	2479
	235-254	NP_001065691	Os11g0136600 [*Oryza sativa Japonica* Group] > gi|33340240|gb|AAQ14593.1| AF319480_1 calcium-dependent calmodulin-independent protein kinase [*Oryza sativa*] > gi|33340242|gb|AAQ14594.1| AF319481_1 calcium-dependent calmodulin-independent protein	1.00		2480

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			kinase [*Oryza sativa*] > gi|77548548|gb|ABA91345.1| Calcium-dependent protein kinase, isoform 2, putative, expressed [*Oryza sativa Japonica* Group] > gi|113644395|dbj|BAF27536.1| Os11g0136600 [*Oryza sativa Japonica* Group]			
Predicted siRNA 56542	452-472	XP_002465086	hypothetical protein SORBIDRAFT_01g031850 [*Sorghum bicolor*] > gi|241918940|gb|EER92084.1| hypothetical protein SORBIDRAFT_01g031850 [*Sorghum bicolor*]	1.00	2056	2481
		NP_001145189	hypothetical protein LOC100278439 [*Zea mays*] > gi|195652469|gb|ACG45702.1| hypothetical protein [*Zea mays*]	0.92	2057	2482
		NP_001050454	Os03g0439700 [*Oryza sativa Japonica* Group] > gi|108709042|gb|ABF96837.1| expressed protein [*Oryza sativa Japonica* Group] > gi|113548925|dbj|BAF12368.1| Os03g0439700 [*Oryza sativa Japonica* Group] > gi|222625197|gb|EEE59329.1| hypothetical protein OsJ_11404 [*Oryza sativa Japonica* Group]	0.78	2058	2483
		AAR89010	expressed protein [*Oryza sativa Japonica* Group]	0.77	2059	
		BAJ96331	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.77	2060	2484
Predicted siRNA 56353	585-608	NP_001183654	hypothetical protein LOC100502248 [*Zea mays*] > gi|238013682|gb|ACR37876.1| unknown [*Zea mays*]	1.00	2061	2485
		XP_002464467	hypothetical protein SORBIDRAFT_01g018940 [*Sorghum bicolor*] > gi|241918321|gb|EER91465.1| hypothetical protein SORBIDRAFT_01g018940 [*Sorghum bicolor*]	0.94	2062	2486
		AAL59033	hypothetical protein [*Oryza sativa Japonica* Group] > gi|31432747|gb|AAP54340.1| expressed protein [*Oryza sativa Japonica* Group]	0.78	2063	
		BAJ89715	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326505214|dbj|BAK02994.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.77	2064	2487
		BAK03788	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.75	2065	2488
		NP_001064892	Os10g0484900 [*Oryza sativa Japonica* Group] > gi|255679504|dbj|BAF26806.2| Os10g0484900 [*Oryza sativa Japonica* Group]	0.76	2066	2489
	23-46	XP_002463222	hypothetical protein SORBIDRAFT_02g040060 [*Sorghum bicolor*] > gi|241926599|gb|EER99743.1| hypothetical protein SORBIDRAFT_02g040060 [*Sorghum bicolor*]	1.00	2067	2490

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)						
Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		NP_001105697	thiazole biosynthetic enzyme 1-2, chloroplastic precursor [*Zea mays*] > gi|2501190|sp|Q41739.1|THI42_MAIZE RecName: Full = Thiazole biosynthetic enzyme 1-2, chloroplastic; Flags: Precursor > gi|596080|gb|AAA96739.1| thiamine biosynthetic enzyme [*Zea mays*]	0.93	2068	2491
		ACF87708	unknown [*Zea mays*] > gi|224033955|gb|ACN36053.1| unknown [*Zea mays*]	0.93	2069	2492
		NP_001105696	thiazole biosynthetic enzyme 1-1, chloroplastic precursor [*Zea mays*] > gi|2501189|sp|Q41738.1|THI41_MAIZE RecName: Full = Thiazole biosynthetic enzyme 1-1, chloroplastic; Flags: Precursor > gi|596078|gb|AAA96738.1| thiamine biosynthetic enzyme [*Zea mays*] > gi|194704634|gb|ACF86401.1| unknown [*Zea mays*]	0.92	2070	2493
		NP_001059841	Os07g0529600 [*Oryza sativa Japonica* Group] > gi|32352138|dbj|BAC78562.1| thiamine biosynthetic enzyme [*Oryza sativa Japonica* Group] > gi|113611377|dbj|BAF21755.1| Os07g0529600 [*Oryza sativa Japonica* Group] > gi|215712225|dbj|BAG94352.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.87	2071	2494
		BAC45141	putative thiamine biosynthesis protein [*Oryza sativa Japonica* Group] > gi|125600511|gb|EAZ40087.1| hypothetical protein OsJ_24530 [*Oryza sativa Japonica* Group]	0.87	2072	2495
		EAZ04139	hypothetical protein OsI_26282 [*Oryza sativa Indica* Group]	0.87	2073	
		XP_002458014	hypothetical protein SORBIDRAFT_03g025520 [*Sorghum bicolor*] > gi|241929989|gb|EES03134.1| hypothetical protein SORBIDRAFT_03g025520 [*Sorghum bicolor*]	0.91	2074	2496
		ACF85034	unknown [*Zea mays*]	0.84	2075	2497
		AAZ93636	pathogen-induced defense-responsive protein 8 [*Oryza sativa Indica* Group]	0.84	2076	2498
	71-94	ACG31888	ubiquitin-conjugating enzyme E2 W [*Zea mays*]	1.00	2077	2499
		NP_001050906	Os03g0681400 [*Oryza sativa Japonica* Group] > gi|57164486|gb|AAK00965.2| AC079736_5 putative ubiquitin-conjugating enzyme E2 [*Oryza sativa Japonica* Group] > gi|108710422|gb|ABF98217.1| Ubiquitin-conjugating enzyme family protein, expressed [*Oryza sativa Japonica* Group] > gi|113549377|dbj|BAF12820.1| Os03g0681400 [*Oryza sativa Japonica* Group]	0.71	2078	2500

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			> gi|215737341|dbj|BAG96270.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222625566|gb|EEE59698.1| hypothetical protein OsJ_12122 [*Oryza sativa Japonica* Group]			
		XP_002464080	hypothetical protein SORBIDRAFT_01g011940 [*Sorghum bicolor*] > gi|241917934|gb|EER91078.1| hypothetical protein SORBIDRAFT_01g011940 [*Sorghum bicolor*]	0.72	2079	2501
		XP_002443656	hypothetical protein SORBIDRAFT_08g022990 [*Sorghum bicolor*] > gi|241944349|gb|EES17494.1| hypothetical protein SORBIDRAFT_08g022990 [*Sorghum bicolor*]	0.71	2080	2502
		NP_001146940	ubiquitin-conjugating enzyme E2 W [*Zea mays*] > gi|195605468|gb|ACG24564.1| ubiquitin-conjugating enzyme E2 W [*Zea mays*]	0.70	2081	2503
Predicted siRNA 59965	614-634	NP_001047323	Os02g0596900 [*Oryza sativa Japonica Group*] > gi|75291091|sp|Q6K908.1|ARP3_ORYSJ RecName: Full = Actin-related protein 3 > gi|190356069|sp|A2X6S3.2|ARP3_ORYSI RecName: Full = Actin-related protein 3 > gi|47847830|dbj|BAD21625.1| putative arp3 [*Oryza sativa Japonica* Group] > gi|113536854|dbj|BAF09237.1| Os02g0596900 [*Oryza sativa Japonica* Group] > gi|218191098|gb|EEC73525.1| hypothetical protein OsI_07915 [*Oryza sativa Indica* Group] > gi|222623169|gb|EEE57301.1| hypothetical protein OsJ_07378 [*Oryza sativa Japonica* Group]	1.00	2082	2504
		ACF87749	unknown [*Zea mays*] > gi|223972725|gb|ACN30550.1| unknown [*Zea mays*]	0.92	2083	2505
		XP_002285370	PREDICTED: hypothetical protein [*Vitis vinifera*]	0.86	2084	2506
		NP_001147580	LOC100281189 [*Zea mays*] > gi|195612296|gb|ACG27978.1| actin-like protein 3 [*Zea mays*]	0.92	2085	2507
		NP_001170315	hypothetical protein LOC100384280 [*Zea mays*] > gi|224034999|gb|ACN36575.1| unknown [*Zea mays*]	0.90	2086	2508
		XP_002315648	predicted protein [*Populus trichocarpa*] > gi|222864688|gb|EEF01819.1| predicted protein [*Populus trichocarpa*]	0.84	2087	2509
		XP_002515041	protein binding protein, putative [*Ricinus communis*] > gi|223546092|gb|EEF47595.1| protein binding protein, putative [*Ricinus communis*]	0.85	2088	2510
		XP_002312654	predicted protein [*Populus trichocarpa*] > gi|222852474|gb|EEE90021.1| predicted protein [*Populus trichocarpa*]	0.84	2089	2511

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		CAM97883	actin-related protein 3 [*Nicotiana tabacum*]	0.83	2090	2512
		NP_172777	actin-related protein 3 [*Arabidopsis thaliana*] > gi|75313139|sp|Q9SAF1.1|ARP3_ARATH RecName: Full = Actin-related protein 3; AltName: Full = Protein DISTORTED TRICHOMES 1 > gi|4850401|gb|AAD31071.1| AC007357_20 Strong similarity to gb|U29610 Actin-like protein (Arp3) from *Acanthamoeba castellanii* and is a member of the PF|00022 Actin family [*Arabidopsis thaliana*] > gi|21427461|gb|AAM53243.1| AF507911_1 actin-related protein 3 [*Arabidopsis thaliana*] > gi|20260500|gb|AAM13148.1| similar to actin-like protein [*Arabidopsis thaliana*] > gi|21489929|tpg|DAA00033.1| TPA_exp: actin-related protein 3; AtARP3 [*Arabidopsis thaliana*] > gi|30387525|gb|AAP31928.1| At1g13180 [*Arabidopsis thaliana*] > gi|332190859|gb|AEE28980.1| actin-related protein 3 [*Arabidopsis thaliana*]	0.81	2091	2513
Predicted siRNA 58872	632-651	ACR34392	unknown [*Zea mays*]	1.00	2092	2514
	315-334	NP_001004443	beta-hexosaminidase subunit alpha precursor [*Rattus norvegicus*] > gi|85701350|sp|Q641X3.1|HEXA_RAT RecName: Full = Beta-hexosaminidase subunit alpha; AltName: Full = Beta-N-acetylhexosaminidase subunit alpha; Short = Hexosaminidase subunit A; AltName: Full = N-acetyl-beta-glucosaminidase subunit alpha; Flags: Precursor > gi|51980341|gb|AAH82097.1| Hexosaminidase A [*Rattus norvegicus*] > gi|149041858|gb|EDL95699.1| hexosaminidase A, isoform CRA_a [*Rattus norvegicus*]	1.00	2093	2515
		NP_034551	beta-hexosaminidase subunit alpha precursor [*Mus musculus*] > gi|497174|gb|AAA18775.1| beta-hexosaminidase [*Mus musculus*] > gi|497196|gb|AAA18777.1| beta-hexosaminidase alpha-subunit [*Mus musculus*] > gi|14789650|gb|AAH10755.1| Hexosaminidase A [*Mus musculus*] > gi|26344774|dbj|BAC36036.1| unnamed protein product [*Mus musculus*] > gi|26344800|dbj|BAC36049.1| unnamed protein product [*Mus musculus*] > gi|74184438|dbj|BAE25744.1| unnamed protein product [*Mus musculus*]	0.94	2094	2516

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			> gi|74204649|dbj|BAE35394.1| unnamed protein product [*Mus musculus*] > gi|148694024|gb|EDL25971.1| hexosaminidase A [*Mus* musculus]			
		BAE35636	unnamed protein product [*Mus musculus*]	0.94	2095	2517
		BAE29566	unnamed protein product [*Mus musculus*]	0.94	2096	2518
		BAE30831	unnamed protein product [*Mus musculus*]	0.94	2097	2519
		BAE35457	unnamed protein product [*Mus musculus*]	0.94	2098	2520
		P29416	RecName: Full = Beta-hexosaminidase subunit alpha; AltName: Full = Beta-N-acetylhexosaminidase subunit alpha; Short = Hexosaminidase subunit A; AltName: Full = N-acetyl-beta-glucosaminidase subunit alpha; Flags: Precursor > gi|51265|emb|CAA45615.1| beta-N-acetylhexosaminidase [*Mus musculus*] > gi|577688|gb|AAC53246.1| beta-N-acetylhexosaminidase, alpha-subunit [*Mus musculus*]	0.94	2099	
		BAC38018	unnamed protein product [*Mus musculus*]	0.94	2100	2521
		BAE39189	unnamed protein product [*Mus musculus*]	0.94	2101	2522
		BAE40146	unnamed protein product [*Mus musculus*]	0.94	2102	2523
	535-554	XP-002526446	heat shock protein, putative [*Ricinus communis*] > gi|223534226|gb|EEF35941.1| heat shock protein, putative [*Ricinus communis*]	1.00	2103	2524
		XP_002328713	predicted protein [*Populus trichocarpa*] > gi|222839011|gb|EEE77362.1| predicted protein [*Populus trichocarpa*]	0.92	2104	2525
		XP_002331133	predicted protein [*Populus trichocarpa*] > gi|222872861|gb|EEF09992.1| predicted protein [*Populus trichocarpa*]	0.92	2105	2526
		XP_002279101	PREDICTED: hypothetical protein [*Vitis vinifera*]	0.93	2106	2527
		ABZ04081	chloroplast heat shock protein 70-2 [*Ipomoea nil*]	0.90	2107	2528
		ABM92419	chloroplast HSP70 [*Cucumis sativus*]	0.90	2108	2529
		ABE79560	Chaperone DnaK [*Medicago truncatula*]	0.90	2109	2530
		CAA52149	heat shock protein 70 [*Cucumis sativus*]	0.89	2110	2531
		Q02028	RecName: Full = Stromal 70 kDa heat shock-related protein, chloroplastic; Flags: Precursor > gi|169023|gb|AAA33637.1| 70 kDa heat shock protein [*Pisum sativum*] > gi|871515|emb|CAA49147.1| Psst70 (stress 70 protein) [*Pisum sativum*]	0.90	2111	
		CAN81065	hypothetical protein VITISV_000728 [*Vitis vinifera*]	0.91	2112	2532

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
Predicted siRNA 54631	1842-1866	YP_024387	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Saccharum* hybrid cultivar SP-80-3280] > gi|50812536|ref|YP_054639.1| ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Saccharum officinarum*] > gi|118614500|ref|YP_899415.1| ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit [*Sorghum bicolor*] > gi|75290174|sp|Q6ENV5.1|RBL_SACOF RecName: Full = Ribulose bisphosphate carboxylase large chain; Short = RuBisCO large subunit; Flags: Precursor > gi|75291223|sp|Q6L391.1|RBL_SACHY RecName: Full = Ribulose bisphosphate carboxylase large chain; Short = RuBisCO large subunit; Flags: Precursor > gi|125987520|sp|A1E9T2.1|RBL_SORBI RecName: Full = Ribulose bisphosphate carboxylase large chain; Short = RuBisCO large subunit; Flags: Precursor > gi|48478681|gb|AAT44701.1| RuBisCO large chain [*Saccharum* hybrid cultivar SP80-3280] > gi|49659520|dbj|BAD27301.1| RuBisCO large subunit [*Saccharum* hybrid cultivar NCo 310] > gi|118201134|gb|ABK79504.1| ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Sorghum bicolor*]	1.00	2113	2533
		NP_043033	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Zea mays*] > gi|1172861|sp|P00874.2|RBL_MAIZE RecName: Full = Ribulose bisphosphate carboxylase large chain; Short = RuBisCO large subunit; Flags: Precursor > gi|18036|emb|CAA78027.1| Ribulose bisphosphate carboxylase [*Zea mays*] > gi|902230|emb|CAA60294.1| ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Zea mays*]	0.99	2114	2534
		ABP01447	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Sorghastrum nutans*]	0.99	2115	2535
		YP_003208195	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Coix lacryma-jobi*] > gi|209361365|gb|ACI43280.1| ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Coix lacryma-jobi*]	0.98	2116	2536
		ABP01443	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Cymbopogon citratus*]	0.98	2117	2537

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		ABP01445	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Pogonatherum* sp. Hodkinson 21]	0.98	2118	2538
		ABP01442	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Coix lacryma-jobi*]	0.97	2119	2539
		ABP01448	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Sorghum halepense*]	0.96	2120	2540
		CAG34130	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Arthraxon* sp. Hodkinson 111]	0.96	2121	2541
		AAA31678	ribulose 1,5-bisphosphate carboxylase/oxygenase [*Cenchrus setiger*] > gi|294104|gb|AAA32020.1| ribulosebiphosphate carboxylase, large subunit [*Pennisetum glaucum*]	0.97	2122	2542
	884-908	ABP01449	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Trachypogon spicatus*]	1.00	2123	2543
		ABP01447	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Sorghastrum nutans*]	1.00	2124	2544
		NP_043033	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Zea mays*] > gi|1172861|sp|P00874.2|RBL_MAIZE RecName: Full = Ribulose bisphosphate carboxylase large chain; Short = RuBisCO large subunit; Flags: Precursor > gi|18036|emb|CAA78027.1| Ribulose bisphosphate carboxylase [*Zea mays*] > gi|902230|emb|CAA60294.1| ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Zea mays*]	0.99	2125	2545
		YP_024387	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Saccharum* hybrid cultivar SP-80-3280] > gi|50812536|ref|YP_054639.1| ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Saccharum officinarum*] > gi|118614500|ref|YP_899415.1| ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit [*Sorghum bicolor*] > gi|75290174|sp|Q6ENV5.1|RBL_SACOF RecName: Full = Ribulose bisphosphate carboxylase large chain; Short = RuBisCO large subunit; Flags: Precursor > gi|75291223|sp|Q6L391.1|RBL_SACHY RecName: Full = Ribulose bisphosphate carboxylase large chain; Short = RuBisCO large subunit; Flags: Precursor > gi|125987520|sp|A1E9T2.1|RBL_SORBI RecName: Full = Ribulose bisphosphate carboxylase large chain;	1.00	2126	2546

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			Short = RuBisCO large subunit; Flags: Precursor > gi|48478681|gb|AAT44701.1| RuBisCO large chain [*Saccharum* hybrid cultivar SP80-3280] > gi|49659520|dbj|BAD27301.1| RuBisCO large subunit [*Saccharum* hybrid cultivar NCo 310] > gi|118201134|gb|ABK79504.1| ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Sorghum bicolor*]			
		ABP01443	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Cymbopogon citratus*]	1.00	2127	2547
		ABP01445	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Pogonatherum* sp. Hodkinson 21]	0.99	2128	2548
		ABP01442	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Coix lacryma-jobi*]	0.98	2129	2549
		YP_003208195	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Coix lacryma-jobi*] > gi|209361365|gb|ACI43280.1| ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Coix lacryma-jobi*]	0.98	2130	2550
		ABP01441	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Bothriochloa ischaemum*]	0.98	2131	2551
		CAG34130	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Arthraxon* sp. Hodkinson 111]	0.96	2132	2552
Predicted siRNA 59846	69-92	XP_002458082	hypothetical protein SORBIDRAFT_03g026670 [*Sorghum bicolor*] > gi|241930057|gb|EES03202.1| hypothetical protein SORBIDRAFT_03g026670 [*Sorghum bicolor*]	1.00	2133	2553
		EEC70994	hypothetical protein OsI_02661 [*Oryza sativa Indica* Group]	0.83	2134	
		NP_001152397	regulator of telomere elongation helicase 1 [*Zea mays*] > gi|195655863|gb|ACG47399.1| regulator of telomere elongation helicase 1 [*Zea mays*]	0.78	2135	2554
		NP_001043456	Os01g0592900 [*Oryza sativa Japonica* Group] > gi|53791584|dbj|BAD52706.1| DEAH helicase isoform 5-like [*Oryza sativa Japonica* Group] > gi|255673416|dbj|BAF05370.2| Os01g0592900 [*Oryza sativa Japonica* Group]	0.70	2136	2555
	85-108	ACR34511	unknown [*Zea mays*]	1.00	2137	2556
		NP_001105187	histone acetyltransferase1 [*Zea mays*] > gi|20977602|gb|AAM28228.1| histone acetyl transferase [*Zea mays*] > gi|223975399|gb|ACN31887.1| unknown [*Zea mays*]	0.99	2138	2557
		Q8LPU4	RecName: Full = Histone acetyltransferase type B catalytic subunit; AltName: Full = Histone acetyltransferase HAT B;	0.99	2139	

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			AltName: Full = Histone acetyltransferase HAT-B-p50 > gi|6288802|gb|AAF06742.1| AF171927_1 histone acetyltransferase HAT-B-p50 [*Zea mays*] > gi|5579441|gb|AAC03423.2| histone acetyltransferase HAT B [*Zea mays*]			
		XP_002460092	hypothetical protein SORBIDRAFT_02g022640 [*Sorghum bicolor*] > gi|241923469|gb|EER96613.1| hypothetical protein SORBIDRAFT_02g022640 [*Sorghum bicolor*]	0.89	2140	2558
		NP_001062946	Os09g0347800 [*Oryza sativa Japonica* Group] > gi|75121858|sp|Q6ES10.1|HAT1_ORYSJ RecName: Full = Probable acetyltransferase type B catalytic subunit; AltName: Full = HAT B > gi|50252375|dbj|BAD28482.1| putative histone acetyltransferase HAT B [*Oryza sativa Japonica* Group] > gi|50252405|dbj|BAD28560.1| putative histone acetyltransferase HAT B [*Oryza sativa Japonica* Group] > gi|113631179|dbj|BAF24860.1| Os09g0347800 [*Oryza sativa Japonica* Group] > gi|215678892|dbj|BAG95329.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.77	2141	2559
		EEC84410	hypothetical protein OsI_30998 [*Oryza sativa Indica* Group]	0.77	2142	
		EEE69531	hypothetical protein OsJ_29003 [*Oryza sativa Japonica* Group]	0.77	2143	
		BAK05443	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.75	2144	2560
	85-108	XP_002460092	hypothetical protein SORBIDRAFT_02g022640 [*Sorghum bicolor*] > gi|241923469|gb|EER96613.1| hypothetical protein SORBIDRAFT_02g022640 [*Sorghum bicolor*]	1.00	2145	2561
		NP_001105187	histone acetyltransferase1 [*Zea mays*] > gi|20977602|gb|AAM28228.1| histone acetyl transferase [*Zea mays*] > gi|223975399|gb|ACN31887.1| unknown [*Zea mays*]	0.90	2146	2562
		Q8LPU4	RecName: Full = Histone acetyltransferase type B catalytic subunit; AltName: Full = Histone acetyltransferase HAT B; AltName: Full = Histone acetyltransferase HAT-B-p50 > gi|6288802|gb|AAF06742.1| AF171927_1 histone acetyltransferase HAT-B-p50 [*Zea mays*] > gi|5579441|gb|AAC03423.2| histone acetyltransferase HAT B [*Zea mays*]	0.90	2147	

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		NP_001062946	Os09g0347800 [*Oryza sativa Japonica* Group] > gi|75121858|sp|Q6ES10.1|HAT1_ORYSJ RecName: Full = Probable acetyltransferase type B catalytic subunit; AltName: Full = HAT B > gi|50252375|dbj|BAD28482.1| putative histone acetyltransferase HAT B [*Oryza sativa Japonica* Group] > gi|50252405|dbj|BAD28560.1| putative histone acetyltransferase HAT B [*Oryza sativa Japonica* Group] > gi|113631179|dbj|BAF24860.1| Os09g0347800 [*Oryza sativa Japonica* Group] > gi|215678892|dbj|BAG95329.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.81	2148	2563
		EEC84410	hypothetical protein OsI_30998 [*Oryza sativa Indica* Group]	0.81	2149	
		EEE69531	hypothetical protein OsJ_29003 [*Oryza sativa Japonica* Group]	0.81	2150	
		BAK05443	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.78	2151	2564
		ACR34511	unknown [*Zea mays*]	0.79	2152	2565
Predicted siRNA 60081	293-311	XP_002460816	hypothetical protein SORBIDRAFT_02g035420 [*Sorghum bicolor*] > gi|241924193|gb|EER97337.1| hypothetical protein SORBIDRAFT_02g035420 [*Sorghum bicolor*]	1.00	2153	2566
		NP_001147287	receptor-like serine-threonine protein kinase [*Zea mays*] > gi|195609532|gb|ACG26596.1| receptor-like serine-threonine protein kinase [*Zea mays*]	0.87	2154	2567
		BAK06110	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.73	2155	2568
	564-582	ACN27203	unknown [*Zea mays*]	1.00	2156	2569
		NP_001150572	RING-H2 finger protein ATL1R [*Zea mays*] > gi|195640284|gb|ACG39610.1| RING-H2 finger protein ATL1R [*Zea mays*]	1.00	2157	2570
		XP_002448400	hypothetical protein SORBIDRAFT_06g026580 [*Sorghum bicolor*] > gi|241939583|gb|EES12728.1| hypothetical protein SORBIDRAFT_06g026580 [*Sorghum bicolor*]	0.80	2158	2571
	374-392	NP_001151643	DNA binding protein [*Zea mays*] > gi|195648318|gb|ACG43627.1| DNA binding protein [*Zea mays*]	1.00	2159	2572
		XP_002468594	hypothetical protein SORBIDRAFT_01g048710 [*Sorghum bicolor*] > gi|241922448|gb|EER95592.1| hypothetical protein SORBIDRAFT_01g048710 [*Sorghum bicolor*]	0.83	2160	2573
		NP_001048832	Os03g0127500 [*Oryza sativa Japonica* Group] > gi|20330751|gb|AAM19114.1|	0.73	2161	2574

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			AC104427_12 Putative bZIP transcription factor [*Oryza sativa Japonica* Group] > gi|108705971|gb|ABF93766.1| bZIP family transcription factor, putative, expressed [*Oryza sativa Japonica* Group] > gi|113547303|dbj|BAF10746.1| Os03g0127500 [*Oryza sativa Japonica* Group]			
		EAZ25438	hypothetical protein OsJ_09254 [*Oryza sativa Japonica* Group]	0.73	2162	
		EAY88362	hypothetical protein OsI_09817 [*Oryza sativa Indica* Group]	0.73	2163	
	365-383	XP_002446810	hypothetical protein SORBIDRAFT_06g023020 [*Sorghum bicolor*] > gi|241937993|gb|EES11138.1| hypothetical protein SORBIDRAFT_06g023020 [*Sorghum bicolor*]	1.00	2164	2575
		NP_001185810	yellow stripe-like transporter 11 [*Zea mays*] > gi|308210134|gb|ADO20998.1| yellow stripe-like transporter 11 [*Zea mays*]	0.90	2165	2576
		CAH67887	OSIGBa0153E02-OSIGBa0093I20.16 [*Oryza sativa Indica* Group] > gi|125549079|gb|EAY94901.1| hypothetical protein OsI_16701 [*Oryza sativa Indica* Group]	0.79	2166	
		Q7X660	RecName: Full = Probable metal-nicotianamine transporter YSL11; AltName: Full = Protein YELLOW STRIPE LIKE 11; Short = OsYSL11 > gi|32487645|emb|CAE05635.1| OSJNBa0038O10.1 [*Oryza sativa Japonica* Group] > gi|57834127|emb|CAI44638.1| OSJNBb0065J09.18 [*Oryza sativa Japonica* Group] > gi|125591037|gb|EAZ31387.1| hypothetical protein OsJ_15515 [*Oryza sativa Japonica* Group]	0.79	2167	
		BAE91891	hypothetical protein [*Oryza sativa Japonica* Group]	0.79	2168	2577
		Q5JQD7	RecName: Full = Probable metal-nicotianamine transporter YSL12; AltName: Full = Protein YELLOW STRIPE LIKE 12; Short = OsYSL12 > gi|116310949|emb|CAH67886.1| OSIGBa0153E02-OSIGBa0093I20.15 [*Oryza sativa Indica* Group]	0.74	2169	
		NP_001185468	yellow stripe-like transporter 12 [*Zea mays*] > gi|308210136|gb|ADO20999.1| yellow stripe-like transporter 12 [*Zea mays*]	0.73	2170	2578
		XP_002452492	hypothetical protein SORBIDRAFT_04g026840 [*Sorghum bicolor*] > gi|241932323|gb|EES05468.1| hypothetical protein SORBIDRAFT_04g026840 [*Sorghum bicolor*]	0.71	2171	2579
		BAE91892	hypothetical protein [*Oryza sativa Japonica* Group]	0.73	2172	2580

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		XP_002446809	hypothetical protein SORBIDRAFT_06g023010 [*Sorghum bicolor*] > gi|241937992|gb|EES11137.1| hypothetical protein SORBIDRAFT_06g023010 [*Sorghum bicolor*]	0.72	2173	2581
	529-547	XP_002464238	hypothetical protein SORBIDRAFT_01g014760 [*Sorghum bicolor*] > gi|241918092|gb|EER91236.1| hypothetical protein SORBIDRAFT_01g014760 [*Sorghum bicolor*]	1.00	2174	2582
		NP_001146578	hypothetical protein LOC100280174 [*Zea mays*] > gi|219887889|gb|ACL54319.1| unknown [*Zea mays*]	0.92	2175	2583
		ACN27618	unknown [*Zea mays*]	0.91	2176	2584
		EAY90980	hypothetical protein OsI_12589 [*Oryza sativa Indica* Group]	0.83	2177	
		NP_001050649	Os03g0609800 [*Oryza sativa Japonica* Group] > gi|37700299|gb|AAR00589.1| putative NPH3 family protein [*Oryza sativa Japonica* Group] > gi|40539093|gb|AAR87349.1| transposon protein, putative, mutator sub-class [*Oryza sativa Japonica* Group] > gi|62733727|gb|AAX95837.1| transposon protein, putative, mutator sub-class [*Oryza sativa Japonica* Group] > gi|108709776|gb|ABF97571.1| transposon protein, putative, Mutator sub-class, expressed [*Oryza sativa Japonica* Group] > gi|108709777|gb|ABF97572.1| transposon protein, putative, Mutator sub-class, expressed [*Oryza sativa Japonica* Group] > gi|113549120|dbj|BAF12563.1| Os03g0609800 [*Oryza sativa Japonica* Group] > gi|125587097|gb|EAZ27761.1| hypothetical protein OsJ_11706 [*Oryza sativa Japonica* Group] > gi|215686957|dbj|BAG89762.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.83	2178	2585
		EAZ21022	hypothetical protein OsJ_36671 [*Oryza sativa Japonica* Group]	0.73	2179	
		NP_001067147	Os12g0583500 [*Oryza sativa Japonica* Group] > gi|77556906|gb|ABA99702.1| transposon protein, putative, Mutator sub-class, expressed [*Oryza sativa Japonica* Group] > gi|113649654|dbj|BAF30166.1| Os12g0583500 [*Oryza sativa Japonica* Group]	0.73	2180	2586
		EAY83679	hypothetical protein OsI_38903 [*Oryza sativa Indica* Group]	0.73	2181	
		BAJ87350	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.71	2182	2587
	3078-3096	NP_001185468	yellow stripe-like transporter 12 [*Zea mays*] > gi|308210136|gb|ADO20999.1| yellow stripe-like transporter 12 [*Zea mays*]	1.00	2183	2588

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		XP_002446809	hypothetical protein SORBIDRAFT_06g023010 [*Sorghum bicolor*] > gi|241937992|gb|EES11137.1| hypothetical protein SORBIDRAFT_06g023010 [*Sorghum bicolor*]	0.93	2184	2589
		Q5JQD7	RecName: Full = Probable metal-nicotianamine transporter YSL12; AltName: Full = Protein YELLOW STRIPE LIKE 12; Short = OsYSL12 > gi|116310949|emb|CAH67886.1| OSIGBa0153E02-OSIGBa0093I20.15 [*Oryza sativa Indica* Group]	0.88	2185	
		BAE91892	hypothetical protein [*Oryza sativa Japonica* Group]	0.87	2186	2590
		XP_002452492	hypothetical protein SORBIDRAFT_04g026840 [*Sorghum bicolor*] > gi|241932323|gb|EES05468.1| hypothetical protein SORBIDRAFT_04g026840 [*Sorghum bicolor*]	0.82	2187	2591
		BAE44205	hypothetical protein [*Oryza sativa Japonica* Group]	0.81	2188	2592
		Q6H7J6	RecName: Full = Probable metal-nicotianamine transporter YSL14; AltName: Full = Protein YELLOW STRIPE LIKE 14; Short = OsYSL14 > gi|49388177|dbj|BAD25303.1| oligopeptide transporter OPT-like [*Oryza sativa Japonica* Group]	0.81	2189	
		BAJ89062	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.80	2190	2593
		BAJ92335	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.80	2191	2594
		ACN34648	unknown [*Zea mays*] > gi|295441975|gb|ADG21035.1| oligopeptide transporter [*Zea mays*] > gi|308210138|gb|ADO21000.1| yellow stripe-like transporter 14A [*Zea mays*]	0.81	2192	2595
Predicted siRNA 59380	1927-1945	XP_002450269	hypothetical protein SORBIDRAFT_05g002900 [*Sorghum bicolor*] > gi|241936112|gb|EES09257.1| hypothetical protein SORBIDRAFT_05g002900 [*Sorghum bicolor*]	1.00	2193	2596
		NP_001130515	hypothetical protein LOC100191614 [*Zea mays*] > gi|194689354|gb|ACF78761.1| unknown [*Zea mays*] > gi|195635013|gb|ACG36975.1| pyruvate kinase, cytosolic isozyme [*Zea mays*] > gi|223947285|gb|ACN27726.1| unknown [*Zea mays*] > gi|238009496|gb|ACR35783.1| unknown [*Zea mays*]	0.98	2194	2597
		NP_001149198	LOC100282820 [*Zea mays*] > gi|195625378|gb|ACG34519.1| pyruvate kinase, cytosolic isozyme [*Zea mays*]	0.97	2195	2598
		BAJ87403	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.95	2196	2599

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		BAJ94667	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.95	2197	2600
		NP_001065749	Os11g0148500 [*Oryza sativa Japonica* Group] > gi|77548686|gb|ABA91483.1| pyruvate kinase family protein, expressed [*Oryza sativa Japonica* Group] > gi|113644453|dbj|BAF27594.1| Os11g0148500 [*Oryza sativa Japonica* Group] > gi|215692631|dbj|BAG88051.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218185248|gb|EEC67675.1| hypothetical protein OsI_35105 [*Oryza sativa Indica* Group] > gi|222615524|gb|EEE51656.1| hypothetical protein OsJ_32969 [*Oryza sativa Japonica* Group]	0.95	2198	2601
		NP_001066148	Os12g0145700 [*Oryza sativa Japonica* Group] > gi|77553678|gb|ABA96474.1| pyruvate kinase family protein, expressed [*Oryza sativa Japonica* Group] > gi|113648655|dbj|BAF29167.1| Os12g0145700 [*Oryza sativa Japonica* Group] > gi|215701048|dbj|BAG92472.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218186432|gb|EEC68859.1| hypothetical protein OsI_37456 [*Oryza sativa Indica* Group] > gi|222616632|gb|EEE52764.1| hypothetical protein OsJ_35209 [*Oryza sativa Japonica* Group]	0.94	2199	2602
		XP_002283911	PREDICTED: hypothetical protein [*Vitis vinifera*]	0.89	2200	2603
		AAM22747	pyruvate kinase-like [*Deschampsia antarctica*]	0.88	2201	2604
		ABE80121	Pyruvate kinase [*Medicago truncatula*]	0.89	2202	
Predicted siRNA 55806	43-66	NP_001052992	Os04g0460600 [*Oryza sativa Japonica* Group] > gi|38344965|emb|CAD40985.2| OSJNBa0072F16.10 [*Oryza sativa Japonica* Group] > gi|108947442|gb|ABF47345.2| NAC domain protein [*Oryza sativa Japonica* Group] > gi|113564563|dbj|BAF14906.1| Os04g0460600 [*Oryza sativa Japonica* Group] > gi|116310448|emb|CAH67453.1| H0219H12.10 [*Oryza sativa Indica* Group] > gi|215692665|dbj|BAG88085.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215737715|dbj|BAG96845.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218194979|gb|EEC77406.1| hypothetical protein OsI_16171 [*Oryza sativa Indica* Group] > gi|222628996|gb|EEE61128.1| hypothetical protein OsJ_15058 [*Oryza sativa Japonica* Group]	1.00	2203	2605

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		BAC53811	OsNAC2 protein [*Oryza sativa*]	0.97	2204	2606
		XP_002446618	hypothetical protein SORBIDRAFT_06g019010 [*Sorghum bicolor*] > gi|241937801|gb|EES10946.1| hypothetical protein SORBIDRAFT_06g019010 [*Sorghum bicolor*]	0.71	2205	2607
Predicted siRNA 57034	2555-2578	NP_001141674	hypothetical protein LOC100273800 [*Zea mays*] > gi|194705506|gb|ACF86837.1| unknown [*Zea mays*]	1.00	2206	2608
		XP_002451554	hypothetical protein SORBIDRAFT_04g003650 [*Sorghum bicolor*] > gi|241931385|gb|EES04530.1| hypothetical protein SORBIDRAFT_04g003650 [*Sorghum bicolor*]	0.74	2207	2609
	95-115	YP_874773	ribosomal protein L14 [*Agrostis stolonifera*] > gi|118430423|ref|YP_874689.1| ribosomal protein L14 [*Hordeum vulgare* subsp. *vulgare*] > gi|159106900|ref|YP_001531318.1| ribosomal protein L14 [*Lolium perenne*] > gi|125987532|sp|A1EA45.1|RK14_AGRST RecName: Full = 50S ribosomal protein L14, chloroplastic > gi|218546804|sp|A1E9M7.1| RK14_HORVU RecName: Full = 50S ribosomal protein L14, chloroplastic > gi|218546811|sp|A8Y9C3.1|RK14_LOLPR RecName: Full = 50S ribosomal protein L14, chloroplastic > gi|118201077|gb|ABK79448.1| ribosomal protein L14 [*Hordeum vulgare* subsp. *vulgare*] > gi|118201247|gb|ABK79616.1| ribosomal protein L14 [*Agrostis stolonifera*] > gi|158934434|emb|CAO86012.1| ribosomal protein L14 [*Lolium perenne*]	1.00	2208	2610
		YP_002364534	ribosomal protein L14 [*Festuca arundinacea*] > gi|215882361|gb|ACJ70791.1| ribosomal protein L14 [*Festuca arundinacea*]	0.99	2209	2611
		NP_114294	ribosomal protein L14 [*Triticum aestivum*] > gi|45477200|sp|Q95H51.1|RK14_WHEAT RecName: Full = 50S ribosomal protein L14, chloroplastic > gi|13928241|dbj|BAB47070.1| ribosomal protein L14 [*Triticum aestivum*]	0.99	2210	2612
		NP_039422	ribosomal protein L14 [*Oryza sativa Japonica* Group] > gi|50234008|ref|YP_052786.1| ribosomal protein L14 [*Oryza nivara*] > gi|109156621|ref|YP_654240.1| ribosomal protein L14 [*Oryza sativa Indica* Group] > gi|253729591|ref|YP_003029775.1| ribosomal protein L14	0.98	2211	2613

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			[*Bambusa oldhamii*] > gi|255961418|ref|YP_003097611.1| ribosomal protein L14 [*Dendrocalamus latiflorus*] > gi|297723921|ref|NP_001174324.1| Os05g0292700 [*Oryza sativa Japonica* Group] > gi|68565732|sp|Q6END7.1|RK14_ORYNI RecName: Full = 50S ribosomal protein L14, chloroplastic > gi|148839610|sp|P0C438.1|RK14_ORYSA RecName: Full = 50S ribosomal protein L14, chloroplastic > gi|148839611|sp|P0C439.1|RK14_ORYSI RecName: Full = 50S ribosomal protein L14, chloroplastic > gi|148839612|sp|P0C440.1|RK14_ORYSJ RecName: Full = 50S ribosomal protein L14, chloroplastic > gi|12023|emb|CAA33932.1| ribosomal protein L14 [*Oryza sativa Japonica* Group] > gi|20160833|dbj|BAB89773.1| Chloroplast ribosomal protein L14 [*Oryza sativa Japonica* Group] > gi|40253571|dbj|BAD05517.1| ribosomal protein L14 [*Oryza sativa Japonica* Group] > gi|42795513|gb|AAS46080.1| ribosomal protein L14 [*Oryza sativa Indica* Group] > gi|49615032|dbj|BAD26815.1| ribosomal protein L14 [*Oryza nivara*] > gi|246367101|gb|ACS94712.1| ribosomal protein L14 [*Bambusa oldhamii*] > gi|255040295|gb|ACT99955.1| ribosomal protein L14 [*Dendrocalamus latiflorus*] > gi|255676212|dbj|BAH93052.1| Os05g0292700 [*Oryza sativa Japonica* Group] > gi|307133922|gb|ADN32927.1| ribosomal protein L14 [*Phyllostachys nigra* var. *henonis*] > gi|309321653|gb|ADO65178.1| ribosomal protein L14 [*Acidosasa purpurea*] > gi|309321737|gb|ADO65261.1| ribosomal protein L14 [*Ferrocalamus rimosivaginus*] > gi|309321821|gb|ADO65344.1| ribosomal protein L14 [*Indocalamus longiauritus*] > gi|309321904|gb|ADO65426.1| ribosomal protein L14 [*Phyllostachys edulis*] > gi|309321989|gb|ADO65510.1| ribosomal protein L14 [*Bambusa emeiensis*] > gi|226644|prf||1603356BU ribosomal protein L14			
		YP_00200522	ribosomal protein L14 [*Brachypodium distachyon*] > gi|218546902|sp|B3TN86.1|RK14_BRADI RecName: Full = 50S	0.98	2212	2614

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			ribosomal protein L14, chloroplastic > gi|193075591|gb|ACF08674.1| ribosomal protein L14 [*Brachypodium distachyon*]			
		ABJ52167	ribosomal protein L14 [*Phyllostachys edulis*]	0.98	2213	2615
		BAC10087	Chloroplast 50S ribosomal protein L14 [*Oryza sativa Japonica* Group] > gi|50510231|dbj|BAD31429.1| Chloroplast 50S ribosomal protein L14 [*Oryza sativa Japonica* Group]	0.98	2214	2616
		YP_003587704	ribosomal protein L14 [*Anomochloa marantoidea*] > gi|251765288|gb|ACT15442.1| ribosomal protein L14 [*Anomochloa marantoidea*]	0.95	2215	2617
		BAD33446	putative ribosomal protein L14 [*Oryza sativa Japonica* Group] > gi|50726203|dbj|BAD33722.1| putative ribosomal protein L14 [*Oryza sativa Japonica* Group]	0.96	2216	2618
		AAT85078	putative 50S ribosomal protein L14 [*Oryza sativa Japonica* Group] > gi|50878445|gb|AAT85219.1| putative 50S ribosomal protein L14 [*Oryza sativa Japonica* Group]	0.94	2217	2619
Predicted siRNA 60387	403-422	XP_002439358	hypothetical protein SORBIDRAFT_09g005070 [*Sorghum bicolor*] > gi|241944643|gb|EES17788.1| hypothetical protein SORBIDRAFT_09g005070 [*Sorghum bicolor*]	1.00	2218	2620
		NP_001140641	hypothetical protein LOC100272716 [*Zea mays*] > gi|194700306|gb|ACF84237.1| unknown [*Zea mays*]	0.88	2219	2621
		ACG56678	tryptophan aminotransferase [*Zea mays*]	0.88	2220	2622
		NP_001151869	alliin lyase 2 [*Zea mays*] > gi|195650459|gb|ACG44697.1| alliin lyase 2 precursor [*Zea mays*]	0.79	2221	2623
	374-393	NP_001140641	hypothetical protein LOC100272716 [*Zea mays*] > gi|194700306|gb|ACF84237.1| unknown [*Zea mays*]	1.00	2222	2624
		ACG56678	tryptophan aminotransferase [*Zea mays*]	1.00	2223	2625
		XP_002439358	hypothetical protein SORBIDRAFT_09g005070 [*Sorghum bicolor*] > gi|241944643|gb|EES17788.1| hypothetical protein SORBIDRAFT_09g005070 [*Sorghum bicolor*]	0.89	2224	2626
		NP_001151869	alliin lyase 2 [*Zea mays*] > gi|195650459|gb|ACG44697.1| alliin lyase 2 precursor [*Zea mays*]	0.77	2225	2627
	155-174	XP_002446287	hypothetical protein SORBIDRAFT_06g013470 [*Sorghum bicolor*] > gi|241937470|gb|EES10615.1| hypothetical protein SORBIDRAFT_06g013470 [*Sorghum bicolor*]	1.00	2226	2628

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		NP_001132422	hypothetical protein LOC100193871 [*Zea mays*] > gi|194694338|gb|ACF81253.1| unknown [*Zea mays*]	0.89	2227	2629
		ACN36503	unknown [*Zea mays*]	0.89	2228	2630
		NP_001144520	hypothetical protein LOC100277514 [*Zea mays*] > gi|195643396|gb|ACG41166.1| hypothetical protein [*Zea mays*]	0.89	2229	2631
		ACN25444	unknown [*Zea mays*]	0.89	2230	2632
		XP_002454376	hypothetical protein SORBIDRAFT_04g029660 [*Sorghum bicolor*] > gi|241934207|gb|EE507352.1| hypothetical protein SORBIDRAFT_04g029660 [*Sorghum bicolor*]	0.83	2231	2633
	302-321	XP_002445712	hypothetical protein SORBIDRAFT_07g024570 [*Sorghum bicolor*] > gi|241942062|gb|EES15207.1| hypothetical protein SORBIDRAFT_07g024570 [*Sorghum bicolor*]	1.00	2232	2634
		NP_001148095	auxin-independent growth promoter [*Zea mays*] > gi|195615748|gb|ACG29704.1| auxin-independent growth promoter [*Zea mays*]	0.95	2233	2635
		BAD10226	putative auxin-independent growth promoter [*Oryza sativa Japonica* Group] > gi|50725540|dbj|BAD33009.1| putative auxin-independent growth promoter [*Oryza sativa Japonica* Group]	0.82	2234	2636
		XP_002460613	hypothetical protein SORBIDRAFT_02g031900 [*Sorghum bicolor*] > gi|241923990|gb|EER97134.1| hypothetical protein SORBIDRAFT_02g031900 [*Sorghum bicolor*]	0.71	2235	2637
	151-170	NP_001144386	hypothetical protein LOC100277314 [*Zea mays*] > gi|195641382|gb|ACG40159.1| hypothetical protein [*Zea mays*]	1.00	2236	2638
	781-800	NP_001151955	senescence-associated protein 15 [*Zea mays*] > gi|195651331|gb|ACG45133.1| senescence-associated protein 15 [*Zea mays*]	1.00	2237	2639
	46-65	XP_002465563	hypothetical protein SORBIDRAFT_01g041190 [*Sorghum bicolor*] > gi|241919417|gb|EER92561.1| hypothetical protein SORBIDRAFT_01g041190 [*Sorghum bicolor*]	1.00	2238	2640
		NP_001049540	Os03g0245700 [*Oryza sativa Japonica* Group] > gi|108707147|gb|ABF94942.1| senescence-associated protein 15, putative, expressed [*Oryza sativa Japonica* Group] > gi|113548011|dbj|BAF11454.1| Os03g0245700 [*Oryza sativa Japonica* Group] > gi|125543096|gb|EAY89235.1| hypothetical protein OsI_10732 [*Oryza sativa Indica* Group] > gi|125585589|gb|EAZ26253.1|	0.88	2239	2641

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			hypothetical protein OsJ_10120 [*Oryza sativa Japonica* Group]			
		BAJ85769	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326514266|dbj|BAJ92283.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.86	2240	2642
		XP_002464724	hypothetical protein SORBIDRAFT_01g025820 [*Sorghum bicolor*] > gi|241918578|gb|EER91722.1| hypothetical protein SORBIDRAFT_01g025820 [*Sorghum bicolor*]	0.76	2241	2643
		AAC34858	senescence-associated protein 15 [*Hemerocallis* hybrid cultivar]	0.70	2242	2644
		EEC66585	hypothetical protein OsI_32794 [*Oryza sativa Indica* Group]	0.74	2243	
		EEE50594	hypothetical protein OsJ_30776 [*Oryza sativa Japonica* Group]	0.74	2244	
		NP_001064196	Os10g0158100 [*Oryza sativa Japonica* Group] > gi|255679225|dbj|BAF26110.2| Os10g0158100 [*Oryza sativa Japonica* Group]	0.73	2245	2645
	400-419	NP_001149275	DNA polymerase epsilon subunit 3 [*Zea mays*] > gi|195625970|gb|ACG34815.1| DNA polymerase epsilon subunit 3 [*Zea mays*] > gi|195628668|gb|ACG36164.1| DNA polymerase epsilon subunit 3 [*Zea mays*] > gi|223942345|gb|ACN25256.1| unknown [*Zea mays*]	1.00	2246	2646
		XP_002461994	hypothetical protein SORBIDRAFT_02g012030 [*Sorghum bicolor*] > gi|241925371|gb|EER98515.1| hypothetical protein SORBIDRAFT_02g012030 [*Sorghum bicolor*]	0.71	2247	2647
	71-90	NP_001141681	hypothetical protein LOC100273808 [*Zea mays*] > gi|238908879|gb|ACF86850.2| unknown [*Zea mays*]	1.00	2248	2648
	106-125	XP_002468642	hypothetical protein SORBIDRAFT_01g049490 [*Sorghum bicolor*] > gi|241922496|gb|EER95640.1| hypothetical protein SORBIDRAFT_01g049490 [*Sorghum bicolor*]	1.00	2249	2649
		ACG46521	F-box protein [*Zea mays*]	0.83	2250	2650
	670-689	XP_002444258	hypothetical protein SORBIDRAFT_07g019090 [*Sorghum bicolor*] > gi|241940608|gb|EES13753.1| hypothetical protein SORBIDRAFT_07g019090 [*Sorghum bicolor*]	1.00	2251	2651
		NP_001131520	hypothetical protein LOC100192859 [*Zea mays*] > gi|194691750|gb|ACF79959.1| unknown [*Zea mays*]	0.95	2252	2652
		ACG32608	peroxisomal coenzyme A diphosphatase NUDT7 [*Zea mays*]	0.95	2253	2653

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		EAZ06644	hypothetical protein OsI_28893 [*Oryza sativa Indica* Group] > gi|125561356|gb|EAZ06804.1| hypothetical protein OsI_29048 [*Oryza sativa Indica* Group]	0.74	2254	
		EAZ42551	hypothetical protein OsJ_27117 [*Oryza sativa Japonica* Group]	0.74	2255	
		EAZ06802	hypothetical protein OsI_29046 [*Oryza sativa Indica* Group]	0.72	2256	
		NP_001061674	Os08g0375900 [*Oryza sativa Japonica* Group] > gi|40253324|dbj|BAD05258.1| putative phosphohydrolase [*Oryza sativa Japonica* Group] > gi|40253358|dbj|BAD05290.1| putative phosphohydrolase [*Oryza sativa Japonica* Group] > gi|113623643|dbj|BAF23588.1| Os08g0375900 [*Oryza sativa Japonica* Group]	0.72	2257	2654
		XP_002444259	hypothetical protein SORBIDRAFT_07g019110 [*Sorghum bicolor*] > gi|241940609|gb|EES13754.1| hypothetical protein SORBIDRAFT_07g019110 [*Sorghum bicolor*]	0.71	2258	2655
	2195-2214	XP_002440313	hypothetical protein SORBIDRAFT_09g029610 [*Sorghum bicolor*] > gi|241945598|gb|EES18743.1| hypothetical protein SORBIDRAFT_09g029610 [*Sorghum bicolor*]	1.00	2259	2656
		ACG34981	glucose-1-phosphate adenylyltransferase large subunit [*Zea mays*] > gi|223948357|gb|ACN28262.1| unknown [*Zea mays*]	0.97	2260	2657
		NP_001056424	Os05g0580000 [*Oryza sativa Japonica* Group] > gi|51854319|gb|AAU10700.1| putative glucose-1-phosphate adenylyltransferase [*Oryza sativa Japonica* Group] > gi|125553462|gb|EAY99171.1| hypothetical protein OsI_21129 [*Oryza sativa Indica* Group] > gi|169244411|gb|ACA50479.1| ADP-glucose pyrophosphorylase large subunit [*Oryza sativa Japonica* Group] > gi|215704797|dbj|BAG94825.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222632685|gb|EEE64817.1| hypothetical protein OsJ_19673 [*Oryza sativa Japonica* Group] > gi|255676601|dbj|BAF18338.2| Os05g0580000 [*Oryza sativa Japonica* Group] > gi|262344368|gb|ACY56044.1| ADP-glucose pyrophosphorylase large subunit [*Oryza sativa Japonica* Group] > gi|262344370|gb|ACY56045.1| ADP-glucose pyrophosphorylase large subunit [*Oryza sativa Japonica* Group] > gi|262344372|gb|ACY56046.1| ADP-glucose pyrophosphorylase large subunit	0.93	2261	2658

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			[*Oryza sativa Japonica* Group] > gi|262344374|gb|ACY56047.1| ADP-glucose pyrophosphorylase large subunit [*Oryza sativa Japonica* Group] > gi|262344376|gb|ACY56048.1| ADP-glucose pyrophosphorylase large subunit [*Oryza sativa Japonica* Group] > gi|262344378|gb|ACY56049.1| ADP-glucose pyrophosphorylase large subunit [*Oryza sativa Japonica* Group] > gi|262344380|gb|ACY56050.1| ADP-glucose pyrophosphorylase large subunit [*Oryza sativa Indica* Group] > gi|262344382|gb|ACY56051.1| ADP-glucose pyrophosphorylase large subunit [*Oryza sativa Indica* Group] > gi|262344384|gb|ACY56052.1| ADP-glucose pyrophosphorylase large subunit [*Oryza sativa Indica* Group] > gi|262344386|gb|ACY56053.1| ADP-glucose pyrophosphorylase large subunit [*Oryza sativa Indica* Group] > gi|262344388|gb|ACY56054.1| ADP-glucose pyrophosphorylase large subunit [*Oryza sativa Indica* Group] > gi|262344390|gb|ACY56055.1| ADP-glucose pyrophosphorylase large subunit [*Oryza sativa Indica* Group] > gi|262344392|gb|ACY56056.1| ADP-glucose pyrophosphorylase large subunit [*Oryza sativa Indica* Group] > gi|262344394|gb|ACY56057.1| ADP-glucose pyrophosphorylase large subunit [*Oryza sativa Indica* Group]			
		BAA23490	ADP glucose pyrophosphorylase large subunit [*Oryza sativa Japonica* Group]	0.92	2262	2659
		AAD39597	10A19I.12 [*Oryza sativa Japonica* Group]	0.93	2263	2660
		P12299	RecName: Full = Glucose-1-phosphate adenylyltransferase large subunit, chloroplastic/amyloplastic; AltName: Full = ADP-glucose pyrophosphorylase; AltName: Full = ADP-glucose synthase; AltName: Full = AGPase S; AltName: Full = Alpha-D-glucose-1-phosphate adenyl transferase; Flags: Precursor > gi|995746|emb|CAA79980.1| ADP-glucose pyrophosphorylase large subunit [*Triticum aestivum*] > gi|110729318|gb|ABG88200.1| ADP-glucose pyrophosphorylase large subunit [*Triticum aestivum*]	0.91	2264	
		P30524	RecName: Full = Glucose-1-phosphate adenylyltransferase large subunit 1, chloroplastic/amyloplastic;	0.91	2265	

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			AltName: Full = ADP-glucose pyrophosphorylase; AltName: Full = ADP-glucose synthase; AltName: Full = AGPase S; AltName: Full = Alpha-D-glucose-1-phosphate adenyl transferase; AltName: Full = BEPL; Flags: Precursor > gi|1279513|emb|CAA47626.1| glucose-1-phosphate adenylyltransferase [*Hordeum vulgare* subsp. *vulgare*] > gi|229610847|emb|CAX51355.1| large subunit of ADP-glucose pyrophosphorylase [*Hordeum vulgare* subsp. *vulgare*] > gi|326527375|dbj|BAK04629.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326528409|dbj|BAJ93393.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326528511|dbj|BAJ93437.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]			
		CAD98749	ADP-glucose pyrophosphorylase large subunit [*Triticum aestivum*]	0.89	2266	2661
		NP_001105717	glucose-1-phosphate adenylyltransferase large subunit 2, chloroplastic/amyloplastic [*Zea mays*] >gi|707928|sp|p55234.1|GLG L2_MAIZE RecName: Full = Glucose-1-phosphate adenylyltransferase large subunit 2, chloroplastic/amyloplastic; AltName: Full = ADP-glucose pyrophosphorylase; AltName: AltName: Full = synthase AltName: Full = AGPase S; AltName: Full = Alpha-D-glucose-1-phosphate adenyl transferase; Flags: Precursor >gi|558365|emb|CAA86227.1| ADP-glucose pyrophosphorylase [*Zea mays*]	0.92	2267	2662
		1909370A	ADP glucose	0.87	2268	
Predicted siRNA 60837	154-171	XP_001545081	hypothetical protie BC1G_16418 [*Botryotinia fuckeliana* B05.10] >gi|150854146|gb|EDN29338.1| hypothetical protein BCIG$_{16418}$[*Botryotinia fuckeliana* B05.10	1.00	2269	2663
	629-646	XP_002441128	hypothetical protein SORBIDRAFT_09g020930 [*Sorghum bicolor*] &gt:g1|241946413|gb|EES19558.1| hypothetical protein SORBIDRAFT_09g020930 [*Sorghum bicolor*]	1.00	2270	2664
		ACR35990	unknown [*Zea mays*]	0.91	2271	2665
		NP_001152387	LOC100286027 [*Zea mays*] >gi|195655783|gb|ACG47359.1| secondary cell wall-related glycosyltransferase family 8 [*Zea mays*]	0.92	2272	2666
		BAJ85213	predicted protein [*Hordeum vulgare* subsp. *vulgare*] >gi|326515442|dbj|BAK03634.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.86	2273	2667

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		AAS90653	putative glycogenin [*Oryza sativa Japonica* Group]	0.84	2274	2668
		EEC79261	hypothetical protein OsI_20036 [*Oryza sativa Indica* Group]	0.84	2275	
		EEE63788	hypothetical protein OsJ_18611 [*Oryza sativa Japonica* Group]	0.83	2276	
		NP_00104491	Os01g0880200 [*Oryza sativa Japonica* Group] >gi|56784626|dbj|BAD81673.1| glycogenin-like protein [*Oryza sativa Japonica* Group] > gi|113534522|dbj|BAF06905.1| Os01g0880200 [*Oryza sativa Japonica* Group]	0.84	2277	2669
		EEC71899	hypothetical protein OsI_04661 [*Oryza sativa Indica* Group]	0.84	2278	
		BAJ87677	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.82	2279	2670
	687-704	EEC83357	hypothetical protein OsI_28763 [*Oryza sativa Indica* Group] > gi|222623167|gb|EEE57299.1| hypothetical protein OsJ_07374 [*Oryza sativa Japonica* Group]	1.00	2280	
		NP_001060995	Os08g0150800 [*Oryza sativa Japonica* Group] > gi|37573038|dbj|BAC98550.1| putative tyrosyl-tRNA synthetase [*Oryza sativa Japonica* Group] > gi|113622964|dbj|BAF22909.1| Os08g0150800 [*Oryza sativa Japonica* Group] > gi|222639916|gb|EEE68048.1| hypothetical protein OsJ_26046 [*Oryza sativa Japonica* Group]	0.94	2281	2671
		ACF82652	unknown [*Zea mays*]	0.87	2282	2672
		NP_001149217	LOC100282839 [*Zea mays*] > gi|195625536|gb|ACG34598.1| tyrosyl-tRNA synthetase [*Zea mays*]	0.86	2283	2673
		NP_001148699	tyrosyl-tRNA synthetase [*Zea mays*] > gi|195621482|gb|ACG32571.1| tyrosyl-tRNA synthetase [*Zea mays*]	0.83	2284	2674
		BAK05692	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326527699|dbj|BAK08124.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326533322|dbj|BAJ93633.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.83	2285	2675
		CAA71881	Tyrosyl-tRNA synthetase [*Nicotiana tabacum*]	0.69	2286	2676
		XP_002517485	tyrosyl-tRNA synthetase, putative [*Ricinus communis*] > gi|223543496|gb|EEF45027.1| tyrosyl-tRNA synthetase, putative [*Ricinus communis*]	0.71	2287	2677
		XP_002274369	PREDICTED: hypothetical protein [*Vitis vinifera*] > gi|297742518|emb|CBI34667.3| unnamed protein product [*Vitis vinifera*]	0.71	2288	2678
		CAN65657	hypothetical protein VITISV_000951 [*Vitis vinifera*]	0.71	2289	2679

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
	796-813	ACG35054	THO complex subunit 4 [*Zea mays*]	1.00	2290	2680
		NP_001146734	hypothetical protein LOC100280336 [*Zea mays*] > gi|194704900|gb|ACF86534.1| unknown [*Zea mays*] > gi|219888533|gb|ACL54641.1| unknown [*Zea mays*]	0.99	2291	2681
		XP_002438180	hypothetical protein SORBIDRAFT_10g009240 [*Sorghum bicolor*] > gi|241916403|gb|EER89547.1| hypothetical protein SORBIDRAFT_10g009240 [*Sorghum bicolor*]	0.87	2292	2682
	310-327	NP_001168358	hypothetical protein LOC100382126 [*Zea mays*] > gi|223947741|gb|ACN27954.1| unknown [*Zea mays*]	1.00	2293	2683
		BAD54151	putative poly(A) polymerase [*Oryza sativa Japonica* Group]	0.81	2294	
		BAJ95542	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.80	2295	2684
		NP_001174846	Os06g0558700 [*Oryza sativa Japonica* Group] > gi|255677141|dbj|BAH93574.1| Os06g0558700 [*Oryza sativa Japonica* Group]	0.80	2296	2685
		AAW68015	putative polynucleotide adenylyltransferase [*Oryza sativa Indica* Group]	0.80	2297	2686
		EAZ37348	hypothetical protein OsJ_21686 [*Oryza sativa Japonica* Group]	0.78	2298	
		EAZ01335	hypothetical protein OsI_23369 [*Oryza sativa Indica* Group]	0.78	2299	
	576-593	XP_002466644	hypothetical protein SORBIDRAFT_01g011560 [*Sorghum bicolor*] > gi|241920498|gb|EER93642.1| hypothetical protein SORBIDRAFT_01g011560 [*Sorghum bicolor*]	1.00	2300	2687
		NP_001169332	hypothetical protein LOC100383199 [*Zea mays*] > gi|224028751|gb|ACN33451.1| unknown [*Zea mays*]	0.96	2301	2688
		NP_001130678	hypothetical protein LOC100191781 [*Zea mays*] > gi|194688930|gb|ACF78549.1| unknown [*Zea mays*]	0.95	2302	2689
		EEC81302	hypothetical protein OsI_24438 [*Oryza sativa Indica* Group] > gi|222636212|gb|EEE66344.1| hypothetical protein OsJ_22634 [*Oryza sativa Japonica* Group]	0.87	2303	
		BAJ99110	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.86	2304	2690
		BAJ86220	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.75	2305	2691
		NP_001063757	Os09g0531900 [*Oryza sativa Japonica* Group] > gi|52075938|dbj|BAD46018.1| glycosyl transferase family 8 protein-like [*Oryza sativa Japonica* Group] > gi|52077221|dbj|BAD46265.1| glycosyl transferase family 8 protein-like [*Oryza sativa Japonica* Group] > gi|113631990|dbj|BAF25671.1|	0.74	2306	2692

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			Os09g0531900 [*Oryza sativa Japonica* Group] > gi|222641970|gb|EEE70102.1| hypothetical protein OsJ_30110 [*Oryza sativa Japonica* Group]			
		EEC84934	hypothetical protein OsI_32147 [*Oryza sativa Indica* Group]	0.74	2307	
		XP_002462717	hypothetical protein SORBIDRAFT_02g030820 [*Sorghum bicolor*] > gi|241926094|gb|EER99238.1| hypothetical protein SORBIDRAFT_02g030820 [*Sorghum bicolor*]	0.75	2308	2693
		CBI38820	unnamed protein product [*Vitis vinifera*]	0.72	2309	
Predicted siRNA 61382	70-89	XP_002446795	hypothetical protein SORBIDRAFT_06g022830 [*Sorghum bicolor*] > gi|241937978|gb|EES11123.1| hypothetical protein SORBIDRAFT_06g022830 [*Sorghum bicolor*]	1.00	2310	2694
		NP_001143685	hypothetical protein LOC100276413 [*Zea mays*] > gi|195624570|gb|ACG34115.1| hypothetical protein [*Zea mays*]	0.86	2311	2695
		ACN29321	unknown [*Zea mays*]	0.86	2312	2696
		NP_001053334	Os04g0520900 [*Oryza sativa Japonica* Group] > gi|21741854|emb|CAD41444.1| OSJNBa0019D11.15 [*Oryza sativa Japonica* Group] > gi|13564905|dbj|BAF15248.1| Os04g0520900 [*Oryza sativa Japonica* Group] > gi|116310729|emb|CAH67525.1| OSIGBa0131L05.6 [*Oryza sativa Indica* Group] > gi|125549050|gb|EAY94872.1| hypothetical protein OsI_16672 [*Oryza sativa Indica* Group] > gi|125591012|gb|EAZ31362.1| hypothetical protein OsJ_15488 [*Oryza sativa Japonica* Group] > gi|215697100|dbj|BAG91094.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.72	2313	2697
	682-701	NP_001143685	hypothetical protein LOC100276413 [*Zea mays*] > gi|195624570|gb|ACG34115.1| hypothetical protein [*Zea mays*]	1.00	2314	2698
		ACN29321	unknown [*Zea mays*]	0.95	2315	2699
		XP_002446795	hypothetical protein SORBIDRAFT_06g022830 [*Sorghum bicolor*] > gi|241937978|gb|EES11123.1| hypothetical protein SORBIDRAFT_06g022830 [*Sorghum bicolor*]	0.90	2316	2700
		NP_001053334	Os04g0520900 [*Oryza sativa Japonica Group*] > gi|21741854|emb|CAD41444.1| OSJNBa0019D11.15 [*Oryza sativa Japonica* Group] > gi|113564905|dbj|BAF15248.1| Os04g0520900 [*Oryza sativa Japonica* Group] > gi|116310729|emb|CAH67525.1|	0.70	2317	2701

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			OSIGBa0131L05.6 [*Oryza sativa Indica* Group] > gi|125549050|gb|EAY94872.1| hypothetical protein OsI_16672 [*Oryza sativa Indica* Group] > gi|125591012|gb|EAZ31362.1| hypothetical protein OsJ_15488 [*Oryza sativa Japonica* Group] > gi|215697100|dbj|BAG91094.1| unnamed protein product [*Oryza sativa Japonica* Group]			
Predicted siRNA 60188	237-254	XP_002459573	hypothetical protein SORBIDRAFT_02g006770 [*Sorghum bicolor*] > gi|241922950|gb|EER96094.1| hypothetical protein SORBIDRAFT_02g006770 [*Sorghum bicolor*]	1.00	2318	2702
		NP_001150031	nucleic acid binding protein [*Zea mays*] > gi|194699002|gb|ACF83585.1| unknown [*Zea mays*] > gi|195636208|gb|ACG37572.1| nucleic acid binding protein [*Zea mays*]	0.98	2319	2703
		NP_001140438	hypothetical protein LOC100272497 [*Zea mays*] > gi|194699514|gb|ACF83841.1| unknown [*Zea mays*]	0.96	2320	2704
		NP_001059216	Os07g0227400 [*Oryza sativa Japonica* Group] > gi|24060154|dbj|BAC21599.1| KH domain-like protein [*Oryza sativa Japonica* Group] > gi|113610752|dbj|BAF21130.1| Os07g0227400 [*Oryza sativa Japonica* Group] > gi|215697533|dbj|BAG91527.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.91	2321	2705
		EAZ39172	hypothetical protein OsJ_23597 [*Oryza sativa Japonica* Group] > gi|218199326|gb|EEC81753.1| hypothetical protein OsI_25419 [*Oryza sativa Indica* Group]	0.91	2322	
		NP_001148920	nucleic acid binding protein [*Zea mays*] > gi|195623320|gb|ACG33490.1| nucleic acid binding protein [*Zea mays*]	0.85	2323	2706
		XP_002466215	hypothetical protein SORBIDRAFT_01g003680 [*Sorghum bicolor*] > gi|241920069|gb|EER93213.1| hypothetical protein SORBIDRAFT_01g003680 [*Sorghum bicolor*]	0.85	2324	2707
		NP_001051685	Os03g0815700 [*Oryza sativa Japonica* Group] > gi|75226290|sp|Q75GR5.1|SPIN1_ORYSJ RecName: Full = KH domain-containing protein SPIN1; AltName: Full = SPL11-interacting protein 1 > gi|37718879|gb|AAR01750.1| expressed protein [*Oryza sativa Japonica* Group] > gi|108711745|gb|ABF99540.1| KH domain-containing protein, putative, expressed [*Oryza sativa Japonica* Group] > gi|113550156|dbj|BAF13599.1|	0.86	2325	2708

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			Os03g0815700 [*Oryza sativa Japonica* Group] > gi|215694514|dbj|BAG89507.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218193980|gb|EEC76407.1| hypothetical protein OsI_14057 [*Oryza sativa Indica* Group] > gi|222626037|gb|EEE60169.1| hypothetical protein OsJ_13097 [*Oryza sativa Japonica* Group]			
		NP_001130116	hypothetical protein LOC100191210 [*Zea mays*] > gi|194688334|gb|ACF78251.1| unknown [*Zea mays*]	0.84	2326	2709
		BAJ96236	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.83	2327	2710
	362-379	XP_002448500	hypothetical protein SORBIDRAFT_06g028030 [*Sorghum bicolor*] > gi|241939683|gb|EES12828.1| hypothetical protein SORBIDRAFT_06g028030 [*Sorghum bicolor*]	1.00	2328	2711
		NP_001148728	protein phosphatase 2C [*Zea mays*] > gi|195621678|gb|ACG32669.1| protein phosphatase 2C [*Zea mays*] > gi|238007398|gb|ACR34734.1| unknown [*Zea mays*]	0.93	2329	2712
		NP_001053823	Os04g0609600 [*Oryza sativa Japonica* Group] > gi|122240832|sp|Q0JAA0.1|P2C44_ORYSJ RecName: Full = Probable protein phosphatase 2C 44; Short = OsPP2C44 > gi|113565394|dbj|BAF15737.1| Os04g0609600 [*Oryza sativa Japonica* Group]	0.91	2330	2713
		5	[*Oryza sativa Japonica* Group]			
		EEC71777	hypothetical protein OsI_04389 [*Oryza sativa Indica* Group]	0.80	2339	
		BAJ99773	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.78	2340	2721
		XP_002458747	hypothetical protein SORBIDRAFT_03g039530 [*Sorghum bicolor*] > gi|241930722|gb|EES03867.1| hypothetical protein SORBIDRAFT_03g039530 [*Sorghum bicolor*]	0.78	2341	2722
		AAC04576	putative high-pI laccase [*Oryza sativa Japonica* Group]	0.79	2342	2723
	725-742	CAE03557	OSJNBa0085I10.2 [*Oryza sativa Japonica* Group] > gi|90265077|emb|CAH67750.1| H0702G05.9 [*Oryza sativa Indica* Group]	1.00	2343	2724
		NP_001053823	Os04g0609600 [*Oryza sativa Japonica* Group] > gi|122240832|sp|Q0JAA0.1|P2C44_ORYSJ RecName: Full = Probable protein phosphatase 2C 44; Short = OsPP2C44 > gi|113565394|dbj|BAF15737.1| Os04g0609600 [*Oryza sativa Japonica* Group] > gi|218195541|gb|EEC77968.1| hypothetical protein OsI_17335	1.00	2344	2725

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			[*Oryza sativa Indica* Group] > gi|222629521|gb|EEE61653.1| hypothetical protein OsJ_16105 [*Oryza sativa Japonica* Group]			
		XP_002448500	hypothetical protein SORBIDRAFT_06g028030 [*Sorghum bicolor*] > gi|241939683|gb|EES12828.1| hypothetical protein SORBIDRAFT_06g028030 [*Sorghum bicolor*]	0.91	2345	2726
		NP_001148728	protein phosphatase 2C [*Zea mays*] > gi|195621678|gb|ACG32669.1| protein phosphatase 2C [*Zea mays*] > gi|238007398|gb|ACR34734.1| unknown [*Zea mays*]	0.90	2346	2727
		CAE03658	OSJNBa0060NO3.23 [*Oryza sativa Japonica* Group]	0.75	2347	2728
		XP_002274944	PREDICTED: hypothetical protein isoform 1 [*Vitis vinifera*] > gi|297745124|emb|CB138963.3| unnamed protein product [*Vitis vinifera*]	0.74	2348	2729
		XP_002514493	protein phosphatase 2c, putative [*Ricinus communis*] > gi|223546392|gb|EEF47893.1| protein phosphatase 2c, putative [*Ricinus communis*]	0.76	2349	2730
		XP_002274981	PREDICTED: hypothetical protein isoform 2 [*Vitis vinifera*]	0.71	2350	2731
	879-896	NP_001054756	Os05g0168700 [*Oryza sativa Japonica* Group] > gi|53982148|gb|AAV25244.1| putative phosphate translocator [*Oryza sativa Japonica* Group] > gi|113578307|dbj|BAF16670.1| Os05g0168700 [*Oryza sativa Japonica* Group] > gi|215686739|dbj|BAG89589.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218196167|gb|EEC78594.1| hypothetical protein OsI_18612 [*Oryza sativa Indica* Group] > gi|222630341|gb|EEE62473.1| hypothetical protein OsJ_17270 [*Oryza sativa Japonica* Group]	1.00	2351	2732
		BAB41206	putative glucose-6-phosphate/phosphate-tranlocat or [*Oryza sativa* (*japonica* cultivar-group)]	0.99	2352	2733
		ACN32013	unknown [*Zea mays*]	0.96	2353	2734
		XP_002440680	hypothetical protein SORBIDRAFT_09g005010 [*Sorghum bicolor*] > gi|241945965|gb|EES19110.1| hypothetical protein SORBIDRAFT_09g005010 [*Sorghum bicolor*]	0.96	2354	2735
		NP_001142411	hypothetical protein LOC100274586 [*Zea mays*] > gi|194707946|gb|ACF88057.1| unknown [*Zea mays*] > gi|194708688|gb|ACF88428.1| unknown [*Zea mays*] > gi|195620476|gb|ACG32068.1| integral membrane protein like [*Zea mays*]	0.95	2355	2736

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		BAK03308	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.95	2356	2737
		NP_001148556	integral membrane protein like [*Zea mays*] > gi|195620390|gb|ACG32025.1| integral membrane protein like [*Zea mays*]	0.87	2357	2738
		NP_001042121	Os01g0167500 [*Oryza sativa Japonica* Group] > gi|13486667|dbj|BAB39904.1| P0028E10.8 [*Oryza sativa Japonica* Group] > gi|15528768|dbj|BAB64810.1| putative glucose-6-phosphate/phosphate-tranlocator [*Oryza sativa Japonica* Group] > gi|20804811|dbj|BAB92494.1| putative glucose-6-phosphate/phosphate-tranlocator [*Oryza sativa Japonica* Group] > gi|113531652|dbj|BAF04035.1| Os01g0167500 [*Oryza sativa Japonica* Group] > gi|215767361|dbj|BAG99589.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218187579|gb|EEC70006.1| hypothetical protein OsI_00550 [*Oryza sativa Indica* Group] > gi|222617800|gb|EEE53932.1| hypothetical protein OsJ_00515 [*Oryza sativa Japonica* Group]	0.92	2358	2739
		NP_001142171	hypothetical protein LOC100274338 [*Zea mays*] > gi|194707458|gb|ACF87813.1| unknown [*Zea mays*]	0.93	2359	2740
		ACN34739	unknown [*Zea mays*]	0.92	2360	2741
	130-147	XP_002448782	hypothetical protein SORBIDRAFT_06g033075 [*Sorghum bicolor*] > gi|241939965|gb|EES13110.1| hypothetical protein SORBIDRAFT_06g033075 [*Sorghum bicolor*]	1.00	2361	2742
		NP_001151057	LOC100284690 [*Zea mays*] > gi|195643970|gb|ACG41453.1| ATP binding protein [*Zea mays*]	0.92	2362	2743
		EAZ32429	hypothetical protein OsJ_16639 [*Oryza sativa Japonica* Group]	0.82	2363	
		NP_001054279	Os04g0679200 [*Oryza sativa Japonica* Group] > gi|38344039|emb|CAE05726.2| OSJNBb0017I01.6 [*Oryza sativa Japonica* Group] > gi|113565850|dbj|BAF16193.1| Os04g0679200 [*Oryza sativa Japonica* Group] > gi|215712397|dbj|BAG94524.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215740866|dbj|BAG97022.1| unnamed protein product [*Oryza sativa Japonica*Group]	0.82	2364	2744
		CAJ86254	H0801D08.12 [*Oryza sativa Indica* Group] > gi|125550244|gb|EAY96066.1| hypothetical protein OsI_17939 [*Oryza sativa Indica* Group]	0.82	2365	2745
		BAJ93433	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.80	2366	2746

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)						
Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
	99-116	XP_002452000	hypothetical protein SORBIDRAFT_04g014390 [*Sorghum bicolor*] > gi|241931831|gb|EES04976.1| hypothetical protein SORBIDRAFT_04g014390 [*Sorghum bicolor*]	1.00	2367	2747
		ACR36123	unknown [*Zea mays*]	0.93	2368	2748
		NP_001145206	hypothetical protein LOC100278461 [*Zea mays*] > gi|195652631|gb|ACG45783.1| hypothetical protein [*Zea mays*]	0.92	2369	2749
		NP_001046716	Os02g0329300 [*Oryza sativa Japonica* Group] > gi|46389946|dbj|BAD15798.1| unknown protein [*Oryza sativa Japonica* Group] > gi|113536247|dbj|BAF08630.1| Os02g0329300 [*Oryza sativa Japonica* Group] > gi|222622747|gb|EEE56879.1| hypothetical protein OsJ_06518 [*Oryza sativa Japonica* Group]	0.86	2370	2750
		EEC73063	hypothetical protein OsI_07020 [*Oryza sativa Indica* Group]	0.85	2371	
		BAK07073	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.81	2372	2751
	736-753	ACN28855	unknown [*Zea mays*]	1.00	2373	2752
		NP_001105875	putative laccase [*Zea mays*] > gi|84618781|emb|CAJ30500.1| putative laccase [*Zea mays*]	0.99	2374	2753
		NP_001146658	hypothetical protein LOC100280258 [*Zea mays*] > gi|219888209|gb|ACL54479.1| unknown [*Zea mays*]	0.93	2375	2754
		XP_002458746	hypothetical protein SORBIDRAFT_03g039520 [*Sorghum bicolor*] > gi|241930721|gb|EES03866.1| hypothetical protein SORBIDRAFT_03g039520 [*Sorghum bicolor*]	0.93	2376	2755
		NP_001044772	Os01g0842400 [*Oryza sativa Japonica* Group] > gi|75321217|sp|Q5N9X2.1|LAC4_ORYSJ RecName: Full = Laccase-4; AltName: Full = Benzenediol:oxygen oxidoreductase 4; AltName: Full = Diphenol oxidase 4; AltName: Full = Urishiol oxidase 4; Flags: Precursor > gi|56784239|dbj|BAD81734.1| putative laccase LAC5-6 [*Oryza sativa Japonica* Group] > gi|113534303|dbj|BAF06686.1| Os01g0842400 [*Oryza sativa Japonica* Group] > gi|215697155|dbj|BAG91149.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.81	2377	2756
		EAZ14115	hypothetical protein OsJ_04039 [*Oryza sativa Japonica* Group]	0.81	2378	
		EEC71777	hypothetical protein OsI_04389 [*Oryza sativa Indica* Group]	0.80	2379	
		BAJ99773	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.78	2380	2757
		XP_002458747	hypothetical protein SORBIDRAFT_03g039530 [*Sorghum bicolor*] > gi|241930722|gb|EES03867.1| hypothetical protein	0.78	2381	2758

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			SORBIDRAFT_03g039530 [*Sorghum bicolor*]			
		AAC04576	putative high-pI laccase [*Oryza sativa Japonica* Group]	0.79	2382	2759
	0-17	NP_001132686	hypothetical protein LOC100194164 [*Zea mays*] > gi|194695090|gb|ACF81629.1| unknown [*Zea mays*]	1.00	2383	2760
		XP_002457397	hypothetical protein SORBIDRAFT_03g006690 [*Sorghum bicolor*] > gi|241929372|gb|EES02517.1| hypothetical protein SORBIDRAFT_03g006690 [*Sorghum bicolor*]	0.81	2384	2761
	1000-1017	NP_001136742	hypothetical protein LOC100216883 [*Zea mays*] > gi|194696868|gb|ACF82518.1| unknown [*Zea mays*] > gi|195648274|gb|ACG43605.1| monoglyceride lipase [*Zea mays*]	1.00	2385	2762
		XP_002450081	hypothetical protein SORBIDRAFT_05g000200 [*Sorghum bicolor*] > gi|241935924|gb|EES09069.1| hypothetical protein SORBIDRAFT_05g000200 [*Sorghum bicolor*]	0.80	2386	2763
		XP_002442631	hypothetical protein SORBIDRAFT_08g000200 [*Sorghum bicolor*] > gi|241943324|gb|EES16469.1| hypothetical protein SORBIDRAFT_08g000200 [*Sorghum bicolor*]	0.80	2387	2764
	296-313	XP_002440680	hypothetical protein SORBIDRAFT_09g005010 [*Sorghum bicolor*] > gi|241945965|gb|EES19110.1| hypothetical protein SORBIDRAFT_09g005010 [*Sorghum bicolor*]	1.00	2388	2765
		ACN32013	unknown [*Zea mays*]	0.99	2389	2766
		NP_001142411	hypothetical protein LOC100274586 [*Zea mays*] > gi|194707946|gb|ACF88057.1| unknown [*Zea mays*] > gi|194708688|gb|ACF88428.1| unknown [*Zea mays*] > gi|195620476|gb|ACG32068.1| integral membrane protein like [*Zea mays*]	0.98	2390	2767
		NP_001054756	Os05g0168700 [*Oryza sativa Japonica* Group] > gi|53982148|gb|AAV25244.1| putative phosphate translocator [*Oryza sativa Japonica* Group] > gi|113578307|dbj|BAF16670.1| Os05g0168700 [*Oryza sativa Japonica* Group] > gi|215686739|dbj|BAG89589.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218196167|gb|EEC78594.1| hypothetical protein OsI_18612 [*Oryza sativa Indica* Group] > gi|222630341|gb|EEE62473.1| hypothetical protein OsJ_17270 [*Oryza sativa Japonica* Group]	0.96	2391	2768

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		BAB41206	putative glucose-6-phosphate/phosphate-tranlocat or [*Oryza sativa* (*japonica* cultivar-group)]	0.95	2392	2769
		BAK03308	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.94	2393	2770
		NP_001148556	integral membrane protein like [*Zea mays*] > gi|195620390|gb|ACG32025.1| integral membrane protein like [*Zea mays*]	0.90	2394	2771
		NP_001042121	Os01g0167500 [*Oryza sativa Japonica* Group] > gi|13486667|dbj|BAB39904.1| P0028E10.8 [*Oryza sativa Japonica* Group] > gi|15528768|dbj|BAB64810.1| putative glucose-6-phosphate/phosphate-tranlocator [*Oryza sativa Japonica* Group] > gi|20804811|dbj|BAB92494.1| putative glucose-6-phosphate/phosphate-tranlocator [*Oryza sativa Japonica* Group] > gi|113531652|dbj|BAF04035.1| Os01g0167500 [*Oryza sativa Japonica* Group] > gi|215767361|dbj|BAG99589.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218187579|gb|EEC70006.1| hypothetical protein OsI_00550 [*Oryza sativa Indica* Group] > gi|222617800|gb|EEE53932.1| hypothetical protein OsJ_00515 [*Oryza sativa Japonica* Group]	0.92	2395	2772
		NP_001142171	hypothetical protein LOC100274338 [*Zea mays*] > gi|194707458|gb|ACF87813.1| unknown [*Zea mays*]	0.92	2396	2773
		ACN34739	unknown [*Zea mays*]	0.91	2397	2774
	1638-1655	NP_001183153	hypothetical protein LOC100501523 [*Zea mays*] > gi|238009674|gb|ACR35872.1| unknown [*Zea mays*]	1.00	2398	2775
	1133-1150	NP_001146658	hypothetical protein LOC100280258 [*Zea mays*] > gi|219888209|gb|ACL54479.1| unknown [*Zea mays*]	1.00	2399	2776
		NP_001105875	putative laccase [*Zea mays*] > gi|84618781|emb|CAJ30500.1| putative laccase [*Zea mays*]	0.95	2400	2777
		ACN28855	unknown [*Zea mays*]	0.92	2401	2778
		XP_002458746	hypothetical protein SORBIDRAFT_03g039520 [*Sorghum bicolor*] > gi|241930721|gb|EES03866.1| hypothetical protein SORBIDRAFT_03g039520 [*Sorghum bicolor*]	0.91	2402	2779
		NP_001044772	Os01g0842400 [*Oryza sativa Japonica* Group] > gi|75321217|sp|Q5N9X2.1|LAC4_ORYSJ RecName: Full = Laccase-4; AltName: Full = Benzenediol:oxygen oxidoreductase 4; AltName: Full = Diphenol oxidase 4; AltName: Full = Urishiol oxidase 4; Flags: Precursor > gi|56784239|dbj|BAD81734.1| putative laccase LAC5-6	0.80	2403	2780

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			[*Oryza sativa Japonica* Group] > gi|113534303|dbj|BAF06686.1| Os01g0842400 [*Oryza sativa Japonica* Group] > gi|215697155|dbj|BAG91149.1| unnamed protein product [*Oryza sativa Japonica* Group]			
		EAZ14115	hypothetical protein OsJ_04039 [*Oryza sativa Japonica* Group]	0.80	2404	
		EEC71777	hypothetical protein OsI_04389 [*Oryza sativa Indica* Group]	0.80	2405	
		BAJ99773	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.78	2406	2781
		AAC04576	putative high-pI laccase [*Oryza sativa Japonica* Group]	0.78	2407	2782
		XP_002458747	hypothetical protein SORBIDRAFT_03g039530 [*Sorghum bicolor*] > gi|241930722|gb|EES03867.1| hypothetical protein SORBIDRAFT_03g039530 [*Sorghum bicolor*]	0.77	2408	2783
	574-591	NP_001053823	Os04g0609600 [*Oryza sativa Japonica* Group] > gi|122240832|sp|Q0JAA0.1|P2C44_ORYSJ RecName: Full = Probable protein phosphatase 2C 44; Short = OsPP2C44 > gi|113565394|dbj|BAF15737.1| Os04g0609600 [*Oryza sativa Japonica* Group] > gi|218195541|gb|EEC77968.1| hypothetical protein OsI_17335 [*Oryza sativa Indica* Group] > gi|222629521|gb|EEE61653.1| hypothetical protein OsJ_16105 [*Oryza sativa Japonica* Group]	1.00	2409	2784
		CAE03557	OSJNBa0085I10.2 [*Oryza sativa Japonica* Group] > gi|90265077|emb|CAH67750.1| H0702G05.9 [*Oryza sativa Indica* Group]	0.99	2410	2785
		XP_002448500	hypothetical protein SORBIDRAFT_06g028030 [*Sorghum bicolor*] > gi|241939683|gb|EES12828.1| hypothetical protein SORBIDRAFT_06g028030 [*Sorghum bicolor*]	0.91	2411	2786
		NP_001148728	protein phosphatase 2C [*Zea mays*] > gi|195621678|gb|ACG32669.1| protein phosphatase 2C [*Zea mays*] > gi|238007398|gb|ACR34734.1| unknown [*Zea mays*]	0.90	2412	2787
		CAE03658	OSJNBa0060N03.23 [*Oryza sativa Japonica* Group]	0.74	2413	2788
		XP_002274944	PREDICTED: hypothetical protein isoform 1 [*Vitis vinifera*] > gi|297745124|emb|CBI38963.3| unnamed protein product [*Vitis vinifera*]	0.73	2414	2789
		XP_002514493	protein phosphatase 2c, putative [*Ricinus communis*] > gi|223546392|gb|EEF47893.1| protein phosphatase 2c, putative [*Ricinus communis*]	0.75	2415	2790
		XP_002274981	PREDICTED: hypothetical protein isoform 2 [*Vitis vinifera*]	0.70	2416	2791

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
	1034-1051	NP_001170532	hypothetical protein LOC100384546 [*Zea mays*] > gi|238005884|gb|ACR33977.1| unknown [*Zea mays*]	1.00	2417	2792
		XP_002438672	hypothetical protein SORBIDRAFT_10g024080 [*Sorghum bicolor*] > gi|241916895|gb|EER90039.1| hypothetical protein SORBIDRAFT_10g024080 [*Sorghum bicolor*]	0.88	2418	2793
		EAZ01659	hypothetical protein OsI_23694 [*Oryza sativa Indica* Group]	0.72	2419	
		EAZ37629	hypothetical protein OsJ_21963 [*Oryza sativa Japonica* Group]	0.72	2420	
		BAD35523	unknown protein [*Oryza sativa Japonica* Group] > gi|51090952|dbj|BAD35555.1| unknown protein [*Oryza sativa Japonica* Group]	0.72	2421	
	1728-1745	AAW66346	YZ1 [*Zea luxurians*]	1.00	2422	2794
		AAW66344	YZ1 [*Zea mays* subsp. *mexicana*]	0.99	2423	2795
		AAW66348	YZ1 [*Zea mays* subsp. *parviglumis*]	0.99	2424	2796
		AAM22634	YZ1 [*Zea mays*]	0.99	2425	2797
		AAM21160	YZ1 [*Zea mays*]	0.98	2426	2798
		ABB29302	YZ1 [*Zea mays*] > gi|78172241|gb|ABB29304.1| YZ1 [*Zea mays*]	0.91	2427	2799
		NP_001043656	Os01g0633400 [*Oryza sativa Japonica* Group] > gi|55296003|dbj|BAD68894.1| putative YZ1 [*Oryza sativa Japonica* Group] > gi|113533187|dbj|BAF05570.1| Os01g0633400 [*Oryza sativa Japonica* Group] > gi|215766352|dbj|BAG98580.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.71	2428	2800
		XP_002456014	hypothetical protein SORBIDRAFT_03g028870 [*Sorghum bicolor*] > gi|241927989|gb|EES01134.1| hypothetical protein SORBIDRAFT_03g028870 [*Sorghum bicolor*]	0.77	2429	2801
		EAY75077	hypothetical protein OsI_02971 [*Oryza sativa Indica* Group]	0.71	2430	
Predicted siRNA 59659	689-710	XP_002443139	hypothetical protein SORBIDRAFT_08g011100 [*Sorghum bicolor*] > gi|241943832|gb|EES16977.1| hypothetical protein SORBIDRAFT_08g011100 [*Sorghum bicolor*]	1.00	2431	2802
		NP_001169596	hypothetical protein LOC100383477 [*Zea mays*] > gi|224030279|gb|ACN34215.1| unknown [*Zea mays*]	0.94	2432	2803
		NP_001066586	Os12g0285600 [*Oryza sativa Japonica* Group] > gi|77554686|gb|ABA97482.1| Oxysterol-binding protein, expressed [*Oryza sativa Japonica* Group]	0.83	2433	2804

TABLE 7-continued

Target genes of up regulated siRNA sequences associated with NUE (Table 3)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			> gi|113649093|dbj|BAF29605.1| Os12g0285600 [*Oryza sativa Japonica* Group] > gi|215697261|dbj|BAG91255.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222616918|gb|EEE53050.1| hypothetical protein OsJ_35782 [*Oryza sativa Japonica* Group]			
		EEC69105	hypothetical protein OsI_38013 [*Oryza sativa Indica* Group]	0.81	2434	
		CBI16832	unnamed protein product [*Vitis vinifera*]	0.71	2435	
		XP_002282089	PREDICTED: similar to oxysterol-binding family protein [*Vitis vinifera*]	0.72	2436	2805

Table 7: Provided are the target Genes of siRNAs Associated with Increased NUE (Table 3) along with their GenBank Accession numbers and sequence identifiers (SEQ ID NO:).

"bind" = binding;

"pos" = position;

"hom" = homologue;

"p.p." = polypeptide;

"p.n." = polynucleotide.

TABLE 8

Target genes of down regulated siRNA sequences associated with NUE (Table 4)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
Predicted siRNA 59123	61-79	EEE65047	hypothetical protein OsJ_20044 [*Oryza sativa Japonica* Group]	1.00	2806	
		NP_001056727	Os06g0136600 [*Oryza sativa Japonica* Group] > gi|55296986|dbj|BAD68461.1| putative enolase [*Oryza sativa Japonica* Group] > gi|55297212|dbj|BAD68886.1| putative enolase [*Oryza sativa Japonica* Group] > gi|113594767|dbj|BAF18641.1| Os06g0136600 [*Oryza sativa Japonica* Group] > gi|218197519|gb|EEC79946.1| hypothetical protein OsI_21538 [*Oryza sativa Indica* Group]	0.97	2807	3082
		NP_001105896	enolase 1 [*Zea mays*] > gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full = Enolase 1; AltName: Full = 2-phospho-D-glycerate hydro-lyase 1; AltName: Full = 2-phosphoglycerate dehydratase 1 > gi|22273|emb|CAA39454.1|enolase [*Zea mays*]	0.92	2808	3083
		ACL53816	unknown [*Zea mays*]	0.92	2809	3084
		ACN26258	unknown [*Zea mays*]	0.88	2810	3085
		ACG31732	enolase [*Zea mays*]	0.87	2811	3086
		XP_002322420	predicted protein [*Populus trichocarpa*] > gi|118484871|gb|ABK94302.1| unknown [*Populus trichocarpa*] > gi|222869416|gb|EEF06547.1| predicted protein [*Populus trichocarpa*]	0.88	2812	3087
		NP_001105371	enolase 2 [*Zea mays*] > gi|1169528|sp|P42895.1|ENO2_MAIZE RecName: Full = Enolase 2; AltName: Full = 2-phospho-D-glycerate hydro-lyase 2; AltName: Full = 2-phosphoglycerate dehydratase 2	0.87	2813	3088

TABLE 8-continued

Target genes of down regulated siRNA sequences associated with NUE (Table 4)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			> gi|602253|gb|AAD04187.1|enolase [*Zea mays*] > gi|37222051|gb|AAQ17040.2|pollen 2-phosphoglycerate dehydrogenase 2 precursor [*Cynodon dactylon*]			
		ACF06525	enolase [*Elaeis guineensis*]	0.87	2814	3089
		BAJ90134	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.87	2815	3090
	45-63	NP_001143947	hypothetical protein LOC100276760 [*Zea mays*] > gi|195630673|gb|ACG36643.1| hypothetical protein [*Zea mays*]	1.00	2816	3091
		ACR36446	unknown [*Zea mays*]	0.97	2817	3092
		NP_001143988	hypothetical protein LOC100276806 [*Zea mays*] > gi|194707932|gb|ACF88050.1| unknown [*Zea mays*] > gi|195619872|gb|ACG31766.1| hypothetical protein [*Zea mays*] > gi|195634969|gb|ACG36953.1| hypothetical protein [*Zea mays*]	0.79	2818	3093
		XP_002450179	hypothetical protein SORBIDRAFT_05g001600 [*Sorghum bicolor*] > gi|241936022|gb|EES09167.1| hypothetical protein SORBIDRAFT_05g001600 [*Sorghum bicolor*]	0.81	2819	3094
		NP_001065630	Os11g0127700 [*Oryza sativa Japonica* Group] > gi|77548485|gb|ABA91282.1| expressed protein [*Oryza sativa Japonica* Group] > gi|113644334|dbj|BAF27475.1| Os11g0127700 [*Oryza sativa Japonica* Group] > gi|125576047|gb|EAZ17269.1| hypothetical protein OsJ_32788 [*Oryza sativa Japonica* Group]	0.70	2820	3095
		EAY79782	hypothetical protein OsI_34938 [*Oryza sativa Indica* Group]	0.70	2821	
	2433-2451	XP_002466271	hypothetical protein SORBIDRAFT_01g004840 [*Sorghum bicolor*] > gi|241920125|gb|EER93269.1| hypothetical protein SORBIDRAFT_01g004840 [*Sorghum bicolor*]	1.00	2822	3096
		NP_001145769	hypothetical protein LOC100279276 [*Zea mays*] > gi|219884363|gb|ACL52556.1| unknown [*Zea mays*]	0.98	2823	3097
		NP_001151633	vacuolar protein sorting 35 [*Zea mays*] > gi|195648240|gb|ACG43588.1| vacuolar protein sorting 35 [*Zea mays*]	0.98	2824	3098
		EAY92214	hypothetical protein OsI_13933 [*Oryza sativa Indica* Group]	0.95	2825	
		NP_001051593	Os03g0801600 [*Oryza sativa Japonica* Group] > gi|29150373|gb|AAO72382.1| putative vacuolar protein sorting-associated protein [*Oryza sativa Japonica* Group] > gi|108711598|gb|ABF99393.1| vacuolar protein sorting-associated protein 35 family protein, putative, expressed [*Oryza sativa Japonica* Group] > gi|113550064|dbj|BAF13507.1| Os03g0801600 [*Oryza sativa Japonica* Group] > gi|125588278|gb|EAZ28942.1| hypothetical protein OsJ_12986 [*Oryza sativa Japonica* Group] > gi|215704706|dbj|BAG94334.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.95	2826	3099
		BAJ89592	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326488479|dbj|BAJ93908.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.95	2827	3100

TABLE 8-continued

Target genes of down regulated siRNA sequences associated with NUE (Table 4)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		XP_002272227	PREDICTED: hypothetical protein isoform 1 [*Vitis vinifera*]	0.82	2828	3101
		XP_002272268	PREDICTED: hypothetical protein isoform 2 [*Vitis vinifera*]	0.81	2829	3102
		BAJ53108	JHL20J20.15 [*Jatropha curcas*]	0.79	2830	
		CBI17331	unnamed protein product [*Vitis vinifera*]	0.81	2831	
	20-38	XP_002442446	hypothetical protein SORBIDRAFT_08g020140 [*Sorghum bicolor*] > gi|241943139|gb|EES16284.1| hypothetical protein SORBIDRAFT_08g020140 [*Sorghum bicolor*]	1.00	2832	3103
		ACF80272	unknown [*Zea mays*]	0.84	2833	3104
		NP_001141063	hypothetical protein LOC100273144 [*Zea mays*] > gi|194702462|gb|ACF85315.1| unknown [*Zea mays*]	0.84	2834	3105
		ACG44331	hypothetical protein [*Zea mays*]	0.84	2835	3106
		BAJ89075	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326533254|dbj|BAJ93599.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.70	2836	3107
Predicted siRNA 57685	713-731	CAI30078	glycosyltransferase [*Sorghum bicolor*]	1.00	2837	3108
		NP_001105165	glycosyltransferase [*Zea mays*] > gi|56409864|emb|CAI30080.1| glycosyltransferase [*Zea mays*]	0.96	2838	3109
		CAI30079	glycosyltransferase [*Saccharum officinarum*]	0.95	2839	3110
		BAJ96053	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.81	2840	3111
		NP_001064930	Os10g0492200 [*Oryza sativa Japonica* Group] > gi|10140717|gb|AAG13551.1|AC023240_24 unknown protein [*Oryza sativa Japonica* Group] > gi|31432816|gb|AAP54403.1| glycosyltransferase, putative, expressed [*Oryza sativa Japonica* Group] > gi|113639539|dbj|BAF26844.1| Os10g0492200 [*Oryza sativa Japonica* Group] > gi|215766456|dbj|BAG98764.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222613059|gb|EEE51191.1| hypothetical protein OsJ_31998 [*Oryza sativa Japonica* Group]	0.77	2841	3112
		EEC67226	hypothetical protein OsI_34143 [*Oryza sativa Indica* Group]	0.76	2842	
		CCA61105	TaGT61_1 [*Triticum aestivum*]	0.70	2843	3113
		BAK04539	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.71	2844	3114
		NP_001046724	Os02g0331200 [*Oryza sativa Japonica* Group] > gi|46390170|dbj|BAD15603.1| putative HGA1 [*Oryza sativa Japonica* Group] > gi|46390974|dbj|BAD16509.1| putative HGA1 [*Oryza sativa Japonica* Group] > gi|113536255|dbj|BAF08638.1| Os02g0331200 [*Oryza sativa Japonica* Group] > gi|215712340|dbj|BAG94467.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215737036|dbj|BAG95965.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.71	2845	3115

TABLE 8-continued

Target genes of down regulated siRNA sequences associated with NUE (Table 4)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
	344-362	YP_588428	hypothetical protein ZeamMp184 [*Zea mays* subsp. *mays*] > gi|40795041|gb|AAR91085.1| hypothetical protein [*Zea mays*] > gi|93116163|gb|ABE98794.1| hypothetical protein [*Zea mays* subsp. *mays*] > gi|102579667|gb|ABF70947.1| hypothetical protein [*Zea mays* subsp. *mays*]	1.00	2846	
		ABE98707	hypothetical protein [*Zea mays* subsp. *mays*]	0.90	2847	
	1201-1219	CAI30079	glycosyltransferase [*Saccharum officinarum*]	1.00	2848	3116
		NP_001105165	glycosyltransferase [*Zea mays*] > gi|56409864|emb|CAI30080.1| glycosyltransferase [*Zea mays*]	0.96	2849	3117
		CAI30078	glycosyltransferase [*Sorghum bicolor*]	0.97	2850	3118
		BAJ96053	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.83	2851	3119
		NP_001064930	Os10g0492200 [*Oryza sativa Japonica* Group] > gi|10140717|gb|AAG13551.1|AC023240_24 unknown protein [*Oryza sativa Japonica* Group] > gi|31432816|gb|AAP54403.1| glycosyltransferase, putative, expressed [*Oryza sativa Japonica* Group] > gi|113639539|dbj|BAF26844.1| Os10g0492200 [*Oryza sativa Japonica* Group] > gi|215766456|dbj|BAG98764.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222613059|gb|EEE51191.1| hypothetical protein OsJ_31998 [*Oryza sativa Japonica* Group]	0.77	2852	3120
		EEC67226	hypothetical protein OsI_34143 [*Oryza sativa Indica* Group]	0.78	2853	
		BAK04539	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.71	2854	3121
		CCA61105	TaGT61_1 [*Triticum aestivum*]	0.70	2855	3122
		BAD15602	putative HGA1 [*Oryza sativa Japonica* Group] > gi|46390975|dbj|BAD16510.1| putative HGA1 [*Oryza sativa Japonica* Group] > gi|215686668|dbj|BAG88921.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.71	2856	
		NP_001046724	Os02g0331200 [*Oryza sativa Japonica* Group] > gi|46390170|dbj|BAD15603.1| putative HGA1 [*Oryza sativa Japonica* Group] > gi|46390974|dbj|BAD16509.1| putative HGA1 [*Oryza sativa Japonica* Group] > gi|113536255|dbj|BAF08638.1| Os02g0331200 [*Oryza sativa Japonica* Group] > gi|215712340|dbj|BAG94467.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215737036|dbj|BAG95965.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.71	2857	3123
Predicted siRNA 59993	Jan-19	XP_002440494	hypothetical protein SORBIDRAFT_09g001910 [*Sorghum bicolor*] > gi|241945779|gb|EES18924.1| hypothetical protein SORBIDRAFT_09g001910 [*Sorghum bicolor*]	1.00	2858	3124
		ACG27529	splicing factor, arginine/serine-rich 7 [*Zea mays*] > gi|223973611|gb|ACN30993.1| unknown [*Zea mays*]	0.87	2859	3125

TABLE 8-continued

Target genes of down regulated siRNA sequences associated with NUE (Table 4)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		NP_001049771	Os03g0285900 [*Oryza sativa Japonica* Group] > gi|108707560|gb|ABF95355.1| RNA recognition motif family protein, expressed [*Oryza sativa Japonica* Group] > gi|113548242|dbj|BAF11685.1| Os03g0285900 [*Oryza sativa Japonica* Group] > gi|222624706|gb|EEE58838.1| hypothetical protein OsJ_10413 [*Oryza sativa Japonica* Group]	0.74	2860	3126
		EEC75006	hypothetical protein OsI_11073 [*Oryza sativa Indica* Group]	0.70	2861	
		NP_001132009	hypothetical protein LOC100193414 [*Zea mays*] > gi|194693184|gb|ACF80676.1| unknown [*Zea mays*]	0.72	2862	3127
		AAY84873	alternative splicing regulator [*Triticum aestivum*]	0.72	2863	3128
	14-32	XP_002458875	hypothetical protein SORBIDRAFT_03g041990 [*Sorghum bicolor*] > gi|241930850|gb|EES03995.1| hypothetical protein SORBIDRAFT_03g041990 [*Sorghum bicolor*]	1.00	2864	3129
		NP_001142991	hypothetical protein LOC100275452 [*Zea mays*] > gi|195612624|gb|ACG28142.1| hypothetical protein [*Zea mays*]	0.92	2865	3130
		NP_001145171	hypothetical protein LOC100278407 [*Zea mays*] > gi|195652179|gb|ACG45557.1| hypothetical protein [*Zea mays*]	0.91	2866	3131
		ACF83626	unknown [*Zea mays*]	0.92	2867	3132
		EAZ14403	hypothetical protein OsJ_04323 [*Oryza sativa Japonica* Group]	0.89	2868	
		EAY76740	hypothetical protein OsI_04696 [*Oryza sativa Indica* Group]	0.90	2869	
		BAK00430	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.84	2870	3133
	2352-2370	NP_001067313	Os12g0623900 [*Oryza sativa Japonica* Group] > gi|77556631|gb|ABA99427.1| 5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase, putative, expressed [*Oryza sativa Japonica* Group] > gi|108862991|gb|ABG22094.1|5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase, putative, expressed [*Oryza sativa Japonica* Group] > gi|113649820|dbj|BAF30332.1| Os12g0623900 [*Oryza sativa Japonica* Group] > gi|125537469|gb|EAY83957.1| hypothetical protein OsI_39179 [*Oryza sativa Indica* Group] > gi|125580128|gb|EAZ21274.1| hypothetical protein OsJ_36926 [*Oryza sativa Japonica* Group]	1.00	2871	3134
		ABG22095	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase, putative, expressed [*Oryza sativa Japonica* Group] > gi|108862993|gb|ABG22096.1|5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase, putative, expressed [*Oryza sativa Japonica* Group]	0.99	2872	
		NP_001067314	Os12g0624000 [*Oryza sativa Japonica* Group] > gi|77556632|gb|ABA99428.1| 5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase, putative, expressed [*Oryza sativa Japonica* Group] > gi|77556633|gb|ABA99429.1|5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase, putative, expressed [*Oryza sativa Japonica* Group]	0.98	2873	3135

TABLE 8-continued

Target genes of down regulated siRNA sequences associated with NUE (Table 4)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			> gi|113649821|dbj|BAF30333.1| Os12g0624000 [*Oryza sativa Japonica* Group] > gi|215695374|dbj|BAG90565.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|218187282|gb|EEC69709.1| hypothetical protein OsI_39180 [*Oryza sativa Indica* Group] > gi|222617511|gb|EEE53643.1| hypothetical protein OsJ_36927 [*Oryza sativa Japonica* Group]			
		ACN28399	unknown [*Zea mays*]	0.95	2874	3136
		AAL33589	methionine synthase [*Zea mays*]	0.94	2875	3137
		ACL54117	unknown [*Zea mays*]	0.94	2876	3138
		NP_001152513	LOC100286153 [*Zea mays*] > gi|195657041|gb|ACG47988.1|5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase [*Zea mays*]	0.94	2877	3139
		CAJ01714	methionine synthase 2 enzyme [*Hordeum vulgare* subsp. *vulgare*] > gi|326512178|dbj|BAJ96070.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.94	2878	3140
		BAJ89541	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.94	2879	3141
		BAJ88127	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.94	2880	3142
	121-139	ACL52492	unknown [*Zea mays*]	1.00	2881	3143
		XP_002465926	hypothetical protein SORBIDRAFT_01g048350 [*Sorghum bicolor*] > gi|241919780|gb|EER92924.1| hypothetical protein SORBIDRAFT_01g048350 [*Sorghum bicolor*]	0.94	2882	3144
		NP_001048855	Os03g0130500 [*Oryza sativa Japonica* Group] > gi|108706005|gb|ABF93800.1| EF hand family protein, expressed [*Oryza sativa Japonica* Group] > gi|113547326|dbj|BAF10769.1| Os03g0130500 [*Oryza sativa Japonica* Group]	0.80	2883	3145
		EAZ25463	hypothetical protein OsJ_09285 [*Oryza sativa Japonica* Group]	0.79	2884	
		BAJ91192	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.80	2885	3146
	49-67	ACV84253	LOX5 [*Sorghum bicolor*]	1.00	2886	3147
		XP_002446554	hypothetical protein SORBIDRAFT_06g018040 [*Sorghum bicolor*] > gi|241937737|gb|EES10882.1| hypothetical protein SORBIDRAFT_06g018040 [*Sorghum bicolor*]	1.00	2887	3148
		ACL81190	tasselseed 1 [*Zea mays*]	0.95	2888	3149
		NP_001105979	tassel seed1 [*Zea mays*] > gi|84626293|gb|ABC59691.1| lipoxygenase [*Zea mays*]	0.95	2889	
		ACL81191	tasselseed 1b [*Zea mays*]	0.91	2890	3150
		NP_001105978	lipoxygenase7 [*Zea mays*] > gi|84626291|gb|ABC59690.1| lipoxygenase [*Zea mays*]	0.90	2891	3151
		Q7XV13	RecName: Full = Putative lipoxygenase 5 > gi|38344820|emb|CAD40882.2| OSJNBa0064H22.1 [*Oryza sativa Japonica* Group] > gi|116310177|emb|CAH67189.1| OSIGBa0152K17.1 [*Oryza sativa Indica* Group]	0.86	2892	

TABLE 8-continued

Target genes of down regulated siRNA sequences associated with NUE (Table 4)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		BAJ94611	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326511025|dbj|BAJ91860.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.85	2893	3152
		CAI84707	lipoxygenase-like protein [*Hordeum vulgare* subsp. *vulgare*]	0.85	2894	3153
		BAK03423	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.85	2895	3154
	117-135	NP_001169757	hypothetical protein LOC100383639 [*Zea mays*] > gi|224031489|gb|ACN34820.1| unknown [*Zea mays*] > gi|238006168|gb|ACR34119.1| unknown [*Zea mays*]	1.00	2896	3155
		ACG49031	ubiquinone biosynthesis methyltransferase COQ5 [*Zea mays*]	0.99	2897	3156
		NP_001151844	ubiquinone biosynthesis methyltransferase COQ5 [*Zea mays*] > gi|195650199|gb|ACG44567.1| ubiquinone biosynthesis methyltransferase COQ5 [*Zea mays*]	0.93	2898	3157
		NP_001045568	Os01g0976600 [*Oryza sativa Japonica* Group] > gi|75320942|sp|Q5JNC0.1|COQ5_ORYSJ RecName: Full = 2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial; AltName: Full = Ubiquinone biosynthesis methyltransferase COQ5; Flags: Precursor > gi|57899522|dbj|BAD87036.1| putative ubiquinone [*Oryza sativa Japonica* Group] > gi|113535099|dbj|BAF07482.1| Os01g0976600 [*Oryza sativa Japonica* Group] > gi|215706368|dbj|BAG93224.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222619975|gb|EEE56107.1| hypothetical protein OsJ_04965 [*Oryza sativa Japonica* Group]	0.87	2899	3158
		EAY77437	hypothetical protein OsI_05431 [*Oryza sativa Indica* Group]	0.87	2900	
		BAJ89795	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.78	2901	3159
		XP_002457083	hypothetical protein SORBIDRAFT_03g000990 [*Sorghum bicolor*] > gi|241929058|gb|EES02203.1| hypothetical protein SORBIDRAFT_03g000990 [*Sorghum bicolor*]	0.72	2902	3160
		XP_002324457	predicted protein [*Populus trichocarpa*] > gi|222865891|gb|EEF03022.1| predicted protein [*Populus trichocarpa*]	0.70	2903	3161
	656-674	XP_002444158	hypothetical protein SORBIDRAFT_07g010240 [*Sorghum bicolor*] > gi|241940508|gb|EES13653.1| hypothetical protein SORBIDRAFT_07g010240 [*Sorghum bicolor*]	1.00	2904	3162
		NP_001168336	hypothetical protein LOC100382104 [*Zea mays*] > gi|223947549|gb|ACN27858.1| unknown [*Zea mays*]	0.85	2905	3163
		EAY97519	hypothetical protein OsI_19447 [*Oryza sativa Indica* Group] > gi|222631101|gb|EEE63233.1| hypothetical protein OsJ_18043 [*Oryza sativa Japonica* Group]	0.80	2906	
		BAJ96779	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.78	2907	3164
		BAK02037	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.78	2908	3165

TABLE 8-continued

Target genes of down regulated siRNA sequences associated with NUE (Table 4)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		BAJ97459	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.78	2909	3166
		AAV44115	unknown protein [*Oryza sativa Japonica* Group]	0.78	2910	
	668-686	NP_001150708	zinc finger, C2H2 type family protein [*Zea mays*] > gi|195641252|gb|ACG40094.1| zinc finger, C2H2 type family protein [*Zea mays*]	1.00	2911	3167
		XP_002460014	hypothetical protein SORBIDRAFT_02g020840 [*Sorghum bicolor*] > gi|241923391|gb|EER96535.1| hypothetical protein SORBIDRAFT_02g020840 [*Sorghum bicolor*]	0.87	2912	3168
		NP_001150040	zinc finger, C2H2 type family protein [*Zea mays*] > gi|195636264|gb|ACG37600.1| zinc finger, C2H2 type family protein [*Zea mays*]	0.78	2913	3169
		BAK04496	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.70	2914	3170
	524-542	NP_001183648	hypothetical protein LOC100502242 [*Zea mays*] > gi|238013654|gb|ACR37862.1| unknown [*Zea mays*]	1.00	2915	3171
	660-678	NP_001150040	zinc finger, C2H2 type family protein [*Zea mays*] > gi|195636264|gb|ACG37600.1| zinc finger, C2H2 type family protein [*Zea mays*]	1.00	2916	3172
		XP_002460014	hypothetical protein SORBIDRAFT_02g020840 [*Sorghum bicolor*] > gi|241923391|gb|EER96535.1| hypothetical protein SORBIDRAFT_02g020840 [*Sorghum bicolor*]	0.78	2917	3173
		NP_001150708	zinc finger, C2H2 type family protein [*Zea mays*] > gi|195641252|gb|ACG40094.1| zinc finger, C2H2 type family protein [*Zea mays*]	0.76	2918	3174
	433-451	NP_001140599	hypothetical protein LOC100272670 [*Zea mays*] > gi|194700138|gb|ACF84153.1| unknown [*Zea mays*]	1.00	2919	3175
	277-295	XP_002468199	hypothetical protein SORBIDRAFT_01g041550 [*Sorghum bicolor*] > gi|241922053|gb|EER95197.1| hypothetical protein SORBIDRAFT_01g041550 [*Sorghum bicolor*]	1.00	2920	3176
		NP_001140579	hypothetical protein LOC100272649 [*Zea mays*] > gi|194700056|gb|ACF84112.1| unknown [*Zea mays*]	0.88	2921	3177
		ACG35337	purple acid phosphatase 1 [*Zea mays*]	0.84	2922	3178
		NP_001049500	Os03g0238600 [*Oryza sativa Japonica* Group] > gi|108707073|gb|ABF94868.1| purple acid phosphatase 1, putative, expressed [*Oryza sativa Japonica* Group] > gi|113547971|dbj|BAF11414.1| Os03g0238600 [*Oryza sativa Japonica* Group] > gi|125543049|gb|EAY89188.1| hypothetical protein OsI_10684 [*Oryza sativa Indica* Group] > gi|125585546|gb|EAZ26210.1| hypothetical protein OsJ_10077 [*Oryza sativa Japonica* Group] > gi|215697901|dbj|BAG92094.1| unnamed protein product [*Oryza sativa*	0.78	2923	3179

TABLE 8-continued

Target genes of down regulated siRNA sequences associated with NUE (Table 4)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			Japonica Group] > gi|215737711|dbj|BAG96841.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215740770|dbj|BAG96926.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215767489|dbj|BAG99717.1| unnamed protein product [*Oryza sativa Japonica* Group]			
		NP_001151094	LOC100284727 [*Zea mays*] > gi|195644254|gb|ACG41595.1|purple acid phosphatase 1 [*Zea mays*]	0.75	2924	3180
		ACF83217	unknown [*Zea mays*]	0.74	2925	3181
		ACN25848	unknown [*Zea mays*]	0.74	2926	3182
		ACL54336	unknown [*Zea mays*]	0.74	2927	3183
		BAI78301	purple acid phosphatase [*Triticum aestivum*]	0.72	2928	3184
		BAK06221	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326500986|dbj|BAJ98724.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326530618|dbj|BAK01107.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.73	2929	3185
	121-139	XP_002465926	hypothetical protein SORBIDRAFT_01g048350 [*Sorghum bicolor*] > gi|241919780|gb|EER92924.1| hypothetical protein SORBIDRAFT_01g048350 [*Sorghum bicolor*]	1.00	2930	3186
		ACL52492	unknown [*Zea mays*]	0.94	2931	3187
		NP_001048855	Os03g0130500 [*Oryza sativa Japonica* Group] > gi|108706005|gb|ABF93800.1| EF hand family protein, expressed [*Oryza sativa Japonica* Group] > gi|113547326|dbj|BAF10769.1| Os03g0130500 [*Oryza sativa Japonica* Group]	0.82	2932	3188
		EAZ25463	hypothetical protein OsJ_09285 [*Oryza sativa Japonica* Group]	0.80	2933	
		BAJ91192	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.81	2934	3189
	2507-2525	XP_002454851	hypothetical protein SORBIDRAFT_04g038540 [*Sorghum bicolor*] > gi|241934682|gb|EES07827.1| hypothetical protein SORBIDRAFT_04g038540 [*Sorghum bicolor*]	1.00	2935	3190
		NP_001183894	hypothetical protein LOC100502487 [*Zea mays*] > gi|238015298|gb|ACR38684.1| unknown [*Zea mays*]	0.90	2936	3191
		BAJ86117	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326521078|dbj|BAJ96742.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.76	2937	3192
		NP_001050813	Os03g0657100 [*Oryza sativa Japonica* Group] > gi|108710182|gb|ABF97977.1| U-box domain containing protein, expressed [*Oryza sativa Japonica* Group] > gi|113549284|dbj|BAF12727.1| Os03g0657100 [*Oryza sativa Japonica* Group] > gi|218193430|gb|EEC75857.1| hypothetical protein OsI_12864 [*Oryza sativa Indica* Group]	0.70	2938	3193
		AAP50990	unknown protein [*Oryza sativa Japonica* Group]	0.70	2939	3194

TABLE 8-continued

Target genes of down regulated siRNA sequences associated with NUE (Table 4)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
	746-764	NP_001140297	hypothetical protein LOC100272342 [*Zea mays*] > gi|194698890|gb|ACF83529.1| unknown [*Zea mays*]	1.00	2940	3195
	49-67	NP_001105978	lipoxygenase7 [*Zea mays*] > gi|84626291|gb|ABC59690.1| lipoxygenase [*Zea mays*]	1.00	2941	3196
		ACL81191	tasselseed 1b [*Zea mays*]	0.98	2942	3197
		XP_002446554	hypothetical protein SORBIDRAFT_06g018040 [*Sorghum bicolor*] > gi|241937737|gb|EES10882.1| hypothetical protein SORBIDRAFT_06g018040 [*Sorghum bicolor*]	0.91	2943	3198
		ACV84253	LOX5 [Sorghum *bicolor*]	0.90	2944	3199
		NP_001105979	tassel seed1 [*Zea mays*] > gi|84626293|gb|ABC59691.1| lipoxygenase [*Zea mays*]	0.91	2945	3200
		ACL81190	tasselseed 1 [*Zea mays*]	0.90	2946	3201
		Q7XV13	RecName: Full = Putative lipoxygenase 5 > gi|38344820|emb|CAD40882.2| OSJNBa0064H22.1 [*Oryza sativa Japonica* Group] > gi|116310177|emb|CAH67189.1| OSIGBa0152K17.1 [*Oryza sativa Indica* Group]	0.83	2947	
		CAI84707	lipoxygenase-like protein [*Hordeum vulgare* subsp. *vulgare*]	0.82	2948	3202
		BAJ94611	predicted protein [*Hordeum vulgare* subsp. *vulgare*] > gi|326511025|dbj|BAJ91860.1| predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.82	2949	3203
		BAK03423	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.82	2950	3204
Predicted siRNA 60012	256-274	XP_002461947	hypothetical protein SORBIDRAFT_02g011010 [*Sorghum bicolor*] > gi|241925324|gb|EER98468.1| hypothetical protein SORBIDRAFT_02g011010 [*Sorghum bicolor*]	1.00	2951	3205
	948-966	XP_002457764	hypothetical protein SORBIDRAFT_03g013140 [*Sorghum bicolor*] > gi|241929739|gb|EES02884.1| hypothetical protein SORBIDRAFT_03g013140 [*Sorghum bicolor*]	1.00	2952	3206
		ACF87582	unknown [*Zea mays*]	0.93	2953	3207
		NP_001105753	Pti1 protein [*Zea mays*] > gi|49188602|gb|AAT57904.1|putative PTI1-like kinase [*Zea mays*]	0.92	2954	3208
		AAT57905	putative PTI1-like kinase [*Zea mays*]	0.92	2955	3209
		AAT57906	putative PTI1-like kinase [*Zea mays*]	0.93	2956	3210
		EAY73772	hypothetical protein OsI_01646 [*Oryza sativa Indica* Group]	0.81	2957	
		NP_001042895	Os01g0323100 [*Oryza sativa Japonica* Group] > gi|12328582|dbj|BAB21241.1| putative Pto kinase interactor 1 [*Oryza sativa Japonica* Group] > gi|29027802|dbj|BAC65877.1| putative Pto kinase interactor 1 [*Oryza sativa Japonica* Group] > gi|113532426|dbj|BAF04809.1| Os01g0323100 [*Oryza sativa Japonica* Group] > gi|125570160|gb|EAZ11675.1| hypothetical protein OsJ_01536 [*Oryza sativa Japonica* Group] > gi|215694472|dbj|BAG89427.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.81	2958	3211

TABLE 8-continued

Target genes of down regulated siRNA sequences associated with NUE (Table 4)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
	1207-1225	XP_002451738	hypothetical protein SORBIDRAFT_04g006950 [*Sorghum bicolor*] > gi|241931569|gb|EES04714.1| hypothetical protein SORBIDRAFT_04g006950 [*Sorghum bicolor*]	1.00	2959	3212
		ACG38564	cerebral protein 1 [*Zea mays*] > gi|238015424|gb|ACR38747.1| unknown [*Zea mays*]	0.96	2960	3213
		NP_001047303	Os02g0593900 [*Oryza sativa Japonica* Group] > gi|113536834|dbj|BAF09217.1| Os02g0593900 [*Oryza sativa Japonica* Group] > gi|125540112|gb|EAY86507.1| hypothetical protein OsI_07887 [*Oryza sativa Indica* Group] > gi|125582717|gb|EAZ23648.1| hypothetical protein OsJ_07349 [*Oryza sativa Japonica* Group]	0.70	2961	3214
	67-85	XP_002449762	hypothetical protein SORBIDRAFT_05g022780 [*Sorghum bicolor*] > gi|241935605|gb|EES08750.1| hypothetical protein SORBIDRAFT_05g022780 [*Sorghum bicolor*]	1.00	2962	3215
		ABA94447	ETO1-like protein 1, putative, expressed [*Oryza sativa Japonica* Group] > gi|125577639|gb|EAZ18861.1| hypothetical protein OsJ_34400 [*Oryza sativa Japonica* Group]	0.93	2963	3216
		EAY81449	hypothetical protein OsI_36620 [*Oryza sativa Indica* Group]	0.93	2964	
		NP_001068166	Os11g0585900 [*Oryza sativa Japonica* Group] > gi|113645388|dbj|BAF28529.1| Os11g0585900 [*Oryza sativa Japonica* Group]	0.90	2965	3217
		NP_001146335	hypothetical protein LOC100279911 [*Zea mays*] > gi|219886675|gb|ACL53712.1| unknown [*Zea mays*]	0.91	2966	3218
		CBI25039	unnamed protein product [*Vitis vinifera*]	0.73	2967	
		XP_002280519	PREDICTED: hypothetical protein [*Vitis vinifera*]	0.72	2968	3219
		AAZ08351	ethylene overproducer-like 1 [*Solanum lycopersicum*]	0.71	2969	3220
		ABB46489	ethylene-overproducer1-like protein [*Solanum lycopersicum*]	0.71	2970	3221
Predicted siRNA 55081	358-381	XP_002466013	hypothetical protein SORBIDRAFT_01g050070 [*Sorghum bicolor*] > gi|241919867|gb|EER93011.1| hypothetical protein SORBIDRAFT_01g050070 [*Sorghum bicolor*]	1.00	2971	3222
		NP_001132709	hypothetical protein LOC100194192 [*Zea mays*] > gi|194695168|gb|ACF81668.1| unknown [*Zea mays*]	0.77	2972	3223
		NP_001148998	xyloglucan endotransglucosylase/hydrolase protein 32 [*Zea mays*] > gi|195623856|gb|ACG33758.1| xyloglucan endotransglucosylase/hydrolase protein 32 precursor [*Zea mays*]	0.76	2973	3224
Predicted siRNA 59032	364-382	XP_002439498	hypothetical protein SORBIDRAFT_09g008130 [*Sorghum bicolor*] > gi|241944783|gb|EES17928.1| hypothetical protein SORBIDRAFT_09g008130 [*Sorghum bicolor*]	1.00	2974	3225
		NP_001141460	hypothetical protein LOC100273570 [*Zea mays*] > gi|194704658|gb|ACF86413.1| unknown [*Zea mays*] > gi|195620084|gb|ACG31872.1|triose	0.88	2975	3226

TABLE 8-continued

Target genes of down regulated siRNA sequences associated with NUE (Table 4)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			phosphate/phosphate translocator [*Zea mays*] > gi|195625418|gb|ACG34539.1| triose phosphate/phosphate translocator [*Zea mays*]			
		ACG32515	triose phosphate/phosphate translocator [*Zea mays*]	0.88	2976	3227
		NP_001055001	Os05g0241200 [*Oryza sativa Japonica* Group] > gi|53980843|gb|AAV24764.1| putative phosphate translocator [*Oryza sativa Japonica* Group] > gi|113578552|dbj|BAF16915.1| Os05g0241200 [*Oryza sativa Japonica* Group] > gi|125551487|gb|EAY97196.1| hypothetical protein OsI_19118 [*Oryza sativa Indica* Group] > gi|215765430|dbj|BAG87127.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.75	2977	3228
		BAJ94007	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.73	2978	3229
	225-243	NP_001168807	hypothetical protein LOC100382608 [*Zea mays*] > gi|223973113|gb|ACN30744.1| unknown [*Zea mays*]	1.00	2979	3230
Predicted siRNA 58721	227-245	XP_002447337	hypothetical protein SORBIDRAFT_06g033160 [*Sorghum bicolor*] > gi|241938520|gb|EES11665.1| hypothetical protein SORBIDRAFT_06g033160 [*Sorghum bicolor*]	1.00	2980	3231
		NP_001142056	hypothetical protein LOC100274212 [*Zea mays*] > gi|194706940|gb|ACF87554.1| unknown [*Zea mays*] > gi|223947485|gb|ACN27826.1| unknown [*Zea mays*]	0.96	2981	3232
		ACG45259	hypothetical protein [*Zea mays*]	0.96	2982	3233
		EEC78262	hypothetical protein OsI_17948 [*Oryza sativa Indica* Group]	0.86	2983	
		EEE61915	hypothetical protein OsJ_16648 [*Oryza sativa Japonica* Group]	0.86	2984	
		BAJ96591	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.86	2985	3234
		CAJ86266	H0901F07.3 [*Oryza sativa Indica* Group]	0.76	2986	3235
	614-632	NP_001183362	hypothetical protein LOC100501771 [*Zea mays*] > gi|238011008|gb|ACR36539.1| unknown [*Zea mays*]	1.00	2987	3236
		XP_002453714	hypothetical protein SORBIDRAFT_04g011130 [*Sorghum bicolor*] > gi|241933545|gb|EES06690.1| hypothetical protein SORBIDRAFT_04g011130 [*Sorghum bicolor*]	0.92	2988	3237
		BAJ91736	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.80	2989	3238
		NP_001043916	Os01g0687800 [*Oryza sativa Japonica* Group] > gi|18844891|dbj|BAB85360.1| FAD binding domain containing protein-like [*Oryza sativa Japonica* Group] > gi|113533447|dbj|BAF05830.1| Os01g0687800 [*Oryza sativa Japonica* Group]	0.76	2990	3239
		EAY75418	hypothetical protein OsI_03321 [*Oryza sativa Indica* Group]	0.75	2991	
	361-379	XP_002441149	hypothetical protein SORBIDRAFT_09g021260 [*Sorghum bicolor*] > gi|241946434|gb|EES19579.1| hypothetical protein SORBIDRAFT_09g021260 [*Sorghum bicolor*]	1.00	2992	3240

TABLE 8-continued

Target genes of down regulated siRNA sequences associated with NUE (Table 4)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		NP_001152458	phosphoribosylanthranilate transferase [*Zea mays*] > gi|195656517|gb|ACG47726.1| phosphoribosylanthranilate transferase [*Zea mays*]	0.97	2993	3241
		BAK04138	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.89	2994	3242
		EEC79273	hypothetical protein OsI_20060 [*Oryza sativa Indica* Group]	0.90	2995	
		NP_001055620	Os05g0429700 [*Oryza sativa Japonica* Group] > gi|55733914|gb|AAV59421.1| putative anthranilate phosphoribosyltransferase [*Oryza sativa Japonica* Group] > gi|113579171|dbj|BAF17534.1| Os05g0429700 [*Oryza sativa Japonica* Group] > gi|215737213|dbj|BAG96142.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222631675|gb|EEE63807.1| hypothetical protein OsJ_18631 [*Oryza sativa Japonica* Group]	0.90	2996	3243
	149-167	XP_002454239	hypothetical protein SORBIDRAFT_04g027330 [*Sorghum bicolor*] > gi|241934070|gb|EES07215.1| hypothetical protein SORBIDRAFT_04g027330 [*Sorghum bicolor*]	1.00	2997	3244
		ACG32582	heat shock 22 kDa protein [*Zea mays*]	0.88	2998	3245
		NP_001105607	low molecular weight heat shock protein precursor [*Zea mays*] > gi|3015621|gb|AAC12279.1|low molecular weight heat shock protein precursor [*Zea mays*] > gi|54299342|gb|AAV32521.1| mitochondrial small heat shock protein 22 [*Zea mays*] > gi|195622718|gb|ACG33189.1|heat shock 22 kDa protein [*Zea mays*]	0.88	2999	3246
		ACF84470	unknown [*Zea mays*]	0.87	3000	3247
		NP_01048175	Os02g0758000 [*Oryza sativa Japonica* Group] > gi|75294195|sp|Q6Z7V2.1|HS24M_ORYSJ RecName: Full = 24.1 kDa heat shock protein, mitochondrial; Short = OsHsp24.1; Flags: Precursor > gi|46805691|dbj|BAD17092.1| putative low molecular weight heat shock protein [*Oryza sativa Japonica* Group] > gi|113537706|dbj|BAF10089.1| Os02g0758000 [*Oryza sativa Japonica* Group] > gi|125541201|gb|EAY87596.1| hypothetical protein OsI_09007 [*Oryza sativa Indica* Group] > gi|125583753|gb|EAZ24684.1| hypothetical protein OsJ_08454 [*Oryza sativa Japonica* Group] > gi|215693891|dbj|BAG89090.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215704321|dbj|BAG93755.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215740605|dbj|BAG97261.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|313575793|gb|ADR66976.1|22 kDa heat shock protein [*Oryza sativa*	0.80	3001	3248

TABLE 8-continued

Target genes of down regulated siRNA sequences associated with NUE (Table 4)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			Japonica Group] > gi|332691639|gb|AEE90022.1| mitochondrial small heat shock protein [*Oryza sativa Japonica* Group]			
	270-288	XP_02444207	hypothetical protein SORBIDRAFT_07g014990 [*Sorghum bicolor*] > gi|241940557|gb|EES13702.1| hypothetical protein SORBIDRAFT_07g014990 [*Sorghum bicolor*]	1.00	3002	3249
		NP_001145845	hypothetical protein LOC100279356 [*Zea mays*] > gi|219884681|gb|ACL52715.1| unknown [*Zea mays*]	0.91	3003	3250
		NP_001061645	Os08g0365900 [*Oryza sativa Japonica* Group] > gi|38636850|dbj|BAD03090.1| putative nucleolar protein [*Oryza sativa Japonica* Group] > gi|113623614|dbj|BAF23559.1| Os08g0365900 [*Oryza sativa Japonica* Group] > gi|215717005|dbj|BAG95368.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|222640447|gb|EEE68579.1| hypothetical protein OsJ_27075 [*Oryza sativa Japonica* Group]	0.77	3004	3251
	40959	436-454 NP_001147431	Redundant master homologue-skipping aconitase2 [*Zea mays*] > gi|195611330|gb|ACG27495.1| aconitate hydratase, cytoplasmic [*Zea mays*] > gi|223948253|gb|ACN28210.1| unknown [*Zea mays*]	1.00	3005	3252
		XP_002445174	hypothetical protein SORBIDRAFT_07g005390 [*Sorghum bicolor*] > gi|241941524|gb|EES14669.1| hypothetical protein SORBIDRAFT_07g005390 [*Sorghum bicolor*]	0.78	3006	3253
		Q6YZX6	RecName: Full = Putative aconitate hydratase, cytoplasmic; Short = Aconitase; AltName: Full = Citrate hydro-lyase > gi|40253814|dbj|BAD05751.1| putative Aconitate hydratase [*Oryza sativa Japonica* Group]	0.77	3007	
		BAJ85661	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.76	3008	3254
		CBE71057	aconitate hydratase 3 [*Citrus clementina*]	0.75	3009	3255
		ADZ57218	aconitase protein [*Litchi chinensis*]	0.74	3010	3256
		XP_002524184	aconitase, putative [*Ricinus communis*] > gi|223536553|gb|EEF38199.1| aconitase, putative [*Ricinus communis*]	0.74	3011	3257
		XP_002278138	PREDICTED: hypothetical protein [*Vitis vinifera*] > gi|297737441|emb|CBI26642.3| unnamed protein product [*Vitis vinifera*]	0.74	3012	3258
		P49608	RecName: Full = Aconitate hydratase, cytoplasmic; Short = Aconitase; AltName: Full = Citrate hydro-lyase > gi|7437043|pir||T10101 aconitate hydratase (EC 4.2.1.3) - cucurbit > gi|868003|dbj|BAA06108.1|aconitase [*Cucurbita* cv. *Kurokawa Amakuri*]	0.75	3013	
		CBE71058	aconitate hydratase 2 [*Citrus clementina*]	0.74	3014	3259
	529-547	XP_002453714	hypothetical protein SORBIDRAFT_04g011130 [*Sorghum bicolor*] > gi|241933545|gb|EES06690.1| hypothetical protein SORBIDRAFT_04g011130 [*Sorghum bicolor*]	1.00	3015	3260
		NP_001183362	hypothetical protein LOC100501771 [*Zea mays*] > gi|238011008|gb|ACR36539.1| unknown [*Zea mays*]	0.85	3016	3261

TABLE 8-continued

Target genes of down regulated siRNA sequences associated with NUE (Table 4)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		BAJ91736	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.80	3017	3262
		NP_001043916	Os01g0687800 [*Oryza sativa Japonica* Group] > gi|18844891|dbj|BAB85360.1| FAD binding domain containing protein-like [*Oryza sativa Japonica* Group] > gi|113533447|dbj|BAF05830.1| Os01g0687800 [*Oryza sativa Japonica* Group]	0.76	3018	3263
		EAY75418	hypothetical protein OsI_03321 [*Oryza sativa Indica* Group]	0.75	3019	
Predicted siRNA 58877	254-273	XP_002489117	hypothetical protein SORBIDRAFT_0057s002150 [*Sorghum bicolor*] > gi|241947368|gb|EES20513.1| hypothetical protein SORBIDRAFT_0057s002150 [*Sorghum bicolor*]	1.00	3020	3264
		XP_002488963	hypothetical protein SORBIDRAFT_1150s002010 [*Sorghum bicolor*] > gi|241946997|gb|EES20142.1| hypothetical protein SORBIDRAFT_1150s002010 [*Sorghum bicolor*]	0.94	3021	3265
		XP_002464695	hypothetical protein SORBIDRAFT_01g023641 [*Sorghum bicolor*] > gi|241918549|gb|EER91693.1| hypothetical protein SORBIDRAFT_01g023641 [*Sorghum bicolor*]	0.84	3022	3266
		XP_002450731	hypothetical protein SORBIDRAFT_05g016471 [*Sorghum bicolor*] > gi|241936574|gb|EES09719.1| hypothetical protein SORBIDRAFT_05g016471 [*Sorghum bicolor*]	0.80	3023	3267
		XP_002450732	hypothetical protein SORBIDRAFT_05g016475 [*Sorghum bicolor*] > gi|241936575|gb|EES09720.1| hypothetical protein SORBIDRAFT_05g016475 [*Sorghum bicolor*]	0.79	3024	3268
Predicted siRNA 57179	632-655	XP_002447941	hypothetical protein SORBIDRAFT_06g018520 [*Sorghum bicolor*] > gi|241939124|gb|EES12269.1| hypothetical protein SORBIDRAFT_06g018520 [*Sorghum bicolor*]	1.00	3025	3269
		NP_001159183	hypothetical protein LOC100304268 [*Zea mays*] > gi|195627604|gb|ACG35632.1| ubiquitin carboxyl-terminal hydrolase 4 [*Zea mays*] > gi|223942511|gb|ACN25339.1| unknown [*Zea mays*]	0.99	3026	3270
		NP_001146737	hypothetical protein LOC100280339 [*Zea mays*] > gi|219888545|gb|ACL54647.1| unknown [*Zea mays*] > gi|223974199|gb|ACN31287.1| unknown [*Zea mays*]	0.99	3027	3271
		ACG34260	ubiquitin carboxyl-terminal hydrolase 4 [*Zea mays*]	0.99	3028	3272
		NP_001052951	Os04g0452400 [*Oryza sativa Japonica* Group] > gi|113564522|dbj|BAF14865.1| Os04g0452400 [*Oryza sativa Japonica* Group] > gi|215695550|dbj|BAG90741.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.97	3029	3273
		BAK02826	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.96	3030	3274

TABLE 8-continued

Target genes of down regulated siRNA sequences associated with NUE (Table 4)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		CAD40853	OSJNBa0086B14.26 [*Oryza sativa Japonica* Group] > gi|116310175|emb|CAH67188.1| H0815C01.9 [Oryza *sativa Indica* Group] > gi|125548525|gb|EAY94347.1| hypothetical protein OsI_16114 [*Oryza sativa Indica* Group] > gi|125590577|gb|EAZ30927.1| hypothetical protein OsJ_15007 [*Oryza sativa Japonica* Group]	0.97	3031	
		XP_002270407	PREDICTED: hypothetical protein [*Vitis vinifera*]	0.87	3032	3275
		XP_002531269	Ubiquitin carboxyl-terminal hydrolase, putative [*Ricinus communis*] > gi|223529154|gb|EEF31133.1| Ubiquitin carboxyl-terminal hydrolase, putative [*Ricinus communis*]	0.88	3033	3276
		CAN67091	hypothetical protein VITISV_006756 [*Vitis vinifera*]	0.86	3034	
Predicted siRNA 55393	490-510	XP_002446760	hypothetical protein SORBIDRAFT_06g021990 [*Sorghum bicolor*] > gi|241937943|gb|EES11088.1| hypothetical protein SORBIDRAFT_06g021990 [*Sorghum bicolor*]	1.00	3035	3277
		ACG37655	anther-specific proline-rich protein APG [*Zea mays*]	0.86	3036	3278
		ACG35356	anther-specific proline-rich protein APG [*Zea mays*]	0.86	3037	3279
		NP_001132075	hypothetical protein LOC100193489 [*Zea mays*] > gi|194693356|gb|ACF80762.1| unknown [*Zea mays*]	0.86	3038	3280
		NP_001141295	hypothetical protein LOC100273386 [*Zea mays*] > gi|194703842|gb|ACF86005.1| unknown [*Zea mays*]	0.87	3039	3281
		NP_001053264	Os04g0507700 [*Oryza sativa Japonica* Group] > gi|32489520|emb|CAE04723.1| OSJNBa0043L24.11 [*Oryza sativa Japonica* Group] > gi|38567850|emb|CAE05693.2| OSJNBb0002J11.20 [*Oryza sativa Japonica* Group] > gi|113564835|dbj|BAF15178.1| Os04g0507700 [*Oryza sativa Japonica* Group] > gi|116310323|emb|CAH67339.1| OSIGBa0157A06.8 [*Oryza sativa Indica* Group] > gi|116310765|emb|CAH67558.1| OSIGBa0101P20.1 [*Oryza sativa Indica* Group] > gi|125548968|gb|EAY94790.1| hypothetical protein OsI_16569 [*Oryza sativa Indica* Group] > gi|125590941|gb|EAZ31291.1| hypothetical protein OsJ_15397 [*Oryza sativa Japonica* Group]	0.75	3040	3282
		BAJ85303	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.73	3041	3283
	66-86	NP_001104926	MADS2 [*Zea mays*] > gi|29611976|gb|AAO85643.1|MADS-box transcription factor MADS2 [*Zea mays*]	1.00	3042	3284
		AAG09919	MADS box protein 2 [*Zea mays*]	1.00	3043	3285
		NP_001047230	Os02g0579600 [*Oryza sativa Japonica* Group] > gi|91207149|sp|Q6EP49.2|MAD27_ORYSJ RecName: Full = MADS-box transcription factor 27; AltName: Full = OsMADS27; AltName: Full = RMADS218 > gi|30313677|gb|AAO47706.1|	0.86	3044	3286

TABLE 8-continued

Target genes of down regulated siRNA sequences associated with NUE (Table 4)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			transcription factor MADS27 [*Oryza sativa Japonica* Group] > gi|113536761|dbj|BAF09144.1| Os02g0579600 [*Oryza sativa Japonica* Group]			
		EEC73475	hypothetical protein OsI_07801 [*Oryza sativa Indica* Group] > gi|222623119|gb|EEE57251.1| hypothetical protein OsJ_07263 [*Oryza sativa Japonica* Group]	0.84	3045	
		BAK01931	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.79	3046	3287
		CAM59078	MIKC-type MADS-box transcription factor WM30 [*Triticum aestivum*]	0.79	3047	3288
		CAD40988	OSJNBa0072F16.13 [*Oryza sativa Japonica* Group]	0.77	3048	
		BAD29571	putative transcription factor MADS27 [*Oryza sativa Japonica* Group]	0.76	3049	
	571-591	NP_001047230	Os02g0579600 [*Oryza sativa Japonica* Group] > gi|91207149|sp|Q6EP49.2|MAD27_ORYSJ RecName: Full = MADS-box transcription factor 27; AltName: Full = OsMADS27; AltName: Full = RMADS218 > gi|30313677|gb|AAO47706.1| transcription factor MADS27 [*Oryza sativa Japonica* Group] > gi|113536761|dbj|BAF09144.1| Os02g0579600 [*Oryza sativa Japonica* Group]	1.00	3050	3289
		EEC73475	hypothetical protein OsI_07801 [*Oryza sativa Indica* Group] > gi|222623119|gb|EEE57251.1| hypothetical protein OsJ_07263 [*Oryza sativa Japonica* Group]	0.98	3051	
		BAD29571	putative transcription factor MADS27 [*Oryza sativa Japonica* Group]	0.90	3052	
		AAG09919	MADS box protein 2 [*Zea mays*]	0.86	3053	3290
		NP_001104926	MADS2 [*Zea mays*] > gi|29611976|gb|AAO85643.1|MADS-box transcription factor MADS2 [*Zea mays*]	0.86	3054	3291
		BAK01931	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.82	3055	3292
		CAD40988	OSJNBa0072F16.13 [*Oryza sativa Japonica* Group]	0.80	3056	
		CAM59078	MIKC-type MADS-box transcription factor WM30 [*Triticum aestivum*]	0.81	3057	3293
	481-501	NP_001132075	hypothetical protein LOC100193489 [*Zea mays*] > gi|194693356|gb|ACF80762.1| unknown [*Zea mays*]	1.00	3058	3294
		ACG35356	anther-specific proline-rich protein APG [*Zea mays*]	1.00	3059	3295
		ACG37655	anther-specific proline-rich protein APG [*Zea mays*]	0.92	3060	3296
		NP_001141295	hypothetical protein LOC100273386 [*Zea mays*] > gi|194703842|gb|ACF86005.1| unknown [*Zea mays*]	0.92	3061	3297
		XP_002446760	hypothetical protein SORBIDRAFT_06g021990 [*Sorghum bicolor*] > gi|241937943|gb|EES11088.1| hypothetical protein SORBIDRAFT_06g021990 [*Sorghum bicolor*]	0.91	3062	3298
		NP_001053264	Os04g0507700 [*Oryza sativa Japonica* Group] > gi|32489520|emb|CAE04723.1| OSJNBa0043L24.11 [*Oryza sativa Japonica* Group] > gi|38567850|emb|CAE05693.2|	0.81	3063	3299

TABLE 8-continued

Target genes of down regulated siRNA sequences associated with NUE (Table 4)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			OSJNBb0002J11.20 [*Oryza sativa Japonica* Group] > gi|113564835|dbj|BAF15178.1| Os04g0507700 [*Oryza sativa Japonica* Group] > gi|116310323|emb|CAH67339.1| OSIGBa0157A06.8 [*Oryza sativa Indica* Group] > gi|116310765|emb|CAH67558.1| OSIGBa0101P20.1 [*Oryza sativa Indica* Group] > gi|125548968|gb|EAY94790.1| hypothetical protein OsI_16569 [*Oryza sativa Indica* Group] > gi|125590941|gb|EAZ31291.1| hypothetical protein OsJ_15397 [*Oryza sativa Japonica* Group]			
		BAJ85303	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.78	3064	3300
Predicted siRNA 59235	55-75	NP_001167787	hypothetical protein LOC100381480 [*Zea mays*] > gi|223943955|gb|ACN26061.1| unknown [*Zea mays*]	1.00	3065	3301
		NP_001143285	hypothetical protein LOC100275819 [*Zea mays*] > gi|195617040|gb|ACG30350.1| hypothetical protein [*Zea mays*]	0.97	3066	3302
Predicted siRNA 60123	512-531	NP_001149853	LOC100283481 [*Zea mays*] > gi|195635075|gb|ACG37006.1|pollen-specific protein like [*Zea mays*]	1.00	3067	3303
		NP_001152271	pollen-specific protein like [*Zea mays*] > gi|195638358|gb|ACG38647.1|pollen-specific protein like [*Zea mays*] > gi|195642016|gb|ACG40476.1|pollen-specific protein like [*Zea mays*] > gi|195654521|gb|ACG46728.1|pollen-specific protein like [*Zea mays*]	0.83	3068	3304
		XP_002457577	hypothetical protein SORBIDRAFT_03g009730 [*Sorghum bicolor*] > gi|241929552|gb|EES02697.1| hypothetical protein SORBIDRAFT_03g009730 [*Sorghum bicolor*]	0.71	3069	3305
Predicted siRNA 56837	1216-1237	XP_002455312	hypothetical protein SORBIDRAFT_03g008220 [*Sorghum bicolor*] > gi|241927287|gb|EES00432.1| hypothetical protein SORBIDRAFT_03g008220 [*Sorghum bicolor*]	1.00	3070	3306
		NP_001145952	hypothetical protein LOC100279478 [*Zea mays*] > gi|219885097|gb|ACL52923.1| unknown [*Zea mays*]	0.88	3071	3307
		NP_001143749	hypothetical protein LOC100276506 [*Zea mays*] > gi|195626214|gb|ACG34937.1| hypothetical protein [*Zea mays*] > gi|195645208|gb|ACG42072.1| hypothetical protein [*Zea mays*]	0.89	3072	3308
		NP_001131959	hypothetical protein LOC100193355 [*Zea mays*] > gi|194693040|gb|ACF80604.1| unknown [*Zea mays*]	0.84	3073	3309
		NP_001041811	Os01g0112100 [*Oryza sativa Japonica* Group] > gi|113531342|dbj|BAF03725.1| Os01g0112100 [*Oryza sativa Japonica* Group] > gi|125568749|gb|EAZ10264.1| hypothetical protein OsJ_00099 [*Oryza sativa Japonica* Group] > gi|215697848|dbj|BAG92041.1| unnamed protein product [*Oryza sativa Japonica* Group] > gi|215704817|dbj|BAG94845.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.72	3074	3310

TABLE 8-continued

Target genes of down regulated siRNA sequences associated with NUE (Table 4)

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		EAY72253	hypothetical protein OsI_00107 [*Oryza sativa Indica* Group]	0.72	3075	
Predicted siRNA 55404	231-252	NP_001149348	serine carboxypeptidase 1 [*Zea mays*] > gi|195626594|gb|ACG35127.1|serine carboxypeptidase 1 precursor [*Zea mays*]	1.00	3076	3311
		NP_001137115	hypothetical protein LOC100217293 [*Zea mays*] > gi|194698414|gb|ACF83291.1| unknown [*Zea mays*]	0.98	3077	3312
		XP_002459781	hypothetical protein SORBIDRAFT_02g010510 [*Sorghum bicolor*] > gi|241923158|gb|EER96302.1| hypothetical protein SORBIDRAFT_02g010510 [*Sorghum bicolor*]	0.72	3078	3313
	1046-1067	NP_001137115	hypothetical protein LOC100217293 [*Zea mays*] > gi|194698414|gb|ACF83291.1| unknown [*Zea mays*]	1.00	3079	3314
		NP_001149348	serine carboxypeptidase 1 [*Zea mays*] > gi|195626594|gb|ACG35127.1|serine carboxypeptidase 1 precursor [*Zea mays*]	0.99	3080	3315
		XP_002459781	hypothetical protein SORBIDRAFT_02g010510 [*Sorghum bicolor*] > gi|241923158|gb|EER96302.1| hypothetical protein SORBIDRAFT_02g010510 [*Sorghum bicolor*]	0.72	3081	3316

Table 8:

Provided are the target Genes of siRNAs Associated with Increased NUE (Table 4) along with their GenBank Accession numbers and sequence identifiers (SEQ ID NO:).

"bind" = binding;

"pos" = position;

"hom" = homologue;

"p.p." = polypeptide;

"p.n." = polynucleotide.

TABLE 9

Target genes of mir395, 397 and 398 to be downregulated

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
zma-miR398b*	322-342	YP_003208225	ribosomal protein S3 [*Coix lacryma-jobi*] & gt;gi|209361951|gb|ACI43310.1| ribosomal protein S3 [*Coix lacryma-jobi*]	1.00	982	1647
		NP_043062	ribosomal protein S3 [*Zea mays*] & gt;gi|48478711|ref|YP_024318.1| ribosomal protein S3 [*Saccharum hybrid cultivar* SP-80-3280] & gt;gi|50812566 |ref|YP_054668.1| ribosomal protein S3 [*Saccharum officinarum*] & gt;gi|118614530|ref|YP_899446.1 ribosomal protein S3 [*Sorghum bicolor*] & gt;gi|33933|sp|P06586.1|RR3_MAIZE RecName: Full = 30S ribosomal protein S3, chloroplastic & gt;gi|68052946|sp|Q6ENS5.1|RR3_SACOF RecName: Full = 30S ribosomal protein S3, chloroplastic & gt;gi|75126330|sp|Q6L3G0.1|RR3_SACHY RecName: Full = 30S ribosomal protein S3, chloroplastic & gt;gi|125987748|sp|A1E9W3.1|RR3_SORBI RecName: Full = 30S ribosomal protein S3, chloroplastic & gt;gi|12469|emb|CAA68427.1|ribosomal protein S3 [*Zea mays*] & gt;gi|902260|emb|CAA60324.1|ribosomal protein S3 [*Zea mays*] & gt;gi|48478613& gt;gi|AAT44633.1 ribosomal protein S3 [*Saccharum hybrid cultivar*	0.99	983	1648

TABLE 9-continued

Target genes of mir395, 397 and 398 to be downregulated

Mir name	Mir Bind. Pos.	Hom. NCBI Access ion	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			SP80-3280] & gt;gi|49659550|dbj|BAD27331.1 ribosomal protein S3 [*Saccharum hybrid* & gt;gi|11820164|gb|ABK79534.1 ribosomal protein S3 [*Sorghum bicolor*]			
		ADN86110	ribosomal protein S3 [*Chasmanthium latifolium*]	0.96	984	1649
		ADN32929	ribosomal protein S3 [*Phyllostachys nigra* var. *henonis*] & gt;gi|309321655|gb|ADO65180.1 ribosomal protein S3 [*Acidosasa purpurea*] & gt;gi|309321739|gb|ADO65263.1 ribosomal protein S3 [*Ferrocalamus rimosivaginus*] & gt;gi|309321823|gb|ADO65346.1 ribosomal protein S3 [*Indocalamus longiauritus*] & gt;gi|309321906|gb|ADO65428.14 ribosomal protein S3 [*Phllostachys edulis*]	0.96	985	
		YP_003097613	ribosomal protein S3 [*Dendrocalamus latiflorus*] & gt;gi|255040297|gb|ACT99957.1 ribosomal protein S3 [*Dendrocalamus latisflorus*]	0.96	986	1650
		ADD63064	ribosomal protein S3 [*Potamophila parviflora*]	0.96	987	1651
		ADD62997	ribosomal protein S3 [*Ortza australiensis*]	0.96	988	1652
		NP_039424	ribosomal protein S3 [*Ortza sativa Japonica* Group] & gt;gi|50234010|ref|YP_052788.1 ribosomal protein S3 [*Ortza nivara*] & gt;gi|09156623|ref|YP_654242.1 ribosomal protein S3 [*Oryza sativa Indica* Group] & gt;gi|68052945|sp|Q6END5.1|RR3_ORYNI RecName: Full = 30S ribosomal protein S3, chloroplastic & gt;gi|48840859|sp|P0C483.1| RR3_ORYSA RecName: Full = 30S ribosomal protein S3, chloroplastic & gt;gi| 148840860|sp|P0C484.1|RR3_ORYSI RecName: Full = 30S ribosomal protein S3, chloroplastic & gt;gi|148840861|sp|P0C485.1|RR3_ORYSA RecName: Full = 30S ribosomal protein S3, chloroplastic & gt;gi|12025|emb|CAA33934.1 ribosomal protein S3 [*Ortza sativa Japonica* Group] & gt;gi|42795515|gb|AAS46082.1 ribosomal protein S3 [*Ortza sativa Indica* Group] & gt;gi|42795581|gb|AAS46147.1 ribosomal protein S3 [*Ortza sativa Japonica* Group] & gt;gi|4279564|gb|AAS46210.1 ribosomal protein S3 [*Ortza sativa Japonica* Group] & gt;gi|49615034|dbj|BAD26817.1 ribosomal protein S3 [*Ortza nivara*] & gt;gi|50725165|dbj|BAD33782.1 ribosomal protein S3 [*Ortza sativa Japonica* Group] & gt;gi|151091521|dbj|BAD36259.1 ribosomal protein S3 [*Ortza sativa Japonica* Group] & gt;gi|8200203|gb|EEC82630.1 hypothetical protein OsI_27221 [*Oryza sativa Indica* Group] & gt;gi|218202023|gb|EEC84450.1 hypothetical protein OsI_31072 [Oryza sativa Indica Group] & gt;gi|290790601|gb|ADD62861.1 ribosomal protein S3 [*Ortza sativa Japonica* Group] & gt;gi|290790670|gb|ADD62929.1 ribosomal protein S3 [*Oryza meridionalis*] & gt;gi|226646|prf| 1603356BW ribosomal protein S3	0.96	989	1653
		ADO65512	ribosomal protein S3 [*Bambusa emeiensis*]	0.95	990	
		BAD05516	ribosomal protein S3 [*Ortza sativa Japonica* Group]	0.95	991	1654
osa-miR395m	426-446	XP_002463896	hypothetical protein SORBIDRAFT_01g008450 [*Sorghum bicolor*] & gt;gi|241917750|gb|EER90894.1 SORBIDRAFT_01g008450 [*Sorghum bicolor*]	1.00	1249	1889
		ACN28609	unknown [*Zea mays*]	0.95	1250	1890
		ACN34023	unknown [*Zea mays*]	0.95	1251	1891
		ACG45192	bifunctional 3-phosphoadenosine 5-phosphosulfate synthtase [*Zea mays*]	0.94	1252	1892
		NP_001104877	ATP sulfurylase [*Zea mays*] & gt;gi|2738750|gb|AAB94542.1 ATP sulfurylase [*Zea mays*]	0.95	1253	1893
		EAY91825	hypothetical protein OsI_13470 [*Oryza sativa Indica* Group]	0.80	1254	
		NP_001051234	Os03g0743900 [*Oryza sativa Japonica* Group] & gt;gi|30017582|gb|AAP13004.1 putative ATP sulfurylase [*Oryza sativa Japonica* Group] & gt;gi|108711024|gb|ABF98819.1	0.80	1255	1894

TABLE 9-continued

Target genes of mir395, 397 and 398 to be downregulated

Mir name	Mir Bind. Pos.	Hom. NCBI Access ion	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
			Bifunctional 3 & apos;-phosphoadenosine 5 & apos;-phosphosulfate synthethase, putative, expressed [*Oryza sativa Japonica* Group] & gt;gi|113549705|dbj|BAF13148.1 Os03g0743900 [*Oryza sativa Japonica* Group] & gt;gi|215704581|dbj|BAG94214.1 unnamed protein product [*Oryza sativa Japonica* Group]			
		BAK05662	predicted protein [*Hordeum vulgare* subsp. *vulgare*] & gt;gi|326502564|dbj|BAJ95345.1 predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.79	1256	1895
		BAA36274	plastidic ATP sulfurylase [*Oryza sativa Indica* Group]	0.80	1257	1896
		EAZ28548	hypothetical protein OsJ_12530 [*Oryza sativa Japonica* Group]	0.77	1258	
	352-372	XP_002441904	hypothetical protein SORBIDRAFT_08g004650 [*Sorghum bicolor*] & gt;gi|241942597|gb|EES15742.1 hypothetical protein SORBIDRAFT_08g004650 [*Sorghum bicolor*]	1.00	1259	1897
		EEE52851	hypothetical protein OsJ_35390 [*Oryza sativa Japonica* Group]	0.71	1260	
		NP_001066285	Os12g0174100 [*Oryza sativa Japonica* Group] & gt;gi|77553790|gb|ABA96586.1 Growth regulator protein, putative, expressed [*Oryza sativa Japonica* Group] & gt;gi|255670095|dbj|BAF29304.2 Os12g0174100 [*Oryza sativa Japonica* Group]	0.71	1261	1898
		EEC68940	hypothetical protein OsI_37646 [*Oryza sativa Indica* Group]	0.70	1262	
	528-548	ACN34023	unknown [*Zea mays*]	1.00	1263	1899
		NP_001104877	ATP sulfurylase [*Zea mays*] & gt;gi|2738750|gb|AAB94542.1 ATP sulfurylase [*Zea mays*]	0.98	1264	1900
		ACN28609	unknown [*Zea mays*]	0.94	1265	1901
		ACG41592	bifunctional 3-phosphoadenosine 5-phosphosulfate synthetase [*Zea mays*]	0.94	1266	1902
		XP_002463896	hypothetical protein SORBIDRAFT_01g008450 [*Sorghum bicolor*] & gt;gi|241917750|gb|EER90894.1 hypothetical protein SORBIDRAFT_01g008450 [*Sorghum bicolor*]	0.94	1267	1903
		BAK05662	predicted protein [*Hordeum vulgare* subsp. *vulgare*] & gt;gi|326502564|dbj|BAJ95345.1 predicted protein [*Hordeum vulgare* subsp. *vulfare*]	0.84	1268	1904
		EAY91825	hypothetical protein OsI_13470 [*Oryza sativa Indica* Group]	0.80	1269	
		NP_001051234	Os03g0743900 [*Oryza sativa Japonica* Group] & gt;gi|30017582|gb|AAP13004.1 putative ATP sulfurylase [*Oryza sativa Japonica* Group] & gt;gi|108711024|gb|ABF98819.1 Bifunctional 3 & apos;-phosphoadenosine 5 & aps;-phosphosulfate synthethase, putative, expressed [*Oryza sativa Japonica* Group] & gt;gi|13549705|dbj|BAF13148.1Os03g0743900 [*Oryza sativa Japonica* Group] & gt;gi|215704581|dbj|BAG94214.1 unnamed protein product [*Oryza sativa Japonica* Group]	0.79	1270	1905
		BAA36274	plastidic ATP sulfurylase [*Oryza sativa Indica* Group]	0.79	1271	1906
		EAZ28548	hypothetical protein OsJ_12530 [*Oryza sativa Japonica* Group]	0.76	1272	
	305-325	ACL53345	unknown [*Zea mays*]	1.00	1273	1907
		XP_002465703	hypothetical protein SORBIDRAFT_01g044100 [*Sorghum bicolor*] & gt;gi|241919557|gb|EER92701.1 hypothetical protein SORBIDRAFT_01g044100 [*Sorghum bicolor*]	0.95	1274	1908
		BAJ85215	predicted protein [*Hordeum vulgare* subsp. *vulgare*] & gt;gi|326511599|dbj|BAJ91944.1 predicted protein [*Hordeum vulgare* subsp. *vulfare*] & gt;gi|25585257|gb|EAZ25921.1 hypothetical protein OsJ_09764 [*Oryza sativa Japonica* Group]	0.85	1275	1909
		AAN59769	Putative sulfate transporter [*Oryza sativa Japonica* Group] & gt;gi|125585257|gb|EAZ25921.1| hypothetical protein OsJ_09764 [*Oryza sativa Japonica* Group]	0.85	1276	
		EEC74682	hypothetical protein OsI_10373 [*Oryza sativa Japonica* Group]	0.85	1277	
		EEC74681	hypothetical protein OsI_10372 [*Oryza sativa Japonica* Group]	0.72	1278	
		EEE58498	hypothetical protein OsJ_09763 [*Oryza sativa Japonica* Group]	0.72	1279	
		NP_001049257	Os03g0195300 [*Oryza sativa Japonica* Group] & gt;gi|108706649|gb|ABF94444.1 Sulfate transporter 2.1, putative, expressed [*Oryza sativa Japonica* Group] & gt;gi|13547728|dbj|BAF11171.1 Os03g0195300 [*Oryza sativa Japonica* Group]	0.72	1280	1910
zma-miR397a	798-818	XP_002458747	hypothetical protein SORBIDRAFT_03g039530 [*Sorghum bicolor*] & gt;gi|241930722|gb|EES03867.1 hypothetical protein SORBIDRAFT_03g039530 [*Sorghum bicolor*]	1.00	1321	1949

TABLE 9-continued

Target genes of mir395, 397 and 398 to be downregulated

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		NP_001147942	L-ascorbate oxidase [*Zea mays*] & gt;gi|195614732|gb|ACG29196.1 L-ascorbate oxidase precursor [*Zea mays*]	0.96	1322	1950
		ACN34362	unknown [*Zea mays*]	0.96	1323	1951
		EEC71780	hypothetical protein OsI_04394 [*Oryza sativa Indica* Group]	0.86	1324	
		NP_001044773	Os03g0842500 [*Oryza sativa Japonica* Group] & gt;gi|19571025|gb|BAB86452.1 putative laccase LAC5-6 [*Oryza sativa Japonica* Group] & gt;gi|13534304|dbj|BAF06687.1 Os01g0842500 [*Oryza sativa Japonica* Group] & gt;gi|125572601|gb|EAZ14116.1 hypothetical protein OsJ_04040 [*Oryza sativa Japonica* Group] & gt;gi|21569481|dbj|NAG90005.1 unnamed protein product [*Oryza sativa Japonica* Group]	0.86	1325	1952
		BAJ84890	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.84	1326	1953
		BAJ96691	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.84	1327	1954
		NP_001105875	putative laccase [*Zea mays*] & gt;gi|8461878|emb|CAJ30500.1 putative laccase [*Zea mays*]	0.79	1328	1955
		ACN28855	unknown [*Zea mays*]	0.79	1329	1956
		XP_002458746	hypothetical protein SORBIDRAFT_03g039520 [*Sorghum bicolor*] & gt;gi|241930721|gb|EES03866.1 hypothetical protein SORBIDRAFT_03g039520 [*Sorghum bicolor*]	0.78	1330	1957
	458-478	ACF87912	unknown [*Zea mays*]	1.00	1331	1958
		NP_001105951	LOC100037774 [*Zea mays*] & gt;gi|1184776|gb|AAA87580.1 cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC4 [*Zea mays*]	0.99	1332	1959
		NP_001105385	glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3 [*Zea mays*] & gt;gi|6166167|sp|Q43247.1G3PE_MAIZE RecName: Full = Glyceraldehyde-3-phosphate dehydrogense, cytosolic 3 & gt;gi|184774|gb|AAA87579.1 cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC3 [*Zea mays*]	0.99	1333	1960
		ACG36109	glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3 [*Zea mays*]	0.99	1334	1961
		ADZ55283	glyceraldehyde-3-phosphate dehydrogenase [*Zea mays*]	0.98	1335	1962
		XP_002452401	hypothetical protein SORBIDRAFT_04g025120 [*Sorghum bicolor*] & gt;gi|241932232|gb|EES05377.1 hypothetical protein SORBIDRAFT_04g025120 [*Sorghum bicolor*]	0.98	1336	1963
		NP_001053139	Os04g0486600 [*Oryza sativa Japonica* Group] & gt;gi|3834606|emb|CAE02009.2 OJ0002233_09.15 [*Oryza sativa Japonica* Group] & gt;gi|90265255|emb|CAD79700.2H0302E05.3 [*Oryza sativa Japonica* Group] & gt;gi|13564710|dbj|BAF15053.1 Os05g0486600 [*Oryza sativa Japonica* Group] & gt;gi|69244439|gb|ACA50493.1 glyceraldehyde-3-phosphate dehydrogenase [*Oryza sativa Japonica* Group] & gt;gi|215694303|dbj|BAG89296.1 unnamed protein product [*Oryza sativa Japonica* Group] & gt;gi|306415975|gb|ADM86862.1 glyceraldehyde-3-phosphate dehydrogenase [*Oryza sativa Japonica* Group]	0.92	1337	1964
		NP_001047348	Os02g0601300 [*Oryza sativa Japonica* Group] & gt;gi|47848293|dbj|BAD22157.1 putative glyceraldehyde-3-phosphate dehydrogenase (phosporylating) [*Oryza sativa Japonica* Group] & gt;gi|13536879|dbj|BAF09262.1 Os02g0601300 [*Oryza sativa Japonica Group*] & gt;gi|119434402|gb|ABL75274.1 glyceralde-3-phosphate dehydrogenase [*Oryza sativa*] & gt;gi|215704481|dbjBAG93915.1| unnamed protein product [*Oryza sativa Japonica* Group] & gt;gi|306415941|gb|ADM86845.1 glyceraldehyde-3-phosphate dehydrogenase [*Oryza sativa Japonica* Group]	0.92	1338	1965
		EEC73541	hypothetical protein OsI_07948 [*Oryza sativa Indica* Group]	0.91	1339	
		ABQ81648	glyceraldehyde-3-phosphate dehydrogenase [*Triticum aestivum*]	0.91	1340	1966
	201-221	XP_002458746	hypothetical protein SORBIDRAFT_03g039520 [*Sorghum bicolor*] & gt;gi|241930721|gb|EES03866.1 hypothetical protein SORBIDRAFT_03g039520 [*Sorghum bicolor*]	1.00	1341	1967
		NP_001105875	putative laccase [*Zea mays*] & gt;gi|84618781|emb|CAJ30500.1 putative laccase [*Zea mays*]	0.94	1342	1968

TABLE 9-continued

Target genes of mir395, 397 and 398 to be downregulated

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		NP_001146658	hypothetical protein LOC100280258 [*Zea mays*] & gt;gi|219888209|gb|ACL54479.1 unknown [*Zea mays*]	0.93	1343	1969
		ACN28855	unknown [*Zea mays*]	0.94	1344	1970
		NP_001044772	Os01g0842400 [*Ortza satuva Japonica* Group] & gt;gi|75321217|sp|Q5N9X2.1|LAC4_ORYSJ RecName: Full = Laccase-4; AltName: Full = Benzenediol: oxygen oxidoreductase 4; AltName: Full = Diphenol oxidase 4; AltName: Full = Urishiol oxidase 4; flags: precursor & gt;gi|56784239|dbj|BAD81734.1| putative laccase LAC5-6 [*Oryza sativa Japonica* Group] & gt;gi|13534303|dbj|BAF06686.1|Os01g0842400 [*Oryza sativa Japonica* Group] & gt;gi|l215697155 |dbj|BAG91149.1| unnamed protein product [*Oryza sativa Japonica* Group]	0.80	1345	1971
		EAZ14115	hypothetical protein OsJ_04039 [*Oryza sativa Japonica* Group]	0.80	1346	
		EEC71777	hypothetical protein OsJ_04389 [*Oryza sativa Indica* Group]	0.80	1347	
		BAJ99773	predicted protein [*Hordeum vulgare* subsp. *vulgare*)	0.78	1348	1972
		XP_002458747	hypothetical protein SORBIDRAFT_03g039530 [*Sorghum bicolor*] & gt;gi|241930722|gb|EES03867.1 hypothetical protein SORBIDRAFT_03g039530 [*Sorghum bicolor*]	0.78	1349	1973
		AAC04576	putative high-pI laccase [*Oryza sativa Japonica* Group]	0.79	1350	1974
mtr-miR395c	426-446	XP_002463896	hypothetical protein SORBIDRAFT_01g008450 [*Sorghum bicolor*] & gt;gi|241917750|gb|EER90894.1 hypothetical protein SORBIDRAFT_01g008450 [*Sorghum bicolor*]	1.00	1351	1975
		ACN28609	unknown [*Zea mays*]	0.95	1352	1976
		ACN34023	unknown [*Zea mays*]	0.95	1353	1977
		ACG45192	bifunctional 3-phosphoadenosine 5-phosphosulfate synthtase [*Zea mays*]	0.94	1354	1978
		NP_001104877	ATP sulfurylase [*Zea mays*] & gt;gi|2738750|gb|AAB94542.1 ATP sulfurylase [*Zea mays*]	0.95	1355	1979
		EAY91825	hypothetical protein OsI_13470 [*Oryza sativa Indica* Group]	0.80	1356	
		NP_001051234	Os03g0743900 [*Oryza sativa Japonica* Group] & gt;gi|30017582|gb|AAP13004.1 putative ATP sulfurylase [*Oryza sativa Japonica* Group] & gt;gi|108711024|gb|ABF98819.1 Bifunctional 3 & apos;-phosphoadenenosine 5 & apos;-phosphosulfate synthethase, putative, expressed [*Oryza sativa Japonica* Group] & gt;gi|13549705|dbj|BAF13148.1 Os03g0743900 [*Oryza sativa Japonica* Group] & gt;gi|215704581|dbj| BAG94214.1 unnamed protein product [*Oryza sativa Japonica* Group]	0.80	1357	1980
		BAK05662	predicted protein [*Hordeum vulfare* subsp. *vulgare*] & gt;gi|326502564|dbj|BAJ95345.1 predicted protein product [*Hordeum vulgare* subsp. *vulgare*]	0.79	1358	1981
		BAA36274	plastidic ATP sulfurylase [*Oryza sativa Indica* Group]	0.80	1359	1982
		EAZ28548	hypothetical protein OsJ_12530 [*Oryza sativa Japonica* Group]	0.77	1360	
	528-548	ACN34023	unknown [*Zea mays*]	1.00	1361	1983
		NP_001104877	ATP sulfurylase [*Zea mays*] & gt;gi|2738750|gb|AAB94542.1 ATP sulfurylase [*Zea mays*]	0.98	1362	1984
		ACN28609	unknown [*Zea mays*]	0.94	1363	1985
		ACG45192	bifunctional 3-phosphoadenosine 5-phosphosulfate synthetase [*Zea mays*]	0.94	1364	1986
		XP_002463896	hypothetical protein SORBIDRAFT_01g008450 [*Sorghum bicolor*] & gt;gi|241917750|gb|EER90894.1 hypothetical protein SORBIDRAFT_01g008450 [*Sorghum bicolor*]	0.94	1365	1987
		BAK05662	predicted protein [*Hordeum vulgare* subsp. *vulgare*] & gt;gi|326502564|dbj|BAJ95345.1 predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.84	1366	1988
		EAY91825	hypothetical protein OsI_13470 [*Oryza sativa Indica* Group]	0.80	1367	
		NP_001051234	Os03g0743900 [*Oryza sativa Japonica* Group] & gt;gi|30017582|gb|AAP13004.1 putative ATP sulfurylase [*Oryza sativa Japonica* Group] & gt;gi|10871102|gb|ABF98819.1 Bifunctional 3 & apos;-phosphoadenosine 5 & apos;-phosphosulfate synthethase, putative, expressed [*Oryza sativa Japonica* Group] & gt;gi|113549705|dbj|BAF13148.1Os03g0743900 [*Oryza sativa Japonica Group*] & gt;gi|215704581|dbj|BAG94214.1 unnamed protein product [*Oryza sativa Japonica* Group]	0.79	1368	1989

TABLE 9-continued

Target genes of mir395, 397 and 398 to be downregulated

Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		BAA36274	plastidic ATP sulfurylase [*Oryza sativa Indica* Group]	0.79	1369	1990
		EAZ28548	hypothetical protein OsJ_12530 [*Oryza sativa Japonica* Group]	0.76	1370	
	359-379	XP_002452295	hypothetical protein SORBIDRAFT_04g023180 [*Sorghum bicolor*] & gt;gi|241932126|gb|EES05271.1 hypothetical protein SORBIDRAFT_04g023180 [*Sorghum bicolor*]	1.00	1371	1991
		NP_001148591	2-hydrozy-3-oxopropionate reductase [*Zea mays*] & gt;gi|95620656|gb|ACG32158.1 2-hydrozy-3-oxopropionate reductase [*Zea mays*]	0.98	1372	1992
		NP_001047154	Os02g0562700 [*Oryza sativa Japonica* Group] & gt;gi|29368238|gb|AAAO72678.1 gamma hydroxybutyrate dehydrogenase-like protein [*Oryza sativa Japonica* Group] & gt;gi|32352132|dbj|BAC78559.1 hypothetical protein [*Oryza sativa Japonica* Group] & gt;gi|46390142|dbj|BAD15576.1 putative gamma hydroxybutyrate dehydrogenase [*Oryza sativa Japonica* Group] & gt;gi|13536685|dbj|BAF09068.1|Os02g562700 [*Oryza sativa Japonica* Group] & gt;gi|215679041|dbj|BAG96471.1 unnamed protein product [*Oryza sativa Japonica* Group] & gt;gi|21501279|dbj|BAG92703.1 unnamed protein product [*Oryza sativa Japonica* Group] & gt;gi|215766587|dbj|BAG98746.1 unnamed protein product [*Oryza sativa Japonica* Group] & gt;gi|l218190991|gb|EEC73418.1 hypothetical protein OsI_07685 [*Oryza sativa Indica* Group] & gt;gi|222623072|gb|EEE57204.1 hypothetical protein OsJ_07161 [*Oryza sativa Japonica* Group]	0.92	1373	1993
		BAJ91168	predicted protein [*Hordeum vulgare* subsp. *vulgare*] & gt;gi|326518654|dbj|BAJ88356.1 predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.90	1374	1994
		XP_002266252	PREDICTED: hypothetical protein isoform 1 [*Vitis vinifera*] & gt;gi|47861759|emb|CAN78910.1 hypothetical protein VITISV_032948 [*Vitis vinifera*] & gt;gi|297736660|emb|CBI25677.3 unnamed protein product [*Vitis vinifera*]	0.80	1375	1995
		ACU2717	unknown [Glycine max]	0.80	1376	1996
		XP_002266296	PREDICTED: hypothetical protein isoform 2 [*Vitis vinifera*]	0.78	1377	1997
		XP_002320548	predicted protein [*Populus trichocarpa*] & gt;gi|222861321|gb|EEE98863.1 predicted protein [*Populus trichocarpa*]	0.76	1378	1998
		BAG16485	succinic semialdehyde reductase isofom1 [*Solanum lycopersicum*]	0.79	1379	1999
		ABK22179	unknown [*Picea sitchensis*]	0.77	1380	2000
	305-325	ACL53345	unknown [*Zea mays*]	1.00	1381	2001
		XP_002465703	hypothetical protein SORBIDRAFT_01g044100 [*Sorghum bicolor*] & gt;gi|241919557|gb|EER92701.1 hypothetical protein SORBIDRAFT_01g044100 [*Sorghum bicolor*]	0.95	1382	2002
		BAJ85215	predicted protein [*Hordeum vulgare* subsp. *vulgare*] & gt;gi|326511599|dbj|BAJ91944.1 predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.85	1383	2003
		AAN59769	Putative sulfate transporter [*Oryza sativa Japonica* Group] & gt;gi|25585257|gb|EAZ25921.1 hypothetical protein OsJ_09764 [*Oryza sativa Japonica* Group]	0.85	1384	
		EEC74682	hypothetical protein OsJ_10373 [*Oryza sativa Indica* Group]	0.85	1385	
		EEC74681	hypothetical protein OsJ_10372 [*Oryza sativa Indica* Group]	0.72	1386	
		EEE58498	hypothetical protein OsJ_09763[*Oryza sativa Japonica* Group]	0.72	1387	
		NP_001049257	Os03g0195300 [*Oryza sativa Japonica* Group] & gt;gi|108706649|gb|ABF94444.1 Sulfate transporter 2.1, putative, expressed [*Oryza sativa Japonica* Group] & gt;gi|13547728|dbj|BAF11171.1Os03g0195300 [*Oryza sativa Japonica* Group]	0.72	1388	2004
Predicted zmamir 50266	201-221	XP_002456833	hypothetical protein SORBIDRAFT_03g043750 [*Sorghum bicolor*] & gt;gi|241928808|gb|EES01953.1 hypothetical protein SORBIDRAFT_03g043750 [*Sorghum bicolor*]	1.00	1311	1939
		NP_001131338	hypothetical protein LOC100192654 [*Zea mays*] & gt;gi|94690154|gb|ACF79161.1 unknown [*Zea mays*] & gt;gi|219884631|gb|ACL52690.1 unknown [*Zea mays*] & gt;gil238908563|gb|ACF79698.2unknown [*Zea mays*]	0.96	1312	1940

TABLE 9-continued

Target genes of mir395, 397 and 398 to be downregulated						
Mir name	Mir Bind. Pos.	Hom. NCBI Accession	Annotation/Organism	Identity	p.p. SEQ ID NO:	p.n. SEQ ID NO:
		ACL52654	unknown [*Zea mays*]	0.92	1313	1941
		ACG35805	selenium-binding protein [*Zea mays*]	0.92	1314	1942
		NP_001045194	Os01g0916400 [*Oryza sativa Japonica* Group] & gt;gi|19386752|dbj|BAB86133.1 putative selenium binding protein [*Oryza sativa Japonica* Group] & gt;gi|20805006|dbj|BAB92682.1 putative selenium binding protein [*Oryza sativa Japonica* Group] & gt;gi|31322241|gb|AAO91777.1 putative selenium binding protein [*Oryza sativa Japonica* Group] & gt;gi|113534725|dbj|BAF07108.1|Os01g0916400 [*Oryza sativa Japonica* Group] & gt;gi|125528845|gb|EAY76959.1| hypothetical protein OsI_04917 [*Oryza sativa Indica* Group] & gt;gi|25573100|gb|EAZ14615.1| hypothetical protein OsJ_04540 [*Oryza sativa Japonica* Group] & gt;gi|13534725|dbj|BAF07108.1OS01g0916400 [*Oryza sativa Japonica* Group]	0.90	1315	1943
		BAJ94729	predicted protein [*Hordeum vulgare* subsp. *vulgare*]	0.88	1316	1944
		BAB40923	putative selenium binding protein [*Oryza sativa* (*japonica cultivar*-group)]	0.88	1317	1945
		XP_002328915	predicted protein [*Populus trichocarpa*] & gt;gi|222839345|gb|EEE77682.1 predicted protein [*Populus trichocarpa*]	0.80	1318	1946
		XP_002298672	predicted protein [*Populus trichocarpa*] & gt;gi|222845930|gb|EEE3477.1 predicted protein [*Populus trichocarpa*]	0.80	1319	1947
		XP_002520613	selenium-binding protein, putative [*Ricinus communis*] & gt;gi|223540174|gb|EEF41749.1 selenium-binding protein, putative [*Ricinus communis*]	0.80	1320	1948

Table 9, provided are target genes to be downregulated, of mirs 395, 397 and 398.

TABLE 10

Abbreviations of plant species
Provided are the abbreviations and full names of plant species.

Abbreviation	Organism Name	Common Name
ahy	*Arachis hypogaea*	Peanut
aly	*Arabidopsis lyrata*	*Arabidopsis lyrata*
aqc	*Aquilegia coerulea*	Rocky Mountain Columbine
ata	*Aegilops taushii*	Tausch's goatgrass
ath	*Arabidopsis thaliana*	*Arabidopsis thaliana*
bdi	*Brachypodium distachyon*	Grass
bna	*Brassica napus*	*Brassica napus* canola ("liftit")
bol	*Brassica oleracea*	*Brassica oleracea* wild cabbage
bra	*Brassica rapa*	*Brassica rapa* yellow mustard
ccl	*Citrus clementine*	Clementine
csi	*Citrus sinensis*	Orange
ctr	*Citrus trifoliata*	Trifoliate orange
gma	*Glycine max*	*Glycine max*
gso	*Glycine soja*	Wild soybean
hvu	*Hordeum vulgare*	Barley
lja	*Lotus japonicus*	*Lotus japonicus*
mtr	*Medicago truncatula*	*Medicago truncatula*—Barrel Clover ("tiltan")
osa	*Oryza sativa*	*Oryza sativa*
pab	*Picea abies*	European spruce
ppt	*Physcomitrella patens*	*Physcomitrella patens* (moss)
pta	*Pinus taeda*	*Pinus taeda*—Loblolly Pine
ptc	*Populus trichocarpa*	*Populus trichocarpa*—black cotton wood
rco	*Ricinus communis*	Castor bean ("kikayon")
sbi	*Sorghum bicolor*	*Sorghum bicolor Dura*
sly	*Solanum lycopersicum*	tomato microtom
smo	*Selaginella moellendorffii*	*Selaginella moellendorffii*
sof	*Saccharum officinarum*	Sugarcane
ssp	*Saccharum spp*	Sugarcane
tae	*Triticum aestivum*	*Triticum aestivum*
tcc	*Theobroma cacao*	cacao tree and cocoa tree
vvi	*Vitis vinifera*	*Vitis vinifera* Grapes
zma	*Zea mays*	corn

Example 3

Gene Cloning and Creation of Binary Vectors for Plant Expression

The predicted target sequences were cloned into binary vectors for the generation of transgenic plants. The full-length open reading frame (ORF) was synthesized by Genscript (Israel). The resultant clone was digested with appropriate restriction enzymes and inserted into the Multi Cloning Site (MCS) of a similarly digested binary vector through ligation using T4 DNA ligase enzyme (Promega, Madison, Wis., USA). FIG. **1** is a plasmid map of the binary vector pORE-E1, used for plant transformation.

Example 4

Generation of Transgenic Model Plants Expressing the Target Genes/Silencing Agents of Some Embodiments of the Invention

Arabidoposis thaliana transformation was performed using the floral dip procedure following a slightly modified version of the published protocol (Clough and Bent, 1998, *Plant J* 16(6): 735-43; Desfeux et al, 2000, *Plant Physiol.* 123(3): 895-904). Briefly, T_0 Plants were planted in small pots filled with soil. The pots were covered with aluminum foil and a plastic dome, kept at 4° C. for 3-4 days, then uncovered and incubated in a growth chamber at 24° C. under 16 hr light:8 hr dark cycles. A week prior to transformation all individual flowering stems were removed to allow for growth of multiple flowering stems instead. A single colony of *Agrobacterium* (GV3101) carrying the binary vectors (pORE-E1), harboring the target gene or silencing sequence was cultured in LB medium supplemented with kanamycin (50 mg/L) and gentamycin (25 mg/L). Three days prior to transformation, each culture was incubated at 28° C. for 48 hrs, shaking at 180 rpm. The starter culture was split the day before transformation into two cultures, which were allowed to grow further at 28° C. for 24 hours at 180 rpm. Pellets containing the *agrobacterium* cells were obtained by centrifugation of the cultures at 5000 rpm for 15 minutes. The pellets were resuspended in an infiltration medium (10 mM $MgCl_2$, 5% sucrose, 0.044 μM BAP (Sigma) and 0.03% Tween 20) in double-distilled water.

Transformation of T_0 plants was performed by inverting each plant into the *Agrobacterium* suspension, keeping the flowering stem submerged for 5 minutes. Following inoculation, each plant was blotted dry for 5 minutes on both sides, and placed sideways on a fresh covered tray for 24 hours at 22° C. Transformed (transgenic) plants were then uncovered and transferred to a greenhouse for recovery and maturation. The transgenic T_0 plants were grown in the greenhouse for 3-5 weeks until the seeds are ready. The seeds were then harvested from plants and kept at room temperature until sowing.

Example 5

Selection of Transgenic *Arabidopsis* Plants Expressing the Nucleic Acid Molecules of Some Embodiments of the Invention According to Expression Level

Arabidopsis seeds were sown. One to 2 weeks old seedlings were sprayed with a non-volatile herbicide, Basta (Bayer) at least twice every few days. Only resistant plants, which are heterozygous for the transgene, survive. PCR on the genomic gene sequence was performed on the surviving seedlings using primers pORE-F2 (fwd, 5'-TTTAGCGATGAACTTCACTC-3'/SEQ ID NO:310) and a custom designed reverse primer based on each target sequence.

Example 6

Evaluating Changes in Root Architecture in Transgenic Plants

Root architecture of the plant governs multiple key agricultural traits. Root size and depth have been shown to logically correlate with drought tolerance and enhanced NUE, since deeper and more branched root systems provide better soil coverage and can access water and nutrients stored in deeper soil layers.

To test whether the transgenic plants produce a modified root structure, plants were grown in agar plates placed vertically. A digital picture of the plates was taken every few days and the maximal length and total area covered by the plant roots were assessed. From every construct created, several independent transformation events were checked in replicates. To assess significant differences between root features, statistical test, such as a Student's t-test, was employed in order to identify enhanced root features and to provide a statistical value to the findings.

Example 7

Testing for Increased Nitrogen Use Efficiency (NUE)

To analyze whether the transgenic *Arabidopsis* plants are more responsive to nitrogen, plants were grown in two different nitrogen concentrations: (1) optimal nitrogen concentration (100% NH_4NO_3, which corresponds to 20.61 mM) or (2) nitrogen deficient conditions (1% or 10% NH_4NO_3, which corresponds to 0.2 and 2.06 mM, respectively). Plants were allowed to grow until seed production followed by an analysis of their overall size, time to flowering, yield, protein content of shoot and/or grain, and seed production. The parameters checked are each of the overall size of the plant, wet and dry weight, the weight of the seeds yielded, the average seed size and the number of seeds produced per plant. Other parameters that are tested include: the chlorophyll content of leaves (as nitrogen plant status and the degree of leaf greenness are highly correlated), amino acid and the total protein content of the seeds or other plant parts such as leaves or shoots and oil content. Transformed plants not exhibiting substantial physiological and/or morphological effects, or exhibiting higher measured parameters levels than wild-type plants, are identified as nitrogen use efficient plants.

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

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

SEQUENCE LISTING

The patent contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US09902956B2). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

What is claimed is:

1. A method of improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of a plant, the method comprising expressing within the plant an exogenous polynucleotide which downregulates an activity or expression of a polypeptide having an amino acid sequence 100% homologous to SEQ ID NOs: 312 and 317, wherein said polypeptide is capable of regulating nitrogen use efficiency of the plant, thereby improving nitrogen use efficiency, abiotic stress tolerance, biomass, vigor or yield of the plant.

2. A transgenic plant exogenously expressing a polynucleotide which downregulates an activity or expression of a polypeptide having an amino acid sequence 100% homologous to SEQ ID NOs: 312 and 317, wherein said polypeptide is capable of regulating nitrogen use efficiency of the plant.

3. A nucleic acid construct comprising a polynucleotide which downregulates an activity or expression of a polypeptide having an amino acid sequence 100% homologous to SEQ ID NOs: 312 and 317, wherein said polypeptide is capable of regulating nitrogen use efficiency of a plant, said nucleic acid sequence being under the regulation of a cis-acting regulatory element.

4. The method of claim **1**, the transgenic plant of claim **2** or the nucleic acid construct of claim **3**, wherein said polynucleotide acts by a mechanism selected from the group consisting of sense suppression, antisense suppression, ribozyme inhibition, gene disruption.

5. The nucleic acid construct of claim **3**, wherein said cis-acting regulatory element comprises a promoter.

6. The nucleic acid construct of claim **5**, wherein said promoter comprises a tissue-specific promoter.

7. The nucleic acid construct of claim **6**, wherein said tissue-specific promoter comprises a root specific promoter.

8. The method of claim **1**, further comprising growing the plant under limiting nitrogen conditions.

9. The method of claim **1**, further comprising growing the plant under abiotic stress.

10. The method of claim **9**, wherein said abiotic stress is selected from the group consisting of salinity, drought, water deprivation, flood, etiolation, low temperature, high temperature, heavy metal toxicity, anaerobiosis, nutrient deficiency, nutrient excess, atmospheric pollution and UV irradiation.

11. The method of claim **1** wherein the plant is a monocotyledon.

12. The method of claim **1**, wherein the plant is a dicotyledon.

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