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(54) **PLANT TERMINATOR SEQUENCES**

FOREIGN PATENT DOCUMENTS

(75) Inventors: **Priyanka Bhyri**, Andhra Pradesh (IN);
Nandini Krishnamurthy, Andhra Pradesh (IN); **Eswar Narayanan**, Andhra Pradesh (IN); **Ajit Nott**, Andhra Pradesh (IN); **Rinku Ranjan Sarangi**, Andhra Pradesh (IN)

WO 0020613 A1 4/2000
WO WO 2006/013072 A2 * 2/2006
WO 2006013072 A2 9/2006

(73) Assignee: **E I DU PONT DE NEMOURS AND COMPANY**, Wilmington, DE (US)

OTHER PUBLICATIONS

(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 267 days.

Lin et al., 2005, Chinese Science Bulletin 50: 1669-1672.*
Oryza sativa chromosome 3 BAC OSJNBa0024F18 genomic sequence, GenBank accession No. AC135594.*
Bieri et al., 2002, Molecular Breeding 10: 107-117.*
Olsen et al., 2005, Trends in Plant Science 10: 79-87.*
Mignone and Pesole, 2011, In: eLS, John Wiley & Sons, pp. 1-5.*
Gilmartin, G., "Eukaryotic mRNA 3' processing: a common means to different ends" Genes and Development, 2005, vol. 19: 2517-2521.
Ingelbrecht, I. et al, "Different 3' End Regions Strongly Influence the Level of Gene Expression in Plant Cells" The Plant Cell, 1989:vol. 1:671-680.
Kobayashi et al "Evidence for an evolutionary force that prevents epigenetic silencing between tail-to-tail rice genes with a short spacer", Gene, 2005, vol. 346:231-240.
Mette, M.F. et al, "Production of aberrant promoter transcripts contributes to methylation and silencing of unlinked homologous promoters in trans" The EMBO Journal, 1999, vol. 18:1, 241-248.
Mette, M.F. et al, "Transcriptional silencing and promoter methylation triggered by double-stranded RNA" The EMBO Journal, 2000, vol. 19:19, 5194-5201.
Mourrain, P. et al, "A single transgene locus triggers both transcriptional and post-transcriptional silencing through double-stranded RNA production" Planta, 2007, vol. 225:365-379.
Peremarti, A. et al, "Promoter diversity in multigene transformation" Plant Molecular Biology, 2010, vol. 73:363-378.
Proudfoot, N. "New perspectives on connecting messenger RNA 3' end formation to transcription" Current Opinion in Cell Biology, 2004, vol. 16:272-278.
Genbank EBI Accession CW845633 2004.
International Search Report PCT/US2012/046686 dated Feb. 1, 2013.
Written Opinion of the International Searching Authority for International Application No. PCT/US2012/046686.

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

(56) **References Cited**

U.S. PATENT DOCUMENTS

2007/0214517 A1* 9/2007 Alexandrov C07K 14/415
800/278
2008/0263722 A1* 10/2008 Hu C07K 14/415
800/278
2009/0320160 A1 12/2009 Li

* cited by examiner

Primary Examiner — Amjad Abraham
Assistant Examiner — Bratislav Stankovic

(57) **ABSTRACT**

This invention relates to gene expression regulatory sequences, specifically transcription terminator sequences. Plant transcription terminator sequences are described herein. Methods for identifying novel plant transcription terminator sequences that can terminate transcription in one orientation or in a bidirectional manner and methods of using these terminator sequences to generate transgenic plants are described herein.

15 Claims, 3 Drawing Sheets

Specification includes a Sequence Listing.

FIG. 1

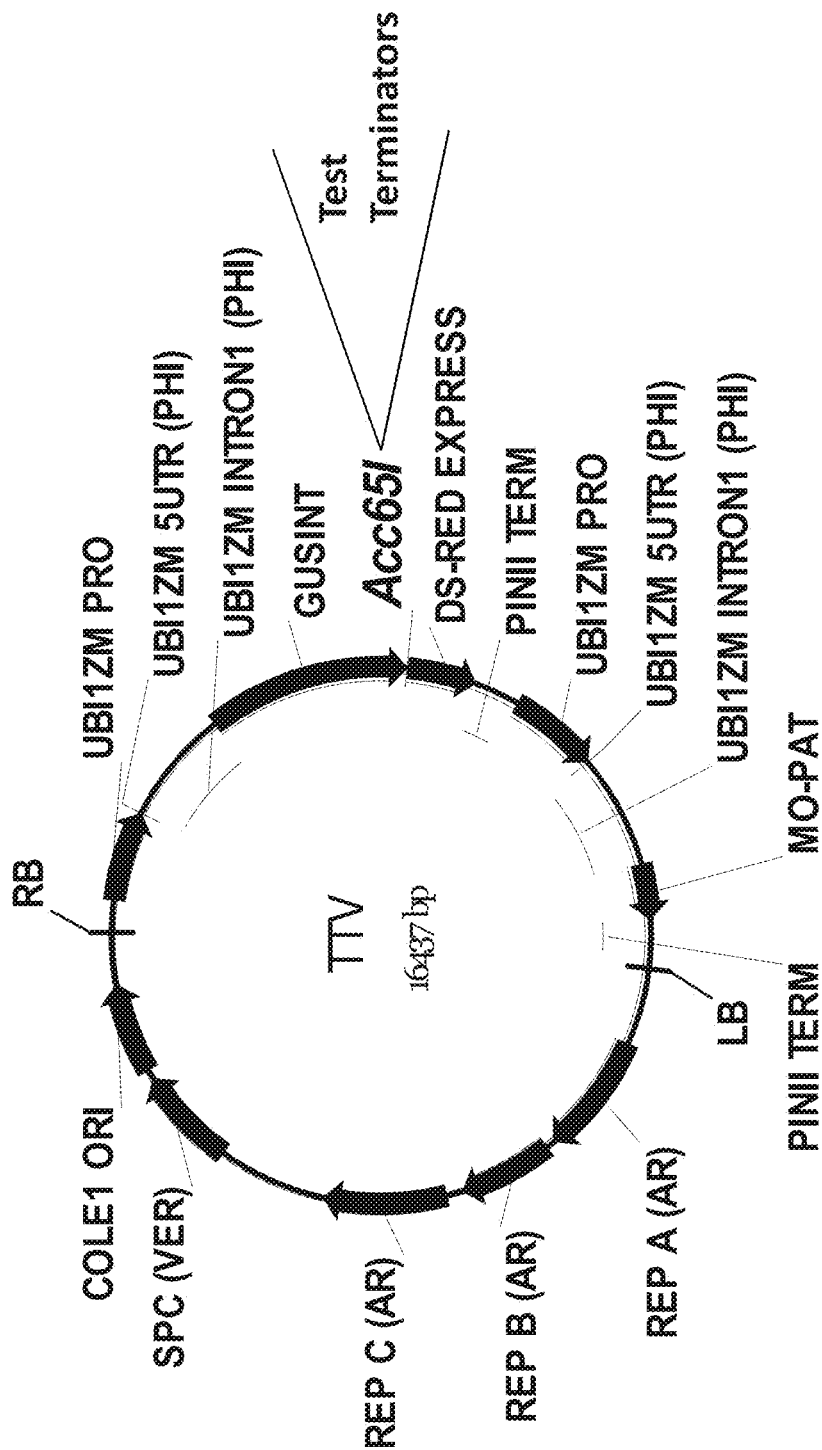


FIG. 2

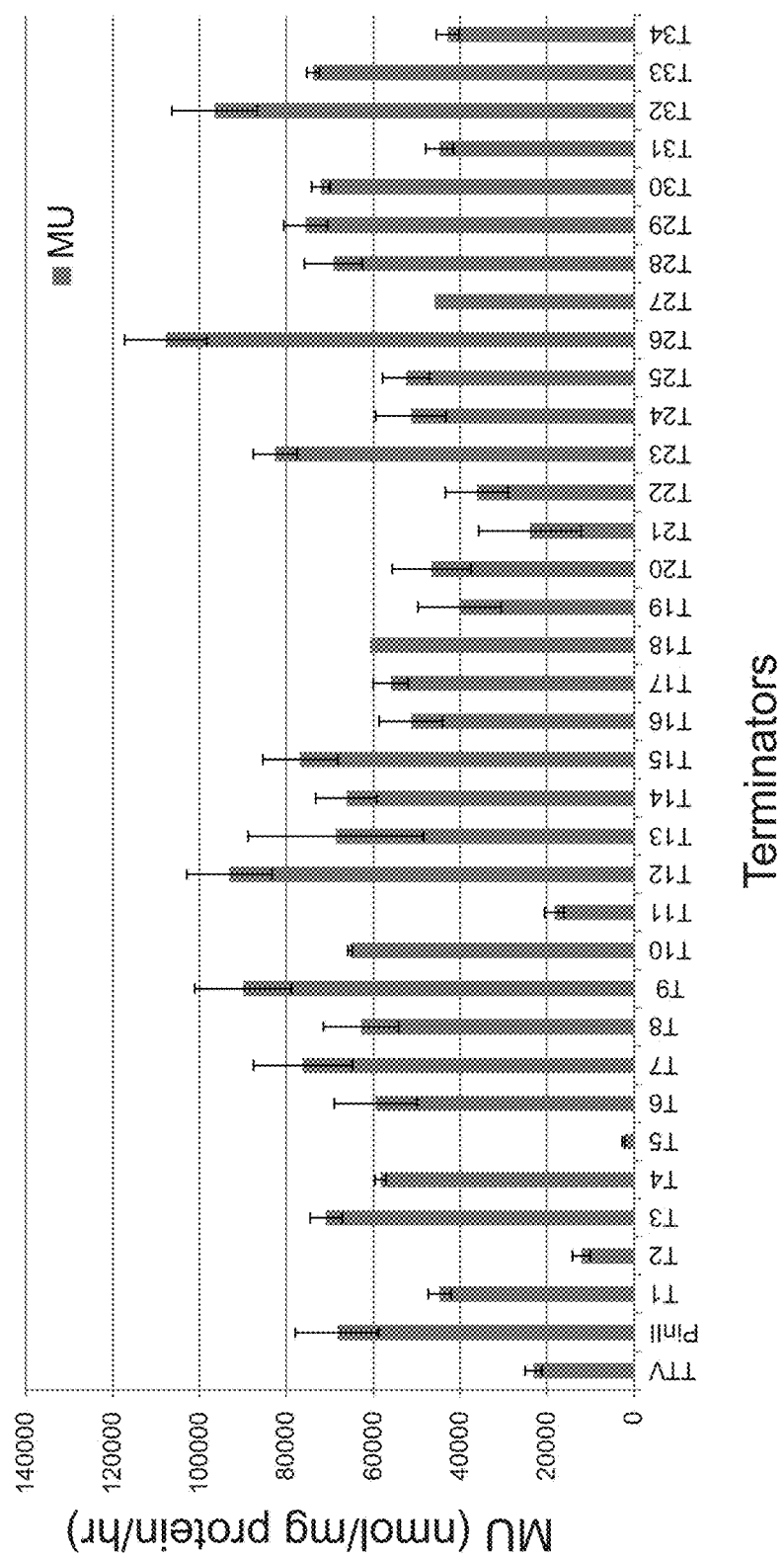
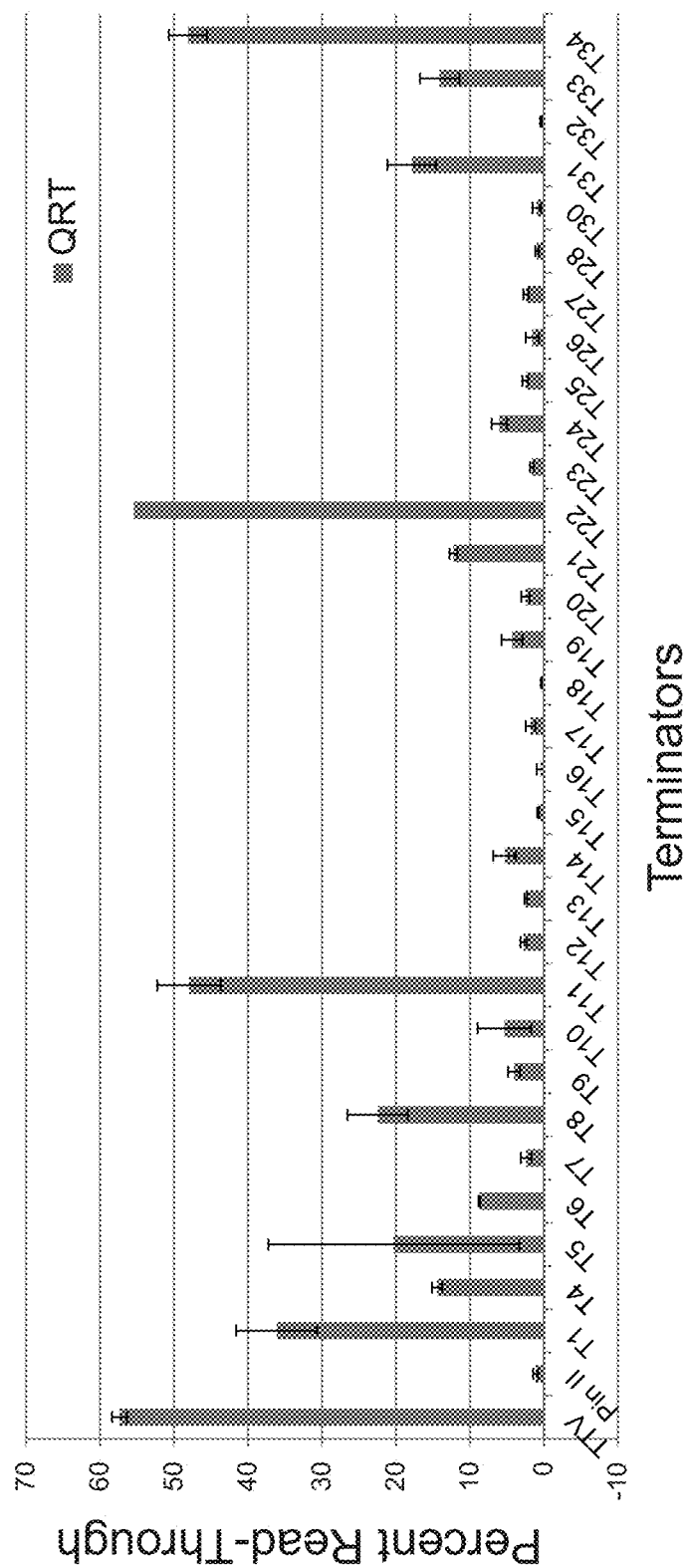


FIG. 3



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PLANT TERMINATOR SEQUENCES

CROSS REFERENCE TO RELATED APPLICATIONS

This application is a U.S. National Stage Entry under 35 U.S.C. § 371 of International Patent Application No. PCT/US2012/046686, filed on Jul. 13, 2012, which claims the benefit of Indian Provisional Application No. 2001/DEL/2011, filed Jul. 15, 2011, and U.S. Provisional Application No. 61/557,433, filed Sep. 11, 2011, the entire contents of each is herein incorporated by reference.

FIELD OF INVENTION

The present invention relates to the field of plant molecular biology and plant genetic engineering. More specifically, it relates to novel plant terminator sequences and their use to regulate gene expression in plants.

BACKGROUND

Recent advances in plant genetic engineering have opened new doors to engineer plants to have improved characteristics or traits. These transgenic plants characteristically have recombinant DNA constructs in their genome that have a protein-coding region operably linked to multiple regulatory regions that allow accurate expression of the transgene. A few examples of regulatory elements that help regulate gene expression in transgenic plants are promoters, introns, terminators, enhancers and silencers.

Plant genetic engineering has advanced to introducing multiple traits into commercially important plants, also known as gene stacking. This can be accomplished by multigene transformation, where multiple genes are transferred to create a transgenic plant that might express a complex phenotype, or multiple phenotypes. But it is important to modulate or control the expression of each transgene optimally. The regulatory elements need to be diverse, to avoid introducing into the same transgenic plant repetitive sequences, which have been correlated with undesirable negative effects on transgene expression and stability (Peremarti et al (2010) *Plant Mol Biol* 73:363-378; Mette et al (1999) *EMBO J* 18:241-248; Mette et al (2000) *EMBO J* 19:5194-5201; Mourrain et al (2007) *Planta* 225:365-379, U.S. Pat. Nos. 7,632,982, 7,491,813, 7,674,950, PCT Application No. PCT/US2009/046968). Therefore it is important to discover and characterize novel regulatory elements that can be used to express heterologous nucleic acids in important crop species. Diverse regulatory regions can be used to control the expression of each transgene optimally.

Regulatory sequences located downstream of protein-coding regions contain signals required for transcription termination and 3' mRNA processing, and are called terminator sequences. The terminator sequences play a key role in mRNA processing, localization, stability and translation (Proudfoot, N. (2004) *Curr Opin Cell Biol* 16:272-278; Gilmartin, G. M. (2005) *Genes Dev.* 19:2517-2521). The 3' regulatory sequences contained in terminator sequences can affect the level of expression of a gene. Optimal expression of a chimeric gene in plant cells has been found to be dependent on the presence of appropriate 3' sequences (Ingelbrecht et al. (1989) *Plant Cell* 1:671-680). Read-through transcription through a leaky terminator of a gene can cause unwanted transcription of one transgene from the promoter of another one. Also, bidirectional, convergent transcription of transgenes in transgenic plants that have

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leaky transcription termination of the convergent genes can lead to overlapping transcription of the convergent genes. Convergent, overlapping transcription can decrease transgene expression, or generate antisense RNA (Bieri, S. et al (2002) *Molecular Breeding* 10:107-117). This underlines the importance of discovering novel and efficient transcriptional terminators.

SUMMARY

Regulatory sequences for modulating gene expression in plants are described. Specifically, regulatory sequences that are transcription terminator sequences are described. Recombinant DNA constructs comprising terminator sequences are provided.

One embodiment is a recombinant construct comprising an isolated polynucleotide comprising (a) a nucleotide sequence as set forth in SEQ ID NO:2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (b) a nucleotide sequence with at least 95% sequence identity to the sequence set forth in SEQ ID NO:2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (c) a functional fragment of either (a) or (b); wherein the isolated polynucleotide functions as a transcriptional terminator in a plant cell. In another embodiment, the isolated polynucleotide is operably linked to the 3' end of a heterologous polynucleotide which is operably linked to a promoter.

One embodiment is a recombinant construct comprising an isolated polynucleotide comprising (a) a nucleotide sequence as set forth in SEQ ID NO:2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (b) a nucleotide sequence with at least 95% sequence identity to the sequence set forth in SEQ ID NO:2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (c) a functional fragment of either (a) or (b); wherein the isolated polynucleotide functions as a bidirectional transcriptional terminator in a plant cell. Another embodiment is the recombinant construct wherein the bidirectional transcriptional terminator is operably linked to (a) the 3' end of a first heterologous polynucleotide which is operably linked to a first promoter; and (b) the 3' end of a second heterologous polynucleotide which is operably linked to a second promoter; wherein the first and the second heterologous polynucleotides are transcribed in a convergent manner.

One embodiment is a method of expressing a heterologous polynucleotide in a plant, comprising the steps of (a) introducing into a regenerable plant cell a recombinant construct wherein the recombinant construct comprises an isolated polynucleotide comprising (i) a nucleotide sequence as set forth in SEQ ID NO:2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (ii) a nucleotide sequence with at least 95% sequence identity to the sequence set forth in SEQ ID NO:2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (iii) a functional fragment of either (i) or (ii); wherein the isolated polynucleotide functions as a transcriptional terminator in a plant cell and further wherein the isolated polynucleotide is operably linked to the 3' end of a heterologous polynucleotide which is operably linked to a promoter; (b) regenerating a transgenic plant from the regenerable plant cell of

(a), wherein the transgenic plant comprises in its genome the recombinant construct; and (c) obtaining a progeny plant from the transgenic plant of step (b), wherein the progeny plant comprises in its genome the recombinant DNA construct and exhibits expression of the heterologous polynucleotide.

Another embodiment provides for a method of regulating the expression of two heterologous polynucleotides in a plant, comprising the steps of: (a) introducing into a regenerable plant cell a recombinant construct, wherein the recombinant construct comprises an isolated polynucleotide comprising (i) a nucleotide sequence as set forth in SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (ii) a nucleotide sequence with at least 95% sequence identity to the sequence set forth in SEQ ID NO:2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (iii) a functional fragment of either (i) or (ii); wherein the isolated polynucleotide functions as a bidirectional transcriptional terminator in a plant cell and further wherein the bidirectional transcriptional terminator is operably linked to the 3' end of a first heterologous polynucleotide which is operably linked to a first promoter and the 3' end of a second heterologous polynucleotide which is operably linked to a second promoter; wherein the first and the second heterologous polynucleotides are transcribed in a convergent manner; (b) regenerating a transgenic plant from the regenerable plant cell of (a), wherein the transgenic plant comprises in its genome the recombinant construct; and (c) obtaining a progeny plant from the transgenic plant of step (b), wherein the progeny plant comprises in its genome the recombinant DNA construct and exhibits expression of both the first heterologous polynucleotide and the second heterologous polynucleotide.

Another embodiment is a vector, cell, microorganism, plant, or seed comprising a recombinant DNA construct comprising a terminator sequences described herein.

Another embodiment is a regenerated, mature and fertile transgenic plants comprising the recombinant DNA constructs described above, transgenic seeds produced therefrom, T1 and subsequent generations. The transgenic plant cells, tissues, plants, and seeds may comprise at least one recombinant DNA construct of interest.

In one embodiment, the plant comprising the terminator sequences described herein is selected from the group consisting of: *Arabidopsis*, maize, soybean, sunflower, *sorghum*, canola, mustard, wheat, alfalfa, cotton, rice, barley, millet, sugar cane and switchgrass.

In one embodiment, the plant comprising the terminator sequences described herein is a monocotyledenous plant. In another embodiment, the plant comprising the terminator sequences described herein is a rice plant.

BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE LISTING

The invention can be more fully understood from the following detailed description and the accompanying drawings and Sequence Listing which form a part of this application. The Sequence Listing contains the one letter code for nucleotide sequence characters and the three letter codes for amino acids as defined in conformity with the IUPAC-IUBMB standards described in Nucleic Acids Research 13:3021-3030 (1985) and in the Biochemical Journal 219 (No. 2): 345-373 (1984), which are herein incorporated by reference in their entirety. The symbols and format used for

nucleotide and amino acid sequence data comply with the rules set forth in 37 C.F.R. § 1.822.

FIG. 1 is a schematic representation of the binary plant transformation vector, the Terminator Test Vector (TTV; PHP49597) used for testing terminators carrying the GUS reporter gene driven by the Maize Ubiquitin promoter. GUSINT is the β -glucuronidase gene with an intron inserted at SnaBI site to prevent bacterial expression. The Acc65I site used for cloning of putative terminator sequences to be tested is also shown.

FIG. 2 depicts the GUS quantitative assay of leaf samples of single-copy stable rice events harboring the constructs.

FIG. 3 shows the qRT-PCR data of single-copy stable rice events harboring TTV constructs containing the candidate terminator sequences: No terminator control (TTV), PINII terminator, T1 (SEQ ID NO:2), T4-T28 (SEQ ID NOS:5-29), T30-T34 (SEQ ID NOS:31-35).

SEQ ID NO:1 is the sequence of the terminator test vector (TTV; PHP49597) carrying GUS (β -glucuronidase) reporter gene driven by the maize ubiquitin promoter.

SEQ ID NO:2-35 are the sequences of the candidate terminator sequences from *Arabidopsis thaliana* and *Oryza sativa*, as given in Table 1.

TABLE 1

SEQ ID NO	Name	Species
2	T1	<i>Arabidopsis thaliana</i>
3	T2	<i>Arabidopsis thaliana</i>
4	T3	<i>Arabidopsis thaliana</i>
5	T4	<i>Arabidopsis thaliana</i>
6	T5	<i>Arabidopsis thaliana</i>
7	T6	<i>Arabidopsis thaliana</i>
8	T7	<i>Arabidopsis thaliana</i>
9	T8	<i>Arabidopsis thaliana</i>
10	T9	<i>Arabidopsis thaliana</i>
11	T10	<i>Arabidopsis thaliana</i>
12	T11	<i>Arabidopsis thaliana</i>
13	T12	<i>Arabidopsis thaliana</i>
14	T13	<i>Arabidopsis thaliana</i>
15	T14	<i>Arabidopsis thaliana</i>
16	T15	<i>Oryza sativa</i>
17	T16	<i>Oryza sativa</i>
18	T17	<i>Oryza sativa</i>
19	T18	<i>Oryza sativa</i>
20	T19	<i>Oryza sativa</i>
21	T20	<i>Oryza sativa</i>
22	T21	<i>Oryza sativa</i>
23	T22	<i>Oryza sativa</i>
24	T23	<i>Oryza sativa</i>
25	T24	<i>Oryza sativa</i>
26	T25	<i>Oryza sativa</i>
27	T26	<i>Oryza sativa</i>
28	T27	<i>Oryza sativa</i>
29	T28	<i>Oryza sativa</i>
30	T29	<i>Oryza sativa</i>
31	T30	<i>Oryza sativa</i>
32	T31	<i>Oryza sativa</i>
33	T32	<i>Oryza sativa</i>
34	T33	<i>Oryza sativa</i>
35	T34	<i>Oryza sativa</i>

SEQ ID NO:36 is the sequence of the PINII terminator.

SEQ ID NOS:37-106 are the primers used for amplifying the candidate terminator sequences and the PINII terminator sequence, as given in Table 2.

SEQ ID NOS:107-113 are the primer sequences used for RT-PCR to determine read through transcription for the candidate terminator sequences.

SEQ ID NOS:114-125 are the sequences of the probes and primers used for qRT-PCR (quantitative reverse transcriptase PCR) for testing the candidate terminator sequences, as given in Table 4.

SEQ ID NOS:126-128 are the sequences of the primers used for polyA mapping.

SEQ ID NOS:129-162 are the sequences of the shorter terminator sequences.

DETAILED DESCRIPTION

The disclosure of each reference set forth herein is hereby incorporated by reference in its entirety.

As used herein and in the appended claims, the singular forms “a”, “an”, and “the” include plural reference unless the context clearly dictates otherwise. Thus, for example, reference to “a plant” includes a plurality of such plants, reference to “a cell” includes one or more cells and equivalents thereof known to those skilled in the art, and so forth.

As used herein:

The terms “monocot” and “monocotyledonous plant” are used interchangeably herein. A monocot includes the Gramineae.

The terms “dicot” and “dicotyledonous plant” are used interchangeably herein. A dicot includes the following families: Brassicaceae, Leguminosae, and Solanaceae.

The terms “full complement” and “full-length complement” are used interchangeably herein, and refer to a complement of a given nucleotide sequence, wherein the complement and the nucleotide sequence consist of the same number of nucleotides and are 100% complementary.

“Transgenic” refers to any cell, cell line, callus, tissue, plant part or plant, the genome of which has been altered by the presence of a heterologous nucleic acid, such as a recombinant DNA construct, including those initial transgenic events as well as those created by sexual crosses or asexual propagation from the initial transgenic event. The term “transgenic” as used herein does not encompass the alteration of the genome (chromosomal or extra-chromosomal) by conventional plant breeding methods or by naturally occurring events such as random cross-fertilization, non-recombinant viral infection, non-recombinant bacterial transformation, non-recombinant transposition, or spontaneous mutation.

“Genome” as it applies to plant cells encompasses not only chromosomal DNA found within the nucleus, but organelle DNA found within subcellular components (e.g., mitochondrial, plastid) of the cell.

“Plant” includes reference to whole plants, plant organs, plant tissues, plant propagules, seeds and plant cells and progeny of same. Plant cells include, without limitation, cells from seeds, suspension cultures, embryos, meristematic regions, callus tissue, leaves, roots, shoots, gametophytes, sporophytes, pollen, and microspores.

“Propagule” includes all products of meiosis and mitosis able to propagate a new plant, including but not limited to, seeds, spores and parts of a plant that serve as a means of vegetative reproduction, such as corms, tubers, offsets, or runners. Propagule also includes grafts where one portion of a plant is grafted to another portion of a different plant (even one of a different species) to create a living organism. Propagule also includes all plants and seeds produced by cloning or by bringing together meiotic products, or allowing meiotic products to come together to form an embryo or fertilized egg (naturally or with human intervention).

“Progeny” comprises any subsequent generation of a plant.

The commercial development of genetically improved germplasm has also advanced to the stage of introducing multiple traits into crop plants, often referred to as a gene stacking approach. In this approach, multiple genes confer-

ring different characteristics of interest can be introduced into a plant. Gene stacking can be accomplished by many means including but not limited to co-transformation, retransformation, and crossing lines with different transgenes.

“Transgenic plant” includes reference to a plant which comprises within its genome a heterologous polynucleotide. For example, the heterologous polynucleotide is stably integrated within the genome such that the polynucleotide is passed on to successive generations. The heterologous polynucleotide may be integrated into the genome alone or as part of a recombinant DNA construct.

“Heterologous” with respect to sequence means a sequence that originates from a foreign species, or, if from the same species, is substantially modified from its native form in composition and/or genomic locus by deliberate human intervention.

“Polynucleotide”, “nucleic acid sequence”, “nucleotide sequence”, or “nucleic acid fragment” are used interchangeably to refer to a polymer of RNA or DNA that is single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases. Nucleotides (usually found in their 5'-monophosphate form) are referred to by their single letter designation as follows: “A” for adenylate or deoxyadenylate (for RNA or DNA, respectively), “C” for cytidylate or deoxycytidylate, “G” for guanylate or deoxyguanylate, “U” for uridylate, “T” for deoxythymidylate, “R” for purines (A or G), “Y” for pyrimidines (C or T), “K” for G or T, “H” for A or C or T, “I” for inosine, and “N” for any nucleotide.

“Polypeptide”, “peptide”, “amino acid sequence” and “protein” are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical analogue of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers. The terms “polypeptide”, “peptide”, “amino acid sequence”, and “protein” are also inclusive of modifications including, but not limited to, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation.

“Messenger RNA (mRNA)” refers to the RNA that is without introns and that can be translated into protein by the cell.

“cDNA” refers to a DNA that is complementary to and synthesized from an mRNA template using the enzyme reverse transcriptase. The cDNA can be single-stranded or converted into the double-stranded form using the Klenow fragment of DNA polymerase I.

“Coding region” refers to the portion of a messenger RNA (or the corresponding portion of another nucleic acid molecule such as a DNA molecule) which encodes a protein or polypeptide. “Non-coding region” refers to all portions of a messenger RNA or other nucleic acid molecule that are not a coding region, including but not limited to, for example, the promoter region, 5' untranslated region (“UTR”), 3' UTR, intron and terminator. The terms “coding region” and “coding sequence” are used interchangeably herein. The terms “non-coding region” and “non-coding sequence” are used interchangeably herein.

An “Expressed Sequence Tag” (“EST”) is a DNA sequence derived from a cDNA library and therefore is a sequence which has been transcribed. An EST is typically obtained by a single sequencing pass of a cDNA insert. The sequence of an entire cDNA insert is termed the “Full-Insert Sequence” (“FIS”). A “Contig” sequence is a sequence assembled from two or more sequences that can be selected

from, but not limited to, the group consisting of an EST, FIS and PCR sequence. A sequence encoding an entire or functional protein is termed a "Complete Gene Sequence" ("CGS") and can be derived from an FIS or a contig.

"Mature" protein refers to a post-translationally processed polypeptide; i.e., one from which any pre- or pro-peptides present in the primary translation product have been removed.

"Precursor" protein refers to the primary product of translation of mRNA; i.e., with pre- and pro-peptides still present. Pre- and pro-peptides may be and are not limited to intracellular localization signals.

"Isolated" refers to materials, such as nucleic acid molecules and/or proteins, which are substantially free or otherwise removed from components that normally accompany or interact with the materials in a naturally occurring environment. Isolated polynucleotides may be purified from a host cell in which they naturally occur. Conventional nucleic acid purification methods known to skilled artisans may be used to obtain isolated polynucleotides. The term also embraces recombinant polynucleotides and chemically synthesized polynucleotides.

"Recombinant" refers to an artificial combination of two otherwise separated segments of sequence, e.g., by chemical synthesis or by the manipulation of isolated segments of nucleic acids by genetic engineering techniques. "Recombinant" also includes reference to a cell or vector, that has been modified by the introduction of a heterologous nucleic acid or a cell derived from a cell so modified, but does not encompass the alteration of the cell or vector by naturally occurring events (e.g., spontaneous mutation, natural transformation/transduction/transposition) such as those occurring without deliberate human intervention.

"Recombinant DNA construct" refers to a combination of nucleic acid fragments that are not normally found together in nature. Accordingly, a recombinant DNA construct may comprise regulatory sequences and coding sequences that are derived from different sources, or regulatory sequences and coding sequences derived from the same source, but arranged in a manner different than that normally found in nature. The terms "recombinant DNA construct" and "recombinant construct" are used interchangeably herein.

The terms "entry clone" and "entry vector" are used interchangeably herein.

"Regulatory sequences" or "regulatory elements" are used interchangeably and refer to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding sequence, and which influence the transcription, RNA processing or stability, or translation of the associated coding sequence. Regulatory sequences may include, but are not limited to, promoters, translation leader sequences, introns, and polyadenylation recognition sequences. The terms "regulatory sequence" and "regulatory element" are used interchangeably herein.

"Promoter" refers to a nucleic acid fragment capable of controlling transcription of another nucleic acid fragment.

"Promoter functional in a plant" is a promoter capable of controlling transcription in plant cells whether or not its origin is from a plant cell.

"Tissue-specific promoter" and "tissue-preferred promoter" are used interchangeably to refer to a promoter that is expressed predominantly but not necessarily exclusively in one tissue or organ, but that may also be expressed in one specific cell.

"Developmentally regulated promoter" refers to a promoter whose activity is determined by developmental events.

Promoters that cause a gene to be expressed in most cell types at most times are commonly referred to as "constitutive promoters".

Inducible promoters selectively express an operably linked DNA sequence in response to the presence of an endogenous or exogenous stimulus, for example by chemical compounds (chemical inducers) or in response to environmental, hormonal, chemical, and/or developmental signals. Examples of inducible or regulated promoters include, but are not limited to, promoters regulated by light, heat, stress, flooding or drought, pathogens, phytohormones, wounding, or chemicals such as ethanol, jasmonate, salicylic acid, or safeners.

"Enhancer sequences" refer to the sequences that can increase gene expression. These sequences can be located upstream, within introns or downstream of the transcribed region. The transcribed region is comprised of the exons and the intervening introns, from the promoter to the transcription termination region. The enhancement of gene expression can be through various mechanisms which include, but are not limited to, increasing transcriptional efficiency, stabilization of mature mRNA and translational enhancement.

An "intron" is an intervening sequence in a gene that is transcribed into RNA and then excised in the process of generating the mature mRNA. The term is also used for the excised RNA sequences. An "exon" is a portion of the sequence of a gene that is transcribed and is found in the mature messenger RNA derived from the gene, and is not necessarily a part of the sequence that encodes the final gene product.

"Operably linked" refers to the association of nucleic acid fragments in a single fragment so that the function of one is regulated by the other. For example, a promoter is operably linked with a nucleic acid fragment when it is capable of regulating the transcription of that nucleic acid fragment.

"Expression" refers to the production of a functional product. For example, expression of a nucleic acid fragment may refer to transcription of the nucleic acid fragment (e.g., transcription resulting in mRNA or functional RNA) and/or translation of mRNA into a precursor or mature protein.

"Overexpression" refers to the production of a gene product in transgenic organisms that exceeds levels of production in a null segregating (or non-transgenic) organism from the same experiment.

"Phenotype" means the detectable characteristics of a cell or organism.

The term "crossed" or "cross" means the fusion of gametes via pollination to produce progeny (e.g., cells, seeds or plants). The term encompasses both sexual crosses (the pollination of one plant by another) and selfing (self-pollination, e.g., when the pollen and ovule are from the same plant). The term "crossing" refers to the act of fusing gametes via pollination to produce progeny.

A "favorable allele" is the allele at a particular locus that confers, or contributes to, a desirable phenotype, e.g., increased cell wall digestibility, or alternatively, is an allele that allows the identification of plants with decreased cell wall digestibility that can be removed from a breeding program or planting ("counterselection"). A favorable allele of a marker is a marker allele that segregates with the favorable phenotype, or alternatively, segregates with the unfavorable plant phenotype, therefore providing the benefit of identifying plants.

The term “introduced” means providing a nucleic acid (e.g., expression construct) or protein into a cell. Introduced includes reference to the incorporation of a nucleic acid into a eukaryotic or prokaryotic cell where the nucleic acid may be incorporated into the genome of the cell, and includes reference to the transient provision of a nucleic acid or protein to the cell. Introduced includes reference to stable or transient transformation methods, as well as sexually crossing. Thus, “introduced” in the context of inserting a nucleic acid fragment (e.g., a recombinant DNA construct/expression construct) into a cell, means “transfection” or “transformation” or “transduction” and includes reference to the incorporation of a nucleic acid fragment into a eukaryotic or prokaryotic cell where the nucleic acid fragment may be incorporated into the genome of the cell (e.g., chromosome, plasmid, plastid or mitochondrial DNA), converted into an autonomous replicon, or transiently expressed (e.g., transfected mRNA).

“Suppression DNA construct” is a recombinant DNA construct which when transformed or stably integrated into the genome of the plant, results in “silencing” of a target gene in the plant. The target gene may be endogenous or transgenic to the plant. “Silencing,” as used herein with respect to the target gene, refers generally to the suppression of levels of mRNA or protein/enzyme expressed by the target gene, and/or the level of the enzyme activity or protein functionality. The terms “suppression”, “suppressing” and “silencing”, used interchangeably herein, include lowering, reducing, declining, decreasing, inhibiting, eliminating or preventing. “Silencing” or “gene silencing” does not specify mechanism and is inclusive, and not limited to, anti-sense, cosuppression, viral-suppression, hairpin suppression, stem-loop suppression, RNAi-based approaches, and small RNA-based approaches.

Standard recombinant DNA and molecular cloning techniques used herein are well known in the art and are described more fully in Sambrook, J., Fritsch, E. F. and Maniatis, T. *Molecular Cloning: A Laboratory Manual*; Cold Spring Harbor Laboratory Press: Cold Spring Harbor, 1989 (hereinafter “Sambrook”).

“Transcription terminator”, “termination sequences”, or “terminator” refer to DNA sequences located downstream of a protein-coding sequence, including polyadenylation recognition sequences and other sequences encoding regulatory signals capable of affecting mRNA processing or gene expression. The polyadenylation signal is usually characterized by affecting the addition of polyadenylic acid tracts to the 3' end of the mRNA precursor. The use of different 3' non-coding sequences is exemplified by Ingelbrecht, I. L., et al., *Plant Cell* 1:671-680 (1989). A polynucleotide sequence with “terminator activity” refers to a polynucleotide sequence that, when operably linked to the 3' end of a second polynucleotide sequence that is to be expressed, is capable of terminating transcription from the second polynucleotide sequence and facilitating efficient 3' end processing of the messenger RNA resulting in addition of poly A tail. Transcription termination is the process by which RNA synthesis by RNA polymerase is stopped and both the processed messenger RNA and the enzyme are released from the DNA template.

Improper termination of an RNA transcript can affect the stability of the RNA, and hence can affect protein expression. Variability of transgene expression is sometimes attributed to variability of termination efficiency (Bieri et al (2002) *Molecular Breeding* 10: 107-117). As used herein, the terms “bidirectional transcriptional terminator” and “bidirectional terminator” refer to a transcription terminator

sequence that has the capability of terminating transcription in both 5' to 3', and 3' to 5' orientations. A single sequence element that acts as a bidirectional transcriptional terminator can terminate transcription initiated from two convergent promoters.

The present invention encompasses functional fragments and variants of the terminator sequences disclosed herein.

A “functional fragment” herein is defined as any subset of contiguous nucleotides of the terminator sequence disclosed herein, that can perform the same, or substantially similar function as the full length promoter sequence disclosed herein. A “functional fragment” with substantially similar function to the full length terminator disclosed herein refers to a functional fragment that retains the ability to terminate transcription largely to the same level as the full-length terminator sequence. A recombinant construct comprising a heterologous polynucleotide operably linked to a “functional fragment” of the terminator sequence disclosed herein exhibits levels of heterologous polynucleotide expression substantially similar to a recombinant construct comprising a heterologous polynucleotide operably linked to the full-length terminator sequence.

A “variant”, as used herein, is the sequence of the terminator or the sequence of a functional fragment of a terminator containing changes in which one or more nucleotides of the original sequence is deleted, added, and/or substituted, while substantially maintaining terminator function. One or more base pairs can be inserted, deleted, or substituted internally to a terminator, without affecting its activity. Fragments and variants can be obtained via methods such as site-directed mutagenesis and synthetic construction.

These terminator functional fragments may comprise at least 50 contiguous nucleotides, at least 75 contiguous nucleotides, at least 100 contiguous nucleotides, at least 150 contiguous nucleotides, at least 200 contiguous nucleotides, at least 250 contiguous nucleotides, at least 300 contiguous nucleotides, at least 350 contiguous nucleotides, at least 400 contiguous nucleotides, at least 450 contiguous nucleotides, at least 500 contiguous nucleotides, at least 550 contiguous nucleotides, at least 600 contiguous nucleotides, at least 650 contiguous nucleotides, at least 700 contiguous nucleotides, at least 750 contiguous nucleotides or at least 800 contiguous nucleotides of the particular terminator nucleotide sequence disclosed herein. Such fragments may be obtained by use of restriction enzymes to cleave the naturally occurring terminator nucleotide sequences disclosed herein; by synthesizing a nucleotide sequence from the naturally occurring terminator DNA sequence; or may be obtained through the use of PCR technology. See particularly, Mullis et al., *Methods Enzymol.* 155:335-350 (1987), and Higuchi, R. In *PCR Technology: Principles and Applications for DNA Amplifications*; Erlich, H. A., Ed.; Stockton Press Inc.: New York, 1989. Again, variants of these terminator fragments, such as those resulting from site-directed mutagenesis, are encompassed by the compositions of the present invention.

The terms “substantially similar” and “corresponding substantially” as used herein refer to nucleic acid fragments, particularly terminator sequences, wherein changes in one or more nucleotide bases do not substantially alter the ability of the terminator to terminate transcription. These terms also refer to modifications, including deletions and variants, of the nucleic acid sequences of the instant invention by way of deletion or insertion of one or more nucleotides that do not substantially alter the functional properties of the resulting terminator relative to the initial, unmodified terminator. It is

therefore understood, as those skilled in the art will appreciate, that the invention encompasses more than the specific exemplary sequences.

Sequence alignments and percent identity calculations may be determined using a variety of comparison methods designed to detect homologous sequences including, but not limited to, the Megalign® program of the LASERGENE® bioinformatics computing suite (DNASTAR® Inc., Madison, Wis.). Unless stated otherwise, multiple alignment of the sequences provided herein were performed using the Clustal V method of alignment (Higgins and Sharp (1989) CABIOS. 5:151-153) with the default parameters (GAP PENALTY=10, GAP LENGTH PENALTY=10). Default parameters for pairwise alignments and calculation of percent identity of protein sequences using the Clustal V method are KTUPLE=1, GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5. For nucleic acids these parameters are KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4. After alignment of the sequences, using the Clustal V program, it is possible to obtain "percent identity" and "divergence" values by viewing the "sequence distances" table on the same program; unless stated otherwise, percent identities and divergences provided and claimed herein were calculated in this manner.

Alternatively, the Clustal W method of alignment may be used. The Clustal W method of alignment (described by Higgins and Sharp, CABIOS. 5:151-153 (1989); Higgins, D. G. et al., *Comput. Appl. Biosci.* 8:189-191 (1992)) can be found in the MegAlign™ v6.1 program of the LASERGENE® bioinformatics computing suite (DNASTAR® Inc., Madison, Wis.). Default parameters for multiple alignment correspond to GAP PENALTY=10, GAP LENGTH PENALTY=0.2, Delay Divergent Sequences=30%, DNA Transition Weight=0.5, Protein Weight Matrix=Gonnet Series, DNA Weight Matrix=IUB. For pairwise alignments the default parameters are Alignment=Slow-Accurate, Gap Penalty=10.0, Gap Length=0.10, Protein Weight Matrix=Gonnet 250 and DNA Weight Matrix=IUB. After alignment of the sequences using the Clustal W program, it is possible to obtain "percent identity" and "divergence" values by viewing the "sequence distances" table in the same program.

As will be evident to one of skill in the art, any heterologous polynucleotide of interest can be operably linked to the terminator sequences described in the current invention. Examples of polynucleotides of interest that can be operably linked to the terminator sequences described in this invention include, but are not limited to, polynucleotides comprising regulatory elements such as introns, enhancers, promoters, translation leader sequences, protein-coding regions from disease and insect resistance genes, genes conferring nutritional value, genes conferring yield and heterosis increase, genes that confer male and/or female sterility, antifungal, antibacterial or antiviral genes, selectable marker genes, herbicide resistance genes and the like. Likewise, the terminator sequences described in the current invention can be used to terminate transcription of any nucleic acid that controls gene expression. Examples of nucleic acids that could be used to control gene expression include, but are not limited to, antisense oligonucleotides, suppression DNA constructs, or nucleic acids encoding transcription factors.

A recombinant DNA construct (including a suppression DNA construct) of the present invention may comprise at least one regulatory sequence. In an embodiment of the present invention, the regulatory sequences disclosed herein can be operably linked to any other regulatory sequence.

Embodiments include the following:

One embodiment is a polynucleotide comprising: (i) a nucleic acid sequence of at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity, based on the Clustal V method of alignment, when compared to SEQ ID NO:2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (ii) a nucleic acid sequence of at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity, based on the Clustal V method of alignment, when compared to a functional fragment of SEQ ID NO:2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (iii) a full complement of the nucleic acid sequence of (i) or (ii), wherein the polynucleotide acts as a terminator in a plant cell.

One embodiment is an isolated polynucleotide comprising a nucleotide sequence, wherein the nucleotide sequence corresponds to an allele of a terminator described herein.

Recombinant DNA constructs comprising terminator sequences are also provided.

One embodiment is a recombinant construct comprising an isolated polynucleotide comprising (a) a nucleotide sequence as set forth in SEQ ID NO:2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (b) a nucleotide sequence with at least 95% sequence identity to the sequence set forth in SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (c) a functional fragment of either (a) or (b); wherein the isolated polynucleotide functions as a transcriptional terminator in a plant cell. In another embodiment, the isolated polynucleotide is operably linked to the 3' end of a heterologous polynucleotide which is operably linked to a promoter.

One embodiment is a recombinant construct comprising an isolated polynucleotide comprising (a) a nucleotide sequence as set forth in SEQ ID NO:2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (b) a nucleotide sequence with at least 95% sequence identity to the sequence set forth in SEQ ID NO: 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (c) a functional fragment of either (a) or (b); wherein the isolated polynucleotide functions as a bidirectional transcriptional terminator in a plant cell. Another embodiment of the current invention is the recombinant construct wherein the bidirectional transcriptional terminator is operably linked to (a) the 3' end of a first heterologous polynucleotide which is operably linked to a first promoter; and (b) the 3' end of a second heterologous polynucleotide which is operably linked to a second promoter; wherein the first and the second heterologous polynucleotides are transcribed in a convergent manner.

One embodiment is a method of expressing a heterologous polynucleotide in a plant, comprising the steps of (a) introducing into a regenerable plant cell a recombinant construct wherein the recombinant construct comprises an isolated polynucleotide comprising (i) a nucleotide sequence as set forth in SEQ ID NO:2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (ii) a nucleotide sequence with at least 95% sequence identity to the sequence set forth in SEQ ID NO:2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26,

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27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (iii) a functional fragment of either (i) or (ii); wherein the isolated polynucleotide functions as a transcriptional terminator in a plant cell and further wherein the isolated polynucleotide is operably linked to the 3' end of a heterologous polynucleotide which is operably linked to a promoter; (b) regenerating a transgenic plant from the regenerable plant cell of (a), wherein the transgenic plant comprises in its genome the recombinant DNA construct and exhibits expression of the heterologous polynucleotide.

One embodiment is a method of expressing a heterologous polynucleotide in a plant, comprising the steps of (a) introducing into a regenerable plant cell a recombinant construct wherein the recombinant construct comprises an isolated polynucleotide comprising (i) a nucleotide sequence as set forth in SEQ ID NO:2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (ii) a nucleotide sequence with at least 95% sequence identity to the sequence set forth in SEQ ID NO:2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (iii) a functional fragment of either (i) or (ii); wherein the isolated polynucleotide functions as a transcriptional terminator in a plant cell and further wherein the isolated polynucleotide is operably linked to the 3' end of a heterologous polynucleotide which is operably linked to a promoter; (b) regenerating a transgenic plant from the regenerable plant cell of (a), wherein the transgenic plant comprises in its genome the recombinant construct; and (c) obtaining a progeny plant from the transgenic plant of step (b), wherein the progeny plant comprises in its genome the recombinant DNA construct and exhibits expression of the heterologous polynucleotide.

Another embodiment provides for a method of regulating the expression of two heterologous polynucleotides in a plant, comprising the steps of: (a) introducing into a regenerable plant cell a recombinant construct, wherein the recombinant construct comprises an isolated polynucleotide comprising (i) a nucleotide sequence as set forth in SEQ ID NO:2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (ii) a nucleotide sequence with at least 95% sequence identity to the sequence set forth in SEQ ID NO:2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (iii) a functional fragment of either (i) or (ii); wherein the isolated polynucleotide functions as a bidirectional transcriptional terminator in a plant cell and further wherein the bidirectional transcriptional terminator is operably linked to the 3' end of a first heterologous polynucleotide which is operably linked to a first promoter and the 3' end of a second heterologous polynucleotide which is operably linked to a second promoter; wherein the first and the second heterologous polynucleotides are transcribed in a convergent manner; (b) regenerating a transgenic plant from the regenerable plant cell of (a), wherein the transgenic plant comprises in its genome the recombinant DNA construct and exhibits expression of both the first heterologous polynucleotide and the second heterologous polynucleotide.

Another embodiment provides for a method of regulating the expression of two heterologous polynucleotides in a plant, comprising the steps of: (a) introducing into a regenerable plant cell a recombinant construct, wherein the recombinant construct comprises an isolated polynucleotide comprising (i) a nucleotide sequence as set forth in SEQ ID

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NO:2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (ii) a nucleotide sequence with at least 95% sequence identity to the sequence set forth in SEQ ID NO:2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 129-161 or 162; or (iii) a functional fragment of either (i) or (ii); wherein the isolated polynucleotide functions as a bidirectional transcriptional terminator in a plant cell and further wherein the bidirectional transcriptional terminator is operably linked to the 3' end of a first heterologous polynucleotide which is operably linked to a first promoter and the 3' end of a second heterologous polynucleotide which is operably linked to a second promoter; wherein the first and the second heterologous polynucleotides are transcribed in a convergent manner; (b) regenerating a transgenic plant from the regenerable plant cell of (a), wherein the transgenic plant comprises in its genome the recombinant construct; and (c) obtaining a progeny plant from the transgenic plant of step (b), wherein the progeny plant comprises in its genome the recombinant DNA construct and exhibits expression of both the first heterologous polynucleotide and the second heterologous polynucleotide.

Another embodiment is a vector, cell, microorganism, plant, or seed comprising a recombinant DNA construct comprising a terminator sequence described herein.

Another embodiment encompasses regenerated, mature and fertile transgenic plants comprising the recombinant DNA constructs described above, transgenic seeds produced therefrom, T1 and subsequent generations. The transgenic plant cells, tissues, plants, and seeds may comprise at least one recombinant DNA construct of interest.

In one embodiment, the plant comprising the terminator sequences described in the present invention is selected from the group consisting of: *Arabidopsis*, maize, soybean, sunflower, *sorghum*, canola, mustard, wheat, alfalfa, cotton, rice, barley, millet, sugar cane and switchgrass.

In one embodiment, the plant comprising the terminator sequences described in the present invention is a monocotyledonous plant. In another embodiment, the plant comprising the terminator sequences described in the present invention is a rice plant.

EXAMPLES

The present invention is further illustrated in the following Examples, in which parts and percentages are by weight and degrees are Celsius, unless otherwise stated. It should be understood that these examples, while indicating embodiments of the invention, are given by way of illustration only. From the above discussion and these Examples, one skilled in the art can ascertain the essential characteristics of this invention, and without departing from the spirit and scope thereof, can make various changes and modifications of the invention to adapt it to various usages and conditions. Furthermore, various modifications of the invention in addition to those shown and described herein will be apparent to those skilled in the art from the foregoing description. Such modifications are also intended to fall within the scope of the appended claims.

Example 1

Identification of Novel Terminator Sequences

The computational strategy to identify convergent gene pairs with high co-expression frequency involved the following steps:

Analysis of *Arabidopsis* and rice genomes for identification of convergent gene pairs.

Analysis of their transcriptomes for identification of convergent genes with high expression.

Identification of samples in which both genes from a convergent pair showed high expression.

Identification of Candidate *Arabidopsis* Terminators:

For identification of convergent gene pairs, the *Arabidopsis* genome GFF (General File Format) file was analyzed to identify adjacent gene models in the convergent orientation with an intergenic distance ranging from 20 bp-1000 bp between them. A total of 3535 convergent gene pairs were identified and their nucleotide sequences were then retrieved. For the transcriptomics analysis, publicly available Affymetrix® array data from the Nottingham *Arabidopsis* Stock Center (NASC's international Affymetrix® service) were downloaded along with their metadata including sample annotations. Samples were scaled to a mean signal value of 100 and those with poor quality and no metadata were discarded. Finally, ~3000 samples were selected for this analysis. For each gene in the shortlisted convergent gene pairs, probes on the Affymetrix® array were identified and only those probes that uniquely mapped to the selected genes were selected for further analysis. Z-scores for each of the samples were calculated using median-centering; if the z-score of a probe in a given sample was greater than two, it was considered as having high expression in that sample. Finally gene pairs were shortlisted based on the criteria that both members of the gene pairs showed high expression in at least one sample. From this analysis, 89 such pairs were identified and they were further shortlisted to 24 gene pairs that showed high co-expression in at least 10 samples. Gene annotation and tissue level expression pattern were also included as additional data for the selected gene pairs. The *Arabidopsis* transcriptome tiling array (Salk Institute Genomic Analysis Laboratory; Yamada et al., 2003, Science, 302 (5646): 842-846) was used to independently evaluate the co-expression data of the 24 gene pairs. Based on a combination of the number of common samples in which a gene pair was showing co-expression and correlation between the expression analyses and the tiling array, 7 gene pairs were finally selected for experimental analysis. The nucleotide sequence between stop codons of each gene pair including the 3'UTRs of both genes and the intergenic region was identified and cloned for testing.

Identification of Candidate Rice Terminators:

A similar approach was used for identifying novel terminators from rice. The entire rice genome was obtained from the MSU Rice Genome Annotation Project Database and was analyzed to identify 2892 convergent gene pairs with an intergenic distance range of 20-1000 bp. Public Affymetrix® microarray data was downloaded from the NCBI expression repository, Gene Expression Omnibus, and good quality samples were selected for analysis. For calculating high expression, the 95th percentile value of signal intensity in each sample was calculated, i.e. only 5% of the genes on the

entire chip exhibited signal intensity values greater than this threshold for the given sample. For each gene pair the samples in which both genes were above the 95th percentile were identified. From this analysis, 82 gene pairs were identified as showing high co-expression in at least one sample; of these, gene pairs showed high co-expression in at least 10 samples and were shortlisted for further experimental analysis. Out of these, the top 10 candidate pairs based on the number of samples in which the gene pairs showed co-expression and presence of a valid gene model were selected for testing. The nucleotide sequence between stop codons of each gene pair including the 3'UTRs of both genes and the intergenic region was identified and used for testing as transcription terminators in plant cells.

Example 2

Amplification and Cloning of *Arabidopsis* and Rice Terminator Sequences

We constructed a terminator test vector (TTV) (PHP49597; FIG. 1; SEQ ID NO:1) carrying GUS (β -glucuronidase) reporter gene driven by the maize ubiquitin promoter using standard molecular biology techniques (Sambrook et al.). A promoterless Ds-RED coding sequence was included downstream of the GUS gene for measurement of read-through transcription. The Ds-Red sequence was followed by a PinII terminator to enable termination and polyadenylation of all read-through transcripts, so we could detect them by reverse-transcription-PCR (RT-PCR) using oligo-dT primer. The Terminator test vector also carried a monocot-optimized phosphinothricin acetyltransferase (MOPAT) gene as a plant selectable marker.

Genomic DNA was isolated from *Arabidopsis thaliana* and *Oryza sativa* leaf tissue using the QIAGEN® DNEASY® Plant Maxi Kit (QIAGEN Inc.) according to the manufacturer's instructions. Candidate terminator sequences were amplified from genomic DNA with PHUSION® DNA polymerase (New England Biolabs Inc.), using the primer sequences listed in Table 2. T1 to T14 sequences (SEQ ID NOS:2-15) were amplified from *Arabidopsis thaliana* and T15 to T34 (SEQ ID NOS:16-35) were amplified from *Oryza sativa* L. var. Nipponbare. T1 to T7 (SEQ ID NOS:2-8) are complementary to sequences T8 to T14 (SEQ ID NOS:9-15) and T15 to T24 (SEQ ID NOS:16-25) are complementary to T25 to T34 (SEQ ID NOS:26-35) (Table 3). The resulting DNA fragments were cloned into the terminator test vector at Acc65I restriction site using In-FUSION™ cloning (Clontech Inc.) and sequenced completely. As a positive control we cloned the potato PINII terminator (SEQ ID NO:36; Keil et al. (1986) *Nucleic Acids Res.* 14:5641-5650) at the same location as the test terminators to produce the plasmid PHP49598.

All constructs were transformed into *Agrobacterium* (LBA4404/pSB1) and selected on spectinomycin and tetracycline. Integrity of the plasmids in 15 *Agrobacterium* was confirmed by restriction digestion analysis from retransformed *E. coli*.

TABLE 2

Primer ID	Terminator	Amplicon Size (bp)	Construct
TETO-1028F (SEQ ID NO: 37)	T1	557	PHP49622
TETO-1029R (SEQ ID NO: 38)	(SEQ ID NO: 2)		
TETO-1207F (SEQ ID NO: 39)	T2	573	PHP51066
TETO-1208R (SEQ ID NO: 40)	(SEQ ID NO: 3)		

TABLE 2-continued

Primer ID	Terminator	Amplicon Size (bp)	Construct
TETO-1209F (SEQ ID NO: 41)	T3	633	PHP51067
TETO-1210R (SEQ ID NO: 42)	(SEQ ID NO: 4)		
TETO-1211F (SEQ ID NO: 43)	T4	639	PHP51068
TETO-1212R (SEQ ID NO: 44)	(SEQ ID NO: 5)		
TETO-1213F (SEQ ID NO: 45)	T5	685	PHP51069
TETO-1214R (SEQ ID NO: 46)	(SEQ ID NO: 6)		
TETO-1215 F (SEQ ID NO: 47)	T6	411	PHP51070
TETO-1216R (SEQ ID NO: 48)	(SEQ ID NO: T7)		
TETO-1030F (SEQ ID NO: 49)	T7	457	PHP49623
TETO-1031R (SEQ ID NO: 50)	(SEQ ID NO: 8)		
TETO-1032F (SEQ ID NO: 51)	T8	557	PHP49624
TETO-1033R (SEQ ID NO: 52)	(SEQ ID NO: 9)		
TETO-1034F (SEQ ID NO: 53)	T9	573	PHP49625
TETO-1035R (SEQ ID NO: 54)	(SEQ ID NO: 10)		
TETO-1217F (SEQ ID NO: 55)	T10	633	PHP51071
TETO-1218R (SEQ ID NO: 56)	(SEQ ID NO: 11)		
TETO-1219F (SEQ ID NO: 57)	T11	639	PHP51072
TETO-1220R (SEQ ID NO: 58)	(SEQ ID NO: 12)		
TETO-1036F (SEQ ID NO: 59)	T12	685	PHP49626
TETO-1037R (SEQ ID NO: 60)	(SEQ ID NO: 13)		
TETO-1038F (SEQ ID NO: 61)	T13	411	PHP49627
TETO-1039R (SEQ ID NO: 62)	(SEQ ID NO: 14)		
TETO-1040F (SEQ ID NO: 63)	T14	457	PHP49628
TETO-1041R (SEQ ID NO: 64)	(SEQ ID NO: 15)		
TETO-986 F (SEQ ID NO: 65)	T15	782	PHP51073
TETO-987 R (SEQ ID NO: 66)	(SEQ ID NO: 16)		
TETO-988 F (SEQ ID NO: 67)	T16	825	PHP51074
TETO-989 R (SEQ ID NO: 68)	(SEQ ID NO: 17)		
TETO-990 F (SEQ ID NO: 69)	T17	776	PHP51075
TETO-991 R (SEQ ID NO: 70)	(SEQ ID NO: 18)		
TETO-992 F (SEQ ID NO: 71)	T18	881	PHP51076
TETO-993 R (SEQ ID NO: 72)	(SEQ ID NO: 19)		
TETO-994 F (SEQ ID NO: 73)	T19	772	PHP51077
TETO-995 R (SEQ ID NO: 74)	(SEQ ID NO: 20)		
TETO-996 F (SEQ ID NO: 75)	T20	827	PHP51078
TETO-997 R (SEQ ID NO: 76)	(SEQ ID NO: 21)		
TETO-998 F (SEQ ID NO: 77)	T21	770	PHP51079
TETO-999 R (SEQ ID NO: 78)	(SEQ ID NO: 22)		
TETO-1000 F (SEQ ID NO: 79)	T22	814	PHP51080
TETO-1001 R (SEQ ID NO: 80)	(SEQ ID NO: 23)		
TETO-1002 F (SEQ ID NO: 81)	T23	834	PHP51081
TETO-1003 R (SEQ ID NO: 82)	(SEQ ID NO: 24)		
TETO-1004 F (SEQ ID NO: 83)	T24	740	PHP51082
TETO-1005 R (SEQ ID NO: 84)	(SEQ ID NO: 25)		
TETO-1006 F (SEQ ID NO: 85)	T25	782	PHP51083
TETO-1007 R (SEQ ID NO: 86)	(SEQ ID NO: 26)		
TETO-1008 F (SEQ ID NO: 87)	T26	825	PHP51084
TETO-1009 R (SEQ ID NO: 88)	(SEQ ID NO: 27)		
TETO-1010 F (SEQ ID NO: 89)	T27	776	PHP51085
TETO-1011 R (SEQ ID NO: 90)	(SEQ ID NO: 28)		
TETO-1012 F (SEQ ID NO: 91)	T28	881	PHP51086
TETO-1013 R (SEQ ID NO: 92)	(SEQ ID NO: 29)		
TETO-1014 F (SEQ ID NO: 93)	T29	772	
TETO-1015 R (SEQ ID NO: 94)	(SEQ ID NO: 30)		
TETO-1016 F (SEQ ID NO: 95)	T30	827	PHP51088
TETO-1017 R (SEQ ID NO: 96)	(SEQ ID NO: 31)		
TETO-1018 F (SEQ ID NO: 97)	T31	770	PHP51089
TETO-1019 R (SEQ ID NO: 98)	(SEQ ID NO: 32)		
TETO-1020 F (SEQ ID NO: 99)	T32	814	
TETO-1021 R (SEQ ID NO: 100)	(SEQ ID NO: 33)		
TETO-1022 F (SEQ ID NO: 101)	T33	834	
TETO-1023 R (SEQ ID NO: 102)	(SEQ ID NO: 34)		
TETO-1024 F (SEQ ID NO: 103)	T34	740	PHP51092
TETO-1025 R (SEQ ID NO: 104)	(SEQ ID NO: 35)		
TETO-420 F (SEQ ID NO: 105)	Pin II	330	PHP49598
TETO-421 R (SEQ ID NO: 106)	(SEQ ID NO: 36)		

TABLE 3

Terminator Sequences in Inverse Orientations		
Orientation 1	Orientation 2	Species
T1 (SEQ ID NO: 2)	T8 (SEQ ID NO: 9)	<i>Arabidopsis thaliana</i>
T2 (SEQ ID NO: 3)	T9 (SEQ ID NO: 10)	<i>Arabidopsis thaliana</i>
T3 (SEQ ID NO: 4)	T10 (SEQ ID NO: 11)	<i>Arabidopsis thaliana</i>
T4 (SEQ ID NO: 5)	T11 (SEQ ID NO: 12)	<i>Arabidopsis thaliana</i>
T5 (SEQ ID NO: 6)	T12 (SEQ ID NO: 13)	<i>Arabidopsis thaliana</i>
T6 (SEQ ID NO: 7)	T13 (SEQ ID NO: 14)	<i>Arabidopsis thaliana</i>
T7 (SEQ ID NO: 8)	T14 (SEQ ID NO: 15)	<i>Arabidopsis thaliana</i>
T15 (SEQ ID NO: 16)	T25 (SEQ ID NO: 26)	<i>Oryza sativa</i>
T16 (SEQ ID NO: 17)	T26 (SEQ ID NO: 27)	<i>Oryza sativa</i>
T17 (SEQ ID NO: 18)	T27 (SEQ ID NO: 28)	<i>Oryza sativa</i>
T18 (SEQ ID NO: 19)	T28 (SEQ ID NO: 29)	<i>Oryza sativa</i>
T19 (SEQ ID NO: 20)	T29 (SEQ ID NO: 30)	<i>Oryza sativa</i>
T20 (SEQ ID NO: 21)	T30 (SEQ ID NO: 31)	<i>Oryza sativa</i>
T21 (SEQ ID NO: 22)	T31 (SEQ ID NO: 32)	<i>Oryza sativa</i>
T22 (SEQ ID NO: 23)	T32 (SEQ ID NO: 33)	<i>Oryza sativa</i>
T23 (SEQ ID NO: 24)	T33 (SEQ ID NO: 34)	<i>Oryza sativa</i>
T24 (SEQ ID NO: 25)	T34 (SEQ ID NO: 35)	<i>Oryza sativa</i>

Example 3

Rice Transformation with Candidate Terminator Sequences

The candidate terminator sequences T1-T34 (SEQ ID NOS:2-35) can be transformed into rice plants by *Agrobacterium*-mediated transformation by using *Agrobacterium* containing the constructs described in Table 2.

Transformation and Regeneration of Rice Callus Via *Agrobacterium* Infection:

O. sativa spp. *japonica* rice var. Nipponbare seeds are sterilized in absolute ethanol for 10 minutes then washed 3 times with water and incubated in 70% Sodium hypochlorite [Fisher Scientific-27908] for 30 minutes. The seeds are then washed 5 times with water and dried completely. The dried seeds are inoculated into NB-CL media [CHU(N6) basal salts (PhytoTechnology-C416) 4 g/l; Eriksson's vitamin solution (1000× PhytoTechnology-E330) 1 ml/l; Thiamine HCl (Sigma-T4625) 0.5 mg/l; 2,4-Dichloro phenoxyacetic acid (Sigma-D7299) 2.5 mg/l; BAP (Sigma-B3408) 0.1 mg/l; L-Proline (PhytoTechnology-P698) 2.5 g/l; Casein acid hydrolysate vitamin free (Sigma-C7970) 0.3 g/l; Myo-inositol (Sigma-I3011) 0.1 g/l; Sucrose (Sigma-S5390) 30 g/l; GELRITE® (Sigma-G1101.5000) 3 g/l; pH 5.8) and kept at 28° C. in dark for callus proliferation.

A single *Agrobacterium* colony containing a desired insert with the candidate terminator sequences (SEQ ID NOS:2-35) or PINII terminator (SEQ ID NO:36) from a freshly streaked plate can be inoculated in YEB liquid media [Yeast extract (BD Difco-212750) 1 g/l; Peptone (BD Difco-211677) 5 g/l; Beef extract (Amresco-0114) 5 g/l; Sucrose (Sigma-S5390) 5 g/l; Magnesium Sulfate (Sigma-M8150) 0.3 g/l at pH-7.0] supplemented with Tetracycline (Sigma-T3383) 5 mg/l, Rifamycin 10 mg/l and Spectinomycin (Sigma-S650) 50 mg/l. The cultures are grown overnight at 28° C. in dark with continuous shaking at 220 rpm. The following day the cultures are adjusted to 0.5 Absorbance at 550 nm in PHI-A(CHU(N6) basal salts (PhytoTechnology-C416) 4 g/l; Eriksson's vitamin solution (1000× PhytoTechnology-E330) 1 ml/l; Thiamine HCl (Sigma-T4625) 0.5 mg/l; 2,4-Dichloro phenoxyacetic acid (Sigma-D7299) 2.5 mg/l; L-Proline (PhytoTechnology-P698) 0.69 mg/l; Sucrose (Sigma-S5390) 68.5 g/l; Glucose-36 g/l (Sigma-G8270); pH 5.8); media supplemented with 200 µM Aceto-

syringone (Sigma-D134406) and incubated for 1 hour at 28° C. with continuous shaking at 220 rpm.

17-21 day old proliferating calli are transferred to a sterile culture flask and *Agrobacterium* solution prepared as described above was added to the flask. The suspension is incubated for 20 minutes with gentle shaking every 2 minutes. The *Agrobacterium* suspension is decanted carefully and the calli are placed on WHATMAN® filter paper No-4. The calli are immediately transferred to NB-CC medium [NB-CL supplemented with 200 µM Acetosyringone (Sigma-D134406) and incubated at 21° C. for 72 hrs. Culture Termination and Selection:

The co-cultivated calli are placed in a dry, sterile, culture flask and washed with 1 liter of sterile distilled water containing Cefotaxime (Duchefa-CO111.0025) 0.250 g/l and Carbenicillin (Sigma-C0109.0025) 0.4 g/l. The washes are repeated 4 times or until the solution appeared clear. The water is decanted carefully and the calli are placed on WHATMAN® filter paper No-4 and dried for 30 minutes at room temperature. The dried calli are transferred to NB-RS medium [NB-CL supplemented with Cefotaxime (Duchefa-CO111.0025) 0.25 g/l; and Carbenicillin (Sigma-C0109.0025) 0.4 g/l and incubated at 28° C. for 4 days.

The calli are then transferred to NB-SB media [NB-RS supplemented with Bialaphos (Meiji Seika K.K., Tokyo, Japan) 5 mg/l and incubated at 28° C. and subcultured into fresh medium every 14 days. After 40-45 days on selection, proliferating, Bialaphos-resistant callus events are easily observable.

Regeneration of Stably Transformed Rice Plants from Transformed Rice Calli:

Transformed callus events are transferred to NB-RG media [CHU(N6) basal salts (PhytoTechnology-C416) 4 g/l; N6 vitamins 1000×1 ml {Glycine (Sigma-47126) 2 g/l; Thiamine HCl (Sigma-T4625) 1 g/l; acid; Kinetin (Sigma-K0753) 0.5 mg/l; Casein acid hydrolysate vitamin free (Sigma-C7970) 0.5 g/l; Sucrose (Sigma-S5390) 20 g/l; Sorbitol (Sigma-S1876) 30 g/l, pH was adjusted to 5.8 and 4 g/l GELRITE® (Sigma-G1101.5000) was added. Post-sterilization 0.1 ml/l of CuSo4 (100 mM concentration, Sigma-C8027) and 100 ml/l 10×AA Amino acids pH free {Glycine (Sigma-G7126) 75 mg/l; L-Aspartic acid (Sigma-A9256) 2.66 g/l; L-Arginine (Sigma-A5006) 1.74 g/l; L-Glutamine (Sigma-G3126) 8.76 g/l) and incubated at 32° C. in light. After 15-20 days, regenerating plantlets can be transferred to magenta boxes or tubes containing NB-RT media [MS basal salts (PhytoTechnology-M524) 4.33 g/L; B5 vitamins 1 ml/l from 1000× stock {Nicotinic acid (Sigma-G7126) 1 g/l, Thiamine HCl (Sigma-T4625) 10 g/l); Myo-inositol (Sigma-I3011) 0.1 g/l; Sucrose (Sigma-S5390) 30 g/l; and IBA (Sigma-I5386) 0.2 mg/l; pH adjusted to 5.8]. Rooted plants obtained after 10-15 days can be hardened in liquid Y media [1.25 ml each of stocks A-F and water sufficient to make 1000 ml. Composition of individual stock solutions: Stock (A) Ammonium Nitrate (HIMEDIA-RM5657) 9.14 g/l, (B) Sodium hydrogen Phosphate (HIMEDIA-58282) 4.03 g, (C) Potassium Sulphate (HIMEDIA-29658-4B) 7.14 g, (D) Calcium Chloride (HIMEDIA-C5080) 8.86 g, (E) Magnesium Sulphate (HIMEDIA-RM683) 3.24 g, (F) (Trace elements) Magnesium chloride tetra hydrate (HIMEDIA-10149) 15 mg, Ammonium Molybdate (HIMEDIA-271974B) 6.74 mg/l, Boric acid (Sigma-136768) 9.34 g/l, Zinc sulphate heptahydrate (Himedia-RM695) 0.35 mg/l, Copper Sulphate heptahydrate (HIMEDIA-C8027) 0.31 mg/l, Ferric chloride hexahydrate (Sigma-236489) 0.77 mg/l, Citric acid monohydrate (HIMEDIA-C4540) 0.119 g/l] at 28° C. for 10-15 days before

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transferring to greenhouse. Leaf samples are collected for histochemical GUS staining with 5-bromo-4-chloro-3-indolyl- β -D-glucuronide (X-Gluc), using standard protocols (Janssen and Gardner, *Plant Mol. Biol.* (1989)14:61-72).

Transgenic plants are analyzed for copy number by southern blotting using standard procedure. All single copy events are transferred to individual pots and further analysis is performed only on these. For all the analysis leaf material from three independent one month old single copy T₀ events are taken.

Example 4

Rice Transformation with Candidate Rice Terminator Sequences

The candidate rice terminator sequences (SEQ ID NOS: 16-35) were tested for their efficacy to function as transcription terminators by transformation into rice plants by *Agrobacterium*-mediated transformation as described in Example 3. The constructs for generating the transgenic plants are described in Table 2.

Example 5A

Assays for Testing of Candidate Rice Terminator Sequences in Stably Transformed Rice Tissues

Reverse Transcriptase-PCR (RT-PCR) as well as quantitative RT-PCR (qRT-PCR) can be done from stably transformed rice plant tissues, to test the ability of candidate terminator sequences to stop transcription (i.e., prevent read-through transcription). QRT-PCR is the preferred way of testing the candidate terminator sequences. SEQ ID NOS:100-113 can be used for doing RT-PCR to determine read-through transcription from the candidate terminator sequences.

Histochemical and Fluorometric GUS Analysis:

Leaf samples from each construct can be used for histochemical GUS staining with 5-bromo-4-chloro-3-indolyl- β -D-glucuronide (X-Gluc), using standard protocols (Janssen and Gardner, *Plant Mol. Biol.* (1989)14:61-72) and three pools of leaf samples from three independent single copy events per construct may be used for quantitative MUG assay using standard protocols (Jefferson, R. A., *Nature*. 342, 837-8 (1989); Jefferson, R. A., Kavanagh, T. A. & Bevan, M. W. *EMBO J.* 6, 3901-3907 (1987).

Example 5B

Testing Of Candidate Rice Terminator Sequences in Stably Transformed Rice Tissues

GUS Fluorometric Analysis of Rice Tissues Stably Transformed with Candidate Rice Terminator Sequences:

When compared with TTV, we observed higher GUS protein expression with PINII as well as test sequences T15, T16, T17, T18, T19, T20, T22, T23, T24, T25, T26, T27, T28, T29, T30, T31, T32, T33 and T34 (SEQ ID NOS:16-21, 23-35 respectively). However, T21 (SEQ ID NO:22) had the same level of GUS expression as TTV (FIG. 2).

Quantitative Reverse Transcriptase PCR (qRT-PCR) to Determine Read Through Transcription Through Test Terminator:

qRT-PCR was performed with leaf tissue from stable transformants. The stably transformed plants were tested for the presence of read-through transcript that had passed

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through the PINII terminator and the test terminators. To assess presence of products that would indicate that transcription was continuing past the terminator, amplification was targeted downstream of the PINII or test terminators, in the filler sequence (Ds Red). The read-through can be measured by the ratio of DsRed to GUS.

At least three pools of leaf samples from three independent single copy events were tested for each construct. The primers and probes are listed in Table 4.

TABLE 4

Probe (SEQ ID NO)	Primer Sequence (SEQ ID NO)	Fluor	qPCR Assay Type
GUS (SEQ ID NO: 114)	GUSFwd primer (SEQ ID NO: 115) GUS Rev primer (SEQ ID NO: 116)	FAM	TAQMAN ®
DsRed (SEQ ID NO: 117)	DsRed Fwd primer (SEQ ID NO: 118) DsRed Rev primer (SEQ ID NO: 119)	FAM	TAQMAN ®

Read-through Transcription from Candidate Rice Sequences:

As expected, read-through transcription was observed in the terminator test vector (TTV (SEQ ID NO:1; PHP49597) as depicted in FIG. 3. The PHP49598 construct with the PINII terminator (SEQ ID NO:36) reduced the transcription read-through significantly (FIG. 3). Candidate terminator sequences from *Oryza sativa* T15, T16, T17, T18, T20, T23, T25, T26, T27, T28, T30 and T32 (SEQ ID NOS:16-19, 21, 24, 26-29, 31 and 33 respectively) were able to terminate transcription efficiently as evidenced by the very low level of read-through transcripts (FIG. 3), comparable to the PINII terminator. As can be seen from Table 3, T14 and T25 (SEQ ID NOS:15 and 26 respectively); T16 and T26 (SEQ ID NOS:17 and 27 respectively); T17 and T27 (SEQ ID NOS:18 and 28 respectively); T18 and T28 (SEQ ID NOS:19 and 29 respectively); T20 and T30 (SEQ ID NOS:21 and 31 respectively) are the same nucleotide sequence but cloned in inverted orientation. Hence these can function as bi-directional terminator sequences. Candidate terminator sequences T19, T21 and T24 (SEQ ID NOS:20, 22 and 25 respectively) also showed less read through compared to the TTV terminator (FIG. 3)

Example 6

Rice Transformation with Candidate *Arabidopsis* Terminator Sequences

The candidate *Arabidopsis* terminator sequences (SEQ ID NOS:2-15) can be transformed into rice plants by *Agrobacterium*-mediated transformation as described in Example 3, to test their efficacy to function as transcription terminators. The constructs are described in Table 2.

Example 7

Testing of Candidate *Arabidopsis* Terminator Sequences in Stably Transformed Rice Tissues

QRT-PCR was done from stably transformed rice plant tissues, to test the ability of candidate *Arabidopsis* terminator sequences (SEQ ID NOS:2-15) to stop transcription (that is prevent transcription read-through transcription) and to

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compare GUS expression as compared to that with PINII terminator, as described in Example 5.

Read-through Transcription from Candidate *Arabidopsis* Sequences:

Terminator sequences from *Arabidopsis thaliana* T7, T9, T10, T12, T13, (SEQ ID NOS:8, 10, 11, 13 and 14 respectively) were able to terminate transcription efficiently as evidenced by the very low level of read-through transcripts (FIG. 3), comparable to the PINII terminator. Terminator sequences T4, T5 and T6 also showed less read through compared to the TTV terminator (FIG. 3).

GUS Fluorometric Analysis of Rice Tissues Stably Transformed with Candidate *Arabidopsis* Terminator Sequences

When compared with TTV, we observed higher GUS protein expression with PINII as well as test sequences T1, T3, T4, T6, T7, T8, T9, T10, T12, T13, and T14 (SEQ ID NOS:2, 4, 5, 7, 8, 10, 13, 14 and 15 respectively). However, T2, T5 and T11 (SEQ ID NOS:3, 6 and 12) had the same level of GUS expression as TTV (FIG. 2).

Example 8

Identification of Shorter Terminator Sequences

Each candidate bidirectional transcriptional terminator might be comprised of two convergent constituent transcriptional terminators. To identify these constituent terminator sequences, polyadenylation sites were mapped as described below.

Mapping Polyadenylation Sites in Terminator Sequences

RNA was extracted from leaf tissue of T₀ single copy event for each construct. cDNA was synthesized using SuperScript® III First-Strand Synthesis System from INVITROGEN™ using adapter ligated oligodT primer (TETO-1527; SEQ ID NO:126) and PCR was performed with GUS internal primer (TETO-1172; SEQ ID NO:127) and adapter reverse primers (TETO-1528; SEQ ID NO:128). The amplified products were cloned using Zero Blunt® TOPO® PCR cloning kit (INVITROGEN™). For each terminator, 40 clones were sequenced. The sequence analysis revealed multiple polyA sites. The sequences of the shorter terminator sequences corresponding to the longer terminator sequences are given in SEQ ID NOS:129-162 and in Table 6.

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TABLE 5

Primer Name	SEQ ID NO	Primer ID
TETO-1527	126	Adap-dT
TETO-1172	127	GUS iF
TETO-1528	128	Adap R

TABLE 6

Orientation 1	Orientation 2	Species	5' terminator	3' terminator
T1 (SEQ ID NO: 2)	T8 (SEQ ID NO: 9)	<i>Arabidopsis thaliana</i>	T1s (SEQ ID NO: 129)	T8s (SEQ ID NO: 136)
T2 (SEQ ID NO: 3)	T9 (SEQ ID NO: 10)	<i>Arabidopsis thaliana</i>	T2s (SEQ ID NO: 130)	T9s (SEQ ID NO: 137)
T3 (SEQ ID NO: 4)	T10 (SEQ ID NO: 11)	<i>Arabidopsis thaliana</i>	T3s (SEQ ID NO: 131)	T10s (SEQ ID NO: 138)
T4 (SEQ ID NO: 5)	T11 (SEQ ID NO: 12)	<i>Arabidopsis thaliana</i>	T4s (SEQ ID NO: 132)	T11s (SEQ ID NO: 139)
T5 (SEQ ID NO: 6)	T12 (SEQ ID NO: 13)	<i>Arabidopsis thaliana</i>	T5s (SEQ ID NO: 133)	T12s (SEQ ID NO: 140)
T6 (SEQ ID NO: 7)	T13 (SEQ ID NO: 14)	<i>Arabidopsis thaliana</i>	T6s (SEQ ID NO: 134)	T13s (SEQ ID NO: 141)
T7 (SEQ ID NO: 8)	T14 (SEQ ID NO: 15)	<i>Arabidopsis thaliana</i>	T7s (SEQ ID NO: 135)	T14s (SEQ ID NO: 142)
T15 (SEQ ID NO: 16)	T25 (SEQ ID NO: 26)	<i>Oryza sativa</i>	T15s (SEQ ID NO: 143)	T25s (SEQ ID NO: 153)
T16 (SEQ ID NO: 17)	T26 (SEQ ID NO: 27)	<i>Oryza sativa</i>	T16s (SEQ ID NO: 144)	T26s (SEQ ID NO: 154)
T17 (SEQ ID NO: 18)	T27 (SEQ ID NO: 28)	<i>Oryza sativa</i>	T17s (SEQ ID NO: 145)	T27s (SEQ ID NO: 155)
T18 (SEQ ID NO: 19)	T28 (SEQ ID NO: 29)	<i>Oryza sativa</i>	T18s (SEQ ID NO: 146)	T28s (SEQ ID NO: 156)
T19 (SEQ ID NO: 20)	T29 (SEQ ID NO: 30)	<i>Oryza sativa</i>	T19s (SEQ ID NO: 147)	T29s (SEQ ID NO: 157)
T20 (SEQ ID NO: 21)	T30 (SEQ ID NO: 31)	<i>Oryza sativa</i>	T20s (SEQ ID NO: 148)	T30s (SEQ ID NO: 158)
T21 (SEQ ID NO: 22)	T31 (SEQ ID NO: 32)	<i>Oryza sativa</i>	T21s (SEQ ID NO: 149)	T31s (SEQ ID NO: 159)
T22 (SEQ ID NO: 23)	T32 (SEQ ID NO: 33)	<i>Oryza sativa</i>	T22s (SEQ ID NO: 150)	T32s (SEQ ID NO: 160)
T23 (SEQ ID NO: 24)	T33 (SEQ ID NO: 34)	<i>Oryza sativa</i>	T23s (SEQ ID NO: 151)	T33s (SEQ ID NO: 161)
T24 (SEQ ID NO: 25)	T34 (SEQ ID NO: 35)	<i>Oryza sativa</i>	T24s (SEQ ID NO: 152)	T34s (SEQ ID NO: 162)

Example 9

Testing of Truncated Terminator Sequences in Stably Transformed *Arabidopsis* Tissue

Based on the polyA data obtained as described in Example 8, the terminators can be truncated and cloned as described in the Example 2.

The truncated terminators (SEQ ID NOS:129-162) can be transformed into *Arabidopsis thaliana* by floral dip method (Kim J Y et al (2003) Development 130: 4351-4362). QRT-PCR and MUG analysis can be done to test the efficiency of the truncated terminators in T1 *Arabidopsis* leaf tissue as described in Example 5.

SEQUENCE LISTING

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<211> LENGTH: 16437

<212> TYPE: DNA

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Vector sequence

<400> SEQUENCE: 1

-continued

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caagcactcc cgaggggaac cctgtggttg gcatgcacat acaaatggac gaacggataa 16380
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<210> SEQ ID NO 2

<211> LENGTH: 557

<212> TYPE: DNA

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<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 2

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aatttcggg atttttagat atctgattct gttgcgaagt ttttttatcc ttattagtgt	120
ctgttgagt tagattgctt ggcgagtagc ccacaataaa gaaataaaaa tggcgaatct	180
ttagctttat ttactctgtt ttcatcgaa acagattcag taatatatac tctgtttttt	240
catcttacat ttgtttgcaa aaccgatatt atcaacttct cagtaacaca attcgttcct	300
gaaagagtgc aaaaaaatg ttctctaca acaccagaag tggttaagagc atcaatcata	360
cactgaaggc caaggattca tgatcacaag tggtaaaagt ttattgtctg acttaaagta	420
agaaacagaa cattaaaagc ttattattc acagttttat tcatggcaag cttaggaaca	480
gtccataact aagatgaag cggagaagaa gcacaagtgc gaaaaagaaa ccaaattgaa	540
agtgttatta aaagtat	557

<210> SEQ ID NO 3

<211> LENGTH: 573

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 3

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ctttatttct ctctgtttgt ttactgttc agtgttttaa gtcttctctt tgtgtttgtt	120
gctgttgtgt ctttgatgga tttttgtgat ccgatttaat aaaagaagtg tgttcaaagt	180
aattctctag tctctttatt tgaattccg gggatagcag attggtttcc gcaacattga	240
ctccaagttt ataatgatct tgatgatggt ctaaaagttt tgaataagct gactctaatt	300
tactaggttc tgtttgttta tataccttca gagagtttca agtcttctcg ttgtggtctt	360
gttctgtttt cttgatgtga tttcttattc attttaacaa aagaagtttg tgcaaagtca	420
caatgcagaa acccacttta tttagatttt agataagcaa agcacacaga tgcattatcc	480
ttaagaaaaa caaaatacaa cactagacca caacttcata aactcacaac ataacttat	540
tcaaatttca gggatatcca gattggttcc aca	573

<210> SEQ ID NO 4

<211> LENGTH: 633

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 4

gagatgaaga aattgctctt atggttctga aaacttctaa tatgtcgagt tgttctgagt	60
tttaagattt tccaaaatgt ctttgtcttt ttttttatat ctttagagtt acttgaacat	120
tgtgactact tctaggggtg ggtttgtgtc aggtctgtta tatcgtgtgg tgggtctgtc	180
taatactgat tcaagttttt gttattcagc taaggaaactt ttcttgtttc tgaacaaatc	240
ttttggttcc ctagagtaaa acttgacttc caaaagatag acttctaag atcactggaa	300
tagataggag tgacaacttg acgtgaaagg tagcttggtc atagtaattt tagatctgac	360
aaaacgagat caagaagtta ataattttca caacaccaat ttgttatcgc ttaaagggtg	420
attgatttgt tcaatagggg gaatcatatt ctgcgatgct cgaaaagggg agagaagatg	480
gaatgaacat aactttaaat cggatgtttg attcaacaac aaaactaaac tcagatagag	540
attatgaagg attccggaat ctgaattaca aaagcaaaat ttaaagctga aaactcctcc	600

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atggtctttac tgtcacctaa agacatttct ttt 633

<210> SEQ ID NO 5
 <211> LENGTH: 639
 <212> TYPE: DNA
 <213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 5

aactgagatg gaagaagaag ttgcaatagt ttttttaaac tagtttcttt ctacgtactc	60
tggtttttct ctgcttggtt catggtttga gtgggcaact actgatcttt cccattttcc	120
tgccggattt gtagaagaat aaaaagggtg aaaatgatca tcttgagatg gtgatgaaac	180
tcttaagatc ctctctctct gcttctcttt ttatttgccg tgcataatg aaaattgcat	240
attcagatgg gcctgtgtgt tgagtaagtg gacctgtgtc cagagagttg attgagatgg	300
gcttcatttt agggccacat gtttatcgat cagggttcatt ctcttcatta tatgaaagtg	360
tcctatatcg caacattctc ttcattaatc attatattag tttatcgcca caaagtccac	420
tattcaaaga ttcgattttt ctctcgcaaa cagaaattta tattgacttt taagaaaaaa	480
tacaaagtat atctatcaca caactcaca aagagatagg tacaacata atgacaaatc	540
acaataagca caccattata ttaaaagtca aatttacctt ttaataaga agatacaaaa	600
atatataaag agacgaccaa gacaatttga cttgagtga	639

<210> SEQ ID NO 6
 <211> LENGTH: 685
 <212> TYPE: DNA
 <213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 6

tgcggtatag ttggcatttg gttttgctgt accctttcga aatctttatg tcgttggtta	60
gtttgttgta ttgcactatc ttcttagact ttgctgaaat tctcaagaga tttttttact	120
caaacatcag tccacttggtg attggcattt atatttcaaa ctattgcctt agttacatct	180
tcaatagtcg acttatgaac gatctttagt aaattctctt attcactcgc ttactaagaa	240
ttaaacctaa agagaatata gaagaattcc ctagagtaag gatttggtgt agtgtaaaac	300
agactcttcc ctctttgtat tggtcagatt ctggaaacat aagatatgtg aatccaatca	360
acacagtact cgagatatgt tctgataaaa aaaatgttgg tactaacaat ttcagtttgg	420
atgggaagga ttatccgaat aaagatatag ctaattctga tcaaaagaga gcgaaaaata	480
gtctctggag tttagattga gaaactaat gtcaacaaac cggaacaaa aaaaaactgt	540
gtcaagtaac aaaaacaaaa gaaaagactc aaagagagta gcagcaacgt aagatttgat	600
tccaaagtgt ctcaacaggg aggaatgagt aatgtactc cctgttttat tcaactcatca	660
caagtccatc aatcaatcta tctct	685

<210> SEQ ID NO 7
 <211> LENGTH: 411
 <212> TYPE: DNA
 <213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 7

gttggtttca tcttattttc tgcgattttt gtacttgctg gatttggaat ccatttggtt	60
tagctctctc gtataagatt gtctcatctt tgcttgtaa ctctatatct tgaatcatca	120
agatatggtt ttgctgttaa tcattgacct tcgatatttt tttgccaac cgttctctct	180

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accaaacctaa gaaaaaatca ctaatatctc acatttagagg gtgcaaaatt tggaagggtct	240
atatcattgt ccaattttct gagtcataca aattctttca tatgattcat tgaacaagac	300
actcatttac ttataaagcg catttatatg ttcacatgat ttgtacaaaa ctcatgagac	360
tgcaccaagc agaaagtatt tatttatctt tacatgtcaa agctttgaga a	411

<210> SEQ ID NO 8
 <211> LENGTH: 457
 <212> TYPE: DNA
 <213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 8

taacatcaaa gagcaggaag tttttaacaa ggaatctggt cgagacatcc atgttctgga	60
ccagacagtt ttttggttta gccttaaaat tccaagggtg tataagaaga acacactgtt	120
tgttattctt tgcggttggt aaccaatata gtaatatcag tatttcgtct caatctctct	180
tgttcttata ataatagaat gagaaatcga aatggaattt tcatgtgaag tggattagta	240
acattatcac aattgataaa acatttgtaa ataactagac aagctttctc ggctatcagt	300
taaaatagaa gttgaattaa cctcacaatt cgttttgtac ggaactaaga gatcacaaat	360
gaaaacggaa aacaacaaca aaaatgaaaa agcgatactt ttttaaacca cctgtcatc	420
ctcatctcaa agagcttctt gacttccatg agtgcta	457

<210> SEQ ID NO 9
 <211> LENGTH: 557
 <212> TYPE: DNA
 <213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 9

atacttttaa taacactttc aatttggttt ctttttcgca attgtgett cttctcgctt	60
tcatcttagt tatggactgt tcctaagctt gccatgaata aaactgtgaa taataaagct	120
tttaagtctc tgtttcttac tttaagtcag acaataaaact tttaacactt gtgatcatga	180
atccttggtc ttcagtgtat gattgatgct cttaacactt ctggtgttgt agaggaaat	240
tttttttgca ctctttcagg aacgaattgt gttactgaga agttgataat atcggttttg	300
caaacaaatg taagatgaaa aaacagagta tatattactg aatctgtttc gatgaaaaac	360
agagtaaata aagctaaaga ttgcgccatt ttatttcttt attgtgggct actcgccaag	420
caatctacac tcaacagaca ctaataagga taaaaaaact tcgcaacaga atcagatatc	480
taaaaatccc ggaaattcac tagatttctt cgattggtac cgagagggtg catcaaattt	540
aacagacttc aagttta	557

<210> SEQ ID NO 10
 <211> LENGTH: 573
 <212> TYPE: DNA
 <213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 10

tgtgaaacca atctggatat ccttgaaatt tgaataagggt tatgttgtga gtttatgaag	60
ttgtggtcta gtgttgtatt ttgtttttct taaggataat gcatctgtgt gctttgctta	120
tctaaaatct aaataaagtg ggtttctgca ttgtgacttt gcacaaactt cttttgttaa	180
aatgaataag aatcacatc aagaaaacag aacaagacca caacgagaag acttgaaact	240
ctctgaaggt atataaaca acagaacctt gtaaattaga gtcagcttat tcaaaacttt	300
tagaccatca tcaagatcat tataaacttg gagtcaatgt tgcggaaacc aatctgctat	360

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ccccggaatt tcaataaag agactagaga attactttga acacacttct tttattaaat 420
cggatcacia aaatccatca aagacacaac agcaacaaac acaaagagaa gacttaaaac 480
actgaagcag taaacaaaca gagagaaata aagtagaatc agcttattca aagtgtgtaa 540
actatcatca aaagatactt aaaatctcca taa 573

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<210> SEQ ID NO 11
<211> LENGTH: 633
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

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<400> SEQUENCE: 11

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aaaagaaatg tctttagggtg acagtaagac catggaggag ttttcagctt taaattttgc 60
ttttgtaatt cagattccgg aatccttcat aatctctatc tgagtttagt tttgtgttg 120
aatcaaacat cggatttaaa gttatgttca ttccatcttc tctccccttt tcgagcatgc 180
gagaatatga ttccccctat tgaacaaatc aatcaacctt taagcgataa caaattgggtg 240
ttgtgaaat tattaacttc ttgatctcgt tttgtcagat ctaaaattac tatagccaag 300
ctacctttca cgtcaagttg tcactcctat ctattccagt gatcttagga agtctatctt 360
ttggaagtca agttttactc tagggaacca aaagatttgt tcagaaacaa gaaaagtacc 420
ttagctgaat aacaaaaact tgaatcagta ttagacagac ccaccacacg atataacaga 480
cctgacacia acccaaccct agaagtagtc acaatgttca agtaactcta aagatataaa 540
aaaaaagaca aagacatttt ggaaaatctt aaaactcaga acaactcgac atattagaag 600
ttttcagaac cataagagca atttcttcat ctc 633

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<210> SEQ ID NO 12
<211> LENGTH: 639
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

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<400> SEQUENCE: 12

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tcactcaagt caaattgtct tggtcgtctc tttatatatt tttgtatctt cttattaaaa 60
aggtaaatgt gacttttaat ataatgggtg gcttattgtg atttgcatt atgtttgtac 120
ctatctcttt tgtgagttgt gtgatagata tactttgtat tttttcttaa aagtcaatat 180
aaatttctgt ttgcgagaga aaaatcgaat ctttgaatag tgaactttgt ggcgataaac 240
taatataatg attaataag agaattgtgc gatataggac actttcatat aatgaagaga 300
atgaacctga tcgataaaca tgtgggccta aaatgaagcc catctcaatc aactctctgg 360
acacaggtec acttactcaa cacacaggcc catctgaata tgcaattttc attatgacac 420
ggcaataaaa aagagaagca gaagaggagg atcttaagag tttcatcacc atctcaagat 480
gatcattttc aaccttttta ttcttctaca aatccggcag gaaaatggga aagatcagta 540
gttgccact caaacatga accaagcaga gaaaaaacag agtacgtaga aagaaactag 600
tttaaaaaaa ctattgcaac ttcttcttcc atctcagtt 639

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<210> SEQ ID NO 13
<211> LENGTH: 685
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

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<400> SEQUENCE: 13

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ttctctcctt gtgagacact ttggaatcaa atcttacgtt gctgctactc tctttgagtc	120
ttttcttttg tttttgttac ttgacacagt ttttttttgt ttccggtttg ttgacattta	180
gtttctcaat ctaaaactoca gagacttatt ttcgctctct tttgatcaga attaggtata	240
tctttattcg gataatcctt cccatccaaa ctgaaattgt tagtaccaac atttttttta	300
tcagaacata tctcgagtac tgtgttgatt ggattcacat atcttatggt tccagaatct	360
gaacaatata aagaggaag agtctgtttt acactacacc aaatccttac tctaggaat	420
tcttctgtat tctctttagg ttttaattctt agtaagcgag tgaataagag aatttactaa	480
agatcggtca taagtggact attgaagatg taactaaggc aatagtttga aatataaatg	540
ccaatcacaa gtggactgat gtttgagtaa aaaaatctct tgagaatttc agcaaagtct	600
aagaagatag tcgaatacaa caaactaac aacgacataa agatttcgaa agggtagagc	660
aaaaccaaat gccaaagtata ccgca	685

<210> SEQ ID NO 14
 <211> LENGTH: 411
 <212> TYPE: DNA
 <213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 14

ttctcaaagc tttgacatgt aaagataaat aaatactttc tgcttgatgc agtctcatga	60
gttttgtaca aatcatgtga acatataaat gcgctttata agtaaatgag tgtcttggtc	120
aatgaatcat atgaagaat ttgtatgact cagaaaattg gacaatgata tagaccttc	180
aaattttgca ccctctaattg tgagatatta gtgatttttt cttagggttg tagagagaac	240
ggattggcaa aaaaatatcg aagggtcaatg attaacagca aaacatattc ttgatgattc	300
aaaatataga gttaacaagc aaagatgaga caatcttata cgagagagct aaaacaaatg	360
gattccaaat ccagcaagta caaaaatcgc agaaaataag atgaaaccaa c	411

<210> SEQ ID NO 15
 <211> LENGTH: 457
 <212> TYPE: DNA
 <213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 15

tagcactcat ggaagtcaag aagctctttg agatgaggat gacaggggtg tttaaaaaag	60
tatcgctttt tcatttttgt tgttgttttc cgttttcatt tgtgatctct tagttccgta	120
caaaacgaat tgtgaggtta attcaacttc tattttaact gatagccgag aaagcttgtc	180
tagttattta caaatgtttt atcaattgtg ataattgtac taatccactt cacatgaaaa	240
ttccatttcg atttctcatt ctattattat aagaacaaga gagattgaga cgaaatactg	300
atattactat attggttacc aaccgcaaag aataacaaac agtgtgttct tcttatataa	360
ccttggaatt ttaaggctaa accaaaaaac tgtctggtcc agaacatgga tgtctcgacc	420
agattccttg ttaaaaactt cctgctcttt gatgtta	457

<210> SEQ ID NO 16
 <211> LENGTH: 782
 <212> TYPE: DNA
 <213> ORGANISM: Oryza Sativa

<400> SEQUENCE: 16

gcattgtttt gatgctgcta cctataaaag tatgagcttc agatgagaat ttagagagct	60
cccctgaggc aatgggttat gactttgtta tcactcttagt actactccta tctaagggac	120

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ggtgtaaggc tgtaatctat gtgcgggtgca atgataaggc taccctttct gcgtttgatc	180
atgacatctc atcgctgttc gattctttct cgctggcgtc tgttatgttg aatgatgcaa	240
ttcttctgta agattccgcc ttaccgaaa tatctctagt atcaaattta aattggagta	300
cggatcctct ttgaacatac ggatctatct gagataatct tgtctgatca tcaacgagaa	360
ctcggaagcg tgccaacctt gtgggtcaat tgtaacgata aagcagggag aatatagttc	420
ccccttttct ctctgatgat gaaatggcag gagaagtgtg gttgagcctg ctgttttggg	480
gaagactgaa atggtatcag aaagtcagaa tccactataa ccaatacaac agcagctgat	540
atataatcat tgatcaagga aaacaactgc agctcataga ttaatgctta ctgctttgt	600
ccatcaatc atacaaaaac cagtccaaca gtcattgtaa ctgtccaaa tcaaagcacg	660
ccagaagttc tcttaacgcc tcacacagca ggaaacacaa caacaaactg gattttattt	720
atctacacat ccatcatatt tacataccaa gggagaatcc gcaggactca ttttccttc	780
tt	782

<210> SEQ ID NO 17
 <211> LENGTH: 825
 <212> TYPE: DNA
 <213> ORGANISM: Oryza Sativa

<400> SEQUENCE: 17

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gtaacatggc cctcaatatt tcatgtgtgc cttgtggaaa aaatagctgg tattggtact	120
gtgtttttta ctctctccag ctaccgacgt tcatgtgttag tgcacaaaat gttcatccat	180
ggtagtttgt ctacattgca gtcattgtaa gttaaacatt cagattttct gtacttttgc	240
atgtgtaact aaatgaaatg gtgtgttaca ttcattcctt caatcaaata atccatagaa	300
acaaactggg ttgtaactat tgtaactagt cgctagtgtc catgggtatt tcatgtgtgg	360
aacataatta gtttaatctg cttcagtata acttaagccg gctttatcct gtgtatgcat	420
cagcttcgct ccattgaaca tccaaacatc agtataagca tttgtgtggc actaatcatc	480
cggagatagg gcaatgcttt ctaccaactg aagagtagag acgtgatgct gtgagatgga	540
atgcaaattt cgcattattg taagaagttg gggaaggatt cgaccactca ctgagaagct	600
agagcatcat ggcacagtaa ttacaatgta acgtagcata ttcttgaaca agaactctg	660
gtcaaatacc aaccgggaaa aaatccacat cgataaagag gtgccgagtg cttacatcaa	720
cgtctttgcc ataatacagaa cactactccg tacaagctaa cagagagca gagattacat	780
ttgcacggat gcaaaagttt ccaagatagg gaactggagt gaagc	825

<210> SEQ ID NO 18
 <211> LENGTH: 791
 <212> TYPE: DNA
 <213> ORGANISM: Oryza Sativa

<400> SEQUENCE: 18

actgagcttt taaaagagtg aggtctaggt tctgttgtct gtctgtccat catccatgtg	60
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aatactagtt ttagcaaaag gctgcgttac ataaggtgat gagaattgag gtaaatgag	180
atctgtacac taaattcatt cagactgttt tggcataaag aataatttgg ccttctgcga	240
tttcagaagc tataaattgc catctcacta aattctcctt ggctcctcatg gcaatgcaac	300

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gacagtgtga agcactgaag cccgtaatgc tctatcacca ccatgtacaa cagaaccata	360
tatgtocata tgtacaactc gagtgttgtt tgagtggcca gcaaactggc tgaccaagcc	420
acacgagaga gaatactata aactcaatca tacataacaa gcccaagcaa cagaagacag	480
aacacaacaa cactcgagtc tgggaacagc aacgccgata cactacagca tactgcaacg	540
acacaaagga attggttaagg aaatggcacc aaaatcttgt agatcttttag cgagtcattc	600
atztatagca tatgttggaa cagacatgag tcacaagatt tatgatagct tagataacag	660
atggtcggaa ttaaccgcgc agagcctata gatgaacaaa aactctgttc caccagtgtt	720
ctcatgctaa aaactttctg aaatacccta cctgtttcac cgaattttctc cacctgttgg	780
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<210> SEQ ID NO 19
 <211> LENGTH: 881
 <212> TYPE: DNA
 <213> ORGANISM: Oryza Sativa

<400> SEQUENCE: 19

ggtgacggcg acgcgatcga acaggtggtg atcgatgctg caacgtgtgt aaatatacag	60
cgccggctgg gtcaagagat ggctcgggtg acgcgcgcgc ggctgtcct ggctgtggcg	120
cgggggcatt ctttagtttt tcactctttc atcatctcag atggtagata caaaacagtg	180
tatgtatgta gctctgtttc tctctataga accccaacaa attttgttgt tgatgttgtt	240
tatcttcata tgctttgatc ttgaaatcgt ctacettact actgccgac gttgctcaaa	300
agtgtggaag tttgaagcat cttccacggg cgttgcctca ctcccatctc gtttcaccac	360
gaaatccctc tcgcatagag gcactctcag cgtacatctc caaaccacg ttctggattc	420
agcaaacgga cggcatatgc cagcggactg actaggattt gtggttcaga ataaaaatat	480
ggtttgcagt gtcaattttc caggagagtg actatgtcat actaacttca tactccaata	540
atgaagctaa gctatctcca tgtacatata aaatacgaaa tcatatccaa gggaactaac	600
acagtcacaa acaacaggta cacagacaat tacagcacia gcgcaggagg gaaataattt	660
taactgaact aggaagaaag gaaacacaa tcatttttta ttgatatatg ttggatgaat	720
ccaataaaac cgatacaagt cagcaaaaat cagactagat gaatccttcg agatcacatg	780
agcaaaagct ttcgacgaaa gctgtcctat agtcgtggaa gcaataacac ttgataaaga	840
taggaattca gacacgagag gttgcagact ataagatgtc a	881

<210> SEQ ID NO 20
 <211> LENGTH: 772
 <212> TYPE: DNA
 <213> ORGANISM: Oryza Sativa

<400> SEQUENCE: 20

ccgtggcaat ggctgtcatg ctttggcaca tactaatagc aaggtagaat ggtacagcta	60
tttcattatt tttgcccttg tatatttgta tcactacatg agtaaagcag gtttagttat	120
cgatagtttt gttatgagt atgaatgatc tgcacgtac tgccaatgcc ttgcattctc	180
aatgggtgc acacttgcac tcatacaaaag ttagtacact ccatcatatt ataaattact	240
tttttttcaa gttaaatttc ctgaaagtgt gataaaattt atagaaaaaa tataacgacg	300
cttataacac taaattaatt tcattacatc taacattaaa catattttga ttttttttg	360
ttttgtgtta aatatattac tatgtttttc tataaacttg attaaacata taaaagtta	420
acttcaaaaa aaagttaaaa tgacttgtaa tataaaacgt aggcagtaca atgcgaatgt	480

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agggtactcc atccagctga ggtaaaccaa ctccaatata tatacaaaaca caaacacgt      540
acccaatttt tactgttaaa atacaggcac aatgcctggg atcacacgtt attaagtaga      600
cagactcgat aaccatgaca cggacaggga cttcttgcca ctggtttacg cacggttaat      660
attacagacc acacatagag agacggctta gctatttgca aataagcttg acaagataga      720
tgatgctcca aaaggatgcg atctcagcag ttgagtactt acgctggttc at              772

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<210> SEQ ID NO 21
<211> LENGTH: 827
<212> TYPE: DNA
<213> ORGANISM: Oryza Sativa

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<400> SEQUENCE: 21

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acaccacctg ctgtctgccc ttgtttgttg ccacggctgc gctacaaaca caagccgtat      60
catctgccga acagctccat cgtagcttc ttttgatgcc ttacatctat cgctggacgt      120
ttatcgctgc tacttgtccc atacagggat tgtgtttgga tgattttag agaggggtact      180
gtatggcata agatccttca tattaatgtt ctgtgggtca catatcaact tgctattatt      240
gtattcagcg gttctctctc tattttgctt taagctgtgg taccatttta agtccagtgc      300
ttgcttttga ttgcttttct gagctttcca ggacatggaa tcgagcctgt gaatgtcgtc      360
ggccgggttta tcttttcgac taataattta aattgtccag tgttggttag gaatggagta      420
tcagattctg gcggtttgca tgcgttttgg tcggcgacgt gccttacct gaagatttat      480
atatagtact ttgattgatg tcaagaagga aatttcttta agaaactttt tacaaatagc      540
gattggtaga actgattaac aacatccacg gctcagaaaa ggaacgcaaa catatttgat      600
tcttccctaa attaatgtgc cattgttatt tttacttgac catccgtcaa aatttacatg      660
aatacacaac gcacggacga acgatttatt catgtgaagg catgatttac atccttaaaa      720
ttctctcgca tctagatata gctagagagt ggccagctgc tgactatgca tggagctggc      780
acggcagtag tgtacaatgc tactgttaatt ttgtattgct acaagta                  827

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<210> SEQ ID NO 22
<211> LENGTH: 770
<212> TYPE: DNA
<213> ORGANISM: Oryza Sativa

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<400> SEQUENCE: 22

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gctgaaattt ggttatctgt tatgagcata tctgatttcg ataccactg ttatgaaact      60
gaataaaccc cattcctgta tctggggaat tttctcgta gtgtacgctc caatactcgt      120
gccgttttca aagacaagca gtgatatgca aagcaatgct gtgtatcttg tgtgttacat      180
caggagtttt ttttaatggt gatttcgttc atagttttca gacatctggt tccgtcacac      240
gttcgtggga atgacttttt tcatatgaaa tgcgcccacg gctgcgcctg aaataatttt      300
acttgtcccg tttgggatga atgaattctt ttcctgttcg ttgttcagta attcacacag      360
agtcataaac ataccggtgg aaacatgctc acaagaaaag aaacatcatg aagtcaggct      420
aaggataaga atagccagca cacctagagc aaaattttac taacatcaga tgcaagaaaag      480
tctacatgag ttctaaaaag gaaactgggg aaaactaatt tacaccaatt atcactaata      540
gtactactaa tataaacgac caagaagggc tctaggaacc cattttgtat ctagcaccg      600
aacgttgaac ctttctcccg ataaaagagg gatcaggcgt gcaacagact ggctctcacg      660
ccagggaaac cacagggtaca aaagaggcag cgaaagaaga acaaaaactt ttcctccggg      720

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gcgaacatat acaacttgag aggaaaaata cacaatggcc gagagacaaa 770

<210> SEQ ID NO 23
 <211> LENGTH: 814
 <212> TYPE: DNA
 <213> ORGANISM: Oryza Sativa

<400> SEQUENCE: 23

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agtgttactt attgttgcta ctatccatat tcgtaccat gcttatcgc gctagattaa    60
aggacatgta ttccagtatg gtcgtgcttt ttgcttggtg ctctggtcac atttgtgatg    120
aatgttcgca gttttcgtgg tcattggtctg gattctacat tccacctaaa gaagttttta    180
cctggttatt taatccttga gttgttgaat tagctcatgg taattgtcag tagtcttcca    240
cttggttctc tctgtggatg atcgttcttg ttctctgttt gcgctgtggc tgattgttct    300
catgttttta aggttttttg gttagtcaact ggtcgcctcg tcaactgtgag ccaaaccata    360
tgccggtagt tttcttcttc accatcatcc gtttgatcct gactgcgga tctcctaate    420
caacttctct cttttttttt tttaatccaa actcacccaa cggtggaac atagcttgga    480
accccttgaa attgaacaga atttatagca ggcaaaaatg taagaaacca cgctagtgtg    540
gcagcgcttac agcggggcaa agcagctttt gtttaagcaac cacttacgtt agagattcag    600
agataagcga tgttactttg tttttaccaa catttacata caagcggtag aacacatatt    660
gccagaaacc acttggtttt ccagccataa tttttgacaa ttcatgacgc gcgcgcgcac    720
acacaatgct ggattcacag ggtcacacag ccatgagcca tcagactgga agggctctgt    780
ttgttcatca catagtcaca gatcgcttg gcct                                814

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<210> SEQ ID NO 24
 <211> LENGTH: 834
 <212> TYPE: DNA
 <213> ORGANISM: Oryza Sativa

<400> SEQUENCE: 24

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ttggcagcct acccactctg gtaggaaaaa tggaaggggc aagaagatac agtcgatgat    60
atgtgatgtg ctacatacca attgtaatat ttcattcata tctagagcta gaaggatatt    120
cacttgattt tcagactctg gttcacgggt taaattgata ttgtggtaga atgctttctt    180
ggatgggtat atagtgtgac tcgttaaaaa tatgacaaaa cggttcagct actctttaca    240
agtgttacgg caaattgtag acccaattgc acttggcggg gagctgcttt gttggagcaa    300
cagggcactg tctgcttgcg tggatgaaaa gctgagtcac ctgaagctag tgaacathtt    360
ttcgtgggct cgctgcgtgt gttttttctc tgattgtggc ccggttgatt atgaaaatga    420
ccagtaagta aagtcacccg accctgctga tttgtttgtt ttgcctaacc tagctcatgc    480
tcggggctgt gaatcgtgct acacttggtg cagctttcgt tttcttgaag agttggaagg    540
tgtcagctta gcttctctgt cgtactagta ttgcagaaga aaacgtaaaa ctgtaccaga    600
gcaagaagac tttgacataa atttgtaaca aggcagatag gtgtgacaaa tcaaggcact    660
cagctgaaca gctcaactga aatgcagaac tgaattgaag agtaaaaatg atccatgcat    720
gacagacaaa ccagtggaca ctgactgaag atggagcaat gaacaaaata aaatcaagac    780
ttgtttttat tggcgcacgc atatttaggg tgatatgatg catgacgaaa tgaa                                834

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<210> SEQ ID NO 25
 <211> LENGTH: 740
 <212> TYPE: DNA
 <213> ORGANISM: Oryza Sativa

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<400> SEQUENCE: 25

ggtgttccat atagatgac agatttctat aaccacatga gtacaatgta gagaattcaa	60
atgttttgta accacgtgag ctttgtacgc tatttgcacc acagttctcc ctgtatgttg	120
ttggctcttt tacaattaag aataatgcat gttgaagtat gagtcttctt gtttgcctct	180
ccttgatgat gaaacgctgc tgcacaaact gattatTTTT cagagaataa acgataaaca	240
aagcacgggtg aagtatcgtg taaccaccca taagtggtag agccgtagag gtaggactgt	300
gcatgctgaa ttgtaattac catggttagt tcagcagaat ttgcaaaaag aggacaacag	360
aattagacca tcgtcatgaa ttaatcaagg tacaaccaa tggttgctgg tacatcagta	420
gcaaattggt gtagcactag cgtgcccata tttatatctc aagcctccaa ggtatacaat	480
acatatTTGA tgtaccgaac aactgaaaaa ggcgcttggg ttggaagcgc actatTTTA	540
aatttatagg ataacttctg acagcctttc ttctaaatga acttttggca accgctctga	600
agccgtgtaa cacaatccaa caaagcaatt tgcagtcaaa atttcgggca tgtgccgttc	660
tagttagaat ttaggatgtg actcactaag taattgtgat tgtttctcta tgcaaacacc	720
agccaacagt attgatttca	740

<210> SEQ ID NO 26

<211> LENGTH: 782

<212> TYPE: DNA

<213> ORGANISM: Oryza Sativa

<400> SEQUENCE: 26

aagaaaggaa aatgagctct gcggattctc ccttggtatg taaatatgat ggatgtgtag	60
ataaataaaa tccagtttgt tgttgtgttt cctgctgtgt gaggcgtaa gagaacttct	120
ggcgtgcttt gatttggagc agttaccatg actgttggac tggtttttgt atgtattgat	180
ggacaaagct agtaagcatt aatctatgag ctgcagttgt ttcccttgat caatgattat	240
atatcagctg ctgttgtatt ggttatagtg gattctgact ttctgatacc atttcagtct	300
tcacaaaaac agcaggctca actacacttc tcctgccatt tcacatcagc aggaaaaagg	360
gggaactata ttctccctgc tttatcgtaa caattgaccc acaaggttgg cagccttccg	420
agttctcgtt gatgatcaga caaaattatc tcaaatagat ccgtatgttc aaagaggatc	480
cgtactccaa tttaaatttg atactagaga tatttcggta aaggcggaa cttacagaag	540
aattgcatca ttcaacataa cagacgccag cgagaaagaa tcgaacagcg atgagatgtc	600
atgatcaaac gcagaaagga tagccttata attgcaccgc acatagatta cagccttaca	660
ccgtccctta gataggagta gtactaagat gataacaaag tcataaccca ttgcctcagg	720
ggagctctct aaattctcat ctgaagctca tacttttata ggtagcagca tcaaaacaat	780
gc	782

<210> SEQ ID NO 27

<211> LENGTH: 825

<212> TYPE: DNA

<213> ORGANISM: Oryza Sativa

<400> SEQUENCE: 27

gcttcactcc agttccctat cttggaaact tttgcatccg tgcaaatgta atctctgctc	60
tcgtgttagc ttgtacggag tagtgttctg attatggcaa agacgttgat gtaagcactc	120
ggcacctctt tategatgtg gattttttcc cggttggtag ttgaccagat gttcttgctc	180

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aagaatatgc tacgtttacat tgtaattact gtgccatgat gctctagctt ctcagtgagt	240
ggtcgaaatcc ttccccaact tcttactaat atgcgaaatt tgcattccat ctcacagcat	300
cacgtctcta ctcttcagtt ggtagaaagc attgccctat ctcggatga ttagtcgcca	360
caaaatgctt atactgatgt ttggatgttc aatggagcga agctgatgca tacacaggat	420
aaagccggct taagttatag tgaagcagat taaactaatt atgttcacaca atcgaaaata	480
ccatggacac tagcgactag ttacaatagt tacaaccag tttgtttcta tggattattt	540
gattgaagga atgaatgtaa cacaccattt catttagtta cacatgcaa agtacagaaa	600
tcgtgaatgt ttaactttac atgactgcaa ttagacaaa ctaccatgga tgaacatttt	660
gtgcactaac actgaacgtc ggtagctgga aggagtaaaa aacacagtac caataccagc	720
tattttttcc acaaggcaac atcgaaatat tgagggccat gttacacatg atctgacttt	780
tcaatttagg ctggatacat gactagttag atactgctgc tgcct	825

<210> SEQ ID NO 28

<211> LENGTH: 776

<212> TYPE: DNA

<213> ORGANISM: Oryza Sativa

<400> SEQUENCE: 28

aatgctgcta tccaacaggt ggagaaatc ggtgaacagg gtagggatt tcagaaagtt	60
tttagcatga gaacactggg ggaacagagt tttgtttcat ctataggctc tcggcgggta	120
attccgacca tctgttatct aagctatcat aaatcttggt actcatgtct gttccaacat	180
atgctataaa tgaatgactc gctaaagatc tacaagattt tgggtgccatt tccttaccaa	240
ttcctttgtg tcgttgacgt atgctgtagt gtatcggcgt tgctgttccc agactcgagt	300
gttgtgtgtg tctgtcttct gttgctggg cttgttatgt atgattgagt ttatagtatt	360
ctctctcgtg tggcttggtc agccagtttg ctggccactc aaacaacact cgagttgtac	420
atatggacat atatggttct gttgtacatg gtggtgtag agcattacgg gcttcagtgc	480
ttcacactgt cgttgcatg ccatgaggac caaggagaat ttagtgagat ggcaatttat	540
agcttctgaa atcgagaag gccaaattat tctttatgcc aaaacagtct gaatgaattt	600
agtgtacaga tctcatTTta cctcaattct catcacctta tgtaacgcag cctttgctac	660
aaactagtat tacaggcaca caaaaactca tctcgtgaag aaaagaagaa acgagttccc	720
tcaacagtca acacatggat gatggacaga cagacaacag aacctagacc tcactc	776

<210> SEQ ID NO 29

<211> LENGTH: 881

<212> TYPE: DNA

<213> ORGANISM: Oryza Sativa

<400> SEQUENCE: 29

tgacatctta tagtctgcaa cctctcgtgt ctgaattcct atctttatca agtggtattg	60
cttcacagac tataggacag ctttcgtcga aagcttttgc tcatgtgac tcgaaggatt	120
catctagtct gatttttcgt gacttgatc ggttttattg gattcatcca acatatatca	180
ataaaaaatg agttgtgttt cctttcttcc tagttcagtt aaaattattt ccctcctgct	240
cttgtgtgtg aattgtctgt gtacctgttg tttgtgactg tgtagttcc cttggatatg	300
atttcgtatt tgatagtac atggagatag cttagcttca ttattggagt atgaagttag	360
tatgacatag tcaactctct ggaaaattga cactgcaaac catattttta ttctgaacca	420
caaatcctag tcagtcctgct ggcataatgc gtccgtttgc tgaatccaga acgtgggttt	480

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ggagatgtac ggctgagatg cctctatgcg aaggggattt cgtggtgaaa cgagatggga	540
gtagagcaac gcccgaggaa gatgcttcaa acttccacac ttttgagcaa cgatcggcag	600
tagtaaggta gacgatttca agatcaaagc atatgaagat aaacaacatc aacaacaaaa	660
tttgttgggg ttctatagag agaacagag ctacatacat acactgtttt gtatctacca	720
tctgagatga tgaagagatg aaaaactaaa gaatgccccg gcgccaacgc caggacacgc	780
cgcgcgcgcg tcacccgagc catctcttga cccagccggc gctgtatatt tacacacgtt	840
gcagcatcga tcaccacctg ttcgatcgcg tcgcgcgcac c	881

<210> SEQ ID NO 30
 <211> LENGTH: 772
 <212> TYPE: DNA
 <213> ORGANISM: Oryza Sativa

<400> SEQUENCE: 30

atgaaccagc gtaagtactc aactgctgag atcgcatcct tttggagcat catctatctt	60
gtcaagctta tttgcaaata gctaagccgt ctctctatgt gtggtctgta atattaaccg	120
tgcgtaaacc agtggcaaga agtccctgtc cgtgtcatgg ttatcgagtc tgtctactta	180
ataacgtgtg ataccaggca ttgtgcctgt attttaacag taaaaattgg gtacgttggt	240
tgtgttttga tatatattgg agttggttta cctcagctgg atggagtacc ctacattcgc	300
attgtactgc ctacgtttta tattacaagt cattttaact tttttttgaa gttaaaacttt	360
tatatgttta atcaagttta tagaaaaaca tagtaataata tttaacacaa aacaaaaaaa	420
aatcaaaata tgtttaatgt tagatgtaat gaaattaatt tagtggtata agcgtcgta	480
tattttttct ataaatttta tcaaactttc aggaaattta acttgaaaa aaagtaattt	540
ataatatgat ggagtgtact aactttgtat gagtgcaagt gtgcaacat ttgagaatgc	600
aaggcattgg cagtacgatg cagatcattc atcactcata acaaaactat cgataactaa	660
acgtcgttta ctcatgtagt gatacaaata tacaagggca aaaataatga aatagctgta	720
ccattctacc ttgctattag tatgtgccaa agcatgacag ccattgccac gg	772

<210> SEQ ID NO 31
 <211> LENGTH: 827
 <212> TYPE: DNA
 <213> ORGANISM: Oryza Sativa

<400> SEQUENCE: 31

tacttgtagc aatacaaaat tacagtagca ttgtacacta ctgccgtgcc agctccatgc	60
atagtcagca gctggccact ctctagctat atctagatgc gagagaattt taaggatgta	120
aatcatgcct tcacatgaat aaatcgttcg tccgtgcgtt gtgtattcat gtaaattttg	180
acggatggtc aagtaaaaat aacaatggca aattaattta gggaagaatc aaatatgttt	240
gcgttccttt tctgagccgt ggaatgtgtt aatcagttct accaatcgct atttgtaaaa	300
agtttcttaa agaaatttcc ttcttgacat caatcaaagt actatatata aatcttcagg	360
ataaggcacg tcgccgacca aacagcatgc aaaccgccag aatctgatac tccattccta	420
accaaacactg gacaatttaa attattagtc gaaaggataa accggccgac gacattcaca	480
ggctcgattc catgtcctgg aaagctcaga aaagcaatca aaagcaagca ctggacttaa	540
aatggtacca cagcttaagg caaaatagag agagaaccgc tgaatacaat aatagcaagt	600
tgatatgtga cccacagaac attaatatga aggatcttat gccatacagt accctctcta	660

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caaatcatcc aacacaaatc cctgtatggg acaagtacgc acgataaacg tccagcgata	720
gatgtaaggc atcaaaagaa gctaacgatg gagctgttcg gcagatgata cggcttgtgt	780
ttgtagcgca gccgtggcaa caaacaagcg cagacagcag gtggtgt	827

<210> SEQ ID NO 32
 <211> LENGTH: 770
 <212> TYPE: DNA
 <213> ORGANISM: Oryza Sativa

<400> SEQUENCE: 32

tttgtctctc ggccattgtg tatttttctt ctcaagttgt atatgttcgc cccggaggaa	60
aagttttgtt tcttctttcg ctgcctcttt tgtacctgtg gtttccctgg cgtgagagcc	120
agtctgttgc acgcctgac cctcttttat cgggagaaa gttcaacgtt cgggtgctag	180
atacaaaatg gggttcctaga gcccttcttg gtcgtttata tttagtgtac tattagtgtat	240
aattgggtga aattagtttt cccagtttc ctttttagaa ctcatgtaga ctttcttgca	300
tctgatgtta gtaaaatttt gctctagggt tgctggctat tcttatcctt agcctgactt	360
catgatgttt ctttctttgt gagcatgttt ccaccgggtat gtttatgact ctgtgtgaat	420
tactgaacaa cgaacaggaa aagaattcat tcatcccaa cgggacaagt aaaattattt	480
caggcgcagc catgggcgca ttcatatga aaaaagtcac tcccacgaac gtgtgacgga	540
aacagatgtc tgaaaactat gaacgaaatc accattaaaa aaaactcctg atgtaacaca	600
caagatacac agcattgtct tgcatatcac tgcttgctt tgaaaacggc acgagtattg	660
gagcgtacac taacgagaaa attcccagca tacaggaatg cggtttattc agtttcataa	720
cagtgggtat cgaatcaga tatgctcata acagataacc aaatttcagc	770

<210> SEQ ID NO 33
 <211> LENGTH: 814
 <212> TYPE: DNA
 <213> ORGANISM: Oryza Sativa

<400> SEQUENCE: 33

aggccaaggc gatctgtgac tatgtgatga acaaacagag cccttccagt ctgatggctc	60
atggctgtgt gacctgtga atccagcatt gtgtgtgcgc gcgcgcgtca tgaattgtca	120
aaaattatgg ctggaaaacc aagtggtttc tggcaatatg tggtgtaccg cttgtatgta	180
aatgttggtg aaacaaagt aacatcgctt atctctgaat ctctaacgta agtgggtgct	240
taacaaaagc tgctttgcc cgtgtgaagc ctgtacact agcgtggtt cttacatttt	300
tgctgtctat aaattctgtt caatttcaag gggttccaag ctatgtttcc aacgttgggt	360
gagtttggtg taaaaaaaaa aaagagagaa gttggattag gagatccgcg agtcaggatc	420
aaacggatga tggtgaagaa gaaaactacc ggcataatgt ttggctcaca gtgacgaagc	480
gaccagtgtc taacccaaaa accttaaaaa catgagaaca atcagccaca gcgcaaacag	540
agaacaagaa cgatcatcca cagagagaac caagtgaag actactgaca attaccatga	600
gctaattcaa caactcaagg attaaataac caggtaaaaa cttctttagg tggaatgtag	660
aatccagacc atgaccacga aaactgcgaa cattcatcac aaatgtgacc agagtaccaa	720
gcaaaaagca cgaccatact ggaatacatg tcctttaatc tagcgtatgat aagcatggta	780
gcgaatatgg atagtagcaa caataagtaa cact	814

<210> SEQ ID NO 34
 <211> LENGTH: 834

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<212> TYPE: DNA

<213> ORGANISM: Oryza Sativa

<400> SEQUENCE: 34

ttcatttcgt catgcatcat atcacccctaa atatgcatgc gccataaaaa acaagtcttg	60
atthttatthtt gttcattgct ccattcttcag tcagtgtcca ctggtttgtc tgtcatgcat	120
ggatcatttt tactcttcaa ttcagttctg catttcagtt gagctgttca gctgagtgcc	180
ttgatttgta ccacctatct gccttggttac aaatttatgt caaagtcttc ttgctctggt	240
acagttttac gttttcttct gcaatactag tacgcacagg aagctaagct gacaccttcc	300
aactcttcaa gaaaacgaaa gctgcaacaa gtgtagcacg attcacgacc ccgagcatga	360
gctagggttag gcaaaacaaa caaatcagca gggtcggatg actttactta ctggtcattt	420
tcataatcaa ccgggccaca atcagagaaa aaacacacgc agcgagccag cgaaaaaatg	480
ttcactagct tcagatgact cagcttttca tccacgcaag cagacagtgc cctgttgctc	540
caacaaagca gctcacgcc aagtgcaatt gggctctaca ttgccgtac cacttgtaaa	600
gagtagctga accgttttgt catattttta acgagtcaca ctatataccc atccaagaaa	660
gcattctacc acaatatcaa tttaaaccgt gaaccagagt ctgaaatata agtgaatatc	720
cttctagctc tagatatgaa tgaatatata caattggatg gtagcacatc aaatatcatc	780
gactgtatct tcttgccct tccatttttc ctaccagagt gggtaggctg ccaa	834

<210> SEQ ID NO 35

<211> LENGTH: 740

<212> TYPE: DNA

<213> ORGANISM: Oryza Sativa

<400> SEQUENCE: 35

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cacatccctaa attctaacta gaacggcaca tgcccgaat tttgactgca aattgctttg	120
ttggattgtg ttacacggct tcagagcggg tgccaaaagt tcatttagaa gaaaggetgt	180
cagaagttag cctataaatt taaaaatagt gcgcttccaa accaagcgcc tttttcagtt	240
gttcgggtaca tcaaatatgt attgtatacc ttggaggctt ggaatataaa tatgggcacg	300
ctagtgttac agccatttgc tactgatgta ccagcaacca ttggtttgta ccttgattaa	360
ttcatgacga tggctcaatt ctgttgctct ctttttgcaa attctgctga actaaccatg	420
gtaattacaa ttcagcatgc acagtccctac ctctacggct ctaccactta tgggtgggta	480
cacgatactt caccgtgctt tgtttatcgt ttattctctg aaaaataatc agttgatgca	540
gcagcgtttc atcatcaagg agaagcaaac aggaagactc atacttcaac atgcattatt	600
cttaattgta aaagagccaa caacatacag ggagaactgt ggtgcaata gcgtacaaag	660
ctcacgtggt taaaaacat ttgaattctc tacattgtac tcatgtgggt atagaaatct	720
gatcatctat atggaacacc	740

<210> SEQ ID NO 36

<211> LENGTH: 330

<212> TYPE: DNA

<213> ORGANISM: Solanum tuberosum

<400> SEQUENCE: 36

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gtatgaaata aaaggatgca cacatagtga catgctaata actataatgt gggcatcaaa	120

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gttgtgtgtt atgtgtaatt actagttatc tgaataaaa agaaagagat catccatatt	180
tcttatccta aatgaatgtc acgtgtcttt ataattcttt gatgaaccag atgcatttca	240
ttaaccaa atccatatacat ataaatatta atcatatata attaatatca attgggtag	300
caaaacaa atctagtctagg tgtgttttgc	330

<210> SEQ ID NO 37
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: T1 fwd primer

<400> SEQUENCE: 37

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<210> SEQ ID NO 38
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: T1 rev primer

<400> SEQUENCE: 38

gccatggatc ggtaccatac ttttaataac actttcaatt tg	42
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<210> SEQ ID NO 39
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: T2 fwd primer

<400> SEQUENCE: 39

aggcaa acaa ggtaccttat ggagatttta agtatctttt g	41
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<210> SEQ ID NO 40
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: T2 rev primer

<400> SEQUENCE: 40

gccatggatc ggtacctgtg aaaccaatct ggatatac	37
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<210> SEQ ID NO 41
 <211> LENGTH: 39
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: T3 fwd primer

<400> SEQUENCE: 41

aggcaa acaa ggtaccgaga tgaagaaatt gctcttatg	39
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<210> SEQ ID NO 42
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: T3 rev primer

<400> SEQUENCE: 42

gccatggatc ggtacaaaa gaaatgtctt taggtgac	38
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<210> SEQ ID NO 43
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T4 fwd primer

<400> SEQUENCE: 43
aggcaaacaa ggtaccaact gagatggaag aagaagttg 39

<210> SEQ ID NO 44
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T4 rev primer

<400> SEQUENCE: 44
gccatggatc ggtacctcac tcaagtcaaa ttgtcttg 38

<210> SEQ ID NO 45
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T5 fwd primer

<400> SEQUENCE: 45
aggcaaacaa ggtacctgcg gtatacttgg catttg 36

<210> SEQ ID NO 46
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T5 rev primer

<400> SEQUENCE: 46
gccatggatc ggtaccagag atagattgat tgaaggac 38

<210> SEQ ID NO 47
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T6 fwd primer

<400> SEQUENCE: 47
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<210> SEQ ID NO 48
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T6 rev primer

<400> SEQUENCE: 48
gccatggatc ggtaccttct caaagctttg acatgtaaag 40

<210> SEQ ID NO 49
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<212> TYPE: DNA
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<220> FEATURE:

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<223> OTHER INFORMATION: T7 fwd primer

<400> SEQUENCE: 49

aggcaaacaa ggtacctaac atcaaagagc aggaagt 37

<210> SEQ ID NO 50
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T7 rev primer

<400> SEQUENCE: 50

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<210> SEQ ID NO 51
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T8 fwd primer

<400> SEQUENCE: 51

aggcaaacaa ggtaccatac ttttaataac actttcaatt tg 42

<210> SEQ ID NO 52
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T8 rev primer

<400> SEQUENCE: 52

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<210> SEQ ID NO 53
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T9 fwd primer

<400> SEQUENCE: 53

aggcaaacaa ggtacctgtg aaaccaatct ggatatccc 39

<210> SEQ ID NO 54
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T9 rev primer

<400> SEQUENCE: 54

gccatggatc ggtaccttat ggagatttta agtatctt 38

<210> SEQ ID NO 55
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T10 fwd primer

<400> SEQUENCE: 55

aggcaaacaa ggtacaaaaa gaaatgtctt taggtgacag 40

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<210> SEQ ID NO 56
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T10 rev primer

<400> SEQUENCE: 56
gccatggatc ggtaccgaga tgaagaaatt gctcttatg 39

<210> SEQ ID NO 57
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T11 fwd primer

<400> SEQUENCE: 57
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<210> SEQ ID NO 58
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T11 rev primer

<400> SEQUENCE: 58
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<210> SEQ ID NO 59
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T12 fwd primer

<400> SEQUENCE: 59
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<210> SEQ ID NO 60
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T12 rev primer

<400> SEQUENCE: 60
gccatggatc ggtacctgcg gtatacttgg catttggt 38

<210> SEQ ID NO 61
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T13 fwd primer

<400> SEQUENCE: 61
aggcaaacaa ggtaccttct caaagcttgg acatgta 37

<210> SEQ ID NO 62
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T13 rev primer

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<400> SEQUENCE: 62

gccatggatc ggtaccgttg gtttcacatt attttctgc 39

<210> SEQ ID NO 63

<211> LENGTH: 36

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: T14 fwd primer

<400> SEQUENCE: 63

aggcaaaca ggtacctagc actcatggaa gtcaag 36

<210> SEQ ID NO 64

<211> LENGTH: 36

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: T14 rev primer

<400> SEQUENCE: 64

gccatggatc ggtacctaac atcaaagagc aggaag 36

<210> SEQ ID NO 65

<211> LENGTH: 38

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: T15 fwd primer

<400> SEQUENCE: 65

aggcaaaca ggtaccgcat tgttttgatg ctgctacc 38

<210> SEQ ID NO 66

<211> LENGTH: 38

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: T15 rev primer

<400> SEQUENCE: 66

gccatggatc ggtaccaaga aaggaaaatg agtcctgc 38

<210> SEQ ID NO 67

<211> LENGTH: 38

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: T16 fwd primer

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<210> SEQ ID NO 68

<211> LENGTH: 38

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: T16 rev primer

<400> SEQUENCE: 68

gccatggatc ggtaccgctt cactccagtt ccctatct 38

<210> SEQ ID NO 69

<211> LENGTH: 38

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T17 fwd primer

<400> SEQUENCE: 69

aggcaaacaa ggtaccgagt gaggtctagg ttctgttg 38

<210> SEQ ID NO 70
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T17 rev primer

<400> SEQUENCE: 70

gccatggatc ggtaccaatg ctgctatcca acaggtgg 38

<210> SEQ ID NO 71
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 71

aggcaaacaa ggtaccgggtg acggcgacgc gatcgaac 38

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<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T18 rev primer

<400> SEQUENCE: 72

gccatggatc ggtacctgac atcttatagt ctgcaacctc 40

<210> SEQ ID NO 73
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T19 fwd primer

<400> SEQUENCE: 73

aggcaaacaa ggtaccccggt ggcaatggct gtcatg 36

<210> SEQ ID NO 74
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T19 rev primer

<400> SEQUENCE: 74

gccatggatc ggtaccatga accagcgtaa gtactcaac 39

<210> SEQ ID NO 75
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T20 fwd primer

<400> SEQUENCE: 75

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aggcaaacaa ggtaccacac cacctgctgt ctgcgctt 38

<210> SEQ ID NO 76
<211> LENGTH: 41
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T20 rev primer

<400> SEQUENCE: 76

gccatggatc ggtacctact tgtagcaata caaaattaca g 41

<210> SEQ ID NO 77
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T21 fwd primer

<400> SEQUENCE: 77

aggcaaacaa ggtaccgctg aaatttggtt atctgtta 38

<210> SEQ ID NO 78
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T21 rev primer

<400> SEQUENCE: 78

gccatggatc ggtacctttg tctctcgcc attgtga 38

<210> SEQ ID NO 79
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T22 fwd primer

<400> SEQUENCE: 79

aggcaaacaa ggtaccagtg ttacttattg ttgctacta 39

<210> SEQ ID NO 80
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T22 rev primer

<400> SEQUENCE: 80

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<210> SEQ ID NO 81
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T23 fwd primer

<400> SEQUENCE: 81

aggcaaacaa ggtaccttgg cagcctaccc actctggt 38

<210> SEQ ID NO 82
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: T23 rev primer

<400> SEQUENCE: 82

gccatggatc ggtaccttca ttctgcatg catcatat 38

<210> SEQ ID NO 83
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T24 fwd primer

<400> SEQUENCE: 83

aggcaaacaa ggtaccgggtg ttccatatag atgatcag 38

<210> SEQ ID NO 84
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T24 rev primer

<400> SEQUENCE: 84

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<210> SEQ ID NO 85
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T25 fwd primer

<400> SEQUENCE: 85

aggcaaacaa ggtaccaaga aaggaaaatg agtcctgc 38

<210> SEQ ID NO 86
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T25 rev primer

<400> SEQUENCE: 86

gccatggatc ggtaccgcat tgttttgatg ctgctacc 38

<210> SEQ ID NO 87
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T26 fwd primer

<400> SEQUENCE: 87

aggcaaacaa ggtaccgctt cactccagtt ccctatct 38

<210> SEQ ID NO 88
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T26 rev primer

<400> SEQUENCE: 88

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<210> SEQ ID NO 89
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 89

aggcaaacaa ggtaccaatg ctgctatcca acaggtgg 38

<210> SEQ ID NO 90
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T27 rev primer

<400> SEQUENCE: 90

gccatggatc ggtaccgagt gaggtctagg ttctgttg 38

<210> SEQ ID NO 91
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T28 fwd primer

<400> SEQUENCE: 91

aggcaaacaa ggtacctgac atcttatagt ctgcaacc 38

<210> SEQ ID NO 92
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T28 rev primer

<400> SEQUENCE: 92

gccatggatc ggtaccgggtg acggcgacgc gatcga 36

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<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T29 fwd primer

<400> SEQUENCE: 93

aggcaaacaa ggtaccatga accagcgtaa gtactcaa 38

<210> SEQ ID NO 94
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T29 rev primer

<400> SEQUENCE: 94

gccatggatc ggtaccccggt ggcaatggct gtcatg 36

<210> SEQ ID NO 95
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: T30 fwd primer

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<400> SEQUENCE: 95

aggcaaacaa ggtacctact tgtagcaata caaaattaca 40

<210> SEQ ID NO 96

<211> LENGTH: 38

<212> TYPE: DNA

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<220> FEATURE:

<223> OTHER INFORMATION: T30 rev primer

<400> SEQUENCE: 96

gccatggatc ggtaccacac cacctgctgt ctgcgctt 38

<210> SEQ ID NO 97

<211> LENGTH: 38

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: T31 fwd primer

<400> SEQUENCE: 97

aggcaaacaa ggtacctttg tctctcgcc attgtgta 38

<210> SEQ ID NO 98

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: T31 rev primer

<400> SEQUENCE: 98

gccatggatc ggtaccgctg aaatttggtt atctgttatg 40

<210> SEQ ID NO 99

<211> LENGTH: 38

<212> TYPE: DNA

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: T32 fwd primer

<400> SEQUENCE: 99

aggcaaacaa ggtaccaggc caaggcgatc tgtgacta 38

<210> SEQ ID NO 100

<211> LENGTH: 40

<212> TYPE: DNA

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: T32 rev primer

<400> SEQUENCE: 100

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<210> SEQ ID NO 101

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<212> TYPE: DNA

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: T33 fwd primer

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aggcaaacaa ggtaccttca tttcgtcatg catcatat 38

<210> SEQ ID NO 102

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<211> LENGTH: 38
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<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: T33 rev primer

<400> SEQUENCE: 102

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<210> SEQ ID NO 103
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<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: T34 fwd primer

<400> SEQUENCE: 103

aggcaaacaa ggtacctgaa atcaatactg ttggctgg 38

<210> SEQ ID NO 104
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<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: T34 rev primer

<400> SEQUENCE: 104

gccatggatc ggtaccggtg ttccatatag atgatcag 38

<210> SEQ ID NO 105
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: PinII fwd primer

<400> SEQUENCE: 105

aggcaaacaa ggtaccctc ggtgacgtgg ggcaac 36

<210> SEQ ID NO 106
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Pin II rev primer

<400> SEQUENCE: 106

gccatggatc ggtaccgcaa aacacaccta gactag 36

<210> SEQ ID NO 107
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: GUS forward primer for RTPCR

<400> SEQUENCE: 107

atggtccgtc ctgtagaaac ccca 24

<210> SEQ ID NO 108
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: GUS reverse primer for RT-PCR

<400> SEQUENCE: 108

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caccgcgtct ttgatcgct	20
<210> SEQ ID NO 110 <211> LENGTH: 20 <212> TYPE: DNA <213> ORGANISM: Artificial sequence <220> FEATURE: <223> OTHER INFORMATION: DsRed iR primer for amplicon B <400> SEQUENCE: 110	
atgtcccagg cgaagggcag	20
<210> SEQ ID NO 111 <211> LENGTH: 20 <212> TYPE: DNA <213> ORGANISM: Artificial sequence <220> FEATURE: <223> OTHER INFORMATION: DsRed iR primer for amplicon C <400> SEQUENCE: 111	
ggaagttcac gccgatgaac	20
<210> SEQ ID NO 112 <211> LENGTH: 21 <212> TYPE: DNA <213> ORGANISM: Artificial sequence <220> FEATURE: <223> OTHER INFORMATION: DsRed iR priemr for amplicon D <400> SEQUENCE: 112	
ggaacaggtg gtggcggccc t	21
<210> SEQ ID NO 113 <211> LENGTH: 21 <212> TYPE: DNA <213> ORGANISM: Artificial sequence <220> FEATURE: <223> OTHER INFORMATION: PinII primer for amplicon E <400> SEQUENCE: 113	
acacacaact ttgatgccca c	21
<210> SEQ ID NO 114 <211> LENGTH: 23 <212> TYPE: DNA <213> ORGANISM: Artificial Sequence <220> FEATURE: <223> OTHER INFORMATION: GUS probe <400> SEQUENCE: 114	
aacgtgctga tggcgacga cca	23
<210> SEQ ID NO 115 <211> LENGTH: 21 <212> TYPE: DNA	

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: forward primer for GUS qRTPCR

<400> SEQUENCE: 115

cttacgtggc aaaggattcg a                21

<210> SEQ ID NO 116
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: reverse primer for GUS qRTPCR

<400> SEQUENCE: 116

gccccaatcc agtccattaa                20

<210> SEQ ID NO 117
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: DsRed probe

<400> SEQUENCE: 117

cggcgtgaac ttcccctccg a                21

<210> SEQ ID NO 118
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: fwd primer DsRed qRTPCR

<400> SEQUENCE: 118

aggacggctc cttcatctac                20

<210> SEQ ID NO 119
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: rev primer DsRed qRTPCR

<400> SEQUENCE: 119

gtcttcttct gcattacggg                20

<210> SEQ ID NO 120
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: MOPAT probe

<400> SEQUENCE: 120

accgtgaact tccgcaccga gc                22

<210> SEQ ID NO 121
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: fwd primer MOPAT qRTPCR

<400> SEQUENCE: 121

cgtgaaccac tacatcgaga c                21

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<210> SEQ ID NO 122
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: rev primer MOPAT qRTPCR

<400> SEQUENCE: 122

gtcgatccac tcctgcgg 18

<210> SEQ ID NO 123
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Gr5 probe sequence

<400> SEQUENCE: 123

ttgaagtcac aaagcca 17

<210> SEQ ID NO 124
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: fwd primer Gr5 qRTPCR

<400> SEQUENCE: 124

ggcagtttgg ttgatgctca t 21

<210> SEQ ID NO 125
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: rev primer Gr5 qRTPCR

<400> SEQUENCE: 125

tgctgtatat ctttgctttg aaccat 26

<210> SEQ ID NO 126
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for polyA mapping

<400> SEQUENCE: 126

gcgacacgac ggcacggttt tttttttttt ttttttttt 39

<210> SEQ ID NO 127
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer for polyA mapping

<400> SEQUENCE: 127

caccgcgtct ttgatcgct 20

<210> SEQ ID NO 128
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: primer for polyA mapping

<400> SEQUENCE: 128

gcgacacgac ggcacggttt 20

<210> SEQ ID NO 129

<211> LENGTH: 313

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 129

taaacttgaa gtctgttaaa ttgatgaca cctctcggtta ccaatcgaag aaatctagtgt 60

aatttccggg atttttagat atctgattct gttgcgaagt ttttttatcc ttattagtgt 120

ctgttgagtgt tagattgctt ggcgagtagc ccacaataaa gaaataaaaa tggcgaatct 180

ttagctttat ttactctgtt ttcatcgaa acagattcag taatatatac tctgtttttt 240

catcttacat ttgtttgcaa aaccgatatt atcaacttct cagtaacaca attcgttcct 300

gaaagagtgc aaa 313

<210> SEQ ID NO 130

<211> LENGTH: 296

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 130

ttatggagat ttaagtatc ttttgatgat agtttacaca ctttgaataa gctgattcta 60

ctttatttct ctctgtttgt ttactgcttc agtgttttaa gtcttctctt tgtgtttgtt 120

gctgttgtgt ctttgatgga tttttgtgat ccgatttaat aaaagaagtgt tgttcaaagt 180

aattctctag tctctttatt tgaattccg gggatagcag attgggttcc gcaacattga 240

ctccaagttt ataatgatct tgatgatggt ctaaaagttt tgaataagct gactct 296

<210> SEQ ID NO 131

<211> LENGTH: 314

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 131

gagatgaaga aattgctctt atggttctga aaacttctaa tatgtcgagt tgttctgagt 60

tttaagattt tccaaaatgt ctttgtcttt ttttttatat ctttagagtt acttgaacat 120

tgtgactact tctagggttg ggtttgtgtc aggtctgtta tatcgtgtgg tgggtctgtc 180

taatactgat tcaagttttt gttattcagc taaggaaactt ttcttgtttc tgaacaaatc 240

ttttgggtcc ctagagtaaa acttgacttc caaaagatag acttcctaag atcactggaa 300

tagataggag tgac 314

<210> SEQ ID NO 132

<211> LENGTH: 346

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 132

aactgagatg gaagaagaag ttgcaatagt ttttttaaac tagtttcttt ctacgtactc 60

tgttttttct ctgcttggtt catggtttga gtgggcaact actgatcttt cccattttcc 120

tgccggattt gtagaagaat aaaaagggtg aaaatgatca tcttgagatg gtgatgaaac 180

tcttaagatc ctctcttctt gcttctcttt ttatttgccg tgtcataatg aaaattgcat 240

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attcagatgg gcctgtgtgt tgagtaagtg gacctgtgtc cagagagttg attgagatgg    300
gcttcatttt aggcccacat gtttatcgat cagggttcatt ctcttc                    346

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<210> SEQ ID NO 133
<211> LENGTH: 333
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

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<400> SEQUENCE: 133

tgcggtatac ttggcatttg gttttgctgt accctttcga aatctttatg tcgttgttta    60
gtttgttgta ttcgactatc ttcttagact ttgctgaaat tctcaagaga tttttttact    120
caaacatcag tccacttgtg attggcattt atatttcaaa ctattgcctt agttacatct    180
tcaatagtcc acctatgaac gatctttagt aaattctctt attcactcgc ttactaagaa    240
ttaaacctaa agagaataca gaagaattcc ctagagtaag gatttggtgt agtgtaaaac    300
agactcttcc ctctttgtat tggttcagatt ctg                                333

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<210> SEQ ID NO 134
<211> LENGTH: 219
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

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<400> SEQUENCE: 134

gttggtttca tcttattttc tgcgattttt gtacttgctg gatttggaat ccatttgttt    60
tagctctctc gtataagatt gtctcatctt tgcttgtaa ctctatatat tgaatcatca    120
agatatggtt ttgctgtaa tcattgacct tcgatatttt ttgccaatc cgttctctct    180
accaacctaa gaaaaaatca ctaatatctc acattagag                                219

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<210> SEQ ID NO 135
<211> LENGTH: 243
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

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<400> SEQUENCE: 135

taacatcaaa gagcaggaag tttttaacaa ggaatctggt cgagacatcc atgttctgga    60
ccagacagtt ttttggttta gccttaaaat tccaagggtg tataagaaga acacactggt    120
tgttattctt tgcggttggt aaccaatata gtaatatcag tatttcgtct caatctctct    180
tgttcttata ataatagaat gagaaatcga aatggaattt tcatgtgaag tggattagta    240
aca                                                243

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<210> SEQ ID NO 136
<211> LENGTH: 244
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

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<400> SEQUENCE: 136

atacttttaa taacactttc aatttggttt ctttttcgca cttgtgcttc ttctccgctt    60
tcatcttagt tatggactgt tcctaagctt gccatgaata aaactgtgaa taataaagct    120
tttaagtctc tgtttcttac tttaagtcag acaataaaact tttaacactt gtgatcatga    180
atccttggcc ttcagtgtat gattgatgct cttaacactt ctggtgttgt agaggaaacat    240
tttt                                                244

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<210> SEQ ID NO 137

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<211> LENGTH: 277
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 137

tgtgaaacca atctggatat ccttgaaatt tgaataaggt tatgttgtga gtttatgaag    60
ttgtgggtcta gtgttgtatt ttgtttttct taaggataat gcatctgtgt gctttgctta    120
tctaaaaatct aaataaagtg ggtttctgca ttgtgacttt gcacaaactt cttttgttaa    180
aatgaataag aatcacatc aagaaaacag aacaagacca caacgagaag acttgaaact    240
ctctgaaggt atataaaca acagaacctt gtaaatt                                277

<210> SEQ ID NO 138
<211> LENGTH: 319
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 138

aaaagaaatg tctttaggtg acagtaagac catggaggag ttttcagctt taaattttgc    60
ttttgtaatt cagattccgg aatccttcat aatctctatc tgagtttagt ttgttgtttg    120
aatcaaacat ccgatttaaa gttatgttca ttccatcttc tctccctttt tcgagcatgc    180
gagaatatga ttccccctat tgaacaaatc aatcaacctt taagcgataa caaattggtg    240
ttgtgaaaat tattaacttc ttgatctcgt ttgtcagat ctaaaattac tatagccaag    300
ctacctttca cgtcaagtt                                319

<210> SEQ ID NO 139
<211> LENGTH: 293
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 139

tcactcaagt caaattgtct tggtcgtctc tttatatatt ttgtatctt cttattaaaa    60
aggtaaatat gacttttaat ataatgggtg gcttattgtg atttgcatt atgtttgtac    120
ctatctcttt tgtgagttgt gtgatagata tactttgtat tttttcttaa aagtcaatat    180
aaatttctgt ttgcgagaga aaaatcgaat ctttgaatag tgaactttgt ggcgataaac    240
taatataatg attaatagag agaatgttgc gatataggac actttcatat aat                                293

<210> SEQ ID NO 140
<211> LENGTH: 352
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 140

agagatagat tgattgatgg acttgtgatg agtgaataaa acagggagta gcattactca    60
ttcctccctt gtgagacact ttggaatcaa atcttacggt gctgctactc tctttgagtc    120
ttttcttttg tttttgttac ttgacacagt ttttttttgt ttccggtttg ttgacattta    180
gtttctcaat ctaaaactca gagacttatt ttcgctctct ttgatcaga attaggtata    240
tctttattcg gataatcctt cccatccaaa ctgaaattgt tagtaccaac atttttttta    300
tcagaacata tctcgagtac tgtgttgatt ggattccat atcttatggt tc                                352

<210> SEQ ID NO 141
<211> LENGTH: 243
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis thaliana

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<400> SEQUENCE: 141

ttctcaaagc tttgacatgt aaagataaat aaatactttc tgcttgatgc agtctcatga	60
gttttgtaca aatcatgtga acatataaat gcgctttata agtaaatgag tgtcttggtc	120
aatgaatcat atgaagaat ttgtatgact cagaaaattg gacaatgata tagaccttcc	180
aaattttgca ccctctaattg tgagatatta gtgatttttt cttagggttg tagagagaac	240
gga	243

<210> SEQ ID NO 142

<211> LENGTH: 286

<212> TYPE: DNA

<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 142

tagcactcat ggaagtcaag aagctctttg agatgaggat gacaggggtg tttaaaaaag	60
tatcgctttt tcatttttgt tgttgttttc cgttttcatt tgtgatctct tagttccgta	120
caaaaacgaat tgtgaggta attcaacttc tattttaact gatagccgag aaagcttgtc	180
tagttattta caaatgtttt atcaattgtg ataattgtac taatccactt cacatgaaaa	240
ttccatttcg atttctcatt ctattattat aagaacaaga gagatt	286

<210> SEQ ID NO 143

<211> LENGTH: 402

<212> TYPE: DNA

<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 143

gcattgtttt gatgctgcta cctataaaag tatgagcttc agatgagaat ttagagagct	60
cccctgaggc aatgggttat gactttgtta tcatcttagt actactccta tctaagggac	120
gggtgaaggc tgtaatctat gtgcggtgca atgataaggc tatcctttct gcgtttgatc	180
atgacatctc atcgctgttc gattctttct cgctggcgtc tgttatgttg aatgatgcaa	240
ttcttctgta agattccgcc tttaccgaaa tatctctagt atcaaattha aattggagta	300
cggatcctct ttgaacatac ggatctatth gagataatth tgtctgatca tcaacgagaa	360
ctcggaagcg tgccaacctt gtgggtcaat tgtaacgata aa	402

<210> SEQ ID NO 144

<211> LENGTH: 482

<212> TYPE: DNA

<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 144

aggcagcagc agtatccaac tagtcatgta tccagcctaa attgaaaagt cagatcatgt	60
gtaacatggc cctcaatatt tcgatgttgc cttgtggaaa aaatagctgg tattggtact	120
gtgtttttta ctctctccag ctaccgacgt tcagtgttag tgcacaaaat gttcatccat	180
ggtagtttgt ctacattgca gtcattgtaa gttaaacatt cagattttct gtacttttgc	240
atgtgttaact aaatgaaatg gtgtgttaca ttcattcctt caatcaaata atccatagaa	300
acaaactggg ttgtaactat tgtaactagt cgctagtgtc catgggtatt tcgattgtgg	360
aacataatta gtttaatctg cttcagtata acttaagccg gctttatcct gtgtatgcat	420
cagcttcgct ccattgaaca tccaaacatc agtataagca ttttgtggcg actaatcatc	480
cg	482

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<210> SEQ ID NO 145
 <211> LENGTH: 396
 <212> TYPE: DNA
 <213> ORGANISM: Oryza sativa

<400> SEQUENCE: 145

gagtgaggtc taggttctgt tgtctgtctg tccatcatcc atgtgttgac tgttgagggg	60
actcgtttct tcttttcttc acgagatgag tttttgtgtg cctgtaatac tagttttag	120
caaaggctgc gttacataag gtgatgagaa ttgaggtaaa atgagatctg tacactaaat	180
tcattcagac tgttttggca taaagaataa ttggccttc tgcgatttca gaagctataa	240
attgccatct cactaaattc tcttgggtcc tcatggcaat gcaacgacag tgtgaagcac	300
tgaagcccgat aatgctctat caccaccatg tacaacagaa ccatatatgt ccatatgtac	360
aactcgagtg ttgtttgagt ggccagcaaa ctggct	396

<210> SEQ ID NO 146
 <211> LENGTH: 415
 <212> TYPE: DNA
 <213> ORGANISM: Oryza sativa

<400> SEQUENCE: 146

ggtgacggcg acgcgatcga acaggtggtg atcgatgctg caacgtgtgt aaatatacag	60
cgccggctgg gtcaagagat ggctcgggtg acgcgcgcgc ggctgtcct ggcttggcg	120
cgggggcatt ctttagtttt tcatcttttc atcatctcag atggtagata caaacagtg	180
tatgtatgta gctctgtttc tctctataga accccaacaa attttgtgtg tgatgttgtt	240
tatcttcata tgctttgatc ttgaaatcgt ctaccttact actgccgac gttgctcaaa	300
agtgtggaag tttgaagcat ctccacggg cgttgcteta ctccatctc gtttcaccac	360
gaaatccct tcgcatagag gcctctcagc cgtacatctc caaaccacg ttctg	415

<210> SEQ ID NO 147
 <211> LENGTH: 290
 <212> TYPE: DNA
 <213> ORGANISM: Oryza sativa

<400> SEQUENCE: 147

ccgtggcaat ggctgtcatg ctttggcaca tactaatagc aaggtagaat ggtacagcta	60
tttcattatt tttgcccttg tatatttga tcactacatg agtaaagcag gtttagttat	120
cgatagtttt gttatgagtg atgaatgac tgcacgtac tgccaatgcc ttgcattctc	180
aaatgggtgc acacttgac tcatacaaaag ttagtacact ccatcatatt ataaattact	240
tttttttcaa gttaaatttc ctgaaagttt gataaaattt atagaaaaaa	290

<210> SEQ ID NO 148
 <211> LENGTH: 443
 <212> TYPE: DNA
 <213> ORGANISM: Oryza sativa

<400> SEQUENCE: 148

acaccacctg ctgtctgcgc ttgtttgttg ccacggctgc gctacaaaac caagccgtat	60
catctgccga acagctccat cgtagcttc ttttgatgcc ttacatctat cgctggacgt	120
ttatcgctgc tacttgtccc atacaggat tgtgtttgga tgattttag agagggtact	180
gtatggcata agatccttca tattaatgtt ctgtgggtca catatcaact tgctattatt	240
gtattcagcg gttctctctc tattttgcct taagctgtgg taccatttta agtccagtgc	300

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ttgcttttga ttgcttttct gagctttcca ggacatggaa tcgagcctgt gaatgtcgtc	360
ggccgggttta tccttttcgac taataattta aattgtccag tgttggttag gaatggagta	420
tcagattctg gcggtttgca tgc	443

<210> SEQ ID NO 149
 <211> LENGTH: 405
 <212> TYPE: DNA
 <213> ORGANISM: Oryza sativa

<400> SEQUENCE: 149

gctgaaattt gggtatctgt tatgagcata tctgatttcg ataccactg ttatgaaact	60
gaataaacgg cattcctgta tgctgggaat tttctcgta gtgtacgctc caataactcg	120
gccgttttca aagacaagca gtgatatgca aagcaatgct gtgtatcttg tgtgttacat	180
caggagtttt ttttaatggg gatttcgttc atagttttca gacatctggt tccgtcacac	240
gttcgtggga atgacttttt tcatatgaaa tgcgcccatt gctgcgcctg aaataatttt	300
acttgtcccg tttgggatga atgaattctt ttcctgttcg ttgttcagta attcacacag	360
agtcataaac ataccggtgg aaacatgctc acaaagaaag aaaca	405

<210> SEQ ID NO 150
 <211> LENGTH: 431
 <212> TYPE: DNA
 <213> ORGANISM: Oryza sativa

<400> SEQUENCE: 150

agtgttactt attgttgcta ctatccatat tcgctaccat gcttatcatc gctagattaa	60
aggacatgta ttccagtatg gtcgtgcttt ttgcttggtg ctctggtcac atttgtgatg	120
aatgttcgca gttttcgtgg tcatggctcg gattctacat tccacctaaa gaagttttta	180
cctggttatt taatccttga gttgttgaat tagctcatgg taattgtcag tagtcttcca	240
cttggttctc tctgtggatg atcggttctg tttctgtttt gcgctgtggc tgattgttct	300
catgttttta aggttttttg gttagtcaat ggtcgcctcg tcaactgtgag ccaaaccata	360
tgccggtagt tttcttcttc accatcatcc gtttgatcct gactcgcgga tctcctaate	420
caacttctct c	431

<210> SEQ ID NO 151
 <211> LENGTH: 423
 <212> TYPE: DNA
 <213> ORGANISM: Oryza sativa

<400> SEQUENCE: 151

ttggcagcct acccactctg gtaggaaaaa tggaaggggc aagaagatac agtcgatgat	60
atttgatgtg ctacatacca attgtaatat ttcattcata tctagagcta gaaggatatt	120
cacttgatatt tcagactctg gttcacgggt taaattgata ttgtggtaga atgctttctt	180
ggatgggtat atagtgtgac tcgttaaaaa tatgacaaaa cggttcagct actctttaca	240
agtgttacgg caaattgtag acccaattgc acttggcggt gagctgcttt gttggagcaa	300
cagggcactg tctgcttgcg tggatgaaaa gctgagtcac ctgaagctag tgaacatttt	360
ttcgtgggt cgctgcgtgt gttttttctc tgattgtggc ccggttgatt atgaaaatga	420
cca	423

<210> SEQ ID NO 152

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<211> LENGTH: 349
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 152

ggtgttccat atagatgatac agatttctat aaccacatga gtacaatgta gagaattcaa      60
atgttttga accacgtgag ctttgtacgc tatttgcacc acagttctcc ctgtatgttg      120
ttggtctttt tacaattaag aataatgcat gttgaagtat gagtcttctt gtttgcctct      180
ccttgatgat gaaacgctgc tgcacaaact gattattttt cagagaataa acgataaaca      240
aagcacgggtg aagtatcgtg taaccaccca taagtggtag agccgtagag gtaggactgt      300
gcatgctgaa ttgtaattac catggttagt tcagcagaat ttgcaaaaa      349

<210> SEQ ID NO 153
<211> LENGTH: 380
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 153

aagaaaggaa aatgagtcct gcggattctc ccttggtatg taaatatgat ggatgtgtag      60
ataaataaaa tccagtttgt tgttgtgttt cctgctgtgt gaggcgttaa gagaacttct      120
ggcgtgcttt gatttggagc agttaccatg actgttggac tggtttttgt atgtattgat      180
ggacaaagct agtaagcatt aatctatgag ctgcagttgt tttccttgat caatgattat      240
atatcagctg ctgttgtatt ggttatagtg gattctgact ttctgatacc atttcagtct      300
tcacaaaaac agcaggctca actacacttc tcttgccatt tcatcatcag aggaaaaagg      360
gggaactata ttctccctgc      380

<210> SEQ ID NO 154
<211> LENGTH: 343
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 154

gcttcactcc agttccctat cttggaaact tttgcatccg tgcaaatgta atctctgctc      60
tcgtgttagc ttgtacggag tagtgttctg attatggcaa agacgttgat gtaagcactc      120
ggcaccctct tctcgtatgt gattttttcc cggttggtat ttgaccagat gttcttgctc      180
aagaatatgc tacgttacat tgtaattact gtgccatgat gctctagctt ctacgtgagt      240
ggtcgaaatc ttccccaact tcttactaat atgcgaaatt tgcattccat ctacagcat      300
cacgtctcta ctcttcagtt ggtagaaagc attgccctat ctc      343

<210> SEQ ID NO 155
<211> LENGTH: 380
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 155

aatgtcgcta tccaacaggt ggagaaatc ggtgaacagg gtagggattt tcagaaagtt      60
tttagcatga gaacactggt ggaacagagt tttgtttcat ctataggctc tcggcgggta      120
attccgacca tctgttatct aagctatcat aaatcttggt actcatgtct gttccaacat      180
atgctataaa tgaatgactc gctaaagatc tacaagattt tgggtgccatt tccttaccaa      240
ttcctttgtg tcgttgacgt atgctgtagt gtatcggcgt tgctgttccc agactcgagt      300
gttgttgtgt tctgtcttct gttgcttggg cttgttatgt atgattgagt ttatagtatt      360

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ctctctcgtg tggtttgggc 380

<210> SEQ ID NO 156
 <211> LENGTH: 466
 <212> TYPE: DNA
 <213> ORGANISM: *Oryza sativa*

<400> SEQUENCE: 156

tgacatctta tagtctgcaa cctctcgtgt ctgaattcct atctttatca agtgttattg	60
cttcacgac tataggacag ctttcgtcga aagcttttgc tcatgtgatc tgaaggatt	120
catctagtct gatttttctg gacttgatc ggttttattg gattcatcca acatatatca	180
ataaaaaatg agttgtgttt cttttcttcc tagttcagtt aaaattattt ccctcctgcg	240
cttgtgtgt aattgtctgt gtacctgttg tttgtgactg tgtagttcc cttggatatg	300
atttcgtatt tgatgtgtac atggagatag cttagcttca ttattggagt atgaagttag	360
tatgacatag tcaactctct ggaaaattga cactgcaaac catattttta ttctgaacca	420
caaactcctag tcagtcctgt ggcatatgcc gtccgtttgc tgaatc	466

<210> SEQ ID NO 157
 <211> LENGTH: 482
 <212> TYPE: DNA
 <213> ORGANISM: *Oryza sativa*

<400> SEQUENCE: 157

atgaaccagc gtaagtactc aactgctgag atcgcatcct tttggagcat catctatctt	60
gtcaagctta tttgcaaata gctaagccgt ctctctatgt gtggtctgta atattaaccg	120
tgcgtaaaac agtggcaaga agtccctgtc cgtgtcatgg ttatcgagtc tgtctactta	180
ataacgtgtg ataccaggca ttgtgcctgt attttaacag taaaaattgg gtacgttggt	240
tgtgttttga tatatattgg agttggttta cctcagctgg atggagtacc ctacattcgc	300
attgtactgc ctacgtttta tattacaagt cattttaact tttttttgaa gttaaacttt	360
tatatgttta atcaagttta tagaaaaaca tagtaataata tttaacacaa aacaaaaaaa	420
aatcaaaata tgtttaatgt tagatgtaat gaaattaatt tagtggtata agcgtcggtta	480
ta	482

<210> SEQ ID NO 158
 <211> LENGTH: 384
 <212> TYPE: DNA
 <213> ORGANISM: *Oryza sativa*

<400> SEQUENCE: 158

tacttgtagc aatacaaaat tacagtagca ttgtacacta ctgccgtgcc agtccatgc	60
atagtcagca gctggccact ctctagctat atctagatgc gagagaattt taaggatgta	120
aatcatgcct tcacatgaat aaatcgttcg tccgtgcgtt gtgtattcat gtaaattttg	180
acggatggtc aagtaaaaat aacaatggca aattaattta gggaagaatc aaatatgttt	240
gcgttccttt tctgagccgt ggatgttgtt aatcagttct accaatcgct atttgtaaaa	300
agtttcttaa agaaatttcc ttcttgacat caatcaaagt actatatata aatcttcagg	360
ataaggcacg tcgccgacca aaca	384

<210> SEQ ID NO 159
 <211> LENGTH: 445
 <212> TYPE: DNA

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<213> ORGANISM: *Oryza sativa*

<400> SEQUENCE: 159

tttgtctctc ggccattgtg tatttttcct ctcaagttgt atatgttcgc cccggaggaa	60
aagttttgtt tcttctttcg ctgcctcttt tgtacctgtg gtttcctgg cgtgagagcc	120
agtctgttgc acgcctgatc cctcttttat cgggagaaag gttcaacgtt cgggtgctag	180
atacaaaatg gggtcctaga gcccttcttg gtcgtttata tttagtgtac tattagtgat	240
aattggtgta aattagtttt cccagtttc ctttttagaa ctcatgtaga ctttcttgca	300
tctgatgtta gtaaaatctt gctctagggt tgctggctat tcttatcctt agcctgactt	360
catgatgttt ctttctttgt gagcatgttt ccaccgggtat gtttatgact ctgtgtgaat	420
tactgaacaa cgaacaggaa aagaa	445

<210> SEQ ID NO 160

<211> LENGTH: 371

<212> TYPE: DNA

<213> ORGANISM: *Oryza sativa*

<400> SEQUENCE: 160

aggccaaggc gatctgtgac tatgtgatga acaaacagag cccttcagct ctgatggctc	60
atggctgtgt gacctgtga atccagcatt gtgtgtgctc gcgcgctca tgaattgtca	120
aaaattatgg ctggaaaacc aagtggtttc tggcaatatg tggtgtaccg cttgtatgta	180
aatgttggtg aaacaaagt aacatcgctt atctctgaat ctctaacgta agtgggtgct	240
taacaaaagc tgctttgccc cgctgtaagc ctgctacact agcgtgggtt cttacatctt	300
tgccctgctat aaattctgtt caatttcaag gggttccaag ctatgtttcc aacgttgggt	360
gagtttggat t	371

<210> SEQ ID NO 161

<211> LENGTH: 411

<212> TYPE: DNA

<213> ORGANISM: *Oryza sativa*

<400> SEQUENCE: 161

ttcatttcgt catgcatcat atcacctaa atatgcatgc gccataaaa acaagtcttg	60
attttatctt gttcattgct ccattctcag tcagtgtcca ctggtttgtc tgtcatgcat	120
ggatcatttt tactcttcaa ttcagttctg catttcagtt gagctgttca gctgagtgcc	180
ttgatttgta ccacctatct gccttggtac aaatttatgt caaagtcttc ttgctctggt	240
acagttttac gttttcttct gcaataactag tacgcacagg aagctaagct gacaccttcc	300
aactcttcaa gaaaacgaaa gctgcaacaa gtgtagcacg attcacgacc ccgagcatga	360
gctagggttag gcaaaacaaa caaatcagca gggtcggatg actttactta c	411

<210> SEQ ID NO 162

<211> LENGTH: 519

<212> TYPE: DNA

<213> ORGANISM: *Oryza sativa*

<400> SEQUENCE: 162

tgaaatcaat actgttggct ggtgtttgca tagagaaaca atcacaatta cttagttagt	60
cacatcctaa attctaacta gaacggcaca tgcccgaaat tttgactgca aattgctttg	120
ttggattgtg ttacacggct tcagagcggg tgccaaaagt tcatttagaa gaaaggctgt	180
cagaagttat cctataaatt taaaaatagt gcgcttccaa accaagcgcc tttttcagtt	240

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gttcggtaca tcaaatatgt attgtatacc ttggaggctt ggaatataaa tatgggcacg	300
ctagtgtctac agccatttgc tactgatgta ccagcaacca ttggtttgta ccttgattaa	360
ttcatgacga tgggtctaatt ctgttgctct ctttttgcaa attctgctga actaaccatg	420
gtaattacaa ttcagcatgc acagtctctac ctctacggct ctaccactta tgggtgggta	480
cacgatactt caccgtgctt tgtttatcgt ttattctct	519

We claim:

1. A recombinant construct comprising a polynucleotide comprising:

(a) a nucleotide sequence as set forth in SEQ ID NO: 29; or

(b) a functional fragment of at least 200 contiguous nucleotides of (a) having terminator activity; wherein the polynucleotide is operably linked to the 3' end of a heterologous polynucleotide, wherein the heterologous polynucleotide is operably linked to a promoter; and further wherein the polynucleotide functions as a transcriptional terminator for the heterologous polynucleotide in a plant cell.

2. The recombinant construct of claim 1 wherein the polynucleotide functions as a bidirectional transcriptional terminator.

3. The recombinant construct of claim 2 wherein the bidirectional transcriptional terminator is operably linked to:

(a) the 3' end of a first heterologous polynucleotide, wherein the heterologous polynucleotide is operably linked to a first promoter; and

(b) the 3' end of a second heterologous polynucleotide, wherein the second heterologous polynucleotide is operably linked to a second promoter;

wherein the first and the second heterologous polynucleotides are in a convergent transcription orientation with respect to one another.

4. A plant comprising in its genome the recombinant construct of claim 1.

5. A seed from the plant of claim 4, wherein the seed comprises said recombinant construct.

6. The plant of claim 4, wherein said plant is selected from the group consisting of: *Arabidopsis*, maize, soybean, sunflower, *sorghum*, canola, mustard, wheat, alfalfa, cotton, rice, barley, millet, sugar cane and switchgrass.

7. The seed of claim 5, wherein said seed is selected from the group consisting of: *Arabidopsis*, maize, soybean, sunflower, *sorghum*, canola, mustard, wheat, alfalfa, cotton, rice, barley, millet, sugar cane and switchgrass.

8. A method of expressing a heterologous polynucleotide in a plant, comprising the steps of:

(a) introducing into a regenerable plant cell the recombinant construct of claim 1;

(b) regenerating a transgenic plant from the regenerable plant cell of (a), wherein the transgenic plant comprises in its genome the recombinant construct of claim 1; and

(c) obtaining a progeny plant from the transgenic plant of step (b), wherein the progeny plant comprises in its genome the recombinant construct of claim 1 and exhibits expression of the heterologous polynucleotide.

9. A method of regulating the expression of two heterologous polynucleotides in a plant, comprising the steps of:

(a) introducing into a regenerable plant cell the recombinant construct of claim 3;

(b) regenerating a transgenic plant from the regenerable plant cell of (a), wherein the transgenic plant comprises in its genome the recombinant construct of claim 3; and

(c) obtaining a progeny plant from the transgenic plant of step (b), wherein the progeny plant comprises in its genome the recombinant construct of claim 3 and exhibits expression of both the first heterologous polynucleotide and the second heterologous polynucleotide.

10. The method of claim 8, wherein said plant is selected from the group consisting of: *Arabidopsis*, maize, soybean, sunflower, *sorghum*, canola, mustard, wheat, alfalfa, cotton, rice, barley, millet, sugar cane and switchgrass.

11. The method of claim 9, wherein said plant is selected from the group consisting of: *Arabidopsis*, maize, soybean, sunflower, *sorghum*, canola, mustard, wheat, alfalfa, cotton, rice, barley, millet, sugar cane and switchgrass.

12. A plant comprising in its genome the recombinant construct of claim 3.

13. A seed from the plant of claim 12, wherein the seed comprises said recombinant construct.

14. The plant of claim 12, wherein said plant is selected from the group consisting of: *Arabidopsis*, maize, soybean, sunflower, *sorghum*, canola, mustard, wheat, alfalfa, cotton, rice, barley, millet, sugar cane and switchgrass.

15. The seed of claim 13, wherein said seed is selected from the group consisting of: *Arabidopsis*, maize, soybean, sunflower, *sorghum*, canola, mustard, wheat, alfalfa, cotton, rice, barley, millet, sugar cane and switchgrass.

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