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(54) **PROMOTERS FROM *BRASSICA NAPUS* FOR SEED SPECIFIC GENE EXPRESSION**

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(52) **U.S. Cl.**

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USPC ..... **536/24.1**; 800/278; 800/298; 435/320.1;  
435/419

(58) **Field of Classification Search**

None  
See application file for complete search history.

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(57) **ABSTRACT**

The present invention is concerned with means and methods for allowing tissue specific and, in particular, seed specific expression of genes. The present invention, accordingly, relates to a polynucleotide comprising an expression control sequence which allows seed specific expression of a nucleic acid of interest being operatively linked thereto. Moreover, the present invention contemplates vectors, host cells, non-human transgenic organisms comprising the aforementioned polynucleotide as well as methods and uses of such a polynucleotide.

**14 Claims, 4 Drawing Sheets**



Fig. 2

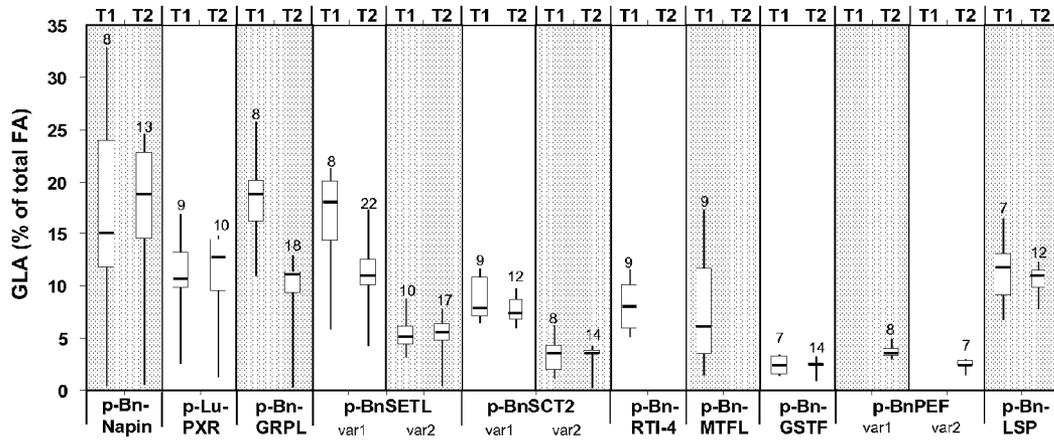


Fig. 3

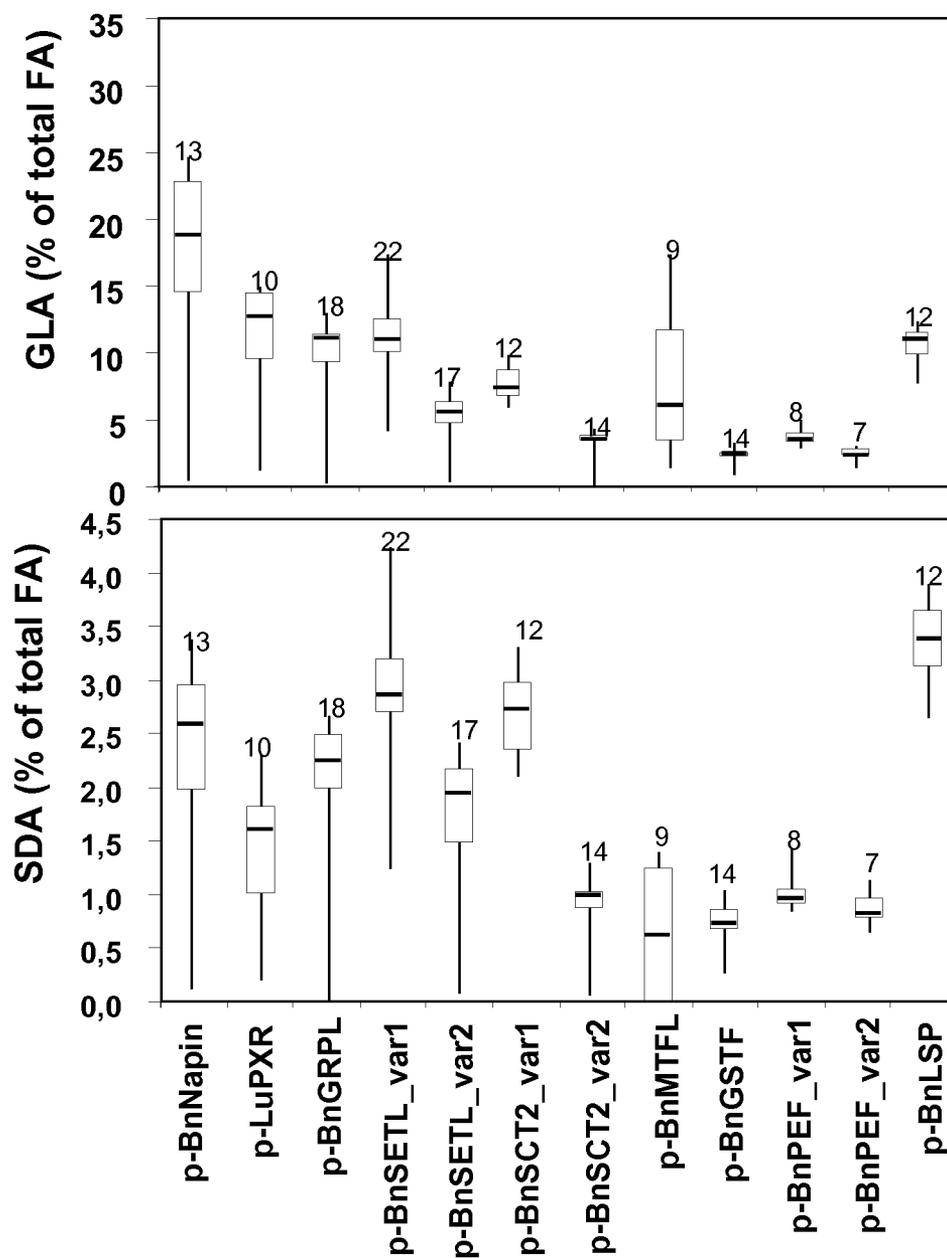
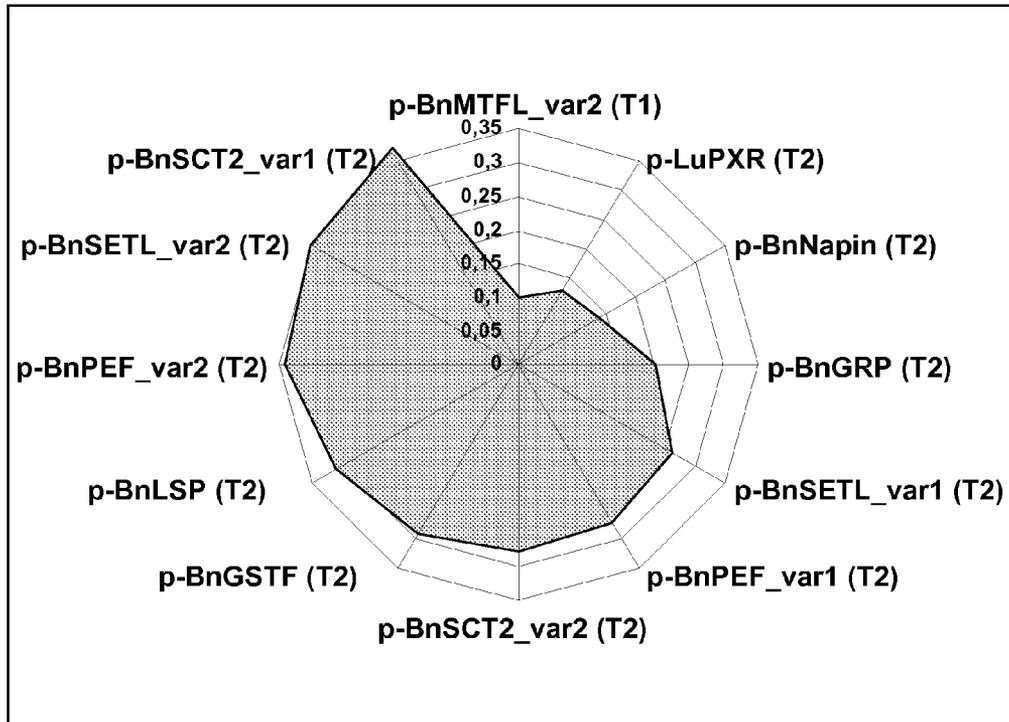


Fig. 4



## PROMOTERS FROM *BRASSICA NAPUS* FOR SEED SPECIFIC GENE EXPRESSION

### RELATED APPLICATIONS

This application is a national stage application (under 35 U.S.C. §371) of PCT/EP2009/058138, filed Jun. 30, 2009, which claims benefit of European application 08159440.0, filed Jul. 1, 2008.

### SUBMISSION OF SEQUENCE LISTING

The Sequence Listing associated with this application is filed in electronic format via EFS-Web and hereby incorporated by reference into the specification in its entirety. The name of the text file containing the Sequence Listing is Sequence\_Listing\_17418\_00062. The size of the text file is 416 KB, and the text file was created on Dec. 28, 2010.

### FIELD OF THE INVENTION

The present invention is concerned with means and methods for allowing tissue specific and, in particular, seed specific expression of genes. The present invention, accordingly, relates to a polynucleotide comprising an expression control sequence which allows seed specific expression of a nucleic acid of interest being operatively linked thereto. Moreover, the present invention contemplates vectors, host cells, non-human transgenic organisms comprising the aforementioned polynucleotide as well as methods and uses of such a polynucleotide.

### BACKGROUND OF THE INVENTION

In the field of "green" (agricultural) biotechnology, plants are genetically manipulated in order to confer beneficial traits. These beneficial traits may be yield increase, tolerance increase, reduced dependency on fertilizers, herbicidal, pesticidal- or fungicidal-resistance, or the capability of producing chemical specialties such as nutrients, drugs, oils for food and petrochemistry etc.

In many cases, it is required to express a heterologous gene in the genetically modified plants at a rather specific location in order to obtain a plant exhibiting the desired beneficial trait. One major location for gene expression is the plant seed. In the seeds, many important synthesis pathways, e.g., in fatty acid synthesis, take place. Accordingly, expression of heterologous genes in seeds allow for the manipulation of fatty acid synthesis pathways and, thus, for the provision of various fatty acid derivatives and lipid-based compounds.

However, for many heterologous genes, a seed specific expression will be required. Promoters which allow for a seed specific expression are known in the art. Such promoters include the oilseed rape napin promoter (U.S. Pat. No. 5,608, 152), the *Vicia faba* USP promoter (Baeumlein et al., Mol Gen Genet, 1991, 225 (3):459-67), the *Arabidopsis* oleosin promoter (WO 98/45461), the *Phaseolus vulgaris* phaseolin promoter (U.S. Pat. No. 5,504,200), the *Brassica* Bce4 promoter (WO 91/13980) or the legumine B4 promoter (LeB4; Baeumlein et al., 1992, Plant Journal, 2 (2):233-9), and promoters which bring about the seed-specific expression in monocotyledonous plants such as maize, barley, wheat, rye, rice and the like. Suitable noteworthy promoters are the barley Ipt2 or Ipt1 gene promoter (WO 95/15389 and WO 95/23230) or the promoters from the barley hordein gene, the rice glutelin gene, the rice oryza gene, the rice prolamine gene, the wheat gliadine gene, the wheat glutelin gene, the

maize zeine gene, the oat glutelin gene, the sorghum kasirin gene or the rye secalin gene, which are described in WO 99/16890.

However, there is a clear need for further expression control sequences such as promoters and terminators which allow for a reliable and efficient control of expression of foreign nucleic acids in seeds.

The technical problem underlying this invention can be seen as the provision of means and methods complying with the aforementioned needs. The technical problem is solved by the embodiments characterized in the claims and herein below.

### BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 shows a developmental expression analysis. Tissue types and developmental stages are given as listed in table 10. Samples 10, 11, 12 were pooled (assigned as 10), as well as samples 13, 14, 15 (assigned as 13).

FIG. 2 shows the 18:3n-6 (GLA) content of seeds-oil of seeds harvested from transgenic plants harboring the T-DNA from vectors described in example 3. Shown are data from T1 seeds and T2 seeds as indicated on top of the figure. Measurements on T1 on seeds are on individual single seeds; measurements on T2 seeds are on seed batches. The black line indicates the minimal and the maximal observation, the box reaches from the 25% quartil to the 75 quartil; the median is indicated as black line within the box. The number of individual measurements is indicated as number above each box.

FIG. 3 shows the 18:3n-6 (GLA) and 18:4n-3 (SDA) content of seeds-oil of seeds harvested from transgenic *Arabidopsis* plants harboring the T-DNA from vectors described in example 3.

FIG. 4 illustrates for the different promoters the different ratios of the omega-3 fatty acid SDA to the omega-6 fatty acid GLA.

### DETAILED DESCRIPTION OF THE INVENTION

Accordingly, the present invention relates to a polynucleotide comprising an expression control sequence which allows seed specific expression of a nucleic acid of interest being operatively linked thereto, said expression control sequence being selected from the group consisting of:

- (a) an expression control sequence having a nucleic acid sequence as shown in any one of SEQ ID NOs: 1, 6, 9, 14, 16, 22, 25, 70, 77, 85, 95, 103, 111, 119, 124 or 131;
- (b) an expression control sequence having a nucleic acid sequence which is at least 80% identical to a nucleic acid sequence shown in any one of SEQ ID NOs: 1, 6, 9, 14, 16, 22, 25, 70, 77, 85, 95, 103, 111, 119, 124 or 131;
- (c) an expression control sequence having a nucleic acid sequence which hybridizes under stringent conditions to a nucleic acid sequence as shown in any one of SEQ ID NOs: 1, 6, 9, 14, 16, 22, 25, 70, 77, 85, 95, 103, 111, 119, 124 or 131;
- (d) an expression control sequence having a nucleic acid sequence which hybridizes to a nucleic acid sequences located upstream of an open reading frame sequence shown in any one of SEQ ID NOs: 5, 13, 20, 21, 27, 28, 71, 78, 86, 96, 104, 112 or 125;
- (e) an expression control sequence having a nucleic acid sequence which hybridizes to a nucleic acid sequences located upstream of an open reading frame sequence being at least 80% identical to an open reading frame sequence as shown in any one of SEQ ID NOs: 5, 13, 20, 21, 27, 28, 71, 78, 86, 96, 104, 112 or 125;

(f) an expression control sequence obtainable by 5' genome walking or by thermal asymmetric interlaced polymerase chain reaction (TAIL-PCR) on genomic DNA from the first exon of an open reading frame sequence as shown in any one of SEQ ID NOs: 5, 13, 20, 21, 27, 28, 71, 78, 86, 96, 104, 112 or 125; and

(g) an expression control sequence obtainable by 5' genome walking or TAIL PCR on genomic DNA from the first exon of an open reading frame sequence being at least 80% identical to an open reading frame as shown in any one of SEQ ID NOs: 5, 13, 20, 21, 27, 28, 71, 78, 86, 96, 104, 112 or 125.

The term "polynucleotide" as used herein refers to a linear or circular nucleic acid molecule. It encompasses DNA as well as RNA molecules. The polynucleotide of the present invention is characterized in that it shall comprise an expression control sequence as defined elsewhere in this specification. In addition to the expression control sequence, the polynucleotide of the present invention, preferably, further comprises at least one nucleic acid of interest being operatively linked to the expression control sequence and/or a termination sequence or transcription. Thus, the polynucleotide of the present invention, preferably, comprises an expression cassette for the expression of at least one nucleic acid of interest. Alternatively, the polynucleotide may comprise in addition to the said expression control sequence a multiple cloning site and/or a termination sequence for transcription. In such a case, the multiple cloning site is, preferably, arranged in a manner as to allow for operative linkage of a nucleic acid to be introduced in the multiple cloning site with the expression control sequence. In addition to the aforementioned components, the polynucleotide of the present invention, preferably, could comprise components required for homologous recombination, i.e. flanking genomic sequences from a target locus. However, also preferably, the polynucleotide of the present invention can essentially consist of the said expression control sequence.

The term "expression control sequence" as used herein refers to a nucleic acid which is capable of governing the expression of another nucleic acid operatively linked thereto, e.g. a nucleic acid of interest referred to elsewhere in this specification in detail. An expression control sequence as referred to in accordance with the present invention, preferably, comprises sequence motifs which are recognized and bound by polypeptides, i.e. transcription factors. The said transcription factors shall upon binding recruit RNA polymerases, preferably, RNA polymerase I, II or III, more preferably, RNA polymerase II or III, and most preferably, RNA polymerase II. Thereby the expression of a nucleic acid operatively linked to the expression control sequence will be initiated. It is to be understood that dependent on the type of nucleic acid to be expressed, i.e. the nucleic acid of interest, expression as meant herein may comprise transcription of RNA polynucleotides from the nucleic acid sequence (as suitable for, e.g., anti-sense approaches or RNAi approaches) or may comprises transcription of RNA polynucleotides followed by translation of the said RNA polynucleotides into polypeptides (as suitable for, e.g., gene expression and recombinant polypeptide production approaches). In order to govern expression of a nucleic acid, the expression control sequence may be located immediately adjacent to the nucleic acid to be expressed, i.e. physically linked to the said nucleic acid at its 5' end. Alternatively, it may be located in physical proximity. In the latter case, however, the sequence must be located so as to allow functional interaction with the nucleic acid to be expressed. An expression control sequence referred to herein, preferably, comprises between 200 and 5,000

nucleotides in length. More preferably, it comprises between 500 and 2,500 nucleotides and, more preferably, at least 1,000 nucleotides. As mentioned before, an expression control sequence, preferably, comprises a plurality of sequence motifs which are required for transcription factor binding or for conferring a certain structure to the polynucleotide comprising the expression control sequence. Sequence motifs are also sometimes referred to as cis-regulatory elements and, as meant herein, include promoter elements as well as enhancer elements. Preferred expression control sequences to be included into a polynucleotide of the present invention have a nucleic acid sequence as shown in any one of SEQ ID NOs: 1, 6, 9, 14, 16, 22, 25, 70, 77, 85, 95, 103, 111, 119, 124 and 131.

Further preferably, an expression control sequence comprised by a polynucleotide of the present invention has a nucleic acid sequence which hybridizes to a nucleic acid sequences located upstream of an open reading frame sequence shown in any one of SEQ ID NOs: 5, 13, 20, 21, 27, 28, 71, 78, 86, 96, 104, 112 and 125, i.e. is a variant expression control sequence. It will be understood that expression control sequences may slightly differ in its sequences due to allelic variations. Accordingly, the present invention also contemplates an expression control sequence which can be derived from an open reading frame as shown in any one of SEQ ID NOs: 5, 13, 20, 21, 27, 28, 71, 78, 86, 96, 104, 112 and 125. Said expression control sequences are capable of hybridizing, preferably under stringent conditions, to the upstream sequences of the open reading frames shown in any one of SEQ ID NOs: 5, 13, 20, 21, 27, 28, 71, 78, 86, 96, 104, 112 and 125, i.e. the expression control sequences shown in any one of SEQ ID NOs: 1, 6, 9, 14, 16, 22, 25, 70, 77, 85, 95, 103, 111, 119, 124 and 131. Stringent hybridization conditions as meant herein are, preferably, hybridization conditions in 6x sodium chloride/sodium citrate (=SSC) at approximately 45° C., followed by one or more wash steps in 0.2xSSC, 0.1% SDS at 53 to 65° C., preferably at 55° C., 56° C., 57° C., 58° C., 59° C., 60° C., 61° C., 62° C., 63° C., 64° C. or 65° C. The skilled worker knows that these hybridization conditions differ depending on the type of nucleic acid and, for example when organic solvents are present, with regard to the temperature and concentration of the buffer. For example, under "standard hybridization conditions" the temperature differs depending on the type of nucleic acid between 42° C. and 58° C. in aqueous buffer with a concentration of 0.1 to 5xSSC (pH 7.2). If organic solvent is present in the abovementioned buffer, for example 50% formamide, the temperature under standard conditions is approximately 42° C. The hybridization conditions for DNA:DNA hybrids are preferably for example 0.1xSSC and 20° C. to 45° C., preferably between 30° C. and 45° C. The hybridization conditions for DNA:RNA hybrids are preferably, for example, 0.1xSSC and 30° C. to 55° C., preferably between 45° C. and 55° C. The abovementioned hybridization temperatures are determined for example for a nucleic acid with approximately 100 bp (=base pairs) in length and a G+C content of 50% in the absence of formamide. Such hybridizing expression control sequences are, more preferably, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the expression control sequences as shown in any one of SEQ ID NOs: 1, 6, 9, 14, 16, 22, 25, 70, 77, 85, 95, 103, 111, 119, 124 and 131. The percent identity values are, preferably, calculated over the entire nucleic acid sequence region. A series of programs based on a variety of algorithms is available to the skilled worker for comparing different sequences. In this context, the algorithms of Needleman and Wunsch or Smith and Waterman give particularly

reliable results. To carry out the sequence alignments, the program PileUp (J. Mol. Evolution., 25, 351-360, 1987, Higgins 1989, CABIOS, 5: 151-153) or the programs Gap and BestFit (Needleman 1970 J. Mol. Biol. 48; 443-453 and Smith 1981, Adv. Appl. Math. 2; 482-489), which are part of the GCG software packet (Genetics Computer Group, 575 Science Drive, Madison, Wis., USA 53711 version 1991), are to be used. The sequence identity values recited above in percent (%) are to be determined, preferably, using the program GAP over the entire sequence region with the following settings: Gap Weight: 50, Length Weight: 3, Average Match: 10.000 and Average Mismatch: 0.000, which, unless otherwise specified, shall always be used as standard settings for sequence alignments.

Moreover, expression control sequences which allow for seed specific expression can not only be found upstream of the aforementioned open reading frames having a nucleic acid sequence as shown in any one of SEQ ID NOs. 5, 13, 20, 21, 27, 28, 71, 78, 86, 96, 104, 112 and 125. Rather, expression control sequences which allow for seed specific expression can also be found upstream of orthologous, paralogous or homologous genes (i.e. open reading frames). Thus, also preferably, a variant expression control sequence comprised by a polynucleotide of the present invention has a nucleic acid sequence which hybridizes to a nucleic acid sequences located upstream of an open reading frame sequence being at least 70%, more preferably, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94% at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to a sequence as shown in any one of SEQ ID NOs: 5, 13, 20, 21, 27, 28, 71, 78, 86, 96, 104, 112 and 125. The said variant open reading shall encode a polypeptide having the biological activity of the corresponding polypeptide being encoded by the open reading frame shown in any one of SEQ ID NOs.: 5, 13, 20, 21, 27, 28, 71, 78, 86, 96, 104, 112 and 125. In this context it should be mentioned that the open reading frame shown in SEQ ID NO: 5 encodes a polypeptide showing similarity to gibberlin responsive proteins, the open reading frame shown in SEQ ID NO: 13 encodes a polypeptide belonging to the pectinesterase family, the open reading frame shown in SEQ ID NO: 20 encodes "sinapoyl choline transferase 1" (SCT1), and the open reading frames shown in SEQ ID NO: 21 encodes "sinapoyl choline transferase 2" (SCT2). These biological activities can be determined by those skilled in the art without further ado. The open reading frames shown in SEQ ID NO: 27 and 28 encode polypeptides showing homology to seed proteins with yet unknown functions.

TABLE 1

Protein function of genes identified to be seed specifically expressed:	
SEQ ID	Protein function
5	putative gibberelin responsive protein
13	putative pectinesterase
20	Sinapoyl choline transferase
21	Sinapoyl choline transferase
27	Seed protein
28	Seed protein
72	Seed protein
80	CRU4 subunit of Cruciferin (seed storage protein)
88	Myrosinase
98	Seed protein
106	serine proteinase inhibitor
114	Transcription factor involved in embryonic development
121	Glutathione S-transferase
133	Seed protein

Also preferably, a variant expression control sequence comprised by a polynucleotide of the present invention is (i) obtainable by 5' genome walking or TAIL PCR from an open reading frame sequence as shown in any one of SEQ ID NOs: 5, 13, 20, 21, 27, 28, 71, 78, 86, 96, 104, 112 and 125 or (ii) obtainable by 5' genome walking or TAIL PCR from an open reading frame sequence being at least 80% identical to an open reading frame as shown in any one of SEQ ID NOs: 5, 13, 20, 21, 27, 28, 71, 78, 86, 96, 104, 112 and 125. Variant expression control sequences are obtainable without further ado by the genome walking technology or by thermal asymmetric interlaced polymerase chain reaction (TAIL-PCR) which can be carried out as described in the accompanying Examples by using, e.g., commercially available kits.

Variant expression control sequences referred to in this specification for the expression control sequence shown in SEQ ID NO: 1, preferably, comprise at least 80, at least 90, at least 100, at least 110, at least 120, at least 130, at least 140 or all of the sequence motifs recited in Table 1. Variant expression control sequences referred to in this specification for the expression control sequence shown in SEQ ID NO: 6, preferably, comprise at least 80, at least 90, at least 100, at least 110 or all of the sequence motifs recited in Table 2. Variant expression control sequences referred to in this specification for the expression control sequence shown in SEQ ID NO: 9, preferably, comprise at least 40, at least 50, at least 60 or all of the sequence motifs recited in Table 3. Variant expression control sequences referred to in this specification for the expression control sequence shown in SEQ ID NO: 14, preferably, comprise at least 50, at least 60, at least 70, at least 80, at least 90 or all of the sequence motifs recited in Table 4. Variant expression control sequences referred to in this specification for the expression control sequence shown in SEQ ID NO: 16, preferably, comprise at least 50, at least 60, at least 70, at least 80, at least 90 or all of the sequence motifs recited in Table 5. Variant expression control sequences referred to in this specification for the expression control sequence shown in SEQ ID NO: 22, preferably, comprise at least 80, at least 90, at least 100, at least 110, at least 120, at least 130 or all of the sequence motifs recited in Table 6. Variant expression control sequences referred to in this specification for the expression control sequence shown in SEQ ID NO: 25, preferably, comprise at least 80, at least 100, at least 120, at least 130, at least 140, at least 150 or all of the sequence motifs recited in Table 7.

Variant expression control sequences referred to in this specification also, preferably, comprise at least the cis-regulatory elements referred to in Table 8, below. Even more preferably, the variant regulatory expression control sequences comprise said elements with the same frequency and distribution as referred to in Table 9 for the individual regulatory sequences.

The term "seed specific" as used herein means that a nucleic acid of interest being operatively linked to the expression control sequence referred to herein will be predominantly expressed in seeds when present in a plant. A predominant expression as meant herein is characterized by a statistically significantly higher amount of detectable transcription in the seeds with respect to other plant tissues. A statistically significant higher amount of transcription is, preferably, an amount being at least two-fold, three-fold, four-fold, five-fold, ten-fold, hundred-fold, five hundred-fold or thousand-fold the amount found in at least one of the other tissues with detectable transcription. Alternatively, it is an expression in seeds whereby the amount of transcription in non-seed tissues is less than 1%, 2%, 3%, 4% or most preferably 5% of the overall (whole plant) amount of expression.

The amount of transcription directly correlates to the amount of transcripts (i.e. RNA) or polypeptides encoded by the transcripts present in a cell or tissue. Suitable techniques for measuring transcription either based on RNA or polypeptides are well known in the art. Seed specific alternatively and, preferably in addition to the above, means that the expression is restricted or almost restricted to seeds, i.e. there is essentially no detectable transcription in other tissues. Almost restricted as meant herein means that unspecific expression is detectable in less than ten, less than five, less than four, less than three, less than two or one other tissue(s). Seed specific expression as used herein includes expression in seed cells or their precursors, such as cells of the endosperm and of the developing embryo.

An expression control sequences can be tested for seed specific expression by determining the expression pattern of a nucleic acid of interest, e.g., a nucleic acid encoding a reporter protein, such as GFP, in a transgenic plant. Transgenic plants can be generated by techniques well known to the person skilled in the art and as discussed elsewhere in this specification. The aforementioned amounts or expression pattern are, preferably, determined by Northern Blot or in situ hybridization techniques as described in WO 02/102970 in *Brassica napus* plants, more preferably, at 20, 25, 30, 35 or 40 days after flowering. Preferred expression pattern for the expression control sequences according to the present invention are shown in the Figure or described in the accompanying Examples, below.

The term "nucleic acid of interest" refers to a nucleic acid which shall be expressed under the control of the expression control sequence referred to herein. Preferably, a nucleic acid of interest encodes a polypeptide the presence of which is desired in a cell or non-human organism as referred to herein and, in particular, in a plant seed. Such a polypeptide may be an enzyme which is required for the synthesis of seed storage compounds or may be a seed storage protein. It is to be understood that if the nucleic acid of interest encodes a polypeptide, transcription of the nucleic acid in RNA and translation of the transcribed RNA into the polypeptide may be required. A nucleic acid of interest, also preferably, includes biologically active RNA molecules and, more preferably, antisense RNAs, ribozymes, micro RNAs or siRNAs. Said biologically active RNA molecules can be used to modify the amount of a target polypeptide present in a cell or non-human organism. For example, an undesired enzymatic activity in a seed can be reduced due to the seed specific expression of an antisense RNAs, ribozymes, micro RNAs or siRNAs. The underlying biological principles of action of the aforementioned biologically active RNA molecules are well known in the art. Moreover, the person skilled in the art is well aware of how to obtain nucleic acids which encode such biologically active RNA molecules. It is to be understood that the biologically active RNA molecules may be directly obtained by transcription of the nucleic acid of interest, i.e. without translation into a polypeptide. It is to be understood that the expression control sequence may also govern the expression of more than one nucleic acid of interest, i.e. at least one, at least two, at least three, at least four, at least five etc. nucleic acids of interest.

The term "operatively linked" as used herein means that the expression control sequence of the present invention and a nucleic acid of interest, are linked so that the expression can be governed by the said expression control sequence, i.e. the expression control sequence shall be functionally linked to said nucleic acid sequence to be expressed. Accordingly, the expression control sequence and, the nucleic acid sequence to be expressed may be physically linked to each other, e.g., by

inserting the expression control sequence at the 5' end of the nucleic acid sequence to be expressed. Alternatively, the expression control sequence and the nucleic acid to be expressed may be merely in physical proximity so that the expression control sequence is capable of governing the expression of at least one nucleic acid sequence of interest. The expression control sequence and the nucleic acid to be expressed are, preferably, separated by not more than 500 bp, 300 bp, 100 bp, 80 bp, 60 bp, 40 bp, 20 bp, 10 bp or 5 bp.

Advantageously, it has been found in the studies underlying the present invention that seed specific expression of a nucleic acid of interest can be achieved by expressing said nucleic acid of interest under the control of an expression control sequence from *Brassica napus* or a variant expression control sequence as specified above. The expression control sequences provided by the present invention allow for a reliable and highly specific expression of nucleic acids of interest. Thanks to the present invention, it is possible to (i) specifically manipulate biochemical processes in seeds, e.g., by expressing heterologous enzymes or biologically active RNAs, or (ii) to produce heterologous proteins in seeds. In principle, the present invention contemplates the use of the polynucleotide, the vector, the host cell or the non-human transgenic organism for the expression of a nucleic acid of interest. Preferably, the envisaged expression is seed specific. More preferably, the nucleic acid of interest to be used in the various embodiments of the present invention encodes a seed storage protein or is involved in the modulation of seed storage compounds.

As used herein, seed storage compounds include fatty acids and triacylglycerides which have a multiplicity of applications in the food industry, in animal nutrition, in cosmetics and the pharmacological sector. Depending on whether they are free saturated or unsaturated fatty acids or else triacylglycerides with an elevated content of saturated or unsaturated fatty acids, they are suitable for various different applications. More preferably, the polynucleotide of the present invention comprising the expression control sequence referred to above is applied for the manufacture of polyunsaturated fatty acids (PUFAs). For the manufacture of PUFAs in seeds, the activity of enzymes involved in their synthesis, in particular, elongases and desaturases, needs to be modulated. This will be achieved by seed specific expression of the nucleic acids of interest encoding the aforementioned enzymes or by seed specific expression of antisense, ribozyme, RNAi molecules which downregulate the activity of the enzymes by interfering with their protein synthesis. PUFAs are seed storage compounds which can be isolated by a subsequently applied purification process using the aforementioned seeds.

Particularly preferred PUFAs in accordance with the present invention are polyunsaturated long-chain  $\omega$ -3-fatty acids such as eicosapentaenoic acid (=EPA, C20:5<sup>Δ5,8,11,14,17</sup>),  $\omega$ -3 eicosetraenoic acid (=ETA, C20:4<sup>Δ8,11,14,17</sup>), arachidonic acid (=ARA C20:4<sup>Δ5,8,11,14</sup>) or docosahexaenoic acid (=DHA, C22:6<sup>Δ4,7,10,13,16,19</sup>). They are important components of human nutrition owing to their various roles in health aspects, including the development of the child brain, the functionality of the eyes, the synthesis of hormones and other signal substances, and the prevention of cardiovascular disorders, cancer and diabetes (Poulos, A Lipids 30:1-14, 14<sup>Δ8,11,14,17</sup>995; Horrocks, L A and Yeo Y K Pharmacol Res 40:211-225, 1999). There is, therefore, a need for the production of polyunsaturated long-chain fatty acids.

Particular preferred enzymes involved in the synthesis of PUFAs are disclosed in WO 91/13972 ( $\Delta$ 9-desaturase), WO 93/11245 ( $\Delta$ 15-desaturase), WO 94/11516 ( $\Delta$ 12-desaturase), EP A 0 550 162, WO 94/18337, WO 97/30582, WO

97/21340, WO 95/18222, EP A 0 794 250, Stukey et al., J. Biol. Chem., 265, 1990: 20144-20149, Wada et al., Nature 347, 1990: 200-203 or Huang et al., Lipids 34, 1999: 649-659.  $\Delta 6$ -Desaturases are described in WO 93/06712, U.S. Pat. No. 5,614,393, U.S. Pat. No. 5,614,393, WO 96/21022, WO 00/21557 and WO 99/27111, and also the application for the production in transgenic organisms is described in WO 98/46763, WO 98/46764 and WO 98/46765. Here, the expression of various desaturases is also described and claimed in WO 99/64616 or WO 98/46776, as is the formation of polyunsaturated fatty acids. As regards the expression efficacy of desaturases and its effect on the formation of polyunsaturated fatty acids, it must be noted that the expression of a single desaturase as described to date has only resulted in low contents of unsaturated fatty acids/lipids such as, for example,  $\gamma$ -linolenic acid and stearidonic acid. Furthermore, mixtures of  $\omega$ -3- and  $\omega$ -6-fatty acids are usually obtained.

Furthermore, the present invention relates to a polynucleotide comprising an expression termination sequence which allows for termination of transcription of a nucleic acid of interest being operatively linked thereto, said expression termination sequence being selected from the group consisting of:

- (a) an expression termination sequence having a nucleic acid sequence as shown in any one of SEQ ID NOs: 2, 7, 10, 15, 17, 23, 71, 78, 86, 96, 104, 112, or 125;
- (b) an expression termination sequence having a nucleic acid sequence which is at least 80% identical to a nucleic acid sequence as shown in any one of SEQ ID NOs: which hybridizes under stringent conditions to a nucleic acid sequence as shown in any one of SEQ ID NOs: 2, 7, 10, 15, 17, 23, 71, 78, 86, 96, 104, 112, or 125;
- (c) an expression termination sequence having a nucleic acid sequence which hybridizes under stringent conditions to a nucleic acid sequence as shown in any one of SEQ ID NOs: 2, 7, 10, 15, 17, 23, 71, 78, 86, 96, 104, 112, or 125;
- (d) an expression termination sequence having a nucleic acid sequence which hybridizes to a nucleic acid sequences located downstream of an open reading frame sequence shown in any one of SEQ ID NOs: 5, 13, 20, 21, 27, 28, 71, 78, 86, 96, 104, 112 or 125;
- (e) an expression termination sequence having a nucleic acid sequence which hybridizes to a nucleic acid sequences located downstream of an open reading frame sequence being at least 80% identical to an open reading frame sequence as shown in any one of SEQ ID NOs: 5, 13, 20, 21, 27, 28, 71, 78, 86, 96, 104, 112 or 125;
- (f) an expression termination sequence obtainable by 3' genome walking or TAIL PCR on genomic DNA from the last exon of an open reading frame sequence as shown in any one of SEQ ID NOs: 5, 13, 20, 21, 27, 28, 71, 78, 86, 96, 104, 112 or 125; and
- (g) an expression termination sequence obtainable by 3' genome walking or TAIL PCR on genomic DNA from the last exon of an open reading frame sequence being at least 80% identical to an open reading frame as shown in any one of SEQ ID NOs: 5, 13, 20, 21, 27, 28, 71, 78, 86, 96, 104, 112 or 125.

The term "expression termination sequence" as used herein refers to a nucleic acid which is capable of governing the termination of the process of RNA transcription of a nucleic acid operatively linked thereto, e.g. a nucleic acid of interest referred to elsewhere in this specification in detail. A termination sequence as referred to in accordance with the present invention, preferably, contains a polyadenylation signal and furthermore mediates dissociation of RNA polymerases, preferably, RNA polymerase I, II or III, more prefer-

ably, RNA polymerase II or III, and most preferably, RNA polymerase II from the transcribed DNA. Thereby the elongation of a RNA transcript, transcribed from a nucleic acid operatively linked to the termination sequence will be terminated and the RNA will be released. In order to govern termination of transcription of a nucleic acid, the expression control sequence may be located immediately adjacent to the nucleic acid whose expression is to be terminated, i.e. physically linked to the said nucleic acid at its 3' end. Alternatively, it may be located in physical proximity. In the latter case, however, the sequence must be located so as to allow functional interaction with the nucleic acid whose transcription is to be terminated. A termination sequence referred to herein, preferably, comprises between 50 and 2,000 nucleotides in length. More preferably, it comprises between 100 and 800 nucleotides and, more preferably, at least 100 nucleotides. Preferred expression termination sequences are those comprised by the polynucleotide referred to above.

Furthermore, the definitions and explanations of the terms made above apply mutatis muandis except as specified herein below.

For termination sequences, the term "operatively linked" means that the termination sequence of the present invention and a nucleic acid of interest, are linked so that the termination of transcription of the mRNA can be governed by said termination sequence, i.e. the termination sequence shall be functionally linked to said nucleic acid sequence whose transcription is to be terminated. Accordingly, the expression control sequence, the nucleic acid sequence to be expressed and the termination sequence may be physically linked to each other, e.g., by inserting the expression control sequence at the 5' end of the nucleic acid sequence to be expressed and/or inserting the termination sequence at the 3' end of the nucleic acid sequence whose transcription is to be terminated. Alternatively, the expression control sequence and the nucleic acid to be expressed may be merely in physical proximity so that the expression control sequence is capable of governing the expression of at least one nucleic acid sequence of interest. The termination sequence and the nucleic acid whose transcription is to be terminated are, preferably, separated by not more than 50 bp, 40 bp, 20 bp, 10 bp or 5 bp.

Advantageously, the polynucleotide of the present invention comprising an expression termination sequence can be also applied for efficient expression control in plants and, in particular, plant seeds. Specifically, the expression termination sequence allows for accurate termination of transcription of the DNA into RNA after the nucleic acid sequence of interest has been transcribed. Thus, the transcription of undesired nucleic acid sequences is avoided.

The present invention also relates to a vector comprising the polynucleotide of the present invention.

The term "vector", preferably, encompasses phage, plasmid, viral or retroviral vectors as well as artificial chromosomes, such as bacterial or yeast artificial chromosomes. Moreover, the term also relates to targeting constructs which allow for random or site-directed integration of the targeting construct into genomic DNA. Such target constructs, preferably, comprise DNA of sufficient length for either homologous or heterologous recombination as described in detail below. The vector encompassing the polynucleotides of the present invention, preferably, further comprises selectable markers for propagation and/or selection in a host. The vector may be incorporated into a host cell by various techniques well known in the art. If introduced into a host cell, the vector may reside in the cytoplasm or may be incorporated into the genome. In the latter case, it is to be understood that the vector may further comprise nucleic acid sequences which allow for

homologous recombination or heterologous insertion. Vectors can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. The terms "transformation" and "transfection", conjugation and transduction, as used in the present context, are intended to comprise a multiplicity of prior-art processes for introducing foreign nucleic acid (for example DNA) into a host cell, including calcium phosphate, rubidium chloride or calcium chloride coprecipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, carbon-based clusters, chemically mediated transfer, electroporation or particle bombardment (e.g., "gene-gun"). Suitable methods for the transformation or transfection of host cells, including plant cells, can be found in Sambrook et al. (Molecular Cloning: A Laboratory Manual, 2<sup>nd</sup> ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989) and other laboratory manuals, such as Methods in Molecular Biology, 1995, Vol. 44, *Agrobacterium* protocols, Ed.: Gartland and Davey, Humana Press, Totowa, N.J. Alternatively, a plasmid vector may be introduced by heat shock or electroporation techniques. Should the vector be a virus, it may be packaged in vitro using an appropriate packaging cell line prior to application to host cells. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host/cells.

Preferably, the vector referred to herein is suitable as a cloning vector, i.e. replicable in microbial systems. Such vectors ensure efficient cloning in bacteria and, preferably, yeasts or fungi and make possible the stable transformation of plants. Those which must be mentioned are, in particular, various binary and co-integrated vector systems which are suitable for the T-DNA-mediated transformation. Such vector systems are, as a rule, characterized in that they contain at least the *vir* genes, which are required for the *Agrobacterium*-mediated transformation, and the sequences which delimit the T-DNA (T-DNA border). These vector systems, preferably, also comprise further cis-regulatory regions such as promoters and terminators and/or selection markers with which suitable transformed host cells or organisms can be identified. While co-integrated vector systems have *vir* genes and T-DNA sequences arranged on the same vector, binary systems are based on at least two vectors, one of which bears *vir* genes, but no T-DNA, while a second one bears T-DNA, but no *vir* gene. As a consequence, the last-mentioned vectors are relatively small, easy to manipulate and can be replicated both in *E. coli* and in *Agrobacterium*. These binary vectors include vectors from the pBIB-HYG, pPZP, pBecks, pGreen series. Preferably used in accordance with the invention are Bin19, pBU1101, pBinAR, pGPTV, pSUN and pCAMBIA. An overview of binary vectors and their use can be found in Hellens et al, Trends in Plant Science (2000) 5, 446-451. Furthermore, by using appropriate cloning vectors, the polynucleotide of the invention can be introduced into host cells or organisms such as plants or animals and, thus, be used in the transformation of plants, such as those which are published, and cited, in: Plant Molecular Biology and Biotechnology (CRC Press, Boca Raton, Fla.), chapter 6/7, pp. 71-119 (1993); F. F. White, Vectors for Gene Transfer in Higher Plants; in: Transgenic Plants, vol. 1, Engineering and Utilization, Ed.: Kung and R. Wu, Academic Press, 1993, 15-38; B. Jenes et al., Techniques for Gene Transfer, in: Transgenic Plants, vol. 1, Engineering and Utilization, Ed.: Kung and R. Wu, Academic Press (1993), 128-143; Potrykus, Annu. Rev. Plant Physiol. Plant Molec. Biol. 42 (1991), 205-225.

More preferably, the vector of the present invention is an expression vector. In such an expression vector, the poly-

nucleotide comprises an expression cassette as specified above allowing for expression in eukaryotic cells or isolated fractions thereof. An expression vector may, in addition to the polynucleotide of the invention, also comprise further regulatory elements including transcriptional as well as translational enhancers. Preferably, the expression vector is also a gene transfer or targeting vector. Expression vectors derived from viruses such as retroviruses, vaccinia virus, adeno-associated virus, herpes viruses, or bovine papilloma virus, may be used for delivery of the polynucleotides or vector of the invention into targeted cell population. Methods which are well known to those skilled in the art can be used to construct recombinant viral vectors; see, for example, the techniques described in Sambrook, Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory (1989) N.Y. and Ausubel, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. (1994).

Suitable expression vector backbones are, preferably, derived from expression vectors known in the art such as Okayama-Berg cDNA expression vector pcDV1 (Pharmacia), pCDM8, pRc/CMV, pcDNA1, pcDNA3 (Invitrogen) or pSPORT1 (GIBCO BRL). Further examples of typical fusion expression vectors are pGEX (Pharmacia Biotech Inc; Smith, D. B., and Johnson, K. S. (1988) Gene 67:31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.), where glutathione S-transferase (GST), maltose E-binding protein and protein A, respectively, are fused with the nucleic acid of interest encoding a protein to be expressed. The target gene expression of the pTrc vector is based on the transcription from a hybrid *trp-lac* fusion promoter by host RNA polymerase. The target gene expression from the pET 11d vector is based on the transcription of a T7-gn10-lac fusion promoter, which is mediated by a co-expressed viral RNA polymerase (T7 gn1). This viral polymerase is provided by the host strains BL21 (DE3) or HMS174 (DE3) from a resident  $\lambda$ -prophage which harbors a T7 gn1 gene under the transcriptional control of the *lacUV 5* promoter. Examples of vectors for expression in the yeast *S. cerevisiae* comprise pYepSec1 (Baldari et al. (1987) Embo J. 6:229-234), pMFa (Kurjan and Herskowitz (1982) Cell 30:933-943), pJRY88 (Schultz et al. (1987) Gene 54:113-123) and pYES2 (Invitrogen Corporation, San Diego, Calif.). Vectors and processes for the construction of vectors which are suitable for use in other fungi, such as the filamentous fungi, comprise those which are described in detail in: van den Hondel, C. A. M. J. J., & Punt, P. J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of fungi, J. F. Peberdy et al., Ed., pp. 1-28, Cambridge University Press: Cambridge, or in: More Gene Manipulations in Fungi (J. W. Bennett & L. L. Lasure, Ed., pp. 396-428: Academic Press: San Diego). Further suitable yeast vectors are, for example, pAG-1, YEp6, YEp13 or pEMBLyE23. As an alternative, the polynucleotides of the present invention can be also expressed in insect cells using baculovirus expression vectors. Baculovirus vectors which are available for the expression of proteins in cultured insect cells (for example Sf9 cells) comprise the pAc series (Smith et al. (1983) Mol. Cell. Biol. 3:2156-2165) and the pVL series (Lucklow and Summers (1989) Virology 170: 31-39).

The polynucleotides of the present invention can be used for expression of a nucleic acid of interest in single-cell plant cells (such as algae), see Falciatore et al., 1999, Marine Biotechnology 1 (3):239-251 and the references cited therein, and plant cells from higher plants (for example Spermatophytes, such as arable crops) by using plant expression vectors. Examples of plant expression vectors comprise those

which are described in detail in: Becker, D., Kemper, E., Schell, J., and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20:1195-1197; and Bevan, M. W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acids Res.* 12:8711-8721; Vectors for Gene Transfer in Higher Plants; in: *Transgenic Plants*, Vol. 1, Engineering and Utilization, Ed.: Kung and R. Wu, Academic Press, 1993, p. 15-38. A plant expression cassette, preferably, comprises regulatory sequences which are capable of controlling the gene expression in plant cells and which are functionally linked so that each sequence can fulfill its function, such as transcriptional termination, for example polyadenylation signals. Preferred polyadenylation signals are those which are derived from *Agrobacterium tumefaciens* T-DNA, such as the gene 3 of the Ti plasmid pTiACH5, which is known as octopine synthase (Gielen et al., *EMBO J.* 3 (1984) 835 et seq.) or functional equivalents of these, but all other terminators which are functionally active in plants are also suitable. Since plant gene expression is very often not limited to transcriptional levels, a plant expression cassette preferably comprises other functionally linked sequences such as translation enhancers, for example the overdrive sequence, which comprises the 5'-untranslated tobacco mosaic virus leader sequence, which increases the protein/RNA ratio (Galie et al., 1987, *Nucl. Acids Research* 15:8693-8711). Other preferred sequences for the use in functional linkage in plant gene expression cassettes are targeting sequences which are required for targeting the gene product into its relevant cell compartment (for a review, see Kermode, *Crit. Rev. Plant Sci.* 15, 4 (1996) 285-423 and references cited therein), for example into the vacuole, the nucleus, all types of plastids, such as amyloplasts, chloroplasts, chromoplasts, the extracellular space, the mitochondria, the endoplasmic reticulum, oil bodies, peroxisomes and other compartments of plant cells.

The abovementioned vectors are only a small overview of vectors to be used in accordance with the present invention. Further vectors are known to the skilled worker and are described, for example, in: *Cloning Vectors* (Ed., Pouwels, P. H., et al., Elsevier, Amsterdam-New York-Oxford, 1985, ISBN 0 444 904018). For further suitable expression systems for prokaryotic and eukaryotic cells see the chapters 16 and 17 of Sambrook, J., Fritsch, E. F., and Maniatis, T., *Molecular Cloning: A Laboratory Manual*, 2<sup>nd</sup> edition, Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

The present invention also contemplates a host cell comprising the polynucleotide or the vector of the present invention.

Host cells are primary cells or cell lines derived from multicellular organisms such as plants or animals. Furthermore, host cells encompass prokaryotic or eukaryotic single cell organisms (also referred to as micro-organisms). Primary cells or cell lines to be used as host cells in accordance with the present invention may be derived from the multicellular organisms referred to below. Host cells which can be exploited are furthermore mentioned in: Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, Calif. (1990). Specific expression strains which can be used, for example those with a lower protease activity, are described in: Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, Calif. (1990) 119-128. These include plant cells and certain tissues, organs and parts of plants in all their phenotypic forms such as anthers, fibers, root hairs, stalks, embryos, calli, cotyledons, petioles, harvested material, plant tissue, reproductive tissue and cell cultures which

are derived from the actual transgenic plant and/or can be used for bringing about the transgenic plant. Preferably, the host cells may be obtained from plants. More preferably, oil crops are envisaged which comprise large amounts of lipid compounds, such as oilseed rape, evening primrose, hemp, thistle, peanut, canola, linseed, soybean, safflower, sunflower, borage, or plants such as maize, wheat, rye, oats, triticale, rice, barley, cotton, cassava, pepper, Tagetes, Solanaceae plants such as potato, tobacco, eggplant and tomato, *Vicia* species, pea, alfalfa, bushy plants (coffee, cacao, tea), *Salix* species, trees (oil palm, coconut) and perennial grasses and fodder crops. Especially preferred plants according to the invention are oil crops such as soybean, peanut, oilseed rape, canola, linseed, hemp, evening primrose, sunflower, safflower, trees (oil palm, coconut). Suitable methods for obtaining host cells from the multicellular organisms referred to below as well as conditions for culturing these cells are well known in the art.

The micro-organisms are, preferably, bacteria or fungi including yeasts. Preferred fungi to be used in accordance with the present invention are selected from the group of the families Chaetomiaceae, Choanephoraceae, Cryptococcaceae, Cunninghamellaceae, Dematiaceae, Moniliaceae, Mortierellaceae, Mucoraceae, Pythiaceae, Saccharomycetaceae, Saprolegniaceae, Schizosacharomycetaceae, Sordariaceae or Tuberculariaceae. Further preferred micro-organisms are selected from the group: Choanephoraceae such as the genera *Blakeslee*, *Choanephora*, for example the genera and species *Blakeslea trispora*, *Choanephora cucurbitarum*, *Choanephora infundibulifera* var. *cucurbitarum*, Mortierellaceae, such as the genus *Mortierella*, for example the genera and species *Mortierella isabeffina*, *Mortierella polycephala*, *Mortierella ramanniana*, *Mortierella vinacea*, *Mortierella zonata*, Pythiaceae such as the genera *Pythium*, *hytophthora* for example the genera and species *Pythium debaryanum*, *Pythium intermedium*, *Pythium irregulare*, *Pythium megalacanthum*, *Pythium paroecandrum*, *Pythium sylvaticum*, *Pythium ultimum*, *Phytophthora cactorum*, *Phytophthora cinnamomi*, *Phytophthora citricola*, *Phytophthora citrophthora*, *Phytophthora cryptogea*, *Phytophthora drechsleri*, *Phytophthora erythroseptica*, *Phytophthora lateralis*, *Phytophthora megasperma*, *Phytophthora nicotianae*, *Phytophthora nicotianae* var. *parasitica*, *Phytophthora palmivora*, *Phytophthora parasitica*, *Phytophthora syringae*, Saccharomycetaceae such as the genera *Hansenula*, *Pichia*, *Saccharomyces*, *Saccharomyces*, *Yarrowia* for example the genera and species *Hansenula anomala*, *Hansenula californica*, *Hansenula canadensis*, *Hansenula capsulata*, *Hansenula ciferrii*, *Hansenula glucozyma*, *Hansenula henricii*, *Hansenula holstii*, *Hansenula minuta*, *Hansenula nonfermentans*, *Hansenula philodendri*, *Hansenula polymorpha*, *Hansenula saturnus*, *Hansenula subpelliculosa*, *Hansenula wickerhamii*, *Hansenula wingei*, *Pichia alcoholophila*, *Pichia angusta*, *Pichia anomala*, *Pichia bispora*, *Pichia burtonii*, *Pichia canadensis*, *Pichia capsulata*, *Pichia carsonii*, *Pichia cellobiosa*, *Pichia ciferrii*, *Pichia farinosa*, *Pichia fermentans*, *Pichia finlandica*, *Pichia glucozyma*, *Pichia guilliermondii*, *Pichia haplophila*, *Pichia henricii*, *Pichia holstii*, *Pichia jadinii*, *Pichia lindnerii*, *Pichia membranaefaciens*, *Pichia methanolica*, *Pichia minuta* var. *minuta*, *Pichia minuta* var. *nonfermentans*, *Pichia norvegensis*, *Pichia ohmeri*, *Pichia pastoris*, *Pichia philodendri*, *Pichia pini*, *Pichia polymorpha*, *Pichia quercuum*, *Pichia rhodanensis*, *Pichia sargentensis*, *Pichia stipitidis*, *Pichia strasburgensis*, *Pichia subpelliculosa*, *Pichia toletana*, *Pichia trehalophila*, *Pichia vini*, *Pichia xylosa*, *Saccharomyces aceta*, *Saccharomyces bailii*, *Saccharomyces bayanus*, *Saccharo-*

*myces bisporus*, *Saccharomyces capensis*, *Saccharomyces carlsbergensis*, *Saccharomyces cerevisiae*, *Saccharomyces cerevisiae* var. *ellipsoideus*, *Saccharomyces chevalieri*, *Saccharomyces delbrueckii*, *Saccharomyces diastaticus*, *Saccharomyces drosophilarum*, *Saccharomyces elegans*, *Saccharomyces ellipsoideus*, *Saccharomyces fermentati*, *Saccharomyces florentinus*, *Saccharomyces fragilis*, *Saccharomyces heterogenicus*, *Saccharomyces hienipiensis*, *Saccharomyces inusitatus*, *Saccharomyces italicus*, *Saccharomyces kluyveri*, *Saccharomyces krusei*, *Saccharomyces lactis*, *Saccharomyces marxianus*, *Saccharomyces microellipsoides*, *Saccharomyces montanus*, *Saccharomyces norbensis*, *Saccharomyces oleaceus*, *Saccharomyces paradoxus*, *Saccharomyces pastorianus*, *Saccharomyces pretoriensis*, *Saccharomyces rosea*, *Saccharomyces rouxii*, *Saccharomyces uvarum*, *Saccharomyces ludwigii*, *Yarrowia lipolytica*, Schizosaccharomycetaceae such as the genera *Schizosaccharomyces* e.g. the species *Schizosaccharomyces japonicus* var. *japonicus*, *Schizosaccharomyces japonicus* var. *versatilis*, *Schizosaccharomyces malidevorans*, *Schizosaccharomyces octosporus*, *Schizosaccharomyces pombe* var. *malidevorans*, *Schizosaccharomyces pombe* var. *pombe*, Thraustochytriaceae such as the genera *Althornia*, *Aplanochytrium*, *Japonochytrium*, *Schizochytrium*, *Thraustochytrium* e.g. the species *Schizochytrium aggregatum*, *Schizochytrium limacinum*, *Schizochytrium mangrovei*, *Schizochytrium minutum*, *Schizochytrium octosporum*, *Thraustochytrium aggregatum*, *Thraustochytrium amoeboideum*, *Thraustochytrium antacticum*, *Thraustochytrium arudimentale*, *Thraustochytrium aureum*, *Thraustochytrium benthicola*, *Thraustochytrium globosum*, *Thraustochytrium indicum*, *Thraustochytrium kerguelense*, *Thraustochytrium kinnei*, *Thraustochytrium motivum*, *Thraustochytrium multirudimentale*, *Thraustochytrium pachydermum*, *Thraustochytrium proliferum*, *Thraustochytrium roseum*, *Thraustochytrium rossii*, *Thraustochytrium striatum* or *Thraustochytrium visurgense*. Further preferred microorganisms are bacteria selected from the group of the families Bacillaceae, Enterobacteriaceae or Rhizobiaceae. Examples of such micro-organisms may be selected from the group: Bacillaceae such as the genera *Bacillus* for example the genera and species *Bacillus acidocaldarius*, *Bacillus acidoterrestris*, *Bacillus alcalophilus*, *Bacillus amyloliquefaciens*, *Bacillus amylolyticus*, *Bacillus brevis*, *Bacillus cereus*, *Bacillus circulans*, *Bacillus coagulans*, *Bacillus sphaericus* subsp. *fusiformis*, *Bacillus galactophilus*, *Bacillus globisporus*, *Bacillus globisporus* subsp. *marinus*, *Bacillus halophilus*, *Bacillus lentimorbus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus polymyxa*, *Bacillus psychrosaccharolyticus*, *Bacillus pumilus*, *Bacillus sphaericus*, *Bacillus subtilis* subsp. *spizizenii*, *Bacillus subtilis* subsp. *subtilis* or *Bacillus thuringiensis*; Enterobacteriaceae such as the genera *Citrobacter*, *Edwardsiella*, *Enterobacter*, *Erwinia*, *Escherichia*, *Klebsiella*, *Salmonella* or *Serratia* for example the genera and species *Citrobacter amalonaticus*, *Citrobacter diversus*, *Citrobacter freundii*, *Citrobacter genomospecies*, *Citrobacter gillenii*, *Citrobacter intermedium*, *Citrobacter koseri*, *Citrobacter murlinae*, *Citrobacter* sp., *Edwardsiella hoshinae*, *Edwardsiella ictaluri*, *Edwardsiella tarda*, *Erwinia alni*, *Erwinia amylovora*, *Erwinia ananatis*, *Erwinia aphidicola*, *Erwinia billingiae*, *Erwinia cacticida*, *Erwinia cancerogena*, *Erwinia carnegiana*, *Erwinia carotovora* subsp. *atroseptica*, *Erwinia carotovora* subsp. *betavasculorum*, *Erwinia carotovora* subsp. *odorifera*, *Erwinia carotovora* subsp. *wasabiae*, *Erwinia chrysanthemi*, *Erwinia cypripedii*, *Erwinia dissolvens*, *Erwinia herbicola*, *Erwinia mallotivora*, *Erwinia milletiae*, *Erwinia nigrifluens*, *Erwinia nimipressuralis*, *Erwinia*

*persicina*, *Erwinia psidii*, *Erwinia pyrifoliae*, *Erwinia quercina*, *Erwinia rhapontici*, *Erwinia rubrifaciens*, *Erwinia salicis*, *Erwinia stewartii*, *Erwinia tracheiphila*, *Erwinia ure-dovora*, *Escherichia adecarboxylata*, *Escherichia anindolica*, *Escherichia aurescens*, *Escherichia blattae*, *Escherichia coli*, *Escherichia coli* var. *communis*, *Escherichia colimutabile*, *Escherichia fergusonii*, *Escherichia hermannii*, *Escherichia* sp., *Escherichia vulneris*, *Klebsiella aerogenes*, *Klebsiella edwardsii* subsp. *atlantae*, *Klebsiella ornithinolytica*, *Klebsiella oxytoca*, *Klebsiella planticola*, *Klebsiella pneumoniae*, *Klebsiella pneumoniae* subsp. *pneumoniae*, *Klebsiella* sp., *Klebsiella terrigena*, *Klebsiella trevisanii*, *Salmonella abony*, *Salmonella arizonae*, *Salmonella bongori*, *Salmonella choleraesuis* subsp. *arizonae*, *Salmonella choleraesuis* subsp. *bongori*, *Salmonella choleraesuis* subsp. *choleraesuis*, *Salmonella choleraesuis* subsp. *diarizonae*, *Salmonella choleraesuis* subsp. *houtenae*, *Salmonella choleraesuis* subsp. *indica*, *Salmonella choleraesuis* subsp. *salamae*, *Salmonella daressalaam*, *Salmonella enterica* subsp. *houtenae*, *Salmonella enterica* subsp. *salamae*, *Salmonella enteritidis*, *Salmonella gallinarum*, *Salmonella heidelberg*, *Salmonella panama*, *Salmonella senftenberg*, *Salmonella typhimurium*, *Serratia entomophila*, *Serratia ficaria*, *Serratia fonticola*, *Serratia grimesii*, *Serratia liquefaciens*, *Serratia marcescens*, *Serratia marcescens* subsp. *marcescens*, *Serratia marinorubra*, *Serratia odorifera*, *Serratia plymouthensis*, *Serratia plymuthica*, *Serratia proteamaculans*, *Serratia proteamaculans* subsp. *quinovora*, *Serratia quinivorans* or *Serratia rubidaea*; Rhizobiaceae such as the genera *Agrobacterium*, *Carbophilus*, *Chelatobacter*, *Ensifer*, *Rhizobium*, *Sinorhizobium* for example the genera and species *Agrobacterium atlanticum*, *Agrobacterium ferrugineum*, *Agrobacterium gelatinovorum*, *Agrobacterium larrymoorei*, *Agrobacterium meteorii*, *Agrobacterium radiobacter*, *Agrobacterium rhizogenes*, *Agrobacterium rubi*, *Agrobacterium stellulatum*, *Agrobacterium tumefaciens*, *Agrobacterium vitis*, *Carbophilus carboxidus*, *Chelatobacter heintzii*, *Ensifer adhaerens*, *Ensifer arboris*, *Ensifer fredii*, *Ensifer kostiensis*, *Ensifer kummerowiae*, *Ensifer medicae*, *Ensifer meliloti*, *Ensifer sahelii*, *Ensifer terengae*, *Ensifer xinjiangensis*, *Rhizobium ciceri*, *Rhizobium etli*, *Rhizobium fredii*, *Rhizobium galegae*, *Rhizobium gallicum*, *Rhizobium giardinii*, *Rhizobium hainanense*, *Rhizobium huakuii*, *Rhizobium huautlense*, *Rhizobium indigoferae*, *Rhizobium japonicum*, *Rhizobium leguminosarum*, *Rhizobium loesense*, *Rhizobium loti*, *Rhizobium lupini*, *Rhizobium mediterraneum*, *Rhizobium meliloti*, *Rhizobium mongolense*, *Rhizobium phaseoli*, *Rhizobium radiobacter*, *Rhizobium rhizogenes*, *Rhizobium rubi*, *Rhizobium sullae*, *Rhizobium tianshanense*, *Rhizobium trifolii*, *Rhizobium tropici*, *Rhizobium undicola*, *Rhizobium vitis*, *Sinorhizobium adhaerens*, *Sinorhizobium arboris*, *Sinorhizobium fredii*, *Sinorhizobium kostiensis*, *Sinorhizobium kummerowiae*, *Sinorhizobium medicae*, *Sinorhizobium meliloti*, *Sinorhizobium morelense*, *Sinorhizobium sahelii* or *Sinorhizobium xinjiangense*.

How to culture the aforementioned micro-organisms is well known to the person skilled in the art.

The present invention also relates to a non-human transgenic organism, preferably a plant or seed thereof, comprising the polynucleotide or the vector of the present invention.

The term "non-human transgenic organism", preferably, relates to a plant, a plant seed, a non-human animal or a multicellular micro-organism. The polynucleotide or vector may be present in the cytoplasm of the organism or may be incorporated into the genome either heterologous or by homologous recombination. Host cells, in particular those obtained from plants or animals, may be introduced into a

developing embryo in order to obtain mosaic or chimeric organisms, i.e. non-human transgenic organisms comprising the host cells of the present invention. Suitable transgenic organisms are, preferably, all organisms which are suitable for the expression of recombinant genes. Preferred plants to be used for making non-human transgenic organisms according to the present invention are all dicotyledonous or monocotyledonous plants, algae or mosses. Advantageous plants are selected from the group of the plant families Adolotheciaceae, Anacardiaceae, Asteraceae, Apiaceae, Betulaceae, Boraginaceae, Brassicaceae, Bromeliaceae, Caricaceae, Cannabaceae, Convolvulaceae, Chenopodiaceae, Crypthecodiniaceae, Cucurbitaceae, Ditrichaceae, Elaeagnaceae, Ericaceae, Euphorbiaceae, Fabaceae, Geraniaceae, Gramineae, Juglandaceae, Lauraceae, Leguminosae, Linaceae, Prasino-phyceae or vegetable plants or ornamentals such as *Tagetes*. Examples which may be mentioned are the following plants selected from the group consisting of: Adolotheciaceae such as the genera *Physcomitrella*, such as the genus and species *Physcomitrella patens*, Anacardiaceae such as the genera *Pistacia*, *Mangifera*, *Anacardium*, for example the genus and species *Pistacia vera* [pistachio], *Mangifer indica* [mango] or *Anacardium occidentale* [cashew], Asteraceae, such as the genera *Calendula*, *Carthamus*, *Centaurea*, *Cichorium*, *Cynara*, *Helianthus*, *Lactuca*, *Locusta*, *Tagetes*, *Valeriana*, for example the genus and species *Calendula offinalis* [common marigold], *Carthamus tinctorius* [safflower], *Centaurea cyanus* [cornflower], *Cichorium intybus* [chicory], *Cynara scolymus* [artichoke], *Helianthus annus* [sunflower], *Lactuca sativa*, *Lactuca crispa*, *Lactuca esculenta*, *Lactuca scariola* L. ssp. *sativa*, *Lactuca scariola* L. var. *integrata*, *Lactuca scariola* L. var. *integrifolia*, *Lactuca sativa* subsp. *romana*, *Locusta communis*, *Valeriana locusta* [salad vegetables], *Tagetes lucida*, *Tagetes erecta* or *Tagetes tenuifolia* [african or french marigold], Apiaceae, such as the genus *Daucus*, for example the genus and species *Daucus carota* [carrot], Betulaceae, such as the genus *Corylus*, for example the genera and species *Corylus avellana* or *Corylus colurna* [hazelnut], Boraginaceae, such as the genus *Borago*, for example the genus and species *Borago officinalis* [borage], Brassicaceae, such as the genera *Brassica*, *Melanosinapis*, *Sinapis*, *Arabidopsis*, for example the genera and species *Brassica napus*, *Brassica rapa* ssp. [oilseed rape], *Sinapis arvensis*, *Brassica juncea*, *Brassica juncea* var. *juncea*, *Brassica juncea* var. *crispifolia*, *Brassica juncea* var. *foliosa*, *Brassica nigra*, *Brassica sinapioides*, *Melanosinapis communis* [mustard], *Brassica oleracea* [fodder beet] or *Arabidopsis thaliana*, Bromeliaceae, such as the genera *Anana*, *Bromelia* (pineapple), for example the genera and species *Anana comosus*, *Ananas ananas* or *Bromelia comosa* [pineapple], Caricaceae, such as the genus *Carica*, such as the genus and species *Carica papaya* [paw-paw], Cannabaceae, such as the genus *Cannabis*, such as the genus and species *Cannabis sativa* [hemp], Convolvulaceae, such as the genera *Ipomea*, *Convolvulus*, for example the genera and species *Ipomea batatas*, *Ipomea pandurata*, *Convolvulus batatas*, *Convolvulus tiliaceus*, *Ipomea fastigiata*, *Ipomea tiliacea*, *Ipomea triloba* or *Convolvulus panduratus* [sweet potato, batate], Chenopodiaceae, such as the genus *Beta*, such as the genera and species *Beta vulgaris*, *Beta vulgaris* var. *altissima*, *Beta vulgaris* var. *Vulgaris*, *Beta maritima*, *Beta vulgaris* var. *perennis*, *Beta vulgaris* var. *conditiva* or *Beta vulgaris* var. *esculenta* [sugarbeet], Crypthecodiniaceae, such as the genus *Crypthecodinium*, for example the genus and species *Crypthecodinium cohnii*, Cucurbitaceae, such as the genus *Cucurbita*, for example the genera and species *Cucurbita maxima*, *Cucurbita mixta*, *Cucurbita pepo* or *Cucurbita moschata* [pumpkin/squash], Cymbellaceae

such as the genera *Amphora*, *Cymbella*, *Okedenia*, *Phaeodactylum*, *Reimeria*, for example the genus and species *Phaeodactylum tricornutum*, Ditrichaceae such as the genera Ditrichaceae, *Astomiopsis*, *Ceratodon*, *Chrysoblastella*, *Ditrichum*, *Distichium*, *Eccremidium*, *Lophidion*, *Philibertiella*, *Pleuridium*, *Saelania*, *Trichodon*, *Skottsbergia*, for example the genera and species *Ceratodon antarcticus*, *Ceratodon columbiae*, *Ceratodon heterophyllus*, *Ceratodon purpureus*, *Ceratodon purpureus* ssp. *convolutus*, *Ceratodon*, *purpureus* spp. *stenocarpus*, *Ceratodon purpureus* var. *rotundifolius*, *Ceratodon ratodon*, *Ceratodon stenocarpus*, *Chrysoblastella chilensis*, *Ditrichum ambiguum*, *Ditrichum brevisetum*, *Ditrichum crispatissimum*, *Ditrichum difficile*, *Ditrichum falcifolium*, *Ditrichum flexicaule*, *Ditrichum giganteum*, *Ditrichum heteromallum*, *Ditrichum lineare*, *Ditrichum lineare*, *Ditrichum montanum*, *Ditrichum montanum*, *Ditrichum pallidum*, *Ditrichum punctulatum*, *Ditrichum pusillum*, *Ditrichum pusillum* var. *tortile*, *Ditrichum rhynchostegium*, *Ditrichum schimperii*, *Ditrichum tortile*, *Distichium capillaceum*, *Distichium hagenii*, *Distichium inclinatum*, *Distichium macounii*, *Eccremidium floridanum*, *Eccremidium whiteleggei*, *Lophidion strictus*, *Pleuridium acuminatum*, *Pleuridium alternifolium*, *Pleuridium holdridgei*, *Pleuridium mexicanum*, *Pleuridium ravenelii*, *Pleuridium subulatum*, *Saelania glaucescens*, *Trichodon borealis*, *Trichodon cylindricus* or *Trichodon cylindricus* var. *oblongus*, Elaeagnaceae such as the genus *Elaeagnus*, for example the genus and species *Olea europaea* [olive], Ericaceae such as the genus *Kalmia*, for example the genera and species *Kalmia latifolia*, *Kalmia angustifolia*, *Kalmia microphylla*, *Kalmia polifolia*, *Kalmia occidentalis*, *Cistus chamaerhodendros* or *Kalmia lucida* [mountain laurel], Euphorbiaceae such as the genera *Manihot*, *Janipha*, *Jatropha*, *Ricinus*, for example the genera and species *Manihot utilissima*, *Janipha manihot*, *Jatropha manihot*, *Manihot aipil*, *Manihot dulcis*, *Manihot manihot*, *Manihot melanobasis*, *Manihot esculenta* [manihot] or *Ricinus communis* [castor-oil plant], Fabaceae such as the genera *Pisum*, *Albizia*, *Cathormion*, *Feuillea*, *Inga*, *Pithecolobium*, *Acacia*, *Mimosa*, *Medicago*, *Glycine*, *Dolichos*, *Phaseolus*, *Soja*, for example the genera and species *Pisum sativum*, *Pisum arvense*, *Pisum humile* [pea], *Albizia berteriana*, *Albizia julibrissin*, *Albizia lebbek*, *Acacia berteriana*, *Acacia littoralis*, *Albizia berteriana*, *Albizia berteriana*, *Cathormion berteriana*, *Feuillea berteriana*, *Inga fragrans*, *Pithecolobium berterianum*, *Pithecolobium fragrans*, *Pithecolobium berterianum*, *Pseudalbizia berteriana*, *Acacia julibrissin*, *Acacia nemu*, *Albizia nemu*, *Feuillea julibrissin*, *Mimosa julibrissin*, *Mimosa speciosa*, *Sericanrda julibrissin*, *Acacia lebbek*, *Acacia macrophylla*, *Albizia lebbek*, *Feuillea lebbek*, *Mimosa lebbek*, *Mimosa speciosa* [silk tree], *Medicago sativa*, *Medicago falcata*, *Medicago varia* [alfalfa], *Glycine max*, *Dolichos soja*, *Glycine gracilis*, *Glycine hispida*, *Phaseolus max*, *Soja hispida* or *Soja max* [soybean], Funariaceae such as the genera *Aphanorrhagma*, *Entosthodon*, *Funaria*, *Physcomitrella*, *Physcomitrium*, for example the genera and species *Aphanorrhagma serratum*, *Entosthodon attenuatus*, *Entosthodon bolanderi*, *Entosthodon bonplandii*, *Entosthodon californicus*, *Entosthodon drummondii*, *Entosthodon jamesonii*, *Entosthodon leibergii*, *Entosthodon neoscoticus*, *Entosthodon rubrisetus*, *Entosthodon spathulifolius*, *Entosthodon tucsoni*, *Funaria americana*, *Funaria bolanderi*, *Funaria calcarea*, *Funaria californica*, *Funaria calvescens*, *Funaria convoluta*, *Funaria flavicans*, *Funaria grotiana*, *Funaria hygrometrica*, *Funaria hygrometrica* var. *arctica*, *Funaria hygrometrica* var. *calvescens*, *Funaria hygrometrica* var. *convoluta*, *Funaria hygrometrica* var. *muralis*, *Funaria*

*hygrometrica* var. *utahensis*, *Funaria microstoma*, *Funaria microstoma* var. *obtusifolia*, *Funaria muhlenbergii*, *Funaria orcuttii*, *Funaria plano-convexa*, *Funaria polaris*, *Funaria ravenelii*, *Funaria rubriseta*, *Funaria serrata*, *Funaria sonorae*, *Funaria sublimbatas*, *Funaria tucsoni*, *Physcomitrella californica*, *Physcomitrella patens*, *Physcomitrella readeri*, *Physcomitrium australe*, *Physcomitrium californicum*, *Physcomitrium collenchymatum*, *Physcomitrium coloradense*, *Physcomitrium cupuliferum*, *Physcomitrium drummondii*, *Physcomitrium euryostomum*, *Physcomitrium flexifolium*, *Physcomitrium hookeri*, *Physcomitrium hookeri* var. *serratum*, *Physcomitrium immersum*, *Physcomitrium kellermanii*, *Physcomitrium megalocarpum*, *Physcomitrium pyriforme*, *Physcomitrium pyriforme* var. *serratum*, *Physcomitrium rufipes*, *Physcomitrium sandbergii*, *Physcomitrium subsphaericum*, *Physcomitrium washingtoniense*, Geraniaceae, such as the genera *Pelargonium*, *Cocos*, *Oleum*, for example the genera and species *Cocos nucifera*, *Pelargonium grossularioides* or *Oleum cocois* [coconut], Gramineae, such as the genus *Saccharum*, for example the genus and species *Saccharum officinarum*, Juglandaceae, such as the genera *Juglans*, *Wallia*, for example the genera and species *Juglans regia*, *Juglans ailanthifolia*, *Juglans sieboldiana*, *Juglans cinerea*, *Wallia cinerea*, *Juglans bixbyi*, *Juglans californica*, *Juglans hindsii*, *Juglans intermedia*, *Juglans jamaicensis*, *Juglans major*, *Juglans microcarpa*, *Juglans nigra* or *Wallia nigra* [walnut], Lauraceae, such as the genera *Persea*, *Laurus*, for example the genera and species *Laurus nobilis* [bay], *Persea americana*, *Persea gratissima* or *Persea persea* [avocado], Leguminosae, such as the genus *Arachis*, for example the genus and species *Arachis hypogaea* [peanut], Linaceae, such as the genera *Linum*, *Adenolinum*, for example the genera and species *Linum usitatissimum*, *Linum humile*, *Linum austriacum*, *Linum bienne*, *Linum angustifolium*, *Linum catharticum*, *Linum flavum*, *Linum grandiflorum*, *Adenolinum grandiflorum*, *Linum lewisii*, *Linum narbonense*, *Linum perenne*, *Linum perenne* var. *lewisii*, *Linum pratense* or *Linum trigynum* [linseed], Lythraeae, such as the genus *Punica*, for example the genus and species *Punica granatum* [pomegranate], Malvaceae, such as the genus *Gossypium*, for example the genera and species *Gossypium hirsutum*, *Gossypium arboreum*, *Gossypium barbadense*, *Gossypium herbaceum* or *Gossypium thurberi* [cotton], Marchantiaceae, such as the genus *Marchantia*, for example the genera and species *Marchantia berteroana*, *Marchantia foliacea*, *Marchantia macropora*, Musaceae, such as the genus *Musa*, for example the genera and species *Musa nana*, *Musa acuminata*, *Musa paradisiaca*, *Musa* spp. [banana], Onagraceae, such as the genera *Camissonia*, *Oenothera*, for example the genera and species *Oenothera biennis* or *Camissonia brevipes* [evening primrose], Palmae, such as the genus *Elacis*, for example the genus and species *Elaeis guineensis* [oil palm], Papaveraceae, such as the genus *Papaver*, for example the genera and species *Papaver orientale*, *Papaver rhoeas*, *Papaver dubium* [poppy], Pedaliaceae, such as the genus *Sesamum*, for example the genus and species *Sesamum indicum* [sesame], Piperaceae, such as the genera *Piper*, *Artanthe*, *Peperomia*, *Steffensia*, for example the genera and species *Piper aduncum*, *Piper amalago*, *Piper angustifolium*, *Piper auriturn*, *Piper betel*, *Piper cubeba*, *Piper longum*, *Piper nigrum*, *Piper retrofractum*, *Artanthe adunca*, *Artanthe elongata*, *Peperomia elongata*, *Piper elongatum*, *Steffensia elongata* [cayenne pepper], Poaceae, such as the genera *Hordeum*, *Secale*, *Avena*, *Sorghum*, *Andropogon*, *Holcus*, *Panicum*, *Oryza*, *Zea* (maize), *Triticum*, for example the genera and species *Hordeum vulgare*, *Hordeum jubatum*, *Hordeum murinum*, *Hordeum secalinum*, *Hordeum distichon*, *Hor-*

*deum aegiceras*, *Hordeum hexastichon*, *Hordeum hexastichum*, *Hordeum irregulare*, *Hordeum sativum*, *Hordeum secalinum* [barley], *Secale cereale* [rye], *Avena sativa*, *Avena fatua*, *Avena byzantina*, *Avena fatua* var. *sativa*, *Avena hybrida* [oats], *Sorghum bicolor*, *Sorghum halepense*, *Sorghum saccharatum*, *Sorghum vulgare*, *Andropogon drummondii*, *Holcus bicolor*, *Holcus sorghum*, *Sorghum aethiopicum*, *Sorghum arundinaceum*, *Sorghum caffrorum*, *Sorghum cernuum*, *Sorghum dochma*, *Sorghum drummondii*, *Sorghum durra*, *Sorghum guineense*, *Sorghum lanceolatum*, *Sorghum nervosum*, *Sorghum saccharatum*, *Sorghum subglabrescens*, *Sorghum verticilliflorum*, *Sorghum vulgare*, *Holcus halepensis*, *Sorghum miliaceum*, *Panicum militaceum* [millet], *Oryza sativa*, *Oryza latifolia* [rice], *Zea mays* [maize], *Triticum aestivum*, *Triticum durum*, *Triticum turgidum*, *Triticum hybernum*, *Triticum macha*, *Triticum sativum* or *Triticum vulgare* [wheat], Porphyridiaceae, such as the genera *Chroothecce*, *Flintiella*, *Petrovanella*, *Porphyridium*, *Rhodella*, *Rhodorus*, *Vanhoeffenia*, for example the genus and species *Porphyridium cruentum*, Proteaceae, such as the genus *Macadamia*, for example the genus and species *Macadamia integrifolia* [macadamia], Prasinophyceae such as the genera *Nephroselmis*, *Prasinococcus*, *Scherffelia*, *Tetraselmis*, *Mantoniella*, *Ostreococcus*, for example the genera and species *Nephroselmis olivacea*, *Prasinococcus capsulatus*, *Scherffelia dubia*, *Tetraselmis chui*, *Tetraselmis suecica*, *Mantoniella squamata*, *Ostreococcus tauri*, Rubiaceae such as the genus *Coffea*, for example the genera and species *Coffea arabica*, *Coffea canephora* or *Coffea liberica* [coffee], Scrophulariaceae such as the genus *Verbascum*, for example the genera and species *Verbascum blattaria*, *Verbascum chaixii*, *Verbascum densiflorum*, *Verbascum lagurus*, *Verbascum longifolium*, *Verbascum lychnitis*, *Verbascum nigrum*, *Verbascum olympicum*, *Verbascum phlomoides*, *Verbascum phoenicum*, *Verbascum pulverulentum* or *Verbascum thapsus* [mullein], Solanaceae such as the genera *Capsicum*, *Nicotiana*, *Solanum*, *Lycopersicon*, for example the genera and species *Capsicum annuum*, *Capsicum annuum* var. *glabriusculum*, *Capsicum frutescens* [pepper], *Capsicum annuum* [paprika], *Nicotiana tabacum*, *Nicotiana alata*, *Nicotiana attenuata*, *Nicotiana glauca*, *Nicotiana langsdorffii*, *Nicotiana obtusifolia*, *Nicotiana quadrivalvis*, *Nicotiana repanda*, *Nicotiana rustica*, *Nicotiana sylvestris* [tobacco], *Solanum tuberosum* [potato], *Solanum melongena* [eggplant], *Lycopersicon esculentum*, *Lycopersicon lycopersicum*, *Lycopersicon pyriforme*, *Solanum integrifolium* or *Solanum lycopersicum* [tomato], Sterculiaceae, such as the genus *Theobroma*, for example the genus and species *Theobroma cacao* [cacao] or Theaceae, such as the genus *Camellia*, for example the genus and species *Camellia sinensis* [tea]. In particular preferred plants to be used as transgenic plants in accordance with the present invention are oil fruit crops which comprise large amounts of lipid compounds, such as peanut, oilseed rape, canola, sunflower, safflower, poppy, mustard, hemp, castor-oil plant, olive, sesame, *Calendula*, *Punica*, evening primrose, mullein, thistle, wild roses, hazelnut, almond, macadamia, avocado, bay, pumpkin/squash, linseed, soybean, pistachios, borage, trees (oil palm, coconut, walnut) or crops such as maize, wheat, rye, oats, triticale, rice, barley, cotton, cassava, pepper, *Tagetes*. Solanaceae plants such as potato, tobacco, eggplant and tomato, *Vicia* species, pea, alfalfa or bushy plants (coffee, cacao, tea), *Salix* species, and perennial grasses and fodder crops. Preferred plants according to the invention are oil crop plants such as peanut, oilseed rape, canola, sunflower, safflower, poppy, mustard, hemp, castor-oil plant, olive, *Calendula*, *Punica*, evening primrose, pumpkin/squash, linseed, soybean, borage, trees (oil palm, coco-

nut). Especially preferred are plants which are high in C18:2-and/or C18:3-fatty acids, such as sunflower, safflower, tobacco, mullein, sesame, cotton, pumpkin/squash, poppy, evening primrose, walnut, linseed, hemp, thistle or safflower. Very especially preferred plants are plants such as safflower, sunflower, poppy, evening primrose, walnut, linseed, or hemp.

Preferred mosses are *Physcomitrella* or *Ceratodon*. Preferred algae are *Isochrysis*, *Mantoniella*, *Ostreococcus* or *Cryptothecodinium*, and algae/diatoms such as *Phaeodactylum* or *Thraustochytrium*. More preferably, said algae or mosses are selected from the group consisting of: *Shewanella*, *Physcomitrella*, *Thraustochytrium*, *Fusarium*, *Phytophthora*, *Ceratodon*, *Isochrysis*, *Aleurita*, *Muscarioides*, *Mortierella*, *Phaeodactylum*, *Cryptothecodinium*, specifically from the genera and species *Thalassiosira pseudonona*, *Euglena gracilis*, *Physcomitrella patens*, *Phytophthora infestans*, *Fusarium gramineum*, *Cryptocodium cohnii*, *Ceratodon purpureus*, *Isochrysis galbana*, *Aleurita farinosa*, *Thraustochytrium* sp., *Muscarioides viallii*, *Mortierella alpina*, *Phaeodactylum tricorutum* or *Caenorhabditis elegans* or especially advantageously *Phytophthora infestans*, *Thalassiosira pseudonona* and *Cryptocodium cohnii*.

Transgenic plants may be obtained by transformation techniques as published, and cited, in: Plant Molecular Biology and Biotechnology (CRC Press, Boca Raton, Fla.), chapter 6/7, pp. 71-119 (1993); F. F. White, Vectors for Gene Transfer in Higher Plants; in: Transgenic Plants, vol. 1, Engineering and Utilization, Ed.: Kung and R. Wu, Academic Press, 1993, 15-38; B. Jenes et al., Techniques for Gene Transfer, in: Transgenic Plants, vol. 1, Engineering and Utilization, Ed.: Kung and R. Wu, Academic Press (1993), 128-143; Potrykus, Annu. Rev. Plant Physiol. Plant Molec. Biol. 42 (1991), 205-225. Preferably, transgenic plants can be obtained by T-DNA-mediated transformation. Such vector systems are, as a rule, characterized in that they contain at least the vir genes, which are required for the *Agrobacterium*-mediated transformation, and the sequences which delimit the T-DNA (T-DNA border). Suitable vectors are described elsewhere in the specification in detail.

Preferably, a multicellular micro-organism as used herein refers to protists or diatoms. More preferably, it is selected from the group of the families Dinophyceae, Turaniellidae or Oxytrichidae, such as the genera and species: *Cryptocodium cohnii*, *Phaeodactylum tricorutum*, *Stylonychia mytilus*, *Stylonychia pustulate*, *Stylonychia putrina*, *Stylonychia notophora*, *Stylonychia* sp., *Colpidium campylum* or *Colpidium* sp.

The present invention also relates to a method for expressing a nucleic acid of interest in a host cell comprising

- (a) introducing the polynucleotide or the vector of the present invention into the host cell, whereby the nucleic acid sequence of interest will be operatively linked to the expression control sequence; and
- (b) expressing the said nucleic acid sequence in said host cell.

The polynucleotide or vector of the present invention can be introduced into the host cell by suitable transfection or transformation techniques as specified elsewhere in this description. The nucleic acid of interest will be expressed in the host cell under suitable conditions. To this end, the host cell will be cultivated under conditions which, in principle, allow for transcription of nucleic acids. Moreover, the host cell, preferably, comprises the exogenously supplied or endogenously present transcription machinery required for expressing a nucleic acid of interest by the expression control

sequence. More preferably, the host cell is a plant cell and, most preferably, a seed cell or precursor thereof.

Moreover, the present invention encompasses a method for expressing a nucleic acid of interest in a non-human organism comprising

- (a) introducing the polynucleotide or the vector of the present invention into the non human organism, whereby the nucleic acid sequence of interest will be operatively linked to the expression control sequence; and
- (b) expressing the said nucleic acid sequence in said non-human transgenic organism.

The polynucleotide or vector of the present invention can be introduced into the non-human transgenic organism by suitable techniques as specified elsewhere in this description. The non-human transgenic organism, preferably, comprises the exogenously supplied or endogenously present transcription machinery required for expressing a nucleic acid of interest by the expression control sequence. More preferably, the non-human transgenic organism is a plant or seed thereof. It is to be understood that the nucleic acid of interest will be expressed, preferably, seed specific in the said non-human transgenic organism.

Further, the present invention relates to a method for the manufacture of stearidonic acid (SDA) in a plant seed comprising the steps of:

- a) growing a transgenic plant expressing a polynucleotide encoding a delta 6 desaturase under the control of the polynucleotide of the present invention; and
- b) obtaining said SDA from the harvested seeds of the said plant.

The SDA may be manufactured in the form of a triglyceride ester, a phospholipid or as Acyl-CoA bound or free fatty acid comprised by seed oil or seed fatty acid preparations obtainable from the harvested seeds of the grown transgenic plants by standard techniques such as an oil mill or chromatographic extraction and/or purification techniques.

Moreover, how to grow transgenic plants and how to harvest their seeds is well known in the art. How to make transgenic plants expressing a gene of interest such as a delta 6 desaturase under the control of the polynucleotide of the present invention is set forth elsewhere herein.

Surprisingly, the polynucleotides of the present invention were found to influence the ratio of the omega-3 fatty acid stearidonic acid (SDA) to the omega-6 fatty acid gamma linolenic acid (GLA). Accordingly, the seeds of the aforementioned transgenic plants expressing a delta 6 desaturase under the control of the promoter comprised by the polynucleotide of the invention are particularly suitable as a source for SDA or SDA enriched fatty acid preparations such as oil.

Thus, the present invention also pertains to the use of the polynucleotide of the present invention driving expression of a delta 6 desaturase in a transgenic plant for increasing (preferably to a statistically significant extent) the amount of SDA at the expense of GLA in plant seeds of said plants.

Moreover, the present invention pertains to seed oil having the said altered SDA to GLA ratio (i.e. an increased SDA amount at the expense of GLA) obtainable by an oil mill from the harvested seeds of a transgenic plant as set forth above. It will be understood that such an oil will be characterized in addition to the altered SDA to GLA ratio by the presence of remaining DNA contaminations including the polynucleotide of the present invention and/or the delta 6 desaturase encoding polynucleotide.

Nucleic acids encoding suitable delta 6 desaturases are well known in the art and are d6-Desaturases d6Des(Cp) from

*Ceratodon purpureus* (WO2000075341), d6Des(OI) from *Ostreococcus lucimarinus* (WO2008040787), d6Des(Ot) from *Ostreococcus tauri* (WO2006069710), d6Des(Pf) from *Primula farinosa* (WO2003072784), d6Des(Pir\_BO) from *Pythium irregulare* (WO2002026946), d6Des(Pir) from *Pythium irregulare* (WO2002026946), d6Des(Plu) from *Primula luteola* (WO2003072784), d6Des(Pp) from *Phycomitrella patens* (WO200102591), d6Des(Pt) from *Phaeodactylum tricorutum* (WO2002057465), d6Des(Pv) from *Primula vialii* (WO2003072784) and d6Des(Tp) from *Thalassiosira pseudonana* (WO2006069710) and, in particular, those mentioned in the accompanying Examples.

Moreover, a transgenic plant expressing a polynucleotide encoding a delta 6 desaturase under the control of the polynucleotide of the present invention may also comprise further desaturases or elongases of the omega-3 pathway which are required for the synthesis of end products such as eicosapentaenoic acid (EPA) or docosahexaenoic acid (DHA).

Thus, a method is provided for increasing stearidonic acid in a plant seed comprising the steps of growing a transgenic

plant expressing a polynucleotide encoding a delta 6 desaturase under the control of the polynucleotide of the present invention.

By increasing the omega-3 pathway substrate SDA at the expense of the omega-6 pathway substrate GLA, further fatty acid products of the omega-3 pathway can be produced more efficiently in the aforementioned transgenic plants. Preferably, the desaturases and/or elongases required for the production of a desired fatty acid can also be expressed under the control of a polynucleotide of the present invention. Most preferably, however, it is envisaged that the delta 6 desaturase and the further desaturases and/or elongases are expressed under the control of polynucleotides of the present invention comprising different expression control sequences with respect to each other.

In the following tables 1 to 9, the cis-regulatory elements found in the expression control sequences of the present invention are shown.

TABLE 1  
cis-regulatory elements of SEQ ID NO: 1

Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_1	P\$AHBP/ATHB9.01	HD-ZIP class III protein ATHB9	0.77	7	17	(-)	1.000	0.772	ttgATGAtttc
SEQ_1	P\$MADS/AGL2.01	AGL2, Arabidopsis MADS-domain protein AGAMOUS-like 2	0.82	57	77	(+)	1.000	0.897	aaaaaCCAAtctttgaaaaacc
SEQ_1	P\$SUCB/SUCROSE.01	Sequence motif from the promoters of different sugar-responsive genes	0.81	57	75	(+)	0.750	0.827	aaaaAccatatttgaaaa
SEQ_1	P\$TELO/ATPURA.01	Arabidopsis Telo-box interacting protein related to the conserved animal protein Pur-alpha	0.85	57	71	(+)	0.750	0.851	aaaaaCCAAtctttg
SEQ_1	P\$GTBX/GT3A.01	Trihelix DNA-binding factor GT-3a	0.83	86	102	(-)	1.000	0.847	accattGTTActccct
SEQ_1	P\$LFBY/LFY.01	Plant specific floral meristem identity gene LEAFY (LFY)	0.93	91	103	(-)	0.914	0.936	tACCAAttgttact
SEQ_1	P\$SEF3/SEF3.01	SEF3, Soybean embryo factor 3	0.87	147	161	(+)	1.000	0.875	accCaACCCaaagag
SEQ_1	P\$CCAF/CCAL.01	Circadian clock associated 1	0.85	177	191	(+)	1.000	0.943	tcagctaaAACTcaa
SEQ_1	P\$LREM/ATCTA.01	Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	184	194	(+)	1.000	0.921	aaATCTaagga
SEQ_1	P\$LEGB/RV.01	RY and Sph motifs conserved in seed-specific promoters	0.87	202	228	(-)	1.000	0.936	ggctactcCATGcaaatattggatgctc
SEQ_1	P\$CAAT/CAAT.01	CAAT-box in plant promoters	0.97	206	214	(+)	1.000	0.983	atCCAAtat
SEQ_1	P\$NCS1/NCS1.01	Modulin consensus sequence 1	0.85	230	240	(+)	0.878	0.865	aaaATgatgcy
SEQ_1	P\$E2FF/E2F.01	E2F class I sites	0.82	234	248	(-)	0.757	0.833	ttgtTTCtGcatca
SEQ_1	P\$LREM/ATCTA.01	Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	274	284	(+)	1.000	0.918	cgATCTacaat

TABLE 1-continued

Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_1	P\$LIBX/PDF2.01	Protodermal factor 2	0.85	278	294	(+)	1.000	0.899	ctacaatATAAtaccaga
SEQ_1	P\$CCAF/CCAL.01	Circadian clock associated 1	0.85	287	301	(+)	1.000	0.881	ataccagaAATCtca
SEQ_1	P\$GTBX/GT1.01	GT1-Box binding factors with a trihelix DNA-binding domain	0.85	330	346	(+)	0.843	0.903	catgagGTGAGtctttt
SEQ_1	P\$OPAQ/GCN4.01	GCN4, conserved in cereal seed storage protein gene promoters, similar to Yeast GCN4 and vertebrate AP-1	0.81	332	348	(+)	1.000	0.830	tgaggTGAGtctttttt
SEQ_1	P\$SALT/ALFIN1.02	Zinc-finger protein in alfalfa roots, regulates salt tolerance	0.95	360	374	(-)	1.000	0.977	ggtatgCGGTGtttc
SEQ_1	P\$NACF/TANAC69.01	Wheat NACdomain DNA binding factor	0.68	367	389	(+)	0.812	0.736	cgcataccagaAAACGtaaagaaa
SEQ_1	P\$DOFF/PBOX.01	Prolamin box, conserved in cereal seed storage protein gene promoters	0.75	375	391	(+)	1.000	0.815	agaaacgtAAAGaaaat
SEQ_1	P\$HEAT/HSE.01	Heat shock element	0.81	375	389	(+)	1.000	0.918	agaaacgtaaAGAAA
SEQ_1	P\$MADS/MADS.01	Binding sites for AP1, AP3-PI and AG dimers	0.75	411	431	(-)	1.000	0.791	ttttcCCATattttttacatt
SEQ_1	P\$TBPF/TATA.01	Plant TATA box	0.88	464	478	(+)	1.000	0.941	aaaatATAaaaaaaa
SEQ_1	P\$GAPB/GAP.01	Cis-element in the GAPDH promoters conferring light inducibility	0.88	474	488	(+)	0.807	0.895	aaaaTTAaaagaaa
SEQ_1	P\$PSRE/GAAA.01	GAAA motif involved in pollen specific transcriptional activation	0.83	480	496	(+)	1.000	0.838	taaaaGAAAattttgac
SEQ_1	P\$WEXF/WRKY.01	WRKY plant specific zinc-finger-type factor associated with pathogen defence, W box	0.92	487	503	(+)	1.000	0.920	aaattTTGAcgctgaaa
SEQ_1	P\$MYBL/MYBP3.01	Myb-like protein of Petunia hybrida	0.80	498	514	(+)	0.750	0.801	ctgaaaccGTAAtctt
SEQ_1	P\$TELO/ATPURA.01	Arabidopsis Telo-box interacting protein related to the conserved animal protein Pur-alpha	0.85	499	513	(+)	0.750	0.863	tgaaACCgtaaatct

TABLE 1-continued

Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core Matrix	
							sim.	Sequence
SEQ_1 P\$CCAF/CCAL.01		Circadian clock associated 1	0.85	501	515	(+)	1.000	aaaccgtaAATCtta
SEQ_1 P\$LIBX/ATML1.01		L1-specific homeodomain protein ATML1 ( <i>A. thaliana</i> meristem layer 1)	0.82	517	533	(+)	0.750	aatcaaCAAAAtgcataa
SEQ_1 P\$LIBX/ATML1.01		L1-specific homeodomain protein ATML1 ( <i>A. thaliana</i> meristem layer 1)	0.82	525	541	(+)	1.000	aatgcaTAAAtgcaaaag
SEQ_1 P\$DOFF/PBOX.01		Prolamin box, conserved in cereal seed storage protein gene promoters	0.75	530	546	(+)	1.000	ataaatgcaAAAGttatt
SEQ_1 P\$AHP/BLR.01		Transcriptional repressor BELLRINGER	0.90	538	548	(+)	0.826	aaagTTAttga
SEQ_1 P\$TBPF/TATA.01		Plant TATA box	0.88	557	571	(-)	1.000	ctaaTATAaaaaatat
SEQ_1 P\$MYBL/GAMYB.01		GA-regulated myb gene from barley	0.91	583	599	(-)	1.000	tagtattttGTTAgcagt
SEQ_1 P\$SPF1/SP8BF.01		DNA-binding protein of sweet potato that binds to the SP8a (ACTGTGTA) and SP8b (TAC-TATT) sequences of sporamin and beta-amylase genes	0.87	593	605	(+)	1.000	aaTACTatacaga
SEQ_1 P\$IDDF/ID1.01		Maize INDETERMINATE1 zinc finger protein	0.92	600	612	(-)	1.000	tgttTTGTctgta
SEQ_1 P\$SUCB/SUCROSE.01		Sequence motif from the promoters of different sugar-responsive genes	0.81	605	623	(+)	0.750	acAAAACacattattaaaa
SEQ_1 P\$AHP/HAHB4.01		Sunflower homeodomain leucine-zipper protein Hahb-4	0.87	611	621	(+)	1.000	cacattATTAA
SEQ_1 P\$GTBX/SBF1.01		SBF-1	0.87	611	627	(+)	1.000	cacattaTTAaaaaaac
SEQ_1 P\$IDDF/ID1.01		Maize INDETERMINATE1 zinc finger protein	0.92	627	639	(-)	1.000	tattTTGTctttg
SEQ_1 P\$GTBX/GT1.01		GT1-Box binding factors with a trihelix DNA-binding domain	0.85	636	652	(-)	1.000	tgatatGTTAatatt

TABLE 1-continued

cis-regulatory elements of SEQ ID NO: 1									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_1	P\$SPF1/SP8BF.01	DNA-binding protein of sweet potato that binds to the SP8a (ACTGTGTA) and SP8b (TAC-TATT) sequences of sporamin and beta-amylase genes	0.87	649	661	(+)	0.814	0.901	atCACTattactta
SEQ_1	P\$LIBX/ATML1.02	<i>Arabidopsis thaliana</i> meristem layer 1	0.76	669	685	(+)	0.890	0.762	acaCAATAaaaaacacca
SEQ_1	P\$CARM/CARICH.01	CA-rich element	0.78	672	690	(+)	1.000	0.815	caataaaaACAccaaaataa
SEQ_1	P\$DOFF/PBF.01	PBF (MPBF)	0.97	698	714	(+)	1.000	0.990	aacaaaataaAGtgatc
SEQ_1	P\$OCSE/OCSL.01	OCS-like elements	0.69	701	721	(+)	0.807	0.729	aaataaaaagtgatcACAaaat
SEQ_1	P\$OCSE/OCSL.01	OCS-like elements	0.69	704	724	(-)	0.769	0.713	gtaattatgtgatcACTTtta
SEQ_1	P\$AHP/HAHB4.01	Sunflower homeodomain leucine-zipper protein Hahb-4	0.87	714	724	(+)	1.000	0.902	cacataATTAC
SEQ_1	P\$GTBX/GT1.01	GT1-Box binding factors with a trihelix DNA-binding domain	0.85	714	730	(-)	0.968	0.867	gataatGTAAattatgtg
SEQ_1	P\$IBOX/GATA.01	Class I GATA factors	0.93	719	735	(-)	1.000	0.942	ttttgGATAAatgtaatt
SEQ_1	P\$MYBS/MYBST1.01	MybSt1 (Myb Solanum tuberosum 1) with a single myb repeat	0.90	722	738	(+)	1.000	0.962	tacattATCCaaaaaat
SEQ_1	P\$SUCB/SUCROSE.01	Sequence motif from the promoters of different sugar-responsive genes	0.81	733	751	(+)	1.000	0.908	aaAAATcataacttttaaca
SEQ_1	P\$GTBX/SBF1.01	SBF-1	0.87	740	756	(-)	1.000	0.967	attgttTTAAaagtat
SEQ_1	P\$MYBS/TAMYB80.01	MYB protein from wheat	0.83	759	775	(+)	1.000	0.857	aacaATATtccgcgcga
SEQ_1	P\$CGCG/OSCET.01	<i>Oryza sativa</i> CaM-binding transcription factor	0.78	768	784	(-)	1.000	0.781	gtcCGCGcttcgcgcgg
SEQ_1	P\$NCS3/NCS3.01	Nodulin consensus sequence 3	0.89	782	792	(+)	1.000	0.913	gaCACCCccct

TABLE 1-continued

cis-regulatory elements of SEQ ID NO: 1									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_1	P\$OPAQ/02_GCN4.01	Recognition site for BZIP transcription factors that belong to the group of Opaque-2 like proteins	0.81	802	818	(-)	1.000	0.829	catacaACATgactaca
SEQ_1	P\$TEPB/TEF1.01	TEF cis acting elements in both RNA polymerase II-dependent promoters and rDNA spacer sequences	0.76	842	862	(-)	0.838	0.843	gcATGGgaaatcaggtccatc
SEQ_1	P\$EINL/TEIL.01	TEIL (tobacco EIN3-like)	0.92	843	851	(+)	0.863	0.966	atTGAacctg
SEQ_1	P\$LEGB/LEGB.01	Legumin box, highly conserved sequence element about 100 bp upstream of the TSS in legumin genes	0.59	847	873	(-)	0.750	0.592	acgactaCTATgcatgggaaatcaggt
SEQ_1	P\$LEGB/RV.01	RY and Sph motifs conserved in seed-specific promoters	0.87	850	876	(+)	1.000	0.944	tgatttccCATGcatagtagtctcat
SEQ_1	P\$MADS/AGL15.01	AGL15, <i>Arabidopsis</i> MADS-domain protein AGAMOUS-like 15	0.79	851	871	(-)	1.000	0.850	gactACTatgcatgggaaatc
SEQ_1	P\$MADS/AGL3.01	AGL3, MADS Box protein	0.83	852	872	(+)	1.000	0.864	atttcCCATgcatagtagtctg
SEQ_1	P\$SPF1/SP8BF.01	DNA-binding protein of sweet potato that binds to the SP8a (ACTGTGTA) and SP8b (TAC-TATT) sequences of sporamin and beta-amylase genes	0.87	858	870	(-)	1.000	0.922	acTACTatgcatg
SEQ_1	P\$GBOX/TGA1.01	<i>Arabidopsis</i> leucine zipper protein TGA1	0.90	861	881	(-)	1.000	0.900	ccgagaTGCgactactatgc
SEQ_1	P\$TELO/ATPURA.01	<i>Arabidopsis</i> Telo-box interacting protein related to the conserved animal protein Pur-alpha	0.85	873	887	(-)	1.000	0.860	ataaACCCgagatga
SEQ_1	P\$OPAQ/02_GCN4.01	Recognition site for BZIP transcription factors that belong to the group of Opaque-2 like proteins	0.81	883	899	(-)	0.829	0.887	gatataACTTgaataaa

TABLE 1-continued

cis-regulatory elements of SEQ ID NO: 1										
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence	
SEQ_1	P\$DOFF/DOF1.01	Dof1/MBE1a - single zinc finger transcription factor	0.98	912	928	(-)	1.000	0.993	ttcagatrrAAAGaacgt	
SEQ_1	P\$MADS/AGL15.01	AGL15, <i>Arabidopsis</i> MADS-domain protein AGAMOUS-like 15	0.79	912	932	(+)	0.925	0.793	acgTTCtTtaactgaaacct	
SEQ_1	P\$AHBP/WUS.01	Homeodomain protein WUSCHEL	0.94	915	925	(+)	1.000	0.963	ttctttTAATct	
SEQ_1	P\$TELO/ATPURA.01	<i>Arabidopsis</i> Telo-box interacting protein related to the conserved animal protein Pur-alpha	0.85	924	938	(+)	1.000	0.876	ctgaaACCCtatcacc	
SEQ_1	P\$STKM/STK.01	Stoakeeper (STK), plant specific DNA binding protein important for tuber-specific and sucrose-inducible gene expression	0.85	937	951	(-)	1.000	0.877	tccTAAAtaaatcgg	
SEQ_1	P\$GTBX/GT1.01	GT1-Box binding factors with a trihelix DNA-binding domain	0.85	968	984	(-)	0.968	0.858	aaagtGTAAttttctg	
SEQ_1	P\$DOFF/PBF.01	PBF (MPBF)	0.97	976	992	(-)	1.000	0.988	gagacagaAAAGtggtgta	
SEQ_1	P\$GTBX/SEF1.01	SEF-1	0.87	999	1015	(+)	1.000	0.907	ctcgttttTTAAttttgggt	
SEQ_1	P\$MIIG/MYBCL1.01	Maize C1 myb-domain protein	0.92	1009	1023	(+)	1.000	0.942	atttgTAGtttcag	
SEQ_1	P\$SPF1/SP8BF.01	DNA-binding protein of sweet potato that binds to the SP8a (ACTGTGTA) and SP8b (TAC-TATT) sequences of sporamin and beta-amylase genes	0.87	1048	1060	(-)	0.814	0.872	aaCACTatgaaaa	
SEQ_1	P\$OPAQ/02_GCN4.01	Recognition site for BZIP transcription factors that belong to the group of Opaque-2 like proteins	0.81	1056	1072	(+)	1.000	0.891	gtgttaACATgttttaag	
SEQ_1	P\$LREM/ATCTA.01	Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	1095	1105	(-)	1.000	0.858	atATCTatggt	

TABLE 1-continued

cis-regulatory elements of SEQ ID NO: 1											
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence		
SEQ_1	P\$MYBL/NTMYBAS1.01	Anther-specific myb gene from tobacco	0.96	1125	1141	(+)	1.000	0.967	tagtggtgGTTAacaaa		
SEQ_1	P\$GTBX/SBF1.01	SBF-1	0.87	1127	1143	(+)	1.000	0.894	gtggtgGTTAcaaaaag		
SEQ_1	P\$MYBL/GAMYB.01	GA-regulated myb gene from barley	0.91	1130	1146	(-)	1.000	0.918	ggccttttGTTAaccac		
SEQ_1	P\$GBOX/BZIP911.01	bZIP transcription factor from Antirrhinum majus	0.77	1138	1158	(-)	0.750	0.781	ataagtTGAAtggccttttg		
SEQ_1	P\$OPAQ/02.01	Opaque-2 regulatory protein	0.87	1141	1157	(+)	0.852	0.882	aaggccattTCAActta		
SEQ_1	P\$NCSI/NCSI.01	Nodulin consensus sequence 1	0.85	1163	1173	(+)	1.000	0.909	tAAAAGataga		
SEQ_1	P\$SUCB/SUCROSE.01	Sequence motif from the promoters of different sugar-responsive genes	0.81	1176	1194	(+)	0.750	0.815	gcAAAGcattgtgataaa		
SEQ_1	P\$DOFF/DOF3.01	Dof3 - single zinc finger transcription factor	0.99	1184	1200	(+)	1.000	0.994	ttggtgatAAAGcctct		
SEQ_1	P\$GAGA/BPC.01	Basic pentacycsteine proteins	1.00	1184	1208	(-)	1.000	1.000	ataaagAGAGaggctttatcaaaaa		
SEQ_1	P\$IBOX/GATA.01	Class I GATA factors	0.93	1184	1200	(+)	1.000	0.938	ttggttGATAAagcctct		
SEQ_1	P\$MYBS/ZMWRP1.01	Zea mays MYB-related protein 1 (transfer cell specific)	0.79	1199	1215	(+)	0.777	0.841	ctctcttTATAaaga		
SEQ_1	P\$TBPF/TATA.01	Plant TATA box	0.88	1199	1213	(-)	1.000	0.958	tttataTAAagagag		
SEQ_1	P\$TBPF/TATA.02	Plant TATA box	0.90	1201	1215	(-)	1.000	0.917	tctttTATAaaagag		
SEQ_1	P\$TBPF/TATA.02	Plant TATA box	0.90	1202	1216	(+)	1.000	0.917	tctttTATAaaagag		
SEQ_1	P\$TBPF/TATA.01	Plant TATA box	0.88	1204	1218	(+)	1.000	0.934	tttataTAAagaggg		
SEQ_1	P\$DOFF/DOF3.01	Dof3 - single zinc finger transcription factor	0.99	1215	1231	(-)	1.000	0.995	aaggcgctAAAGccctt		
SEQ_1	P\$WBXF/WRKY.01	WRKY plant specific zinc-finger-type factor associated with pathogen defence, W box	0.92	1236	1252	(+)	1.000	0.975	atgctTTGActttacct		

TABLE 1-continued

Seq. name	Family/matrix	Further Information	cis-regulatory elements of SEQ ID NO: 1				Core Matrix sim.	Seq. Sequence	
			Opt. thresh.	Start pos.	End pos.	Strand			
SEQ_1	P\$TELO/RPFX.01	Ribosomal protein box, appears unique to plant RP genes and genes associated with gene expression	0.84	1260	1274	(-)	1.000	0.842	cgaaaCCCTtcactt
SEQ_1	P\$L1BX/ATML1.01	L1-specific homeodomain protein ATML1 ( <i>A. thaliana</i> meristem layer 1)	0.82	1317	1333	(+)	0.750	0.830	caagaaTCAAtgtaagc
SEQ_1	P\$CCAF/CCA1.01	Circadian clock associated 1	0.85	1332	1346	(-)	1.000	0.879	caactatAATctgc
SEQ_1	P\$MYBL/MYBPH3.02	Myb-like protein of <i>Petunia hybrida</i>	0.76	1338	1354	(+)	0.817	0.929	tatagtTTGTTagtttt
SEQ_1	P\$MYBL/MYBPH3.02	Myb-like protein of <i>Petunia hybrida</i>	0.76	1342	1358	(+)	1.000	0.818	gtttgtTAGTTTTtttcag
SEQ_1	P\$MYBL/MYBPH3.02	Myb-like protein of <i>Petunia hybrida</i>	0.76	1382	1398	(-)	1.000	0.818	aggcgtTAGTtcagaaa
SEQ_1	P\$MYBL/NTMYBAS1.01	Anther-specific myb gene from tobacco	0.96	1386	1402	(-)	1.000	0.967	tcaaaggcGTTAgttca
SEQ_1	P\$MADS/SQUA.01	MADS-box protein SQUAMOSA	0.90	1400	1420	(-)	1.000	0.902	attgaccATTTTTttttttca
SEQ_1	P\$WXP/BRE.01	Elicitor response element	0.89	1408	1424	(-)	1.000	0.973	gtcaatTGACcattttt
SEQ_1	P\$GTBX/GT3A.01	Trihelix DNA-binding factor GT-3a	0.83	1425	1441	(-)	1.000	0.897	ttagtgGTTAcaatggc
SEQ_1	P\$GTBX/GT1.01	GT1-Box binding factors with a trihelix DNA-binding domain	0.85	1432	1448	(-)	1.000	0.882	catgtgGTTAgTgggta
SEQ_1	P\$MIIG/PALBOXP.01	Putative cis-acting element in various PAL and 4CL gene promoters	0.81	1433	1447	(-)	0.936	0.820	atGTGtttagtggtt
SEQ_1	P\$LEGB/RV.01	RY and Sph motifs conserved in seed-specific promoters	0.87	1445	1471	(-)	1.000	0.944	tgtgtttgCATGcatagccagtgcatg
SEQ_1	P\$LEGB/RV.01	RY and Sph motifs conserved in seed-specific promoters	0.87	1452	1478	(+)	1.000	0.909	tggctatgCATGcaaacacaatgagat
SEQ_1	P\$SPF1/SP8BF.01	DNA-binding protein of sweet potato that binds to the SP8a (ACTGTGTA) and SP8b (TACTATT) sequences of sporamin and beta-amylase genes	0.87	1488	1500	(-)	1.000	0.871	ttTACTctttaggc
SEQ_1	P\$MYBL/MYBPH3.02	Myb-like protein of <i>Petunia hybrida</i>	0.76	1493	1509	(-)	0.778	0.838	caaaagtTGGTTtactct
SEQ_1	P\$MADS/AGL1.01	AGL1, <i>Arabidopsis</i> MADS-domain protein AGAMOUS-like 1	0.84	1495	1515	(-)	0.975	0.840	ggaTTCaaagtTggtttact
SEQ_1	P\$MADS/AGL2.01	AGL2, <i>Arabidopsis</i> MADS-domain protein AGAMOUS-like 2	0.82	1496	1516	(+)	0.968	0.845	gtaaaCCAActttggaatccc

TABLE 1-continued

Seq. name	Family/matrix	Further Information	cis-regulatory elements of SEQ ID NO: 1		Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
			Seq. name	Seq. name							
SEQ_1	P\$STKM/STK.01	Storekeeper (STK), plant specific DNA binding protein important for tuber-specific and sucrose-inducible gene expression	0.85	1513	1527	(+)	0.833	0.873	tccCAAAAaaattata		
SEQ_1	P\$ERSE/ERSE.I.01	ERSE I (ER stress-response element I)-like motif	0.79	1515	1533	(+)	0.750	0.803	ccaaaaaattatagcCATG		
SEQ_1	P\$GEOX/EMBPI.01	bZIP transcription factor implicated in ABA induced gene expression	0.84	1522	1542	(-)	0.750	0.854	agaacgacACATggctataat		
SEQ_1	P\$LEGE/LEGB.01	Legumin box, highly conserved sequence element about 100 bp upstream of the TSS in legumin genes	0.59	1522	1548	(+)	1.000	0.609	attatagCCAgtgctcgctcttgatga		
SEQ_1	P\$ABRE/ABFI.01	ABA (abscisic acid) inducible transcriptional activator	0.79	1525	1541	(-)	1.000	0.853	gaacgACACatggctat		
SEQ_1	P\$OCSE/OCSL.01	OCS-like elements	0.69	1549	1569	(-)	0.807	0.693	aaattttattggaaaACGAatt		
SEQ_1	P\$GTBX/SBF1.01	SBF-1	0.87	1562	1578	(-)	0.826	0.872	ttgttttCTAAatttta		
SEQ_1	P\$MIIG/PALBOXP.01	Putative cis-acting element in various PAL and 4CL gene promoters	0.81	1570	1584	(-)	0.936	0.819	ttGTGGttttgtttct		
SEQ_1	P\$SPF1/SP8BF.01	DNA-binding protein of sweet potato that binds to the SP8a (ACTGTGTA) and SP8b (TACTATT) sequences of sporamin and beta-amylase genes	0.87	1586	1598	(-)	1.000	0.881	atTACTtttgtatt		
SEQ_1	P\$OCSE/OCSL.01	OCS-like elements	0.69	1589	1609	(-)	0.769	0.716	taagttaaaaaattACTTtgt		
SEQ_1	P\$AHP/BLR.01	Transcriptional repressor BELLINGER	0.90	1591	1601	(-)	1.000	0.976	aaaATTActtt		
SEQ_1	P\$STKM/STK.01	Storekeeper (STK), plant specific DNA binding protein important for tuber-specific and sucrose-inducible gene expression	0.85	1593	1607	(-)	1.000	0.901	agtTAAAAaattact		
SEQ_1	P\$MADS/MADS.01	Binding sites for API, AP3-PI and AG dimers	0.75	1599	1619	(-)	1.000	0.777	tttccCCATTtaagttaaaaa		
SEQ_1	P\$L1BX/PDF2.01	Protodermal factor 2	0.85	1602	1618	(+)	1.000	0.864	ttaactTAAAtggggaa		
SEQ_1	P\$I1BX/TBOX.01	I-Box in rbcS genes and other light regulated genes	0.81	1640	1656	(+)	1.000	0.824	aaagaGATAgggcttaa		
SEQ_1	P\$TELO/RPBX.01	Ribosomal protein box, appears unique to plant RP genes and genes associated with gene expression	0.84	1642	1656	(-)	1.000	0.886	ttaagCCCTatctct		

TABLE 1-continued

cis-regulatory elements of SEQ ID NO: 1									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_1	P\$DOFF/DOF2.01	Dof2 - single zinc finger transcription factor	0.98	1647	1663	(+)	1.000	0.994	tagggcttrAAAGcagca
SEQ_1	P\$NACF/TANAC69.01	Wheat NACdomain DNA binding factor	0.68	1673	1695	(-)	0.812	0.695	aacgaaaaacgAAACGtataccag
SEQ_1	P\$MYEL/GAMYB.01	GA-regulated myb gene from barley	0.91	1689	1705	(+)	1.000	0.963	tttcgttttGTTAtcaca
SEQ_1	P\$IBOX/GATA.01	Class I GATA factors	0.93	1691	1707	(-)	1.000	0.931	attgtCAATAcacaaacga
SEQ_1	P\$GTBX/S1F.01	S1F, site 1 binding factor of spinach rps1 promoter	0.79	1707	1723	(+)	1.000	0.851	tttcATGGactataac
SEQ_1	P\$TBPF/TATA.02	Plant TATA box	0.90	1713	1727	(+)	1.000	0.901	ggactATATAcattt
SEQ_1	P\$LIBX/ATML1.01	L1-specific homeodomain protein ATML1 (A. thaliana meristem layer 1)	0.82	1718	1734	(-)	1.000	0.875	ctaagcTAAAtgtatat
SEQ_1	P\$PSRE/GAAA.01	GAAA motif involved in pollen specific transcriptional activation	0.83	1739	1755	(+)	1.000	0.847	caaaaGAAAccatctac
SEQ_1	P\$LREM/ATCTA.01	Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	1748	1758	(+)	1.000	0.854	ccATCTactttg
SEQ_1	P\$AHBP/ATHE1.01	Arabidopsis thaliana homeo box protein 1	0.90	1768	1778	(-)	1.000	0.990	ggaATTAttgt
SEQ_1	P\$AHBP/ATHB5.01	HDZip class I protein ATHB5	0.89	1768	1778	(+)	0.829	0.940	acaATAAttcc

TABLE 2

cis-regulatory elements of SEQ ID NO: 6									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_6	P\$SEF3/SEF3.01	SEF3, Soybean embryo factor 3	0.87	5	19	(+)	1.000	0.921	ctataACCCCaaccca
SEQ_6	P\$SEF3/SEF3.01	SEF3, Soybean embryo factor 3	0.87	10	24	(+)	1.000	0.891	acccaACCCCaaccca
SEQ_6	P\$GTEX/SBF1.01	SBF-1	0.87	22	38	(-)	1000	0.880	aggatacTTAAactfgt
SEQ_6	P\$MYBL/ATMYB77.01	R2R3-type myb-like transcription factor (I-type binding site)	0.87	35	51	(-)	1000	0.892	ttttgtCGGtttcagga
SEQ_6	P\$DREB/CRT_DRE.01	C-repeat/dehydration response element	0.89	38	52	(+)	1.000	0.902	tgaaaCCCGAcaaaa
SEQ_6	P\$DOFF/PBF.01	PBF (MPBF)	0.97	41	57	(+)	1000	0.986	aaccgacaAAAGagaat
SEQ_6	P\$IDDF/ID1.01	Maize INDETERMINATE1 zinc finger protein	0.92	41	53	(-)	1.000	0.987	tctttTGTcgggt
SEQ_6	P\$EPPF/ZPT22.01	Member of the EPF family of zinc finger transcription factors	0.75	50	72	(-)	1.000	0.770	agtcaaaaaagaCAGtattctctt
SEQ_6	P\$SPF1/SP8BF.01	DNA-binding protein of sweet potato that binds to the SP8a (ACTGTGTA) and SP8b (TACTATT) sequences of sporamin and beta-amylase genes	0.87	55	67	(+)	1.000	0.881	aaTACTgtctttt
SEQ_6	P\$NCS2/NCS2.01	Modulin consensus sequence 2	0.79	57	71	(+)	0.750	0.795	tactgtCITtttgac
SEQ_6	P\$WBXF/WRKY.01	WRKY plant specific zinc-finger-type factor associated with pathogen defence, W box	0.92	62	78	(+)	1.000	0.965	tctttTTGActtttcctg
SEQ_6	P\$HEAT/HSE.01	Heat shock element	0.81	72	86	(-)	0.826	0.819	agattattcaGGAAA
SEQ_6	P\$AHBP/BLR.01	Transcriptional repressor BELLINGER	0.90	77	87	(-)	1000	0.901	aagATTAttca
SEQ_6	P\$DOFF/PBOX.01	Prolamins box, conserved in cereal seed storage protein gene promoters	0.75	80	96	(-)	1.000	0.769	tatttttAAAGattat
SEQ_6	P\$GTEX/SBF1.01	SBF-1	0.87	80	96	(+)	1.000	0.892	ataatctTTAAaaaata

TABLE 2-continued

cis-regulatory elements of SEQ ID NO: 6										
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence	
SEQ_6	P\$GAGA/BPC.01	Basic pentacycysteine proteins	1.00	88	112	(-)	1.000	1000	ttccagAGAGaaactgatattttta	
SEQ_6	P\$PSRE/GAAA.01	GAAA motif involved in pollen specific transcriptional activation	0.83	105	121	(+)	1000	0.878	ctctgGAAAatagtaaag	
SEQ_6	P\$SPF1/SP8BF.01	DNA-binding protein of sweet potato that binds to the SP8a (ACTGTGTA) and SP8b (TACTATT) sequences of sporamin and beta-amylase genes	0.87	108	120	(-)	1.000	0.943	ttTACTattttcca	
SEQ_6	P\$OCSE/OC SL.01	OCS-like elements	0.69	116	136	(-)	0.769	0.700	ttgcatcagttcttACTttac	
SEQ_6	P\$HOCT/HOCT.01	Octamer motif found in plant histone H3 and H4 genes	0.76	145	161	(+)	0.750	0.762	atcaccgATCTacgaag	
SEQ_6	P\$LREM/ATCTA.01	Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	150	160	(+)	1.000	0.864	cgATCTacgaa	
SEQ_6	P\$MSAE/MSA.01	M-phase-specific activators (NtmybA1, NtmybA2, NtmybB)	0.80	174	188	(-)	1.000	0.834	aaaaaACGggtgga	
SEQ_6	P\$AHBP/HAHB4.01	Sunflower homeodomain leucine-zipper protein Hahb-4	0.87	187	197	(+)	1.000	0.934	ttgatcATTAT	
SEQ_6	P\$CGG/ATSRI.01	<i>Arabidopsis thaliana</i> signal-responsive gene1, Ca2+/calmodulin binding protein homolog to NtER1 (tobacco early ethylene-responsive gene)	0.84	194	210	(-)	1.000	0.912	aagCCGtaccgataataa	
SEQ_6	P\$OCSE/OC SL.01	OCS-like elements	0.69	196	216	(-)	0.807	0.709	gtttttaagcgcgtACGAtat	
SEQ_6	P\$GTBX/SBF1.01	SBF-1	0.87	202	218	(+)	1.000	0.875	tacgcgcTTAAaaacct	
SEQ_6	P\$MYBL/MYBPH3.02	Myb-like protein of <i>Petunia hybrida</i>	0.76	217	233	(-)	0.778	0.781	tttagtTCGTaaaaaag	
SEQ_6	P\$DOFF/PBOX.01	Prolamin box, conserved in cereal seed storage protein gene promoters	0.75	245	261	(-)	1000	0.831	ttatctgaAAAGtaaaa	
SEQ_6	P\$IBOX/GATA.01	Class I GATA factors	0.93	252	268	(+)	1000	0.933	tttcaGATaatgttgca	

TABLE 2-continued

cis-regulatory elements of SEQ ID NO: 6										
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence	
SEQ_6	P\$AGP1/AGP1.01	AG-motif binding protein 1	0.91	284	294	(-)	1.000	0.988	acaGATCtctac	
SEQ_6	P\$AGP1/AGP1.01	AG-motif binding protein 1	0.91	285	295	(+)	1000	0.920	ataGATCtctgtt	
SEQ_6	P\$GARP/ARR10.01	Type-B response regulator (ARR10), member of the GARP-family of plant myb-related DNA binding motifs	0.97	287	295	(+)	1.000	0.970	AGATctgtt	
SEQ_6	P\$CAAT/CAAT.01	CCAAT-box in plant promoters	0.97	298	306	(+)	1.000	0.973	ttCCAAtga	
SEQ_6	P\$LFB/LFY.01	Plant specific floral meristem identity gene LEAFY (LFY)	0.93	298	310	(+)	1000	0.930	tTCCRatgagaat	
SEQ_6	P\$CCAF/CCAL.01	Circadian clock associated 1	0.85	300	314	(+)	1.000	0.864	ccaatgagAACTctgt	
SEQ_6	P\$GARP/ARR10.01	Type-B response regulator (ARR10), member of the GARP-family of plant myb-related DNA binding motifs	0.97	304	312	(-)	1.000	0.971	AGATtctca	
SEQ_6	P\$RAV5/RAV1-5.01	5'-part of bipartite RAV1 binding site, interacting with AP2 domain	0.96	308	318	(-)	1.000	0.960	aacAACAgatt	
SEQ_6	P\$IDDF/ID1.01	Maize INDETERMINATE1 zinc finger protein	0.92	339	351	(-)	1.000	0.934	tattTTGTCagat	
SEQ_6	P\$CAAT/CAAT.02	CCAAT-box in plant promoters	1.00	400	408	(-)	1000	1000	gtCCAATta	
SEQ_6	P\$WXXF/WRKY.01	WRKY plant specific zinc-finger-type factor associated with pathogen defence, W box	0.92	405	421	(-)	1.000	0.957	cacatTTGActatgtcc	
SEQ_6	P\$MYCL/ICE.01	ICE (inducer of CBF expression 1), AtMYC2 (rd22BFL)	0.95	407	425	(-)	1.000	0.953	ccaacACATtgactatgt	
SEQ_6	P\$CARM/CARICH.01	CA-rich element	0.78	412	430	(-)	1.000	0.785	aaagtcCAACAcatttgac	
SEQ_6	P\$GTBX/SBF1.01	SBF-1	0.87	424	440	(-)	1.000	0.875	tcggaatTTAAagtcc	
SEQ_6	P\$SUCB/SUCROSE.01	Sequence motif from the promoters of different sugar-responsive genes	0.81	439	457	(+)	1000	0.913	gaAAATcattaaaaacaat	

TABLE 2-continued

cis-regulatory elements of SEQ ID NO: 6										
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence	
SEQ_6	P\$AHBP/ATHB5.01	HDZip class I protein ATHB5	0.89	440	450	(-)	0.829	0.902	ttaATGAtttt	
SEQ_6	P\$AHBP/HAHB4.01	Sunflower homeodomain leucine-zipper protein Hahb-4	0.87	440	450	(+)	1.000	0.967	aaatcATTAA	
SEQ_6	P\$GTEx/SBF1.01	SBF-1	0.87	440	456	(+)	1.000	0.886	aaatcATTAAaaaa	
SEQ_6	P\$GTEx/SBF1.01	SBF-1	0.87	441	457	(-)	1000	0.888	attgtttTTAAtgattt	
SEQ_6	P\$LIBX/ATML1.02	<i>Arabidopsis thaliana</i> meristem layer 1	0.76	442	458	(+)	1000	0.789	aatCATTaaaaacaatt	
SEQ_6	P\$AHBP/WUS.01	Homeodomain protein WUSCHEL	0.94	444	454	(-)	1.000	1000	gttttTAATga	
SEQ_6	P\$MYBL/MYBP3.01	Myb-like protein of <i>Petunia hybrida</i>	0.80	448	464	(+)	0.750	0.812	taaaaacaATTAAAA	
SEQ_6	P\$TEPB/TEF1.01	TEF cis acting elements in both RNA polymerase II-dependent promoters and rDNA spacer sequences	0.76	467	487	(+)	0.838	0.839	taATGGagatttttgaatta	
SEQ_6	P\$CCAF/CCA1.01	Circadian clock associated 1	0.85	471	485	(-)	1.000	0.948	attacaaaaATCtcc	
SEQ_6	P\$GTEx/SBF1.01	SBF-1	0.87	478	494	(+)	1.000	0.905	tttgaattTAAttggaa	
SEQ_6	P\$CAAT/CAAT.02	CCAAT-box in plant promoters	1.00	486	494	(-)	1.000	1000	ttcCAATta	
SEQ_6	P\$MADS/AGL15.01	AGL15, <i>Arabidopsis</i> MADS-domain protein AGAMOUS-like 15	0.79	509	529	(-)	1.000	0.886	ctaTACTattaaagggaaaga	
SEQ_6	P\$MADS/AGL3.02	AGL3, MADS Box protein	0.80	510	530	(+)	0.790	0.859	ctttcCCTTtaatagtataga	
SEQ_6	P\$SPF1/SP8BF.01	DNA-binding protein of sweet potato that binds to the SP8a (ACTGTGTA) and SP8b (TACTATT) sequences of sporamin and beta-amylase genes	0.87	516	528	(-)	1.000	0.956	taTACTattaaag	
SEQ_6	P\$LREM/ATCTA.01	Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	523	533	(-)	1.000	0.902	atATCTatact	

TABLE 2-continued

Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core Matrix	
							sim.	Sequence
SEQ_6 P\$LIBX/ATML1.01		L1-specific homeodomain protein ATML1 ( <i>A. thaliana</i> meristem layer 1)	0.82	573	589	(-)	0.750	0.844 taattttAACTgcaact
SEQ_6 P\$GTBX/SBF1.01		SBF-1	0.87	574	590	(+)	1000	0.954 gttgcagTTAAaattac
SEQ_6 P\$NACF/TANAC69.01		Wheat NACdomain DNA binding factor	0.68	577	599	(+)	1000	0.707 gcagttaaaatTACGaatcatgg
SEQ_6 P\$MADS/AGL2.01		AGL2, <i>Arabidopsis</i> MADS-domain protein AGA-MOUS-like 2	0.82	584	604	(-)	1.000	0.820 ggagcCCATgatttcgtaattt
SEQ_6 P\$LREM/ATCTA.01		Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	604	614	(+)	1.000	0.897 ctATCTatatt
SEQ_6 P\$MYBS/ZMMRP1.01		<i>Zea mays</i> MYB-related protein 1 (transfer cell specific)	0.79	604	620	(+)	0.777	0.905 ctatctatATTTttacat
SEQ_6 P\$DOFF/PBOX.01		Prolamin box, conserved in cereal seed storage protein gene promoters	0.75	608	624	(-)	0.761	0.835 tgtgatgrAAAAtatag
SEQ_6 P\$DOFF/DOF2.01		Dof2 - single zinc finger transcription factor	0.98	619	635	(+)	1.000	0.995 atcacaatAAAGctata
SEQ_6 P\$TBPF/TATA.02		Plant TATA box	0.90	628	642	(+)	1.000	0.903 aagcTATAatcatt
SEQ_6 P\$LFYB/LFY.01		Plant specific floral meristem identity gene LFY (LFY)	0.93	634	646	(-)	0.914	0.936 cACCAatgatata
SEQ_6 P\$CAAT/CAAT.01		CCAAT-box in plant promoters	0.97	638	646	(-)	1.000	0.988 caCCRAAtga
SEQ_6 P\$IDDF/ID1.01		Maize INDETERMINATE1 zinc finger protein	0.92	657	669	(-)	1000	0.921 gggTTGTcttcca
SEQ_6 P\$TELO/RPBX.01		Ribosomal protein box, appears unique to plant RP genes and genes associated with gene expression	0.84	662	676	(+)	1.000	0.981 acaaaCCCTaaactc
SEQ_6 P\$AHBP/HAHB4.01		Sunflower homeodomain leucine-zipper protein Hahb-4	0.87	684	694	(-)	1.000	0.923 cttattATTAG

TABLE 2-continued

Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_6	P\$MYCL/ICE.01	ICE (inducer of CBF expression 1), AtMYC2 (rd22BP1)	0.95	694	712	(+)	0.954	0.972	gcaaaACActtgattccaa
SEQ_6	P\$MADS/SQUA.01	MADS-box protein SQUAMOSA	0.90	711	731	(-)	1.000	0.906	ggtcgctATTgtttctgttt
SEQ_6	P\$IBOX/GATA.01	Class I GATA factors	0.93	733	749	(+)	1.000	0.958	tgcaCGATAatagatag
SEQ_6	P\$LREM/ATCTA.01	Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	739	749	(-)	1.000	0.853	ctATCTattat
SEQ_6	P\$HMGF/HMG_IY.02	High mobility group I/Y-like protein isolated from pea	1.00	755	769	(-)	1.000	1.000	tattTATTtttccaaa
SEQ_6	P\$CCAF/CCA1.01	Circadian clock associated 1	0.85	774	788	(-)	1.000	0.864	aaccaagaAATctga
SEQ_6	P\$SPF1/SP8BF.01	DNA-binding protein of sweet potato that binds to the SP8a (ACTGTGTA) and SP8b (TACTATT) sequences of sporamin and beta-amylase genes	0.87	787	799	(-)	1.000	0.909	ttTACTgtttaaa
SEQ_6	P\$DOFF/DOF2.01	Dof2 - single zinc finger transcription factor	0.98	790	806	(+)	1.000	0.981	aaacagtaAAAGctaata
SEQ_6	P\$LIBX/ATML1.02	<i>Arabidopsis thaliana</i> meristem layer 1	0.76	790	806	(+)	0.808	0.780	aaCAGTaaaaagctaata
SEQ_6	P\$CARM/CARICH.01	CA-rich element	0.78	800	818	(-)	1.000	0.836	tttttgaaACACattagct
SEQ_6	P\$MYBL/MYBPH3.01	Myb-like protein of <i>Petunia hybrida</i>	0.80	823	839	(+)	0.750	0.818	aaaaaacacTAAaagct
SEQ_6	P\$SPF1/SP8BF.01	DNA-binding protein of sweet potato that binds to the SP8a (ACTGTGTA) and SP8b (TACTATT) sequences of sporamin and beta-amylase genes	0.87	823	835	(-)	1.000	0.905	ttTACTgtttttt
SEQ_6	P\$DOFF/DOF2.01	Dof2 - single zinc finger transcription factor	0.98	826	842	(+)	1.000	0.981	aaacagtaAAAGctaata
SEQ_6	P\$LIBX/ATML1.02	<i>Arabidopsis thaliana</i> meristem layer 1	0.76	826	842	(+)	0.808	0.780	aaCAGTaaaaagctaata
SEQ_6	P\$GAPB/GAP.01	Cis-element in the GAPDH promoters conferring light inducibility	0.88	843	857	(+)	1.000	0.984	acacATGAgacaag

TABLE 2-continued

Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_6 P\$LREM/ATCTA.01		Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	863	873	(-)	1.000	0.912	aaATCTataag
SEQ_6 P\$CCAF/CCA1.01		Circadian clock associated 1	0.85	866	880	(-)	1.000	0.885	gtgggtaaaATctat
SEQ_6 P\$GTBX/SBF1.01		SBF-1	0.87	867	883	(-)	0.782	0.889	tttTgggTAAaatcta
SEQ_6 P\$MYBL/MYBP3.02		Myb-like protein of Petunia hybrida	0.76	877	893	(-)	0.817	0.846	acaagtTTGTTTTgtgg
SEQ_6 P\$MADS/AGL2.01		AGL2, Arabidopsis MADS-domain protein AGA-MOUS-like 2	0.82	906	926	(-)	0.968	0.856	agaagCCAacattggcaacga
SEQ_6 P\$MADS/AG.01		Agamous, required for normal flower development, similarity to SRF (human) and MCM (yeast) proteins	0.80	907	927	(+)	0.902	0.806	cgtTCCcaatgtggcttctt
SEQ_6 P\$LFBY/LFY.01		Plant specific floral meristem identity gene LFY (LFY)	0.93	910	922	(+)	0.885	0.938	tGCCAatgttggc
SEQ_6 P\$DOFF/PBOX.01		Prolamin box, conserved in cereal seed storage protein gene promoters	0.75	920	936	(-)	1.000	0.801	tgtgtggAAAGaagcc
SEQ_6 P\$SALT/ALFIN1.01		Zinc-finger protein in alfalfa roots, regulates salt tolerance	0.93	926	940	(-)	1.000	0.986	tttGTGTGGtgaaa
SEQ_6 P\$TEPB/TEF1.01		TEF cis acting elements in both RNA polymerase II-dependent promoters and rDNA spacer sequences	0.76	931	951	(-)	0.838	0.781	taACGtcatatttGTgtggt
SEQ_6 P\$WEXF/ERE.01		Elicitor response element	0.89	937	953	(+)	1.000	0.897	caaatATGACcgtaag
SEQ_6 P\$MYBL/ATMYB77.01		R2R3-type myb-like transcription factor (I-type binding site)	0.87	940	956	(+)	0.857	0.916	atatgaCCGTTaagact
SEQ_6 P\$MSAE/MSA.01		M-phase-specific activators (NtmybA1, NtmybA2, NtmybB)	0.80	941	955	(-)	1.000	0.889	gtcttAACGgtcata

TABLE 2-continued

cis-regulatory elements of SEQ ID NO: 6										
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence	
SEQ_6	P\$AHBP/HAHB4.01	Sunflower homeodomain leucine-zipper protein Habb-4	0.87	968	978	(+)	1.000	0.916	tttataATTAC	
SEQ_6	P\$GTBX/GT1.01	GT1-Box binding factors with a trihelix DNA-binding domain	0.85	968	984	(-)	0.968	0.859	catgtaGTAAttataaa	
SEQ_6	P\$LEGB/RV.01	RY and Sph motifs conserved in seed-specific promoters	0.87	970	996	(-)	1.000	0.952	atTTtataCATGcatgtagtaattata	
SEQ_6	P\$LIBX/ATML1.01	L1-specific homeodomain protein ATML1 ( <i>A. thaliana</i> meristem layer 1)	0.82	973	989	(+)	0.750	0.846	aattactACATgcatgt	
SEQ_6	P\$LEGB/RV.01	RY and Sph motifs conserved in seed-specific promoters	0.87	973	999	(+)	1.000	0.952	aattactaCATGcatgtataaaatcta	
SEQ_6	P\$LIBX/ATML1.01	L1-specific homeodomain protein ATML1 ( <i>A. thaliana</i> meristem layer 1)	0.82	980	996	(-)	0.750	0.855	atTTtataCATgcatgt	
SEQ_6	P\$CCAF/CCA1.01	Circadian clock associated 1	0.85	986	1000	(+)	1.000	0.922	atgtataaaATCtat	
SEQ_6	P\$LREM/ATCTA.01	Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	993	1003	(+)	1.000	0.897	aaaTCTataga	
SEQ_6	P\$LREM/ATCTA.01	Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	996	1006	(-)	1.000	0.877	cgATCTataga	

TABLE 3  
cis-regulatory elements of SEQ ID NO: 9

Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_9	P\$SUCB/SUCROSE.01	Sequence motif from the promoters of different sugar-responsive genes	0.81	17	35	(+)	0.750	0.859	caAAATtcaggtagcttaag
SEQ_9	P\$MIIG/MYBC1.01	Maize C1 myb-domain protein	0.92	21	35	(+)	1.000	0.928	ttcagGTAGcttaag
SEQ_9	P\$MADS/AGL3.01	AGL3, MADS Box protein	0.83	30	50	(-)	0.973	0.858	agccaCCAAtttagagcttaag
SEQ_9	P\$CAAT/CAAT.01	CCAAT-box in plant promoters	0.97	39	47	(-)	1.000	0.981	caCCAAtta
SEQ_9	P\$DOFF/DOF3.01	Dof3 - single zinc finger transcription factor	0.99	44	60	(-)	1.000	0.995	tattacctAAAAGccacc
SEQ_9	P\$MYBL/MYBP3.02	Myb-like protein of Petunia hybrida	0.76	69	85	(+)	0.817	0.794	ctcagTGTGtaaatgta
SEQ_9	P\$LIBX/ATML1.01	L1-specific homeodomain protein ATML1 (A. thaliana meristem layer 1)	0.82	72	88	(+)	1.000	0.925	agtttGTAAAtgtagtt
SEQ_9	P\$MYBL/MYBP3.02	Myb-like protein of Petunia hybrida	0.76	78	94	(+)	1.000	0.794	taaatGTAGTtaaaact
SEQ_9	P\$GTBX/SBF1.01	SBF-1	0.87	80	96	(+)	1.000	0.929	aatgtagTTAAAacttt
SEQ_9	P\$NCSI/NCSI.01	Nodulin consensus sequence 1	0.85	88	98	(-)	1.000	0.850	cAAAAGtcttta
SEQ_9	P\$SALT/ALFIN1.01	Zinc-finger protein in alfalfa roots, regulates salt tolerance	0.93	93	107	(+)	1.000	0.948	cttttGTGGtgtaaa
SEQ_9	P\$DOFF/PBOX.01	Prolamin box, conserved in cereal seed storage protein gene promoters	0.75	97	113	(+)	0.776	0.793	tgtggtGTAAAtcatgt
SEQ_9	P\$GTBX/GT1.01	GT1-Box binding factors with a trihelix DNA-binding domain	0.85	97	113	(+)	0.968	0.857	tgtggtGTAAAtcatgt
SEQ_9	P\$CAAT/CAAT.01	CCAAT-box in plant promoters	0.97	121	129	(-)	1.000	0.979	aaCCAAtcgc
SEQ_9	P\$GTBX/GT1.01	GT1-Box binding factors with a trihelix DNA-binding domain	0.85	121	137	(+)	1.000	0.866	cgattGTAAataaaaa
SEQ_9	P\$SEF4/SEF4.01	Soybean embryo factor 4	0.98	129	139	(-)	1.000	0.985	actTTTtatta
SEQ_9	P\$OPAQ/GCN4.01	GCN4, conserved in cereal seed storage protein gene promoters, similar to yeast GCN4 and vertebrate AP-1	0.81	141	157	(+)	1.000	0.813	gttgatGAGTtaaaaa
SEQ_9	P\$MYBL/MYBP3.02	Myb-like protein of Petunia hybrida	0.76	158	174	(+)	1.000	0.805	caaaatTAGTtgcagtt
SEQ_9	P\$AHP/BLR.01	Transcriptional repressor BELLINGER	0.90	159	169	(+)	1.000	0.981	aaaATTAGttg

TABLE 3-continued

Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_9	F\$LIBX/ATML1.01	L1-specific homeodomain protein ATML1 ( <i>A. thaliana</i> meristem layer 1)	0.82	165	181	(-)	0.750	0.844	taatttTACTgcaact
SEQ_9	F\$GTBX/SBF1.01	SBF-1	0.87	166	182	(+)	1.000	0.954	gttgcagTAAaattac
SEQ_9	F\$NACF/TANAC69.01	wheat NACdomain DNA binding factor	0.68	169	191	(+)	1.000	0.707	gcagttaaaatTACGaatcatgg
SEQ_9	F\$MADS/AGL2.01	AGL2, <i>Arabidopsis</i> MADS-domain protein AGA-MOUs-like 2	0.82	176	196	(-)	1.000	0.820	ggagccCAngattcgttaattt
SEQ_9	F\$LREM/ATCTA.01	Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	196	206	(+)	1.000	0.897	ctATCTatatt
SEQ_9	F\$MYBS/ZMRP1.01	<i>Zea mays</i> MYB-related protein 1 (transfer cell specific)	0.79	196	212	(+)	0.777	0.905	ctattctaTATTtcaat
SEQ_9	F\$DOFF/PBOX.01	Prolamin box, conserved in cereal seed storage protein gene promoters	0.75	200	216	(-)	0.761	0.834	tgtaatgtAAAAtatag
SEQ_9	F\$DOFF/DOF2.01	Dof2 - single zinc finger transcription factor	0.98	211	227	(+)	1.000	0.988	attacaatAAAGctttt
SEQ_9	F\$DOFF/DOF2.01	Dof2 - single zinc finger transcription factor	0.98	242	258	(+)	1.000	0.995	attacaatAAAGctata
SEQ_9	F\$TBPF/TATA.02	Plant TATA box	0.90	251	265	(+)	1.000	0.913	aagcTATatcact
SEQ_9	F\$MYBS/ZMRP1.01	<i>Zea mays</i> MYB-related protein 1 (transfer cell specific)	0.79	272	288	(-)	0.777	0.827	ttgtcttTATTtcaagat
SEQ_9	F\$DOFF/DOF1.01	Dof1/MNB1a - single zinc finger transcription factor	0.98	273	289	(+)	1.000	0.984	tctgaaatAAAGacaaa
SEQ_9	F\$IDDF/IDI.01	Maize INDETERMINATE1 zinc finger protein	0.92	280	292	(-)	1.000	0.940	gggtTTGTcttta
SEQ_9	F\$TELO/RPBX.01	Ribosomal protein box, appears unique to plant RP genes and genes associated with gene expression	0.84	285	299	(+)	1.000	0.864	acaaaCCCTgaactc
SEQ_9	F\$AHBP/ATHB1.01	<i>Arabidopsis thaliana</i> homeo box protein 1	0.90	307	317	(-)	1.000	0.989	ctaATTAtttc
SEQ_9	F\$AHBP/HAHB4.01	Sunflower homeodomain leucine-zipper protein Hahb-4	0.87	307	317	(+)	1.000	0.943	gaaataATTAg
SEQ_9	F\$MYCL/ICE.01	ICE (inducer of CBF expression 1), AtMYC2 (rd22BP1)	0.95	317	335	(+)	0.954	0.972	gccaaaCACTtgattccaa
SEQ_9	F\$MADS/SQUA.01	MADS-box protein SQUAMOSA	0.90	334	354	(-)	1.000	0.906	ggtcgtATTGttttctgttt
SEQ_9	F\$ERSE/ERSE_I.01	ERSE I (ER stress-response element I)-like motif	0.79	343	361	(+)	1.000	0.799	caaatagcgaccttaacACG
SEQ_9	F\$IBOX/GATA.01	Class I GATA factors	0.93	356	372	(+)	1.000	0.958	aacacGATAatagatag

TABLE 3-continued

cis-regulatory elements of SEQ ID NO: 9										
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence	
SEQ_9	P\$LREM/ATCTA.01	Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	362	372	(-)	1.000	0.853	ctATCTatttat	
SEQ_9	P\$AHBP/BLR.01	Transcriptional repressor BELLRINGER	0.90	383	393	(-)	1.000	0.928	tatATTAtttt	
SEQ_9	P\$IBOX/IBOX.01	I-Box in rbcS genes and other light regulated genes	0.81	385	401	(+)	0.750	0.817	aatAATATAaggatcag	
SEQ_9	P\$CCAF/CCA1.01	Circadian clock associated 1	0.85	398	412	(-)	1.000	0.864	aaccaagaaATCtga	
SEQ_9	P\$SPF1/SP8BF.01	DNA-binding protein of sweet potato that binds to the SP8a (ACTGTGTA) and SP8b (TACTATT) sequences of sporamin and beta-amylase genes	0.87	411	423	(-)	1.000	0.909	ttTACTgttttaa	
SEQ_9	P\$GABP/GAP.01	Cis-element in the GAPDH promoters conferring light inducibility	0.88	431	445	(+)	1.000	0.984	acacATGAgacaag	
SEQ_9	P\$SUCB/SUCROSE.01	Sequence motif from the promoters of different sugar-responsive genes	0.81	448	466	(+)	1.000	0.815	aaaaATtatagattttaca	
SEQ_9	P\$LREM/ATCTA.01	Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	452	462	(-)	1.000	0.912	aaaTCTataat	
SEQ_9	P\$CCAF/CCA1.01	Circadian clock associated 1	0.85	455	469	(-)	1.000	0.889	ttttgtaaaATCtat	
SEQ_9	P\$DOFF/PBOX.01	Prolamin box, conserved in cereal seed storage protein gene promoters	0.75	455	471	(-)	0.761	0.841	tgttttgtAAAActtat	
SEQ_9	P\$MADS/AGL2.01	AGL2, <i>Arabidopsis</i> MADS-domain protein AGA-MOUS-like 2	0.82	496	516	(-)	0.968	0.856	agaagCCAacattggcaacga	
SEQ_9	P\$MADS/AG.01	Agamous, required for normal flower development, similarity to SRF (human) and MCM (yeast) proteins	0.80	497	517	(+)	0.902	0.806	cgtTGCCaatgttggttctt	
SEQ_9	P\$LFBY/LFY.01	Plant specific floral meristem identity gene LFY (LFY)	0.93	500	512	(+)	0.885	0.938	TGCCAatgtttggc	
SEQ_9	P\$DOFF/PBOX.01	Prolamin box, conserved in cereal seed storage protein gene promoters	0.75	510	526	(-)	1.000	0.801	tgtggtggAAAAGaagcc	
SEQ_9	P\$SALT/ALFIN1.01	Zinc-finger protein in alfalfa roots, regulates salt tolerance	0.93	516	530	(-)	1.000	0.986	tttgtGTGGtgga	
SEQ_9	P\$TEPB/TEF1.01	TEF cis acting elements in both RNA polymerase II-dependent promoters and rDNA spacer sequences	0.76	521	541	(-)	0.838	0.781	taACGGtcacattttgtggt	
SEQ_9	P\$WBXF/ERE.01	Elicitor response element	0.89	527	543	(+)	1.000	0.897	caaatATGACcgtaag	

TABLE 3-continued

cis-regulatory elements of SEQ ID NO: 9									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_9	P\$MYBL/ATMYB77.01	R2R3-type myb-like transcription factor (I-type binding site)	0.87	530	546	(+)	0.857	0.916	atatgaCCGTTaaagact
SEQ_9	P\$MSAE/MSA.01	M-phase-specific activators (NtmybA1, NtmybA2, NtmybB)	0.80	531	545	(-)	1.000	0.889	gtcttAACGgtcata
SEQ_9	P\$AHBP/HAHB4.01	Sunflower homeodomain leucine-zipper protein Hahb-4	0.87	558	568	(+)	1.000	0.916	tttataATTAc
SEQ_9	P\$GTBX/GT1.01	GT1-Box binding factors with a trihelix DNA-binding domain	0.85	558	574	(-)	0.968	0.859	catgtaCTAAttataaa
SEQ_9	P\$OPAQ/O2_GCN4.01	Recognition site for BZIP transcription factors that belong to the group of Opaque-2 like proteins	0.81	564	580	(+)	1.000	0.823	attactACATggatgta
SEQ_9	P\$HMGF/HMG_IY.01	High mobility group I/Y-like proteins	0.89	577	591	(-)	1.000	0.912	tataTATtttataca
SEQ_9	P\$MYBS/ZMMRP1.01	Zea mays MYB-related protein 1 (transfer cell specific)	0.79	580	596	(-)	0.777	0.793	cgatctaTATAttttat
SEQ_9	P\$TBPF/TATA.02	Plant TATA box	0.90	581	595	(-)	1.000	0.909	gatcTATAtatttta
SEQ_9	P\$LREM/ATCTA.01	Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	586	596	(-)	1.000	0.882	cgATCTatata
SEQ_9	P\$LIBX/PDF2.01	Protodermal factor 2	0.85	617	633	(-)	1.000	0.891	gagaaaTAAAtggtcga

TABLE 4

cis-regulatory elements of SEQ ID NO: 14									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_14 P\$OCSE/OCSE.01		OCS-like elements	0.69	7	27	(-)	1.000	0.702	caaaagtgtgactatACGTTTT
SEQ_14 P\$DOFF/DOF3.01		Dof3 - single zinc finger transcription factor	0.99	31	47	(-)	1.000	0.997	catagtcaAAGcaca
SEQ_14 P\$WBXF/WRKY.01		WRKY plant specific zinc-finger-type factor associated with pathogen defence, W box	0.92	34	50	(+)	1.000	0.961	tgctttTGAactatgtgt
SEQ_14 P\$MYBS/ZMRRP1.01		Zea mays MYB-related protein 1 (transfer cell specific)	0.79	43	59	(+)	1.000	0.833	ctatgtGTATCgtttcc
SEQ_14 P\$LREM/ATCTA.01		Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	59	69	(-)	1.000	0.892	cgATCTataag
SEQ_14 P\$MADS/AG.01		Agamous, required for normal flower development, similarity to SRF (human) and MCM (yeast) proteins	0.80	92	112	(-)	0.962	0.820	tagTCCcaaacggttccaa
SEQ_14 P\$MIIG/MYBC1.01		Maize C1 myb-domain protein	0.92	104	118	(-)	1.000	0.935	tgttgGTAGttccca
SEQ_14 P\$MADS/AGL2.01		AGL2, Arabidopsis MADS-domain protein AGAMOUS-like 2	0.82	108	128	(+)	0.968	0.828	aactaCCAaccacaagcaatgc
SEQ_14 P\$NCS2/NCS2.01		Nodulin consensus sequence 2	0.79	130	144	(-)	1.000	0.817	ttttgcCTCTctaag
SEQ_14 P\$SPF1/SP8BF.01		DNA-binding protein of sweet potato that binds to the SP8a (ACTGTGTA) and SP8b (TACTATT) sequences of sporamin and beta-amylase genes	0.87	139	151	(-)	1.000	0.918	atTACTctttttgc
SEQ_14 P\$DOFF/PBF.01		PBF (MPBF)	0.97	145	161	(+)	1.000	0.990	gagtaataAAAGagagg
SEQ_14 P\$NCS1/NCS1.01		Nodulin consensus sequence 1	0.85	163	173	(+)	1.000	0.862	gAAAAGttttg

TABLE 4-continued

cis-regulatory elements of SEQ ID NO: 14									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_14 P\$WBXF/WRKY.01		WRKY plant specific zinc-finger-type factor associated with pathogen defence, W box	0.92	166	182	(-)	1.000	0.942	atagTTGAcAAAaactt
SEQ_14 P\$IDDF/ID1.01		Maize INDETERMINATE1 zinc finger protein	0.92	167	179	(+)	1.000	0.935	agttTTGTcaaac
SEQ_14 P\$OCSE/OCSE.01		OCS-like elements	0.69	194	214	(-)	0.769	0.721	aaaagttagatcttACTTtct
SEQ_14 P\$OCSE/OCSE.01		OCS-like elements	0.69	195	215	(+)	0.769	0.766	gaaagtaagatctaACTTttt
SEQ_14 P\$AGP1/AGP1.01		AG-motif binding protein 1	0.91	199	209	(-)	1.000	0.915	ttaGATCttac
SEQ_14 P\$AGP1/AGP1.01		AG-motif binding protein 1	0.91	200	210	(+)	1.000	0.983	taaGATCtaac
SEQ_14 P\$LREM/ATCTA.01		Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	202	212	(+)	1.000	0.910	agATCTaactt
SEQ_14 P\$MYBL/MYBP3.01		Myb-like protein of Petunia hybrida	0.80	202	218	(-)	1.000	0.819	aaaaaaaGTTAgatct
SEQ_14 P\$MYBL/NTMYEAS1.01		Anther-specific myb gene from tobacco	0.96	222	238	(+)	1.000	0.976	tttgggatGTTAggctt
SEQ_14 P\$TELO/ATPURA.01		Arabidopsis Telo-box interacting protein related to the conserved animal protein Pur-alpha	0.85	227	241	(-)	0.750	0.868	caaaaAGCCTaacatc
SEQ_14 P\$DOFF/DOF3.01		Dof3 - single zinc finger transcription factor	0.99	231	247	(-)	1.000	0.997	agccttcaAAAAGcctaa
SEQ_14 P\$SUCB/SUCROSE.01		Sequence motif from the promoters of different sugar-responsive genes	0.81	238	256	(-)	0.750	0.836	aaaaaacatagccttcaaa
SEQ_14 P\$LEGB/LEGB.01		Legumin box, highly conserved sequence element about 100 bp up-stream of the TSS in legumin genes	0.59	268	294	(-)	0.750	0.593	accttgcACATgatctaaagaaaaaga

TABLE 4-continued

cis-regulatory elements of SEQ ID NO: 14									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_14 P\$LREM/ATCTA.01		Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	274	284	(-)	1.000	0.921	tgATCTaaagaa
SEQ_14 P\$CARM/CARICH.01		CA-rich element	0.78	286	304	(-)	1.000	0.816	acaatttcAACAccttgac
SEQ_14 P\$LIBX/PDF2.01		Protodermal factor 2	0.85	308	324	(+)	1.000	0.903	atgtaaaTAAAtgttatt
SEQ_14 P\$OCSE/OCSE.01		OCS-like elements	0.69	314	334	(-)	0.807	0.714	gcagctgagtaataACAItta
SEQ_14 P\$OCSE/OCSE.01		OCS-like elements	0.69	322	342	(+)	1.000	0.717	attaactcagctgctACGTtta
SEQ_14 P\$CCAF/CCA1.01		Circadian clock associated 1	0.85	368	382	(-)	1.000	0.852	tttacataAATCTca
SEQ_14 P\$DOFF/PBOX.01		Prolamin box, conserved in cereal seed storage protein gene promoters	0.75	372	388	(+)	0.761	0.751	atttatgtAAAAtcccat
SEQ_14 P\$IBOX/GATA.01		Class I GATA factors	0.93	399	415	(-)	1.000	0.973	aaatgGATAagattgat
SEQ_14 P\$MYBS/HVMCB1.01		Hordeum vulgare Myb-related CAB-promoter-binding protein 1	0.93	402	418	(+)	1.000	0.963	aatcttATCCattttct
SEQ_14 P\$AHP/WUS.01		Homeodomain protein WUSCHEL	0.94	420	430	(+)	1.000	0.963	ctgatTAAAtct
SEQ_14 P\$AHP/WUS.01		Homeodomain protein WUSCHEL	0.94	421	431	(-)	1.000	0.963	cagatTAAAtca
SEQ_14 P\$ABRE/ABRE.01		ABA response elements	0.82	428	444	(-)	1.000	0.850	taattgcACGTtgcaga
SEQ_14 P\$MYBL/MYBP3.02		Myb-like protein of Petunia hybrida	0.76	437	453	(+)	1.000	0.782	tgcaatTAGTttgatca
SEQ_14 P\$TEFB/TEF1.01		TEF cis acting elements in both RNA polymerase II-dependent promoters and rDNA spacer sequences	0.76	450	470	(-)	0.838	0.779	ccATGGcctaattgtttgat
SEQ_14 P\$GBOX/UPRE.01		UPRE (unfolded protein response element) like motif	0.86	493	513	(-)	0.767	0.862	cttcgtCCAAGtcaacataaag

TABLE 4-continued

cis-regulatory elements of SEQ ID NO: 14									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_14 P\$RAV5/RAV1-5.01		5'-part of bipartite RAV1 binding site, interacting with Ap2 domain	0.96	493	503	(-)	1.000	0.960	gtcAACATAag
SEQ_14 P\$GBOX/BZIP911.01		bZIP transcription factor from Antirrhinum majus	0.77	494	514	(+)	1.000	0.833	ttatgtTGACTtggacgaaga
SEQ_14 P\$OPAQ/O2.01		Opaque-2 regulatory protein	0.87	495	511	(-)	0.852	0.895	tcgtccaagTCAAacata
SEQ_14 P\$DOFF/DOF2.01		Dof2 - single zinc finger transcription factor	0.98	544	560	(-)	1.000	1.000	tatttattAAAQcaaaa
SEQ_14 P\$L1BX/ATML1.01		L1-specific homeodomain protein ATML1 (A. thaliana meristem layer 1)	0.82	549	565	(+)	1.000	0.853	ctttaaATAAataaagt
SEQ_14 P\$SUCB/SUCROSE.01		Sequence motif from the promoters of different sugar-responsive genes	0.81	559	577	(-)	0.750	0.816	caCAATcatttacttata
SEQ_14 P\$AHP/ATHB5.01		HDZip class I protein ATHB5	0.89	566	576	(+)	0.829	0.904	agaATGattgt
SEQ_14 P\$AHP/ATHB5.01		HDZip class I protein ATHB5	0.89	566	576	(-)	0.936	0.977	acaATCattct
SEQ_14 P\$IDDF/ID1.01		Maize INDETERMINATE1 zinc finger protein	0.92	575	587	(+)	1.000	0.926	gtgtTTGTcttct
SEQ_14 P\$GTBX/SEF1.01		SEF-1	0.87	581	597	(-)	1.000	0.885	tctgtgaTTAAgaagac
SEQ_14 P\$AHP/WUS.01		Homeodomain protein WUSCHEL	0.94	583	593	(+)	1.000	0.963	cttctTAAAtca
SEQ_14 P\$SPF1/SP8BF.01		DNA-binding protein of sweet potato that binds to the SP8a (ACTGTGTA) and SP8b (TACTATT) sequences of sporamin and beta-amylase genes	0.87	590	602	(-)	1.000	0.876	aaTACTctgtgat
SEQ_14 P\$AHP/WUS.01		Homeodomain protein WUSCHEL	0.94	610	620	(-)	1.000	0.963	aacctTAAAtct

TABLE 4-continued

cis-regulatory elements of SEQ ID NO: 14									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_14 P\$OCSE/OCSE.01		OCS-like elements	0.69	614	634	(+)	1.000	0.699	taaggtttgaatgaACGTcgt
SEQ_14 P\$EINL/TEIL.01		TEIL (tobacco EIN3-like)	0.92	624	632	(+)	0.964	0.932	atGAAcgtc
SEQ_14 P\$GBOX/TGA1.01		Arabidopsis leucine zipper protein TGA1	0.90	633	653	(+)	1.000	0.903	gtaaaaTGACggttatgctcg
SEQ_14 P\$MYBL/ATMYB77.01		R2R3-type myb-like transcription factor (I-type binding site)	0.87	636	652	(+)	1.000	0.970	aaatgaCGGttatgctc
SEQ_14 P\$TEFE/TEF1.01		TEF cis acting elements in both RNA polymerase II-dependent promoters and rDNA spacer sequences	0.76	639	659	(+)	0.938	0.778	tgACGttatgctcgtgagag
SEQ_14 P\$PREM/MGPROTORE.01		Promoter elements involved in MgProto (Mg-protoporphyrin IX) and light-mediated induction	0.77	641	671	(-)	1.000	0.792	taagCGACgattctctcagcagcataaccgt
SEQ_14 P\$IBOX/GATA.01		Class I GATA factors	0.93	668	684	(+)	1.000	0.982	cttacGTAaggacgaa
SEQ_14 P\$MYBL/GAMYB.01		GA-regulated myb gene from barley	0.91	690	706	(+)	1.000	0.936	atttgattGTTAtcagg
SEQ_14 P\$MYBL/NTMYBAS1.01		Anther-specific myb gene from tobacco	0.96	701	717	(+)	1.000	0.967	atcaggttGTTAaaagt
SEQ_14 P\$GTEX/SEF1.01		SEF-1	0.87	703	719	(+)	1.000	0.921	caggttgTTAAaagttg
SEQ_14 P\$NCS1/NCS1.01		Nodulin consensus sequence 1	0.85	711	721	(+)	1.000	0.861	tAAAAGttgag
SEQ_14 P\$AREF/ARE.01		Auxin Response Element	0.93	715	727	(-)	1.000	0.932	gttTGTCtcaact
SEQ_14 P\$IDDF/ID1.01		Maize INDETERMINATE1 zinc finger protein	0.92	717	729	(-)	1.000	0.927	tcgtTTGTctcaa
SEQ_14 P\$MYCL/ICE.01		ICE (inducer of CBF expression 1), AtMYC2 (rd22BP1)	0.95	747	765	(-)	0.954	0.972	acgtaACAcctgttttagtc

TABLE 4-continued

cis-regulatory elements of SEQ ID NO: 14									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_14 P\$MYCL/ICE.01		ICE (inducer of CBF expression 1), AtMYC2 (rd22BP1)	0.95	748	766	(+)	0.863	0.954	actaaaACAGgtgttaacgtt
SEQ_14 P\$GBOX/HBP1B.01		Wheat bZIP transcription factor HBP1B (histone gene binding protein 1b)	0.83	753	773	(-)	1.000	0.857	aatgtgaaACGfaaacacctgt
SEQ_14 P\$GTBX/GT3A.01		Trihelix DNA-binding factor GT-3a	0.83	753	769	(+)	1.000	0.858	acaggtGTTAcgttttca
SEQ_14 P\$ABRE/ABRE.01		ABA response elements	0.82	755	771	(+)	1.000	0.820	aggtgttACGTTtcaca
SEQ_14 P\$NACF/TANAC69.01		Wheat NACdomain DNA binding factor	0.68	755	777	(-)	0.812	0.708	aaccaatgtgaaACGtaaacacct
SEQ_14 P\$LFYB/LFY.01		Plant specific floral meristem identity gene LEAFY (LFY)	0.93	765	777	(-)	0.914	0.947	aCCAAtgtgaaa
SEQ_14 P\$CAAT/CAAT.01		CCAAT-box in plant promoters	0.97	769	777	(-)	1.000	0.982	aaCCAAtgt
SEQ_14 P\$GTBX/GT1.01		GT1-Box binding factors with a trihelix DNA-binding domain	0.85	790	806	(+)	1.000	0.906	cttgaaGTTActctatt
SEQ_14 P\$AHP/BLR.01		Transcriptional repressor BELL- RINGER	0.90	793	803	(+)	0.826	0.914	gaaGTTActct
SEQ_14 P\$MYBL/MYBP3.01		Myb-like protein of Petunia hybrida	0.80	802	818	(-)	1.000	0.828	ttggaccgGTTAaatag
SEQ_14 P\$WEXF/ERE.01		Elicitor response element	0.89	824	840	(-)	1.000	0.894	ttaacccTGAccgggttgg
SEQ_14 P\$GTBX/GT1.01		GT1-Box binding factors with a trihelix DNA-binding domain	0.85	830	846	(+)	1.000	0.854	ggtcagGTTAacaaaaac
SEQ_14 P\$MYBL/GAMYB.01		GA-regulated myb gene from barley	0.91	833	849	(-)	1.000	0.930	agtgttttGTTaacctg
SEQ_14 P\$MYBL/GAMYB.01		GA-regulated myb gene from barley	0.91	845	861	(+)	1.000	0.910	acaactgaaGTTAgccgc
SEQ_14 P\$GCCF/GCC-BOX.01		GCC-box, ethylene-responsive element (ERE)	0.86	853	865	(+)	1.000	1.000	gttAGCCGCCaac

TABLE 4-continued

cis-regulatory elements of SEQ ID NO: 14									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_14 P\$GBOX/HBP1B.01		Wheat bZIP transcription factor HBP1B (histone gene binding protein 1b)	0.83	867	887	(+)	1.000	0.842	cgcttattACGfaaacggtag
SEQ_14 P\$NACF/TANAC69.01		Wheat NACdomain DNA binding factor	0.68	868	890	(-)	1.000	0.728	tggctaccgttTACGtaataaagc
SEQ_14 P\$OCSE/OCSE.01		OCS-like elements	0.69	872	892	(-)	1.000	0.710	cggtgctaccgtttACGTaat
SEQ_14 P\$MSAE/MSA.01		M-phase-specific activators (NemybA1, NmybA2, NmybE)	0.80	875	889	(+)	1.000	0.827	acgtaAACGgtagcc
SEQ_14 P\$GBOX/GBF1.01		bZIP protein G-Box binding factor 1	0.94	881	901	(-)	1.000	0.943	tgctcgaaACGTgggtaccgt
SEQ_14 P\$GBOX/HBP1A.01		HBP-1a, suggested to be involved in the cell cycle-dependent expression	0.88	882	902	(+)	1.000	0.943	cggtagcCAGGtttcgagcac
SEQ_14 P\$MYCL/MYCRS.01		Myc recognition sequences	0.93	882	900	(-)	1.000	0.936	gctcgaaACGTgggtaccg
SEQ_14 P\$NACF/TANAC69.01		Wheat NACdomain DNA binding factor	0.68	883	905	(-)	0.812	0.717	gcagtgcgcgaaACGTgggtacc
SEQ_14 P\$ABRE/ABRE.01		ABA response elements	0.82	884	900	(-)	1.000	0.864	gctcgaaACGTgggtacc
SEQ_14 P\$IDDF/ID1.01		Maize INDETERMINATE1 zinc finger protein	0.92	912	924	(+)	1.000	0.921	taatTTGTcttca
SEQ_14 P\$LEGB/LEGB.01		Legumin box, highly conserved sequence element about 100 bp up-stream of the TSS in legumin genes	0.59	975	1001	(-)	0.750	0.657	teactagCCTTgcattgcgaatcagtag
SEQ_14 P\$LEGB/RV.01		RY and Sph motifs conserved in seed-specific promoters	0.87	978	1004	(+)	1.000	0.899	ctgattcgcATGcaaggctagtgacac

TABLE 5

cis-regulatory elements of SEQ ID NO: 16									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_16 P\$OCSE/OCSE.01		OCS-like elements	0.69	7	27	(-)	1.000	0.702	caaatgtgactatACGtttt
SEQ_16 P\$DOFF/DOF3.01		Dof3 - single zinc finger transcription factor	0.99	31	47	(-)	1.000	0.997	catagtcaAAAGcaca
SEQ_16 P\$WEXF/WRKY.01		WRKY plant specific zinc-finger-type factor associated with pathogen defence, W box	0.92	34	50	(+)	1.000	0.961	tgcttTTGActatgtgt
SEQ_16 P\$MYBS/ZMRP1.01		Zea mays MYB-related protein 1 (transfer cell specific)	0.79	43	59	(+)	1.000	0.833	ctatgtTATCTgttcc
SEQ_16 P\$LREM/ATCTA.01		Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	59	69	(-)	1.000	0.892	cgATCTataag
SEQ_16 P\$MADS/AG.01		Agamous, required for normal flower development, similarity to SRF (human) and MCM (Yeast) proteins	0.80	92	112	(-)	0.962	0.820	tagTTCcacaaccggttccaa
SEQ_16 P\$MIIG/WVBC1.01		Maize C1 myb-domain protein	0.92	104	118	(-)	1.000	0.935	tgttgGTAGttccca
SEQ_16 P\$MADS/AGL2.01		AGL2, Arabidopsis MADS-domain protein AGAMOUS-like 2	0.82	108	128	(+)	0.968	0.828	aactaCCAAcacaagcaatgc
SEQ_16 P\$GAGA/BPC.01		Basic pentacycysteine proteins	1.00	129	153	(+)	1.000	1.000	tcttagAGAGagaaaaagagtaataa
SEQ_16 P\$GAGA/BPC.01		Basic pentacycysteine proteins	1.00	131	155	(+)	1.000	1.000	ttagagAGAGaaaaagagtaataaaa
SEQ_16 P\$DOFF/PBF.01		PBF (MPBF)	0.97	134	150	(+)	1.000	0.988	gagagagAAAAGagtaa
SEQ_16 P\$SPF1/SP8BF.01		DNA-binding protein of sweet potato that binds to the SP8a (ACTGTGA) and SP8b (TACTATT) sequences of sporamin and beta-amylase genes	0.87	139	151	(-)	1.000	0.919	atTACTcttttct
SEQ_16 P\$NCS1/NCS1.01		Nodulin consensus sequence 1	0.85	140	150	(+)	1.000	0.855	gAAAAGagtaa
SEQ_16 P\$DOFF/PBF.01		PBF (MPBF)	0.97	145	161	(+)	1.000	0.990	gagtaataAAAAGagagag
SEQ_16 P\$NCS1/NCS1.01		Nodulin consensus sequence 1	0.85	163	173	(+)	1.000	0.862	gAAAAGttttg
SEQ_16 P\$WEXF/WRKY.01		WRKY plant specific zinc-finger-type factor associated with pathogen defence, W box	0.92	166	182	(-)	1.000	0.942	agagtTTGAcacaaactt
SEQ_16 P\$IDDF/ID1.01		Maize INDETERMINATE1 zinc finger protein	0.92	167	179	(+)	1.000	0.935	agttTTGtcaaac
SEQ_16 P\$OCSE/OCSE.01		OCS-like elements	0.69	194	214	(-)	0.769	0.708	gaaagttagacttACTTtct

TABLE 5 -continued  
cis-regulatory elements of SEQ ID NO: 16

Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core Matrix sim.	Matrix sim.	Sequence
SEQ_16	P\$OCSE/OC SL.01	OCS-like elements	0.69	195	215	(+)	0.769	0.733	gaaagtcaagatcttaAATTtct
SEQ_16	P\$AGP1/AGP1.01	AG-motif binding protein 1	0.91	199	209	(-)	1.000	0.915	ttaGATCttac
SEQ_16	P\$AGP1/AGP1.01	AG-motif binding protein 1	0.91	200	210	(+)	1.000	0.983	taaGATCtaac
SEQ_16	P\$LREM/ATCTA.01	Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	202	212	(+)	1.000	0.910	agATCTaaactt
SEQ_16	P\$MYEL/NTMYBAS1.01	Anther-specific myb gene from tobacco	0.96	228	244	(+)	1.000	0.976	tttgggatGTTAggctt
SEQ_16	P\$TELO/ATPURA.01	<i>Arabidopsis</i> Telo-box interacting protein related to the conserved animal protein Pur-alpha	0.85	233	247	(-)	0.750	0.868	caaaaGCCTaacatc
SEQ_16	P\$DOFF/DOF3.01	Dof3 - single zinc finger transcription factor	0.99	237	253	(-)	1.000	0.997	agccttcaAAA Gcctaa
SEQ_16	P\$SUCB/SUCROSE.01	Sequence motif from the promoters of different sugar-responsive genes	0.81	244	262	(-)	0.750	0.836	aaAAAACatagccttcaaa
SEQ_16	P\$LEGB/LEGB.01	Legumin box, highly conserved sequence element about 100 bp upstream of the TSS in legumin genes	0.59	274	300	(-)	0.750	0.593	accttcgACATgactctaagaacaaaaga
SEQ_16	P\$LREM/ATCTA.01	Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	280	290	(-)	1.000	0.921	tgATCTaagaa
SEQ_16	P\$CARM/CARICH.01	CA-rich element	0.78	292	310	(-)	1.000	0.787	acaacttcAACAccttcgac
SEQ_16	P\$CARM/CARICH.01	CA-rich element	0.78	300	318	(-)	1.000	0.829	tacgtcccAACAccttcaaca
SEQ_16	P\$OCSE/OC SL.01	OCS-like elements	0.69	311	331	(-)	1.000	0.695	taataaacattttattACGTcca
SEQ_16	P\$LIBX/PDF2.01	Protodermal factor 2	0.85	314	330	(+)	1.000	0.903	acgtaaTAAATgttatt
SEQ_16	P\$OCSE/OC SL.01	OCS-like elements	0.69	320	340	(-)	0.807	0.714	gcagctgagtaataACAAtta
SEQ_16	P\$OCSE/OC SL.01	OCS-like elements	0.69	328	348	(+)	1.000	0.717	attactcagctgctACGTtta
SEQ_16	P\$CCAF/CCA1.01	Circadian clock associated 1	0.85	374	388	(-)	1.000	0.852	tttacataAATCtea
SEQ_16	P\$SUCB/SUCROSE.01	Sequence motif from the promoters of different sugar-responsive genes	0.81	386	404	(+)	1.000	0.818	aaAAAATccgcaactttatc
SEQ_16	P\$IBOX/GATA.01	Class I GATA factors	0.93	393	409	(-)	1.000	0.973	aaatgGATAagattgcg

TABLE 5 -continued  
cis-regulatory elements of SEQ ID NO: 16

Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_16 P\$MYBS/HVMCB1.01		Hordeum vulgare Myb-related CAB-promoter-binding protein 1	0.93	396	412	(+)	1.000	0.963	aatcttATCCattttct
SEQ_16 P\$AHBP/WUS.01		Homeodomain protein WUSCHEL	0.94	414	424	(+)	1.000	0.963	ctgatTAATct
SEQ_16 P\$AHBP/WUS.01		Homeodomain protein WUSCHEL	0.94	415	425	(-)	1.000	0.963	cagatTAATca
SEQ_16 P\$ABRE/ABRE.01		ABA response elements	0.82	422	438	(-)	1.000	0.850	taattgcACGTTgcaga
SEQ_16 P\$MYBL/MYBPH3.02		Myb-like protein of Petunia hybrida	0.76	431	447	(+)	1.000	0.782	tgcaatTAGTttgatca
SEQ_16 P\$HMGF/HMG_IY.01		High mobility group I/Y-like proteins	0.89	441	455	(-)	1.000	0.907	atatTATTTgatcaa
SEQ_16 P\$AHBP/BLR.01		Transcriptional repressor BELLINGER	0.90	446	456	(-)	1.000	0.928	aatATTATttg
SEQ_16 P\$RAV5/RAV1-5.01		5'-part of bipartite RAV1 binding site, interacting with AP2 domain	0.96	487	497	(-)	1.000	0.960	gtCAACAAtaag
SEQ_16 P\$OPAQ/O2.01		Opaque-2 regulatory protein	0.87	489	505	(-)	0.852	0.895	tcctccaagTCAAcata
SEQ_16 P\$DOFF/DOF3.01		Dof3 - single zinc finger transcription factor	0.99	538	554	(-)	1.000	0.994	tatttataAAAGcaaac
SEQ_16 P\$L1BX/ATML1.01		L1-specific homeodomain protein ATML1 (A. thaliana meristem layer 1)	0.82	538	554	(-)	1.000	0.859	tatttaTAAAgcaaac
SEQ_16 P\$L1BX/ATML1.01		L1-specific homeodomain protein ATML1 (A. thaliana meristem layer 1)	0.82	543	559	(+)	1.000	0.834	cttttaTAAAtataagt
SEQ_16 P\$TBPF/TATA.01		Plant TATA box	0.88	543	557	(+)	1.000	0.971	ctttTATAaatataa
SEQ_16 P\$SUCB/SUCROSE.01		Sequence motif from the promoters of different sugar-responsive genes	0.81	553	571	(-)	0.750	0.816	caCAATcattctacttata
SEQ_16 P\$AHBP/ATHB5.01		HDZip class I protein ATHB5	0.89	560	570	(+)	0.829	0.904	sgaATGAttgt
SEQ_16 P\$AHBP/ATHB5.01		HDZip class I protein ATHB5	0.89	560	570	(-)	0.936	0.977	acaATCAttct
SEQ_16 P\$IDDF/ID1.01		Maize INDETERMINATE1 zinc finger protein	0.92	569	581	(+)	1.000	0.926	gtgtTTGTcttct
SEQ_16 P\$SPF1/SP8BF.01		DNA-binding protein of sweet potato that binds to the SP8a (ACTGTGTA) and SP8b (TACTATT) sequences of sporamin and beta-amylase genes	0.87	586	598	(-)	1.000	0.876	aaTACTctgtgat
SEQ_16 P\$AHBP/WUS.01		Homeodomain protein WUSCHEL	0.94	606	616	(-)	1.000	0.963	aacctTAATct
SEQ_16 P\$GBOX/TGA1.01		Arabidopsis leucine zipper protein TGA1	0.90	625	645	(+)	1.000	0.903	gtaaaaTGACGggttatgctcog

TABLE 5 -continued

cis-regulatory elements of SEQ ID NO: 16									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_16 P\$MYBL/ATMYB77.01		R2R3-type myb-like transcription factor (I-type binding site)	0.87	628	644	(+)	1.000	0.970	aaatgacGGTtatgctc
SEQ_16 P\$TEPB/TEF1.01		TEF cis acting elements in both RNA polymerase II-dependent promoters and yDNA spacer sequences	0.76	631	651	(+)	0.838	0.778	tgACGGttatgctcgtgagag
SEQ_16 P\$IBOX/GATA.01		Class I GATA factors	0.93	660	676	(+)	1.000	0.950	cttgcGATAaggaagaa
SEQ_16 P\$MYBL/GAMYB.01		GA-regulated myb gene from barley	0.91	682	698	(+)	1.000	0.986	atttggttGTTAtcagg
SEQ_16 P\$MIIG/PALBOXL.01		Cis-acting element conserved in various PAL and 4CL promoters	0.80	693	707	(+)	0.750	0.818	atcaggttGTTGaaa
SEQ_16 P\$MYBL/MYBP3.02		Myb-like protein of Petunia hybrida	0.76	693	709	(+)	0.817	0.777	atcaggTTGTTgaaaga
SEQ_16 P\$NCS2/MCS2.01		Nodulin consensus sequence 2 GCN4, conserved in cereal seed storage protein gene promoters, similar to yeast	0.79	705	719	(-)	0.750	0.801	gtttgtCTCActttt
SEQ_16 P\$PQAQ/GCN4.01		GCN4 and vertebrate AP-1	0.81	705	721	(+)	1.000	0.846	aaagaTGAGacaaaacga
SEQ_16 P\$AREF/ARE.01		Auxin Response Element	0.93	707	719	(-)	1.000	0.951	gttTGTctcatct
SEQ_16 P\$IDDF/ID1.01		Maize INDETERMINATE1 zinc finger protein	0.92	709	721	(-)	1.000	0.927	tcgtTTGTctcat
SEQ_16 P\$MYCL/ICE.01		ICE (inducer of CBF expression 1), AtMYC2 (rd22BFL)	0.95	739	757	(-)	0.954	0.972	acgtaACA Cctgtttagtc
SEQ_16 P\$MYCL/ICE.01		ICE (inducer of CBF expression 1), AtMYC2 (rd22BFL)	0.95	740	758	(+)	0.863	0.954	actaaACAGgtgtaacgtt
SEQ_16 P\$GBOX/HBP1B.01		Wheat bZIP transcription factor HBP1B (histone gene binding protein 1b)	0.83	745	765	(-)	1.000	0.857	aatgtaaaACGTAaacacctgt
SEQ_16 P\$GTBX/GT3A.01		Trihelix DNA-binding factor GT-3a	0.83	745	761	(+)	1.000	0.858	acaggtGTTAagtttcca
SEQ_16 P\$ABRE/ABRE.01		ABA response elements	0.82	747	763	(+)	1.000	0.820	aggtgttACGtttcaca
SEQ_16 P\$NACF/TANAC69.01		Wheat NACdomain DNA binding factor	0.68	747	769	(-)	0.812	0.708	aaccaatgtaAACGtaaacct
SEQ_16 P\$LFYB/LFY.01		Plant specific floral meristem identity gene LEAFY (LFY)	0.93	757	769	(-)	0.914	0.947	aACCAatgtgaaa
SEQ_16 P\$CAAT/CAAT.01		CCAAT-box in plant promoters	0.97	761	769	(-)	1.000	0.982	aaCCAAtgt
SEQ_16 P\$MYBL/MYBP3.01		Myb-like protein of Petunia hybrida	0.80	794	810	(-)	1.000	0.818	cgggaccgGTTAaatag

TABLE 5 -continued

cis-regulatory elements of SEQ ID NO: 16									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core Matrix sim.	Matrix sim.	Sequence
SEQ_16 P\$IDDF/ID1.01		Maize INDETERMINATE1 zinc finger protein	0.92	809	821	(-)	1.000	0.929	agtttTGtcaacc
SEQ_16 P\$GCCF/BRE_JERE.01		Ethylene-responsive elements (ERE) and jasmonate- and elicitor-responsive elements (JERE)	0.85	826	838	(+)	1.000	0.907	aaaaggCGCCaac
SEQ_16 P\$GBOX/HBP1B.01		Wheat bZIP transcription factor HBP1B (histone gene binding protein 1b)	0.83	840	860	(+)	1.000	0.858	cgcttgTtACGTaaacggtag
SEQ_16 P\$NACF/TANAC69.01		Wheat NACdomain DNA binding factor	0.68	841	863	(-)	1.000	0.764	tggtaccggtTACGtaacaagc
SEQ_16 P\$OCSE/OCSE.01		OCS-like elements	0.69	845	865	(-)	1.000	0.710	cgTggctaccgTtTACGTaac
SEQ_16 P\$MSAE/MSA.01		M-phase-specific activators (NtmybA1, NtmybA2, NtmybB)	0.80	848	862	(+)	1.000	0.827	acgtaAACGgtagcc
SEQ_16 P\$GBOX/GBF1.01		bZIP protein G-Box binding factor 1	0.94	854	874	(-)	1.000	0.944	tgctcaaaaACGTggctaccgt
SEQ_16 P\$GBOX/HBP1A.01		HBP-1a, suggested to be involved in the cell cycle-dependent expression	0.88	855	875	(+)	1.000	0.914	cggtagcCACGgttttgagcac
SEQ_16 P\$NACF/TANAC69.01		Wheat NACdomain DNA binding factor	0.68	856	878	(-)	0.812	0.712	gcagtgctcaaaACGtggtacc
SEQ_16 P\$ABRE/ABRE.01		ABA response elements	0.82	857	873	(-)	1.000	0.860	gctcaaaaACGTggctac
SEQ_16 P\$MYCL/MYCRS.01		Myc recognition sequences	0.93	872	890	(+)	0.863	0.946	gcactgcATGtgcataatt
SEQ_16 P\$IDDF/ID1.01		Maize INDETERMINATE1 zinc finger protein	0.92	885	897	(+)	1.000	0.921	taatTTGtctca
SEQ_16 P\$TCPP/ATTCP20.01		TCP class I transcription factor (Arabidopsis)	0.94	924	936	(-)	1.000	0.947	ttaagCCCaagtg
SEQ_16 P\$MYBL/MYBP3.02		Myb-like protein of Petunia hybrida	0.76	940	956	(-)	1.000	0.781	attaatTAGTtccacga
SEQ_16 P\$AHBP/WUS.01		Homeodomain protein WUSCHEL	0.94	948	958	(+)	1.000	1.000	ctaatTAATga
SEQ_16 P\$AHBP/ATHB5.01		HDZip class I protein ATHB5	0.89	952	962	(+)	0.829	0.902	ttaATGAttcg
SEQ_16 P\$AHBP/HAHB4.01		Sunflower homeodomain leucine-zipper protein Hahb-4	0.87	952	962	(-)	1.000	0.979	cgaatcAATAa
SEQ_16 P\$LEGB/LEGB.01		Legumin box, highly conserved sequence element about 100 by upstream of the TSS in legumin genes	0.59	952	978	(-)	0.750	0.657	tcactagCCTTgcatgcgaatcattaa
SEQ_16 P\$LEGB/RV.01		RY and Sph motifs conserved in seed-specific promoters	0.87	955	981	(+)	1.000	0.899	atgattcgCATGccaaggctagtcacac

TABLE 6

Seq. name	Family/matrix	Further Information	cis-regulatory elements of SEQ_ID NO: 22				Core Matrix sim.	Sequence
			Opt. thresh.	Start pos.	End pos.	Strand		
SEQ_22 P\$AHBP/BLR.01		Transcriptional repressor BELL-RINGER	0.90	4	14	(+)	0.826 0.936 gaaGTTAtttag	
SEQ_22 P\$MYBL/CARE.01		CAACTC regulatory elements, GA-inducible	0.83	27	43	(-)	1.000 0.875 gttggctAGTTgtaagt	
SEQ_22 P\$WEXF/WRKY.01		WRKY plant specific zinc-finger-type factor associated with pathogen defence, W box	0.92	49	65	(-)	1.000 0.975 catgtTTGAcctctaca	
SEQ_22 P\$OPAQ/02_GCN4.01		Recognition site for BZIP transcription factors that belong to the group of Opaque-2 like proteins	0.81	56	72	(-)	1.000 0.853 ttgttaACAATgttttgac	
SEQ_22 P\$GTBX/GT3A.01		Trihelix DNA-binding factor GT-3a	0.83	59	75	(+)	1.000 0.867 aaacatGTTAcaaacctc	
SEQ_22 P\$MYBL/MYBPH3.02		Myb-like protein of Petunia hybrida	0.76	61	77	(-)	0.817 0.798 ttgagttTGTaacatgt	
SEQ_22 P\$HMGF/HMG_IY.02		High mobility group I/Y-like protein isolated from pea	1.00	72	86	(-)	1.000 1.000 cttttTATTTTTtgagt	
SEQ_22 P\$PSRE/GAAA.01		GAAA motif involved in pollen specific transcriptional activation	0.83	81	97	(+)	1.000 0.879 taaaagAAAacagtgagag	
SEQ_22 P\$LFBY/LFY.01		Plant specific floral meristem identity gene LEAFY (LFY)	0.93	85	97	(-)	1.000 0.969 cTCCActgttttct	
SEQ_22 P\$GTBX/GT1.01		GT1-Box binding factors with a trihelix DNA-binding domain	0.85	100	116	(-)	1.000 0.904 gttcagGTTActcgatt	
SEQ_22 P\$MYCL/ICE.01		ICE (inducer of CBF expression 1), AtMYC2 (rd22BP1)	0.95	109	127	(-)	0.954 0.972 atcaaaCACcctgttcagggt	
SEQ_22 P\$MYCL/ICE.01		ICE (inducer of CBF expression 1), AtMYC2 (rd22BP1)	0.95	110	128	(+)	0.863 0.954 cctgaaCAGgtgttttgatc	
SEQ_22 P\$CARM/CAR1CH.01		CA-rich element	0.78	112	130	(-)	1.000 0.809 ttgatecaAACAcctgttcca	
SEQ_22 P\$MYBL/MYBPH3.02		Myb-like protein of Petunia hybrida	0.76	140	156	(-)	1.000 0.781 aagagaTAGTgacacac	
SEQ_22 P\$MYBS/ZMRRP1.01		Zea mays MYB-related protein 1 (transfer cell specific)	0.79	142	158	(+)	1.000 0.824 gtgtcacTATctcttgg	
SEQ_22 P\$DOFF/DOF1.01		Dof1/MNB1a - single zinc finger transcription factor	0.98	169	185	(+)	1.000 0.984 acacaaaATAAGaccct	

TABLE 6-continued

cis-regulatory elements of SEQ ID NO: 22										
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence	
SEQ_22	P\$MIIG/PALBOXL.01	Cis-acting element conserved in various PAL and 4CL promoters	0.80	188	202	(-)	0.785	0.801	agcagcttGGTTagg	
SEQ_22	P\$CAAT/CAAT.01	CCAAT-box in plant promoters	0.97	204	212	(+)	1.000	0.985	atCCAAatcc	
SEQ_22	P\$OPAQ/02_GCNA.01	Recognition site for BZIP transcription factors that belong to the group of Opaque-2 like proteins	0.81	206	222	(-)	0.829	0.819	tgtgtgACTTggattgg	
SEQ_22	P\$LIBX/PDF2.01	Protodermal factor 2	0.85	229	245	(+)	1.000	0.921	cagctaTAAAtgaaaca	
SEQ_22	P\$TBPF/TATA.02	Plant TATA box	0.90	229	243	(+)	1.000	0.935	cagcTATAaatgaaa	
SEQ_22	P\$MYBL/WYBPH3.01	Myb-like protein of Petunia hybrida	0.80	250	266	(-)	1.000	0.808	attcaatctGTTAagtt	
SEQ_22	P\$GAPP/GAP.01	Cis-element in the GAPDH promoters conferring light inducibility	0.88	257	271	(+)	1.000	0.964	acagATGAatactag	
SEQ_22	P\$HEAT/HSE.01	Heat shock element	0.81	284	298	(-)	1.000	0.811	aggagacactAGAAc	
SEQ_22	P\$AREF/ARE.01	Auxin Response Element	0.93	288	300	(+)	1.000	0.961	tagTGTctcctca	
SEQ_22	P\$NCS2/NCS2.01	Nodulin consensus sequence 2	0.79	288	302	(+)	0.750	0.819	tagtgtCTCctcatt	
SEQ_22	P\$ROOT/RHE.01	Root hair-specific element with a 2-nucleotid spacer between left part (LP) and right part (RP)	0.77	298	322	(-)	1.000	0.852	atcgtagcttgaattCACGtaatga	
SEQ_22	P\$MYBL/WYBPH3.02	Myb-like protein of Petunia hybrida	0.76	317	333	(-)	1.000	0.775	ttgagatAGTgctcgta	
SEQ_22	P\$MYBL/CARE.01	CAACTC regulatory elements, GA-inducible	0.83	326	342	(-)	1.000	0.838	atgtaggAGTTgagata	
SEQ_22	P\$LEGB/LEGB.01	Legumin box, highly conserved sequence element about 100 by upstream of the TSS in legumin genes	0.59	357	383	(+)	0.750	0.595	tacaaaaCTATgcacaaaaaacaagc	
SEQ_22	P\$EIML/TEIL.01	TEIL (tobacco EIN3-like)	0.92	380	388	(-)	1.000	0.934	aTGTAgctt	
SEQ_22	P\$LREM/ATCTA.01	Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	385	395	(+)	1.000	0.931	acATCTaatac	
SEQ_22	P\$CEIF/ABI4.01	ABA insensitive protein 4 (ABI4)	0.87	432	444	(+)	1.000	0.872	caatCACCCgtcga	
SEQ_22	P\$MYBL/WYBPH3.01	Myb-like protein of Petunia hybrida	0.80	450	466	(+)	1.000	0.849	aggattcaGTTAattga	

TABLE 6-continued

Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core Matrix sim.	Sequence
SEQ_22 P\$CGG/OSCFT.01		Oryza sativa CaM-binding transcription factor	0.78	475	491	(-)	0.817	cttCCGAGtttgatcgga
SEQ_22 P\$ROOT/RHE.02		Root hair-specific element with a 3-nucleotid spacer between left part (LP) and right part (RP)	0.77	486	510	(+)	1.000	tcgaagactggtgagCACGaggacg
SEQ_22 P\$NCS2/NCS2.01		Modulin consensus sequence 2	0.79	525	539	(-)	0.750	0.823 tgttgtATCTtcgag
SEQ_22 P\$CCAF/CCAL.01		Circadian clock associated 1	0.85	539	553	(+)	1.000	0.859 aagcaagaaAATctac
SEQ_22 P\$LREM/ATCTA.01		Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	546	556	(+)	1.000	0.869 aaATCTactga
SEQ_22 P\$LIBX/ATML1.02		<i>Arabidopsis thaliana</i> meristem layer 1	0.76	563	579	(-)	0.890	0.767 cgcCAATAaacttcagga
SEQ_22 P\$AHP/BLR.01		Transcriptional repressor BELL-RINGER	0.90	567	577	(+)	0.826	0.936 gaaGTTAttgg
SEQ_22 P\$LIBX/HDG9.01		Homeodomain glabrous 9	0.77	595	611	(-)	0.796	0.777 ccgaaaTTAAttcggat
SEQ_22 P\$LIBX/HDG9.01		Homeodomain glabrous 9	0.77	597	613	(+)	0.750	0.796 ccgaatTAAAttcgggg
SEQ_22 P\$AHP/BLR.01		Transcriptional repressor BELL-RINGER	0.90	599	609	(-)	1.000	1.000 gaaTTAattc
SEQ_22 P\$IBOX/GATA.01		Class I GATA factors	0.93	614	630	(+)	1.000	0.961 aaaaGATAaattagat
SEQ_22 P\$NCS1/NCS1.01		Modulin consensus sequence 1	0.85	614	624	(+)	1.000	0.948 aAAAAGataaa
SEQ_22 P\$LREM/ATCTA.01		Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	622	632	(-)	1.000	0.921 gtATCTaattt
SEQ_22 P\$ABRE/ABF1.01		ABA (abscisic acid) inducible transcriptional activator	0.79	657	673	(+)	0.750	0.797 aagaaaCAGgtggcaat
SEQ_22 P\$TCPF/ATTCP20.01		TCP class I transcription factor ( <i>Arabidopsis</i> )	0.94	670	682	(-)	1.000	0.949 tccaGCCCaattg
SEQ_22 P\$OCSE/OCSE.01		OCS-like elements	0.69	715	735	(+)	0.807	0.693 aaaaaaacggataACATatt
SEQ_22 P\$MSE/MSA.01		M-phase-specific activators (NtmybA1, NtmybA2, NtmybB)	0.80	716	730	(+)	1.000	0.851 aaaaaACGgataac

TABLE 6-continued

cis-regulatory elements of SEQ ID NO: 22									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_22 P\$MYBL/MYBPH3.01		Myb-like protein of Petunia hybrida	0.80	717	733	(+)	0.750	0.845	aaaaaacgGATAacata
SEQ_22 P\$MYBS/MYBST1.01		MybST1 (Myb Solanum tuberosum 1) with a single myb repeat	0.90	717	733	(-)	1.000	0.962	tatgTtATCCGtttttt
SEQ_22 P\$IBOX/GATA.01		Class I GATA factors	0.93	720	736	(+)	1.000	0.935	aaacgGATAacataattt
SEQ_22 P\$MYBL/GAMYB.01		GA-regulated myb gene from barley	0.91	722	738	(-)	1.000	0.920	ataaatatGTTAtccgt
SEQ_22 P\$CCAF/CCAL.01		Circadian clock associated 1	0.85	764	778	(-)	0.757	0.857	aaaaagaaaATAtct
SEQ_22 P\$MYBL/GAMYB.01		GA-regulated myb gene from barley	0.91	771	787	(+)	1.000	0.914	ttctttttGTTAggaaa
SEQ_22 P\$SEF4/SEF4.01		Soybean embryo factor 4	0.98	772	782	(+)	1.000	0.981	tcTTTTtgta
SEQ_22 P\$HEAT/HSE.01		Heat shock element	0.81	783	797	(+)	1.000	0.873	ggaaaattttAGAAA
SEQ_22 P\$HMGF/HMG_IY.01		High mobility group I/Y-like proteins	0.89	790	804	(-)	1.000	0.895	ccatTATtttctaaa
SEQ_22 P\$SUCB/SUCROSE.01		Sequence motif from the promoters of different sugar-responsive genes	0.81	794	812	(+)	1.000	0.851	gaaaATaatggaaataaaa
SEQ_22 P\$AHP/ATHB5.01		HDZip class I protein ATHB5	0.89	795	805	(-)	1.000	0.918	tccATTAtttt
SEQ_22 P\$GTBX/S1F.01		S1F, site 1 binding factor of spinach rps1 promoter	0.79	797	813	(+)	1.000	0.841	aataATGgaaattaaaat
SEQ_22 P\$GTBX/SBF1.01		SBF-1	0.87	801	817	(+)	1.000	0.908	atggaaaTTAAatagcg
SEQ_22 P\$L1BX/HDG9.01		Homeodomain glabrous 9	0.77	803	819	(+)	1.000	0.822	ggaaaTAAAtagcgat
SEQ_22 P\$GTBX/GT3A.01		Trihelix DNA-binding factor GT-3a	0.83	817	833	(+)	1.000	0.843	gattatGTTAcaagata
SEQ_22 P\$OCSE/OCSE.01		OCS-like elements	0.69	819	839	(+)	0.807	0.707	ttatgttacaagatACGAtca
SEQ_22 P\$GARP/ARR10.01		Type-B response regulator (ARR10), member of the GARP-family of plant myb-related DNA binding motifs	0.97	829	837	(+)	1.000	0.985	AGATacgat
SEQ_22 P\$ROOT/RHE.02		Root hair-specific element with a 3-nucleotid spacer between left part (LP) and right part (RP)	0.77	838	862	(-)	0.750	0.777	tagcattttgcaactgCCCCgatgctg
SEQ_22 P\$NCS1/NCS1.01		Modulin consensus sequence 1	0.85	877	887	(-)	0.804	0.899	aaaaAGgatcaa
SEQ_22 P\$MYBL/GAMYB.01		GA-regulated myb gene from barley	0.91	882	898	(+)	1.000	0.926	ctttttggGTTAtctcc
SEQ_22 P\$MYBL/MYBPH3.02		Myb-like protein of Petunia hybrida	0.76	903	919	(+)	1.000	0.785	gacaatTAGTtttaggat

TABLE 6-continued

cis-regulatory elements of SEQ ID NO: 22									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_22 P\$STRM/STK.01		Storekeeper (STK), plant specific DNA binding protein important for tuber-specific and sucrose-inducible gene expression	0.85	904	918	(-)	1.000	0.865	tccTAAActaattgt
SEQ_22 P\$TELO/ATPURA.01		<i>Arabidopsis</i> Telo-box interacting protein related to the conserved animal protein Pur-alpha	0.85	909	923	(-)	0.750	0.867	caaaaATCCTaaacta
SEQ_22 P\$AHP/BLR.01		Transcriptional repressor BELL-RINGER	0.90	929	939	(+)	1.000	0.930	tatATTAAatac
SEQ_22 P\$IBOX/GATA.01		Class I GATA factors	0.93	935	951	(-)	1.000	0.932	tgtcggATAAatagtatt
SEQ_22 P\$SPF1/SP8BF.01		DNA-binding protein of sweet potato that binds to the SP8a (ACTGTGTA) and SP8b (TACTATT) sequences of sporamin and beta-amylase genes	0.87	935	947	(+)	1.000	0.995	aatTACTattatccc
SEQ_22 P\$MYBS/MYBST1.01		MybS1 (Myb Solanum tuberosum 1) with a single myb repeat	0.90	938	954	(+)	1.000	0.943	actattATCCgacaaca
SEQ_22 P\$IDDF/ID1.01		Maize INDETERMINATE1 zinc finger protein	0.92	944	956	(-)	1.000	0.922	agtgTTGtcggat
SEQ_22 P\$MYCL/ICE.01		ICE (inducer of CBF expression 1), AtMYC2 (rd22BP1)	0.95	946	964	(-)	0.954	0.972	ctgaaaCAAgtgttgcgg
SEQ_22 P\$MYCL/ICE.01		ICE (inducer of CBF expression 1), AtMYC2 (rd22BP1)	0.95	947	965	(+)	0.954	0.984	cgacaaCACcttgtttcagc
SEQ_22 P\$GTBX/GT3A.01		Trihelix DNA-binding factor GT-3a	0.83	968	984	(-)	1.000	0.839	aaaaatGTTAaaaaaag
SEQ_22 P\$MYBL/MYBP3.01		Myb-like protein of Petunia hybrida	0.80	970	986	(-)	1.000	0.807	caaaaaatGTTAaaaaa
SEQ_22 P\$CCAF/CCA1.01		Circadian clock associated 1	0.85	975	989	(-)	0.766	0.872	aaacaaaaAATGtta
SEQ_22 P\$GTBX/S1F.01		S1F, site 1 binding factor of spinach rps1 promoter	0.79	997	1013	(-)	1.000	0.821	gctgATGGgaagaagaa
SEQ_22 P\$GTBX/SBF1.01		SBF-1	0.87	1016	1032	(+)	1.000	0.875	tttctttTTAaaaaaatt
SEQ_22 P\$STRM/STK.01		Storekeeper (STK), plant specific DNA binding protein important for tuber-specific and sucrose-inducible gene expression	0.85	1021	1035	(+)	1.000	0.881	tttTAAaaaaattgaa

TABLE 6-continued

cis-regulatory elements of SEQ ID NO: 22									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_22 P\$NCSI/MCS1.01		Nodulin consensus sequence 1	0.85	1039	1049	(-)	1.000	0.852	aAAAAGttaa
SEQ_22 P\$GTEX/SBF1.01		SBF-1	0.87	1042	1058	(-)	1.000	0.874	gaaattttTAAAaagtt
SEQ_22 P\$OPAQ/O2.01		Opaque-2 regulatory protein	0.87	1066	1082	(-)	1.000	0.898	tccataataatCAAtctga
SEQ_22 P\$AGP1/AGP1.01		AG-motif binding protein 1	0.91	1080	1090	(-)	1.000	0.915	tgaGATcttcc
SEQ_22 P\$AGP1/AGP1.01		AG-motif binding protein 1	0.91	1081	1091	(+)	1.000	0.911	gaagATctcaa
SEQ_22 P\$LIBX/PDF2.01		Protodermal factor 2	0.85	1090	1106	(+)	1.000	0.897	aagagTAAAAtgtatcc
SEQ_22 P\$MYBS/OSMYBS.01		Rice MYB proteins with single DNA binding domains, binding to the amylase element (TATCCA)	0.82	1097	1113	(+)	1.000	0.897	aaatgTATCcatcttgg
SEQ_22 P\$LIBX/PDF2.01		Protodermal factor 2	0.85	1111	1127	(-)	0.848	0.899	ccggttTAAAtgcccc
SEQ_22 P\$LIBX/ATML1.02		Arabidopsis thaliana meristem layer 1	0.76	1113	1129	(+)	1.000	0.854	gggCATTaaaccgggtg
SEQ_22 P\$AHP/WUS.01		Homeodomain protein WUSCHEL	0.94	1115	1125	(-)	1.000	1.000	ggttttTAAATgc
SEQ_22 P\$IBOX/GATA.01		Class I GATA factors	0.93	1133	1149	(+)	1.000	0.949	gggatGATRAaatacaga
SEQ_22 P\$LIBX/PDF2.01		Protodermal factor 2	0.85	1134	1150	(+)	1.000	0.855	ggatgTAAAAtacagac
SEQ_22 P\$ROOT/RHE.02		Root hair-specific element with a 3-nucleotid spacer between left part (LP) and right part (RP)	0.77	1172	1196	(+)	1.000	0.804	gtaattcaatattatCACGttgcta
SEQ_22 P\$NACF/TANAC69.01		Wheat NACdomain DNA binding factor	0.68	1176	1198	(+)	0.895	0.684	tccataatttatCACGttgctaaa
SEQ_22 P\$GBOX/HBP1B.01		Wheat bZIP transcription factor HBP1B (histone gene binding protein 1b)	0.83	1179	1199	(-)	1.000	0.835	ttttagcaACGTgataaatat
SEQ_22 P\$MYCL/MYCRS.01		Myc recognition sequences	0.93	1180	1198	(-)	1.000	0.967	tttagcaACGTgataaata
SEQ_22 P\$ABRE/ABRE.01		ABA response elements	0.82	1181	1197	(+)	1.000	0.826	atttatcACGTTtgctaa
SEQ_22 P\$OPAQ/O2_GC4.01		Recognition site for bZIP transcription factors that belong to the group of Opaque-2 like proteins Storekeeper (STK), plant specific	0.81	1182	1198	(+)	0.951	0.830	tttatacACGTTgctaaa

TABLE 6-continued

cis-regulatory elements of SEQ ID NO: 22									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_22 P\$STRM/STK.01		DNA binding protein important for tuber-specific and sucrose-inducible gene expression	0.85	1192	1206	(+)	1.000	0.888	tgctAAAAaaattat
SEQ_22 P\$LEGB/LEGB.01		Legumin box, highly conserved sequence element about 100 bp upstream of the TSS in legumin genes	0.59	1223	1249	(+)	0.750	0.609	acaaaatCAATtaagagaagaaga
SEQ_22 P\$DOFF/DOF1.01		Dof1/MNF1a - single zinc finger transcription factor	0.98	1227	1243	(+)	1.000	0.991	aatcaattAAAAGagaaa
SEQ_22 P\$GAGA/GAGABP.01		(GA)n/(CT)n binding proteins (GBP, soybean, BBR, barley)	0.75	1231	1255	(+)	1.000	0.790	aattaaAGAGaaagaagaacgca
SEQ_22 P\$NCS2/NCS2.01		Nodulin consensus sequence 2	0.79	1232	1246	(-)	1.000	0.808	ttcttttCTCTTtaaat
SEQ_22 P\$OCSE/OCSE.01		OCS-like elements	0.69	1283	1303	(+)	0.769	0.735	taaaataaaaaattaACGCatg
SEQ_22 P\$SEF4/SEF4.01		Soybean embryo factor 4	0.98	1285	1295	(-)	1.000	0.983	aaTTTTtattt
SEQ_22 P\$OPAQ/O2_GCNA.01		Recognition site for BZIP transcription factors that belong to the group of Opaque-2 like proteins	0.81	1294	1310	(-)	1.000	0.825	cattcaACATgcgttaa
SEQ_22 P\$IDRE/IDE1.01		Iron-deficiency-responsive element 1	0.77	1297	1311	(+)	1.000	0.773	acGCATgttgaatgc
SEQ_22 P\$GBOX/BZIP910.02		BZIP transcription factor from Antirrhinum majus	0.84	1300	1320	(+)	1.000	0.864	catgttgaatgcTGCatgtc
SEQ_22 P\$GBOX/BZIP910.01		BZIP transcription factor from Antirrhinum majus	0.77	1306	1326	(+)	1.000	0.784	gaatgcTGCatgtcagtatg
SEQ_22 P\$ABRE/ABF1.03		ABA (abscisic acid) inducible transcriptional activator	0.82	1307	1323	(+)	0.750	0.829	aatgctgaCATGtcagt
SEQ_22 P\$OPAQ/O2.01		Opaque-2 regulatory protein	0.87	1307	1323	(-)	0.794	0.901	actgacatgTCAGcatt
SEQ_22 P\$GTEx/S1F.01		S1F, site 1 binding factor of spinach rps1 promoter	0.79	1319	1335	(-)	1.000	0.818	attcATGGacatactga
SEQ_22 P\$ROOT/RHE.01		Root hair-specific element with a 2-nucleotid spacer between left part (LP) and right part (RP)	0.77	1322	1346	(+)	1.000	0.844	gtatgtccatgaaatccACGtatcaa
SEQ_22 P\$GBOX/GEF1.01		BZIP protein G-Box binding factor 1	0.94	1329	1349	(-)	1.000	0.956	cgcttgatACGTggattcatg

TABLE 6-continued

cis-regulatory elements of SEQ ID NO: 22						
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Core Matrix sim.
SEQ_22 P\$GBOX/HBP1A.01		HBP-1a, suggested to be involved in the cell cycle-dependent expression	0.88	1330	1350 (+)	1.000 0.899 atgaatccACGtatcaagcgc
SEQ_22 P\$ABRE/ABRE.01		ABA response elements	0.82	1332	1348 (-)	1.000 0.866 gcttgatACGTggattc
SEQ_22 P\$L1BX/ATML1.01		L1-specific homeodomain protein ATML1 ( <i>A. thaliana</i> meristem layer 1)	0.82	1370	1386 (+)	1.000 0.889 tctttcTAAAtgaaaac
SEQ_22 P\$GAPB/GAP.01		Cis-element in the GAPDH promoters conferring light inducibility	0.88	1375	1389 (+)	1.000 0.958 ctaaATGAAAaacaac
SEQ_22 P\$URNA/USE.01		Upstream sequence elements in the promoters of U-snrRNA genes of higher plants	0.75	1387	1403 (+)	0.750 0.781 aacttcACACatcacaac
SEQ_22 P\$MYBL/MYBPH3.02		Myb-like protein of <i>Petunia hybrida</i>	0.76	1396	1412 (-)	0.817 0.771 tattgtTTGTTgtgatg
SEQ_22 P\$DPBF/DPBF.01		bZIP factors DPBF-1 and 2 (Dc3 promoter binding factor-1 and 2)	0.89	1413	1423 (+)	1.000 0.898 cACACAagacc
SEQ_22 P\$GAGA/BPC.01		Basic pentacysteine proteins	1.00	1413	1437 (-)	1.000 1.000 aacgagAGAGagggggcttctgtgtg
SEQ_22 P\$GAGA/GAGABP.01		(GA)n/(CT)n binding proteins (GBP, soybean; BBR, barley)	0.75	1423	1447 (-)	0.750 0.805 gcagagAGACaacgagagagagggg
SEQ_22 P\$GAGA/BPC.01		Basic pentacysteine proteins	1.00	1425	1449 (-)	1.000 1.000 tggcagAGAGacaacgagagagaggg
SEQ_22 P\$PREM/MGPROTORE.01		Promoter elements involved in Mgproto (Mg-protoporphyrin IX) and light-mediated induction	0.77	1447	1477 (+)	1.000 0.794 ccagCGACcaaatcgaagcttgagaagaaca

TABLE 7

cis-regulatory elements of SEQ_ID NO: 25									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_25	P\$IBOX/GATA.01	Class I GATA factors	0.93	27	43	(+)	1.000	0.946	aaaaaGATAaccacccc
SEQ_25	P\$NCS1/NCS1.01	Modulin consensus sequence 1	0.85	27	37	(+)	1.000	0.948	AAAAGataaac
SEQ_25	P\$MYBL/GAMYB.01	GA-regulated myb gene from barley	0.91	29	45	(-)	1.000	0.980	agggggtgGTTAtcttt
SEQ_25	P\$SALT/ALFIN1.02	Zinc-finger protein in alfalfa roots, regulates salt tolerance	0.95	34	48	(-)	1.000	0.977	gctagggGGTggtta
SEQ_25	P\$SUCB/SUCROSE.01	Sequence motif from the promoters of different sugar-responsive genes	0.81	57	75	(+)	1.000	0.852	ccAAATcataaactatcaga
SEQ_25	P\$AHBP/ATHB9.01	HD-ZIP class III protein ATHB9	0.77	58	68	(-)	1.000	0.772	gttATGAtttg
SEQ_25	P\$MYBL/MYBPH3.02	Myb-like protein of <i>Petunia hybrida</i>	0.76	60	76	(-)	1.000	0.808	ttctgaTAGTtatgatt
SEQ_25	P\$IBOX/GATA.01	Class I GATA factors	0.93	76	92	(+)	1.000	0.975	acaaaGATAaaaaagccc
SEQ_25	P\$DOFF/DOF3.01	Dof3 - single zinc finger transcription factor	0.99	78	94	(+)	1.000	0.996	aaagataaaaAAAGcccga
SEQ_25	P\$SBPD/SBP.01	SQUA promoter binding proteins	0.88	99	115	(-)	1.000	0.882	ctatgGTACaacatggg
SEQ_25	P\$NCS3/NCS3.01	Modulin consensus sequence 3	0.89	119	129	(+)	1.000	0.893	caCACCCtcta
SEQ_25	P\$LEGB/LEGB.01	Legumin box, highly conserved sequence element about 100 by upstream of the TSS in legumin genes	0.59	122	148	(-)	0.750	0.626	ttcataaCTATgtatgagatagagggg
SEQ_25	P\$MYBL/MYBPH3.02	Myb-like protein of <i>Petunia hybrida</i>	0.76	133	149	(+)	1.000	0.778	catacaTAGTtatgaat
SEQ_25	P\$MIIG/P_Act.01	Maize activator P of flavonoid biosynthetic genes	0.93	150	164	(-)	1.000	0.977	ttacGGTAGgtttca
SEQ_25	P\$MYBL/ATMYB77.01	R2R3-type myb-like transcription factor (I-type binding site)	0.87	172	188	(-)	1.000	0.909	ttgtggCGGtccctgct

TABLE 7-continued

cis-regulatory elements of SEQ ID NO: 25									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_25 P\$DRBB/HVDRF1.01		H. vulgare dehydration-response factor 1	0.89	175	189	(+)	1.000	0.953	aggAACCGccacaat
SEQ_25 P\$GCCF/ERE_JERE.01		Ethylene-responsive elements (ERE) and jasmonate- and elicitor-responsive elements (JERE)	0.85	175	187	(+)	1.000	0.865	aggAACCGCCaca
SEQ_25 P\$MYBS/TAMYB80.01		MYB protein from wheat	0.83	191	207	(-)	1.000	0.874	gcttATATtccccctcac
SEQ_25 P\$TEPB/TEF1.01		TEF cis acting elements in both RNA polymerase II-dependent promoters and rDNA spacer sequences	0.76	192	212	(+)	1.000	0.796	tgAGGGgaatataagccaaaag
SEQ_25 P\$LEGB/LEGB.01		Legumin box, highly conserved sequence element about 100 by upstream of the TSS in legumin genes	0.59	206	232	(+)	0.750	0.649	gccaaaagCCCTgcaattttcagtggaga
SEQ_25 P\$TEPB/TEF1.01		TEF cis acting elements in both RNA polymerase II-dependent promoters and rDNA spacer sequences	0.76	230	250	(+)	0.956	0.795	agAAGGgtaagattattaag
SEQ_25 P\$AHBP/HAHB4.01		Sunflower homeodomain leucine-zipper protein Hahb-4	0.87	238	248	(+)	1.000	0.903	aagattATTaa
SEQ_25 P\$DOFF/DOF1.01		Dof1/MN1a - single zinc finger transcription factor	0.98	239	255	(+)	1.000	0.980	agattattAAAGgcagc
SEQ_25 P\$L1EX/ATML1.01		L1-specific homeodomain protein ATML1 ( <i>A. thaliana</i> meristem layer 1)	0.82	240	256	(+)	1.000	0.835	gattatTAAGgcagcc
SEQ_25 P\$DRBB/CRT_DRE.01		C-repeat/dehydration response element	0.89	262	276	(-)	1.000	0.968	ctttgCCGAcattgt
SEQ_25 P\$URNA/USE.01		Upstream sequence elements in the promoters of U-snrRNA genes of higher plants	0.75	284	300	(-)	1.000	0.858	aatgtccCACctcgaat

TABLE 7-continued

cis-regulatory elements of SEQ ID NO: 25									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_25 P\$GTGX/SBF1.01		SBF-1	0.87	292	308	(+)	1.000	0.908	tgggacattTAAatttaa
SEQ_25 P\$LIBX/HDG9.01		Homeodomain glabrous 9	0.77	292	308	(-)	0.796	0.792	ttaaatTTAAAtgtccca
SEQ_25 P\$LIBX/PDF2.01		Protodermal factor 2	0.85	294	310	(+)	1.000	0.851	ggacatTAAAttttaaaa
SEQ_25 P\$AHBP/WUS.01		Homeodomain protein WUSCHEL	0.94	296	306	(-)	1.000	1.000	aaattTAAAtgt
SEQ_25 P\$GTGX/SBF1.01		SBF-1	0.87	298	314	(+)	1.000	0.875	attaaatTTAAAaaagaa
SEQ_25 P\$GTGX/SBF1.01		SBF-1	0.87	299	315	(-)	1.000	0.885	cttcctttTTAAatttaa
SEQ_25 P\$IDRE/IDE1.01		Iron-deficiency-responsive element 1	0.77	325	339	(-)	0.809	0.806	aagCTTgctactttc
SEQ_25 P\$AGP1/AGP1.01		AG-motif binding protein 1	0.91	376	386	(+)	1.000	0.912	caaGATcttcc
SEQ_25 P\$AHBP/WUS.01		Homeodomain protein WUSCHEL	0.94	383	393	(+)	1.000	0.963	ttcctTAAAtcc
SEQ_25 P\$GTGX/S1F.01		S1F, site 1 binding factor of spinach rps1 promoter	0.79	383	399	(-)	1.000	0.810	tgttATGGattaaggaa
SEQ_25 P\$MADS/AGL2.01		AGL2, <i>Arabidopsis</i> MADS-domain protein AGAMOUS-like 2	0.82	387	407	(+)	1.000	0.865	ttaatCCATAacaagaagtcc
SEQ_25 P\$AHBP/ATHB5.01		HDZip class I protein ATHB5	0.89	435	445	(+)	0.829	0.940	acaATGAtttct
SEQ_25 P\$AHBP/ATHB5.01		HDZip class I protein ATHB5	0.89	435	445	(-)	0.936	0.941	agaATCAttgt
SEQ_25 P\$SUCB/SUCROSE.01		Sequence motif from the promoters of different sugar-responsive genes	0.81	444	462	(+)	1.000	0.875	ctAAATcatacatattacc
SEQ_25 P\$MADS/AGL15.01		AGL15, <i>Arabidopsis</i> MADS-domain protein AGAMOUS-like 15	0.79	487	507	(-)	0.850	0.804	tttTGCTacacctggttagtag
SEQ_25 P\$MYCL/ICE.01		ICE (inducer of CBF expression 1), AtMYC2 (rd22BP1)	0.95	487	505	(-)	0.954	0.966	ttgctACACctggttagtag

TABLE 7-continued

cis-regulatory elements of SEQ ID NO: 25									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_25 P\$MADS/AGL2.01		AGL2, <i>Arabidopsis</i> MADS-domain protein AGAMOUS-like 2	0.82	488	508	(+)	0.869	0.855	tactaCCAGgtgtagcaaaat
SEQ_25 P\$L1BX/PDF2.01		Protodermal factor 2	0.85	510	526	(+)	1.000	0.880	cccgatTAAAttcataa
SEQ_25 P\$AHP/WUS.01		Homeodomain protein WUSCHEL	0.94	512	522	(-)	1.000	0.963	gaattTAATcg
SEQ_25 P\$RAV5/RAV1-5.01		5'-part of bipartite RAV1 binding site, interacting with AP2 domain	0.96	537	547	(-)	1.000	0.974	agcACAaaaat
SEQ_25 P\$CARM/CARICH.01		CA-rich element	0.78	548	566	(+)	1.000	0.837	accttcaAACAcagatgc
SEQ_25 P\$MYCL/ICE.01		ICE (inducer of CBF expression 1), AtMYC2 (rd22BP1)	0.95	554	572	(+)	0.863	0.954	aaacaACAGatgctcgcaa
SEQ_25 P\$RAV5/RAV1-5.01		5'-part of bipartite RAV1 binding site, interacting with AP2 domain	0.96	555	565	(+)	1.000	0.961	aacACAgatg
SEQ_25 P\$MYBL/MYBP3.02		Myb-like protein of <i>Fetunia hybrida</i>	0.76	596	612	(+)	1.000	0.771	tctagcTAGTaaagacc
SEQ_25 P\$MYBL/NTMYBAS1.01		Anther-specific myb gene from tobacco	0.96	600	616	(-)	1.000	0.975	gttaggtcGTTActagc
SEQ_25 P\$MYBL/GMYB.01		GA-regulated myb gene from barley	0.91	608	624	(-)	1.000	0.927	atagtgttGTTAggtcg
SEQ_25 P\$MIIG/PALBOXL.01		Cis-acting element conserved in various PAL and 4CL promoters	0.80	622	636	(-)	1.000	0.812	atctgtttGGTGata
SEQ_25 P\$CARM/CARICH.01		CA-rich element	0.78	623	641	(+)	1.000	0.788	atcaccacaAACAGataaaca
SEQ_25 P\$MYBL/CARE.01		CAACTC regulatory elements, GA-inducible	0.83	646	662	(+)	1.000	0.834	tctagcAGTTccagca
SEQ_25 P\$CEIF/ABI4.01		ABA insensitive protein 4 (ABI4)	0.87	680	692	(+)	1.000	0.900	tcgcACCcgacga
SEQ_25 P\$DREB/CRT_DRE.01		C-repeat/dehydration response element	0.89	681	695	(+)	1.000	0.914	cgccaCCGAcgatta

TABLE 7-continued

cis-regulatory elements of SEQ ID NO: 25									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_25 P\$PREM/MGPROTORE.01		Promoter elements involved in MgProto (Mg-protoporphyrin IX) and light-mediated induction	0.77	683	713	(+)	1.000	0.774	ccacCGACgattatcgattccactaaagctac
SEQ_25 P\$DOFF/DOF1.01		Dof1/MNE1a - single zinc finger transcription factor	0.98	698	714	(+)	1.000	1.000	gattcactAAAGctaca
SEQ_25 P\$CGCG/ATSRI.01		Arabidopsis thaliana signal-responsive gene1, Ca2+/calmodulin binding protein homolog to NtER1 (tobacco early ethylene-responsive gene)	0.84	714	730	(-)	1.000	0.865	ccaCGCGtgacttggt
SEQ_25 P\$CE3S/CE3.01		Coupling element 3 (CE3), non-ACGT ABRE	0.77	715	733	(-)	1.000	0.787	tatccaCGCGtgacttggt
SEQ_25 P\$CGCG/ATSRI.01		Arabidopsis thaliana signal-responsive gene1, Ca2+/calmodulin binding protein homolog to NtER1 (tobacco early ethylene-responsive gene)	0.84	721	737	(+)	1.000	0.870	acaCGCGtgatagtagg
SEQ_25 P\$MYBS/MYBST1.01		MybST1 (Myb <i>Solanum tuberosum</i> 1) with a single myb repeat	0.90	722	738	(-)	1.000	0.936	tccactATCCacgcgtg
SEQ_25 P\$HOCT/HOCT.01		Octamer motif found in plant histone H3 and H4 genes	0.76	723	739	(-)	1.000	0.768	ttccactATCCacgcgt
SEQ_25 P\$MYBS/ZMRRP1.01		<i>Zea mays</i> MYB-related protein 1 (transfer cell specific)	0.79	732	748	(-)	0.777	0.852	atttctcTATccacta
SEQ_25 P\$NCS2/NCS2.01		Nodulin consensus sequence 2	0.79	746	760	(+)	0.750	0.803	aattgcCTGTcaac
SEQ_25 P\$MSAE/MSA.01		M-phase-specific activators (NtmybA1, NtmybA2, NtmybB)	0.80	753	767	(+)	1.000	0.875	tgttcaACGgggsga

TABLE 7-continued

cis-regulatory elements of SEQ ID NO: 25									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	sim.	Core Matrix sim.	Sequence
SEQ_25 P\$PREM/MGPROTORE.01		Promoter elements involved in MgProto (Mg-protoporphyrin IX) and light-mediated induction	0.77	786	816	(+)	1.000	0.801	atagCGACAagggaggagcgatattgcta
SEQ_25 P\$IDDF/ID1.01		Maize INDETERMINATE1 zinc finger protein	0.92	787	799	(-)	1.000	0.921	ctccTTGTegcta
SEQ_25 P\$MYBS/MYBST1.01		MybST1 (Myb Solanum tuberosum 1) with a single myb repeat	0.90	810	826	(+)	1.000	0.928	attgctATCCggaagt
SEQ_25 P\$DREE/HVDRF1.01		<i>H. vulgare</i> dehydration-response factor 1	0.89	842	856	(+)	0.826	0.914	actcGCCGCCcatata
SEQ_25 P\$GARP/ARR10.01		Type-B response regulator (ARR10), member of the GARP-family of plant myb-related DNA binding motifs	0.97	857	865	(-)	1.000	0.970	AGATccttg
SEQ_25 P\$SALT/ALFIN1.01		Zinc-finger protein in alfalfa roots, regulates salt tolerance	0.93	872	886	(-)	1.000	0.930	ccttgGTGGccgct
SEQ_25 P\$PREM/MGPROTORE.01		Promoter elements involved in MgProto (Mg-protoporphyrin IX) and light-mediated induction	0.77	888	918	(-)	1.000	0.774	actaCGACggcgatgaggggtgaccattcgag
SEQ_25 P\$NCS3/NCS3.01		Nodulin consensus sequence 3	0.89	896	906	(+)	1.000	0.947	gtCACCCctcat
SEQ_25 P\$AHBP/ATHB9.01		HD-ZIP class III protein ATHB9	0.77	920	930	(+)	0.750	0.773	gtattGAtctc
SEQ_25 P\$GARP/ARR10.01		Type-B response regulator (ARR10), member of the GARP-family of plant myb-related DNA binding motifs	0.97	941	949	(+)	1.000	0.973	AGATcctgg
SEQ_25 P\$ABRE/ABF1.03		ABA (abscisic acid) inducible transcriptional activator	0.82	952	968	(-)	1.000	0.833	ggcggagcCGTGgctca

TABLE 7-continued

cis-regulatory elements of SEQ ID NO: 25									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core Matrix sim.	sim.	Sequence
SEQ_25 P\$LIBX/ATML1.02		Arabidopsis thaliana meristem layer 1	0.76	987	1003	(-)	1.000	0.791	aggCAITcaaatctggc
SEQ_25 P\$LIBX/PDF2.01		Protodermal factor 2	0.85	989	1005	(+)	0.787	0.854	cagattTGAATgcctcc
SEQ_25 P\$HEAT/HSE.01		Heat shock element	0.81	1015	1029	(-)	1.000	0.822	gcatactctccAGAAAT
SEQ_25 P\$MYBL/MYBP3.02		Myb-like protein of Petunia hybrida	0.76	1076	1092	(+)	0.817	0.775	gagagATTGtgctttc
SEQ_25 P\$CCAF/CCA1.01		Circadian clock associated 1	0.85	1077	1091	(-)	1.000	0.893	aaagcaacAATCtct
SEQ_25 P\$GT3A.01		Trihelix DNA-binding factor GT-3a	0.83	1107	1123	(+)	1.000	0.847	atcagTGTTActtcgat
SEQ_25 P\$CCAF/CCA1.01		Circadian clock associated 1	0.85	1126	1140	(-)	1.000	0.898	gcaaacagAATCtca
SEQ_25 P\$GAGA/BPC.01		Basic pentacysteine proteins	1.00	1128	1152	(-)	1.000	1.000	cgagagAGAGagggcaaacagaatct
SEQ_25 P\$GAGA/BPC.01		Basic pentacysteine proteins	1.00	1130	1154	(-)	1.000	1.000	aacgagAGAGagggcaaacagaat
SEQ_25 P\$HEAT/HSE.01		Heat shock element	0.81	1130	1144	(-)	1.000	0.855	agaggcaaacAGAAAT
SEQ_25 P\$GAGA/GAGABP.01		(GA)n/(CT)n binding proteins (GBP, soybean; BBR, barley)	0.75	1134	1158	(-)	0.750	0.760	ccagaaCGAGagagagggcaaaaca
SEQ_25 P\$GAGA/GAGABP.01		(GA)n/(CT)n binding proteins (GBP, soybean; BBR, barley)	0.75	1138	1162	(-)	0.750	0.757	gaaaccAGAAcggagagagagaggca
SEQ_25 P\$PSRE/GAAA.01		GAAA motif involved in pollen specific transcriptional activation	0.83	1164	1180	(+)	1.000	0.843	ctgtagAAAaacttttt
SEQ_25 P\$NCS1/NCS1.01		Nodulin consensus sequence 1	0.85	1170	1180	(-)	1.000	0.853	aAAAAGttttt
SEQ_25 P\$PSRE/GAAA.01		GAAA motif involved in pollen specific transcriptional activation	0.83	1185	1201	(-)	1.000	0.838	ctaaacGAAAatgttcgc

TABLE 7-continued

cis-regulatory elements of SEQ ID NO: 25										
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence	
SEQ_25 P\$DOFF/DOF1.01		Dof1/MBE1a - single zinc finger transcription factor	0.98	1191	1207	(-)	1.000	0.984	ttgggcctAAAAGaaaat	
SEQ_25 P\$TCPF/ATTCP20.01		TCP class I transcription factor ( <i>Arabidopsis</i> )	0.94	1198	1210	(+)	1.000	0.968	ttagGCCcaaaagt	
SEQ_25 P\$TCPF/ATTCP20.01		TCP class I transcription factor ( <i>Arabidopsis</i> )	0.94	1208	1220	(-)	1.000	0.943	aaaagCCcaaaact	
SEQ_25 P\$DOFF/DOF3.01		Dof3 - single zinc finger transcription factor	0.99	1211	1227	(-)	1.000	0.994	cgttattAAAAGcccaa	
SEQ_25 P\$LIBX/HDG9.01		Homeodomain glabrous 9	0.77	1211	1227	(-)	1.000	0.818	cgttatTAAAagcccaa	
SEQ_25 P\$GTEx/SBF1.01		SBF-1	0.87	1213	1229	(-)	1.000	0.927	ggcgttatTAAAagccc	
SEQ_25 P\$DOFF/DOF3.01		Dof3 - single zinc finger transcription factor	0.99	1223	1239	(+)	1.000	0.995	taacgcctAAAAGcccaa	
SEQ_25 P\$CAAT/CAAT.01		CCAAT-box in plant promoters	0.97	1250	1258	(-)	1.000	0.979	acCCAAtaa	
SEQ_25 P\$TEFB/TEF1.01		TEF cis acting elements in both RNA polymerase II-dependent promoters and rDNA spacer sequences	0.76	1288	1308	(+)	0.956	0.767	atAAGGGgaatctatttattt	
SEQ_25 P\$MADS/SQUA.01		MADS-box protein SQUAMOSA	0.90	1294	1314	(+)	1.000	0.917	ggaatctATTTatttattt	
SEQ_25 P\$STKM/STK.01		Storekeeper (STK), plant specific DNA binding protein important for tuber-specific and sucrose-inducible gene expression	0.85	1298	1312	(-)	1.000	0.859	aatTAAATAaaataga	
SEQ_25 P\$LIBX/HDG9.01		Homeodomain glabrous 9	0.77	1299	1315	(-)	1.000	0.791	aacaatTAAATAaatag	
SEQ_25 P\$HMGF/HMG.IY.01		High mobility group I/Y-like proteins	0.89	1300	1314	(+)	1.000	0.907	tattTATTTaatgt	

TABLE 7-continued

cis-regulatory elements of SEQ ID NO: 25									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_25	P\$GTEX/SBF1.01	SBF-1	0.87	1307	1323	(+)	1.000	0.872	ttaattgTTAATcattc
SEQ_25	P\$AHBP/WUS.01	Homeodomain protein WUSCHEL	0.94	1310	1320	(+)	1.000	0.963	attgtTAATca
SEQ_25	P\$OCSE/OCSL.01	OCS-like elements	0.69	1310	1330	(+)	1.000	0.712	attgtaatacattcACGTTga
SEQ_25	P\$LEGB/LEGB.01	Legumin box, highly conserved sequence element about 100 bp up-stream of the TSS in legumin genes	0.59	1311	1337	(+)	0.750	0.625	ttgttaaTCATTcaccgttgaccattga
SEQ_25	P\$AHBP/ATHB5.01	HDZip class I protein ATHB5	0.89	1314	1324	(+)	0.936	0.939	ttaATCattca
SEQ_25	P\$AHBP/HAHB4.01	Sunflower homeodomain leucine-zipper protein Hahb-4	0.87	1314	1324	(-)	1.000	0.945	tgaatgATTTaa
SEQ_25	P\$GBOX/HBP1B.01	Wheat bZIP transcription factor HBP1B (histone gene binding protein 1b)	0.83	1315	1335	(-)	1.000	0.834	aatggtcaACGTgaatgatta
SEQ_25	P\$OPAQ/02_GCN4.01	Recognition site for bZIP transcription factors that belong to the group of Opaque-2 like proteins	0.81	1317	1333	(-)	0.951	0.842	tggtcaACGTgaatgat
SEQ_25	P\$WBXF/ERE.01	Elicitor response element	0.89	1322	1338	(+)	1.000	0.917	tcacgtTGACcattgaa
SEQ_25	P\$HEAT/HSE.01	Heat shock element	0.81	1328	1342	(+)	1.000	0.826	tgaccattgaaAGAAc
SEQ_25	P\$NCS1/NCS1.01	Modulin consensus sequence 1	0.85	1373	1393	(-)	0.804	0.896	cAAAGgatcaa
SEQ_25	P\$MADS/AGL2.01	AGL2, <i>Arabidopsis</i> MADS-domain protein AGAMOUS-like 2	0.82	1408	1428	(+)	0.869	0.838	tgtctCCAGctctagtaatga
SEQ_25	P\$MYBL/MYBPH3.02	Myb-like protein of <i>Petunia hybrida</i>	0.76	1427	1443	(+)	1.000	0.785	gacaatTAGTtttagttt

TABLE 7-continued

cis-regulatory elements of SEQ ID NO: 25									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_25 P\$STKM/STK.01		Storekeeper (STK), plant specific DNA binding protein important for tuber-specific and sucrose-inducible gene expression	0.85	1428	1442	(-)	1.000	0.864	aacTAAActaattgt
SEQ_25 P\$SPF1/SP8BF.01		DNA-binding protein of sweet potato that binds to the SP8a (ACTGTGTA) and SP8b (TACTATT) sequences of sporamin and beta-amylase genes	0.87	1459	1471	(-)	1.000	0.989	aatACTattacac
SEQ_25 P\$GTEX/SBF1.01		SBF-1	0.87	1495	1511	(-)	1.000	0.886	aaaattgTTAAataata
SEQ_25 P\$MYBL/WYBPH3.01		Myb-like protein of <i>Petunia hybrida</i>	0.80	1497	1513	(-)	1.000	0.809	agaaaaattGTTAataaa
SEQ_25 P\$E2FF/E2F.01		E2F class I sites	0.82	1527	1541	(+)	1.000	0.832	ttttTTCagcaacg
SEQ_25 P\$GTEX/SBF1.01		SBF-1	0.87	1548	1564	(+)	1.000	0.874	tgaattttTAAAacttg
SEQ_25 P\$SUCB/SUCROSE.01		Sequence motif from the promoters of different sugar-responsive genes	0.81	1552	1570	(-)	0.750	0.832	aaATATcaagtttttaaaaa
SEQ_25 P\$CCAF/CCA1.01		Circadian clock associated 1	0.85	1568	1582	(-)	1.000	0.854	ttaaaaaaaATCaaa
SEQ_25 P\$AHBP/BLR.01		Transcriptional repressor BELL-RINGER	0.90	1581	1591	(-)	1.000	0.976	taaaTTActtt
SEQ_25 P\$GTEX/SBF1.01		SBF-1	0.87	1583	1599	(-)	1.000	0.900	tttgcattTAAAttact
SEQ_25 P\$L1BX/ATML1.01		L1-specific homeodomain protein ATML1 ( <i>A. thaliana</i> meristem layer 1)	0.82	1584	1600	(+)	1.000	0.918	gtaattTAAAtgcaaaa
SEQ_25 P\$NCS1/NCS1.01		Nodulin consensus sequence 1	0.85	1606	1616	(+)	0.878	0.862	CAAAAtgatatt
SEQ_25 P\$MYBL/CARE.01		CAACTC regulatory elements, GA-inducible	0.83	1625	1641	(+)	1.000	0.834	actcaagAGTTgtgtga
SEQ_25 P\$NCS2/NCS2.01		Nodulin consensus sequence 2	0.79	1653	1667	(-)	1.000	0.809	acttgcCTCttgccc
SEQ_25 P\$TEPB/TEF1.01		TEF cis acting elements in both RNA polymerase II-dependent promoters and rDNA spacer sequences	0.76	1665	1685	(-)	0.956	0.816	agAAGGatacacaccagtgcact

TABLE 7-continued

cis-regulatory elements of SEQ ID NO: 25									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core sim.	Matrix sim.	Sequence
SEQ_25 P\$MYBS/HVMCB1.01		Hordeum vulgare Myb-related CAB-promoter-binding protein 1	0.93	1672	1688	(+)	1.000	0.933	tggtgtrATCCTcttcg
SEQ_25 P\$GTBX/SBF1.01		SBF-1	0.87	1686	1702	(+)	1.000	0.878	cggggCGTTAAAaccgt
SEQ_25 P\$NCS3/MCS3.01		Modulin consensus sequence 3	0.89	1702	1712	(-)	1.000	0.965	gtCACcttcca
SEQ_25 P\$MYBL/MYBPH3.01		Myb-like protein of <i>Petunia hybrida</i>	0.80	1704	1720	(-)	0.750	0.832	attaaacgGTCaccttc
SEQ_25 P\$MSAE/MSA.01		M-phase-specific activators (NtmybA1, NtmybA2, NtmybB)	0.80	1707	1721	(-)	1.000	0.897	tattaAACGgtcacc
SEQ_25 P\$LIBX/HDG9.01		Homeodomain glabrous 9	0.77	1708	1724	(-)	1.000	0.791	atgatatTAAAacggtcac
SEQ_25 P\$OPAQ/O2_GCN4.01		Recognition site for BZIP transcription factors that belong to the group of Opaque-2 like proteins	0.81	1716	1732	(-)	1.000	0.834	agatagACATgtattaa
SEQ_25 P\$LREM/ATCTA.01		Motif involved in carotenoid and tocopherol biosynthesis and in the expression of photosynthesis-related genes	0.85	1727	1737	(+)	1.000	0.853	ctATCTattat
SEQ_25 P\$ROOT/RHE.02		Root hair-specific element with a 3-nucleotid spacer between left part (LP) and right part (RP)	0.77	1747	1771	(+)	1.000	0.774	gtacttcaatagctatCACGttgctc
SEQ_25 P\$GEOX/HP1B.01		Wheat bZIP transcription factor HP1B (histone gene binding protein 1b)	0.83	1754	1774	(-)	1.000	0.843	gaggagcaACGTgatagctat
SEQ_25 P\$OCSE/OCSE.01		OCS-like elements	0.69	1760	1780	(-)	1.000	0.700	atttgtgaggagcaACGTgat
SEQ_25 P\$SUCB/SUCROSE.01		Sequence motif from the promoters of different sugar-responsive genes	0.81	1799	1817	(+)	1.000	0.911	gcAAAATcaattttataaag
SEQ_25 P\$TBPF/TATA.01		Plant TATA box	0.88	1807	1821	(+)	1.000	0.910	atTTTATAaagacgc
SEQ_25 P\$GTBX/GT3A.01		Trihelix DNA-binding factor GT-3a	0.83	1820	1836	(-)	1.000	0.865	tcagctGTTActcatgc
SEQ_25 P\$MYBL/MYBPH3.01		Myb-like protein of <i>Petunia hybrida</i>	0.80	1822	1838	(-)	1.000	0.823	attcaagctGTTActcat

TABLE 7-continued

cis-regulatory elements of SEQ ID NO: 25									
Seq. name	Family/matrix	Further Information	Opt. thresh.	Start pos.	End pos.	Strand	Core Matrix sim.	Matrix sim.	Sequence
SEQ_25 P\$DOFF/PBF.01		PBF (MPBF)	0.97	1834	1850	(+)	1.000	0.988	tgaataaaaaAGagagg
SEQ_25 P\$IDRE/IDE1.01		Iron-deficiency-responsive element 1	0.77	1856	1870	(+)	1.000	0.777	acGCAgttgattgc
SEQ_25 P\$GBOX/BZIP910.02		bZIP transcription factor from <i>Antirrhinum majus</i>	0.84	1859	1879	(+)	1.000	0.962	catgttgattgcTGAcgtgtc
SEQ_25 P\$OCSE/OCSL.01		OCS-like elements	0.69	1859	1879	(+)	1.000	0.751	catgttgattgctgACGTgtc
SEQ_25 P\$GBOX/HBP1B.01		Wheat bZIP transcription factor HBP1B (histone gene binding protein 1b)	0.83	1864	1884	(-)	1.000	0.973	ctacggacACGTcagcaatca
SEQ_25 P\$GBOX/GBF1.01		bZIP protein G-Box binding factor 1	0.94	1865	1885	(+)	1.000	0.999	gattgctgACGTgtccgtagg
SEQ_25 P\$ABRE/ABF1.03		ABA (abscisic acid) inducible transcriptional activator	0.82	1866	1882	(+)	1.000	0.960	attgctgaCGTgtccgt
SEQ_25 P\$OPAQ/RITA1.01		Rice transcription activator-1 (RITA), basic leucine zipper protein, highly expressed during seed development	0.95	1866	1882	(-)	1.000	0.956	acggacACGTcagcaat
SEQ_25 P\$OPAQ/RITA1.01		Rice transcription activator-1 (RITA), basic leucine zipper protein, highly expressed during seed development	0.95	1867	1883	(+)	1.000	0.958	ttgctgACGTgtccgta
SEQ_25 P\$EINL/TEIL.01		TEIL (tobacco EIN3-like)	0.92	1882	1890	(-)	0.863	0.966	aTGGAccta
SEQ_25 P\$GAGA/BPC.01		Basic pentacysteine proteins	1.00	1937	1961	(-)	1.000	1.000	ctcgagAGAGaggggacttatgatg

In the following table 9, cis-regulatory element families commonly found in at least 13 of the listed expression control sequences of the present invention are shown. Table 8 describes the cis-regulatory element families.

TABLE 8

Description of cis-regulatory elements families commonly found in expression control sequences of the present invention.	
TF-Family	Description
OSVTBP	Vertebrate TATA binding protein vector
P\$AHBP	Arabidopsis homeobox protein
P\$DOFF	DNA binding with one finger (DOF)
P\$GTBX	GT-box elements
P\$IBOX	Plant I-Box sites
P\$LIBX	L1 box, motif for L1 layer-specific expression
P\$LREM	Light responsive element motif, not modulated by different light qualities
P\$MYBL	MYB-like proteins
P\$MYBS	MYB proteins with single DNA binding repeat
P\$NCS1	Nodulin consensus sequence 1
P\$CCAF	Circadian control factors
P\$GBOX	Plant G-box/C-box bZIP proteins

TABLE 8-continued

Description of cis-regulatory elements families commonly found in expression control sequences of the present invention.	
TF-Family	Description
5	P\$IDDF D domain factors, the ID domain includes a cluster of three different types of zinc fingers separated from a fourth C2H2 finger by a long spacer
	P\$MADS floral determination
10	P\$MYCL Myc-like basic helix-loop-helix binding factors
	P\$OPAQ Opaque-2 like transcriptional activators
	P\$SPF1 Sweet potato DNA-binding factor with two WRKY-domains
	P\$SUCB Sucrose box
	P\$WBXF W Box family
	OSINRE Core promoter initiator elements
15	OSPTBP Plant TATA binding protein vector
	P\$ABRE ABA response elements
	P\$LEGB Legumin Box family
	P\$NACF Plant specific NAC [NAM (no apical meristem), ATAF172, CUC2 (cup-shaped cotyledons 2)] transcription factors
20	P\$OCSE Enhancer element first identified in the promoter of the octopine synthase gene (OCS) of the <i>Agrobacterium tumefaciens</i> T-DNA

TABLE 9

Cis-regulatory elements families commonly found in expression control sequences in at least 13 of the listed expression control sequences of the present invention.

TF-Family	No of occurrences									
	p-BnSCP (SEQ-ID 70)	p-BnGRPL (SEQ-ID 1)	p-BnCRU4 (SEQ-ID 77)	p-BnMYR (SEQ-ID 85)	p-BnSETL-var1 (SEQ-ID 22)	p-BnSETL-var2 (SEQ-ID 25)	p-BnSCT2-var1 (SEQ-ID 14)	p-BnSCT2-var2 (SEQ-ID 16)	p-BnMDP (SEQ-ID 95)	
OSVTBP	7	18	17	39	6	10	5	8	19	
P\$AHBP	16	8	22	25	6	12	7	9	15	
P\$DOFF	14	8	11	9	2	7	5	5	4	
P\$GTBX	12	13	10	16	10	12	5	1	7	
P\$IBOX	4	4	4	2	4	2	2	2	7	
P\$LIBX	9	7	11	18	10	10	2	3	10	
P\$LREM	6	4	4	6	3	1	3	3	5	
P\$MYBL	9	11	12	7	16	14	9	7	9	
P\$MYBS	9	3	8	2	4	5	2	2	10	
P\$NCS1	2	2	4	3	3	4	2	2	2	
P\$CCAF	4	4	4	2	3	3	1	1	3	
P\$GBOX	9	3	12	2	5	5	7	5	3	
P\$IDDF	3	2	1	1	1	1	4	5	3	
P\$MADS	6	9	9	2	0	5	2	2	7	
P\$MYCL	1	0	6	3	5	2	3	3	3	
P\$OPAQ	9	5	7	3	6	4	1	2	4	
P\$SPF1	2	6	1	5	1	1	2	2	2	
P\$SUCB	6	4	3	7	1	4	2	3	0	
P\$WBXF	2	3	1	0	1	1	3	2	1	
OSINRE	5	1	1	2	1	4	0	0	1	
OSPTBP	2	7	8	24	1	1	0	1	5	
P\$ABRE	1	1	3	0	4	2	3	3	1	
P\$LEGB	6	4	8	2	1	2	2	2	7	
P\$NACF	2	2	2	1	1	0	3	3	2	
P\$OCSE	3	4	3	5	3	3	7	7	3	

TF-Family	No of occurrences					
	p-BnRTI-4 (SEQ-ID 103)	p-BnMTFL (SEQ-ID 111)	p-BnGSTF (SEQ-ID 119)	p-BnPEF-var1 (SEQ-ID 6)	p-BnPEF-var2 (SEQ-ID 9)	p-BnLSP (SEQ-ID 125)
OSVTBP	9	10	13	28	4	12
P\$AHBP	22	9	9	18	5	14
P\$DOFF	8	6	4	10	8	5
P\$GTBX	8	10	5	22	5	10
P\$IBOX	3	1	1	8	2	3

TABLE 9-continued

Cis-regulatory elements families commonly found in expression control sequences in at least 13 of the listed expression control sequences of the present invention.

PSLIBX	10	2	1	10	3	9
PSLREM	6	2	2	8	4	5
PSMYBL	10	9	15	18	5	6
PSMYBS	13	3	4	5	3	5
PSNCS1	1	3	2	1	1	2
PSCCAF	4	3	3	9	2	0
PSGBOX	12	1	5	2	0	7
PSIDDF	1	3	3	3	1	0
PSMADS	12	6	3	8	5	6
PSMYCL	3	1	6	4	1	1
PSOPAQ	12	0	5	4	2	7
PSSPF1	3	0	2	7	1	2
PSSUCB	1	2	1	7	2	3
PSWBXF	1	2	1	3	1	5
OSINRE	2	4	2	7	2	2
OSPTBP	4	3	8	7	2	0
PSABRE	3	1	3	1	0	4
PSLEGB	3	0	1	2	0	2
PSNACF	3	1	0	1	1	1
PSOCSE	7	0	4	4	0	3

All references cited in this specification are herewith incorporated by reference with respect to their entire disclosure content and the disclosure content specifically mentioned in this specification.

The invention will now be illustrated by the following Examples which are not intended, whatsoever, to limit the scope of this application.

Example 1

General Cloning Methods

General Cloning Methods including enzymatic digestion by restriction enzymes, agarous gel electrophoresis, purification of DNA fragments, transfer of nucleic acids to nitro-cellulose on nylon membranes, maligation of DNA fragments, transformation of *E. coli* bacteria as well as culture of bacteria and sequence analysis of recombinant DNA have been carried out as described in Sambrook et al. (1989, Cold Spring Harbour Laboratory Press. ISBN 0-87969-309-6).

Example 2

Cloning of Promotor Elements from *Brassica napus*

For the analysis of seed specific expressed genes in *Brassica napus*, different tissues of various developmental stages (table 10) have been investigated.

TABLE 10

tissue types used for transcript analysis  
Specific developmental stages are given using the Biologische Bundesanstalt, Bundessortenamt, and Chemical Industry (BBCH) code (Meier, 1997)

Sample Nr.	Tissue	Developmental stage	type sample
1	immature embryos	walking stick	purpose prio 1
2	immature embryos	fully developped (approx 20 days)	purpose prio 1
3	immature embryos	fully developped pre dessic. green	purpose prio 1
4	immature embryos	fully developped. start dessic Yellow	control/purpose prio 2

TABLE 10-continued

tissue types used for transcript analysis  
Specific developmental stages are given using the Biologische Bundesanstalt, Bundessortenamt, and Chemical Industry (BBCH) code (Meier, 1997)

Sample Nr.	Tissue	Developmental stage	type sample
5	embryo sac complete	heart	control/purpose prio 2
6	immature seed coat and endosperm	weight mix sample 1-3	control/purpose prio 2
7	flower buds	BBCH 57	control/purpose prio 2
8	anthers and stigma	BBCH 68	control/purpose prio 2
9	flowers (exclude anthers and stigma)	BBCH 67	control
10	leaves	BBCH 32	control
11	leaves	BBCH 75	control
12	leaves	BBCH 80, senescing (yellow)	control
13	stem	BBCH 32	control
14	stem	BBCH 75	control
15	stem	BBCH 80, senescing (yellow)	control
16	seedling: hypocotyl and cotyledons	BBCH 12	control
17	seedling: roots (sand)	BBCH 12	control
18	empty siliques	weight mix sample 1-3	control

To this end, *Brassica napus* cv. Kumily plants were raised under standard conditions (Moloney et al. 1992, Plant Cell Reports 8: 238-242). The tissues where harvested at the indicated developmental stages (table 10) and used for the preparation of RNA (RNAeasy, Qiagen) according to the manufactures manual. To identify in further experiments seed specifically expressed mRNA transcripts, three pools were created by mixing the RNA. A seed specific pool P-S was created from sample 1, 2, 3 (see table 10). A control pool P-C1 was created from sample 9, 10, 11, 12, 13, 14, 15, 16, 17, 18. A third pool P-C2 consisting of sample 4, 5, 6, 7, 8 was used as a more stringent control: transcripts not expressed in control pool P-C2 are solely expressed in early seed development and in no other tissue/developmental stage. Using the amplified fragment length polymorphism (AFLP) method, known to a person skilled in the art, 384 primer combinations were

used to identify 96 candidate transcript fragments being present solely in pool P-S and/or also weakly in pool P-C2 but absent on pool P-C1. A selection of 42 primer combinations that identified the 55 most promising transcript fragments were used to analyse in detail all samples listed in table 10, resulting in 26 fragment with confirmed expression solely in the developing embryo samples 1, 2, 3 and 4. Sequencing of those candidate fragments resulted in 20 unique sequences. Basic Local Alignment Search Tool (BLAST) was used to identify the putative full length transcripts corresponding to the identified transcript fragments. Surprisingly, besides genes known in the art for seed specific expression, e.g. napin and 3-ketoacyl-CoA synthase, a number of fragments listed in table 11 showed no homology to any known *Brassica* sequence, or to genes which were not known to be seed specifically expressed and/or to genes with unknown sequence upstream of the known mRNA sequence.

TABLE 11

Candidate fragments and homologue sequences identified using BLAST.				
Candidate	fragment length	SEQ-ID	<i>Brassica</i> homologue	<i>Arabidopsis</i> homologue
BnSCP	157 bp	58		At5g36100 (unknown protein)
BnGRPL	174 bp	4		At3g10185 (similar to gibberelin responsive protein)
BnCRU4	127 bp	59	BnCRU4m (Cruciferin)	
BnMYR	101 bp	60	BnMYRmc (Myrosinase)	
BnSETL	120 bp	26		At1g03270 (unknown protein)
BnSCT2	172 bp	19	BnSCT2 (Sinapoyl-cholin transferase 2)	
BnMDP	273 bp	61		At3g20370 (unknown, similar)
BnRTI-4	237 bp	62	BnRTI-4 (Trypsin Inhibitor family)	
BnMTFL	144 bp	63		At2g21650 (put. Myb factor transcr. Factor)
BnGSTF	186 bp	64		At3g62760 (AtGSTF13)
BnSRP	131 bp	65		
BnPEF	121 bp	12	Pectinesterase family protein	At5g47500 (pectinesterase family protein)
BnWSP	83 bp	66		
BnLSP	164 bp	67		At5g62200 (weak similarity to embryo-specific protein 3)

From leaf material of *Brassica napus* cv. Kumily, genomic DNA has been isolated using the DNAeasy kit (Qiagen) according to the manufacturer's manual. Culture conditions for the *Brassica napus* cv. Kumily were as discussed above. Using this genomic DNA, as template, multiple rounds of thermal asymmetric intercalated polymerase chain reaction (TAIL-PCR)—a method known to a person skilled in the art—was performed to isolate sequences 5' upstream and 3' downstream of the 20 identified expressed fragments. The amplified products were either sequences directly, or subcloned into the pGEM-T (Promega) vector prior sequencing. Subcloning was required in some cases, as *Brassica napus* is amphidiploid, that is, *Brassica napus* contains 10 chromosomes common with *Brassica rapa* (A genome) and 9 chromosomes common with *Brassica oleracea* (C genome). Subcloning of PCR products containing a mixture of two

sequences amplified from both genomes allows to separate these two sequences. Sequencing was done by standard techniques (laser fluorescent DNA-sequencing, ABI according to the method of Sanger et al. 1977 Proc. Natl. Acad. Sci. USA 74, 5463-5467).

For candidate expressed sequences where no *Brassica* gene was known to the art, the open reading frame was identified with help of software prediction and using alignments with homologues genes from *Arabidopsis*. The following *Brassica napus* open reading frames have been identified (Table 12):

TABLE 12

Open reading frames (ORF) identified in <i>Brassica napus</i> cDNA sequences.		
<i>Brassica napus</i> Sequence	ORF in bp	SEQ ID NO:
BnGRPL	360	5
BnPEF	1083	13
BnSCT1	1401	20
BnSCT2	1401	21
BnSETL1	1512	27
BnSETL2	1512	28
BnSCP	773	72
BnCRU4	1107	80
BnMYR	1644	88
BnMDP	1152	98
BnRTI-4	300	106
BnMTFL	303	114
BnGSTF	660	121
BnLSP	574	133

For the expressed sequence SEQ-ID 126, no open reading frame could be identified.

The following *Brassica napus* sequences upstream of the expressed sequence SEQ-ID 126 or the identified expressed open reading frames (ORF) have been obtained (Table 13).

TABLE 13

Genomic 5' upstream sequences from the <i>Brassica napus</i> cDNA sequences.		
<i>Brassica napus</i> Sequence	genomic 5' sequence in bp	SEQ ID NO:
p-BnGRPL	1790	1
p-BnPEF-var1	2027	6
p-BnPEF-var2	636	9
p-BnSCT2-var1	1019	14
p-BnSCT2-var2	996	16
p-BnSETL-var1	1490	22
p-BnSETL-var2	2010	25
p-BnSCP	2052	70
p-BnCRU4	1951	77
p-BnMYR	1360	85
p-BnMDP	1428	95
p-BnRTI-4	1820	103
p-BnMTFL	1335	111
p-BnGSTF	1565	119
p-BnSRP	2447	124
p-BnLSP	1593	121

The analysis of the 5' upstream sequences using Genomatrix software Gems-Launcher showed that the sequences comprised promoter elements. This was confirmed by the presence of a TATA-Box which is required for transcription by RNA-polymerases. Also in the isolated fragments elements specific for seed-transcription factors (e.g. Prolamin-box, legumin box, RITA etc.) were found.

The following *Brassica napus* sequences downstream of the identified expressed open reading frames (ORF) have been obtained (Table 14).

TABLE 14

Genomic 3' downstream sequences from the <i>Brassica napus</i> cDNA sequences.		
<i>Brassica napus</i> Sequence	genomic 3' sequence in bp	SEQ ID NO:
t-BnGRPL	581	2
t-BnPEF-var1	477	7
t-BnPEF-var2	538	10
t-BnSCT2-var1	573	15
t-BnSCT2-var2	576	17
t-BnSETL-var1	614	23
t-BnSCP	587	71
t-BnCRU4	514	78
t-BnMYR	652	86
t-BnMDP	483	96
t-BnRTI-4	572	104
t-BnMTFL	521	112
t-BnSRP	865	125

Example 3

## Production of Test Constructs for Demonstrating Promoter Activity

5 For the testing of the promoter elements in a first step  
10 promoter terminator cassettes were generated. To this end,  
fusion PCRs have been used wherein via two PCR steps  
promoter elements were linked with terminator elements. At  
15 the same time, a multiple cloning site was introduced in  
between the promoter and terminator elements. The primers  
used to generate cassettes using corresponding native *Bras-*  
*sica* terminators are shown in Table 15, Table 16 list the  
generated cassettes using the OCS terminator.

TABLE 15

Primer pairs used for the generation of promoter-multiple cloning site-terminated-cassettes via Fusion-PCR using native <i>Brassica</i> terminator sequences.			
<i>Brassica napus</i> Promoter/Terminator cassette	Primer pair 1. PCR Promoter	Primer pair 1. PCR Terminator	Primer pair 2. PCR
p-BnGRP_MCS_t-BnGRP	Forw: ataccgggga-tacctgcagggt-tagggcggccacaa-aacgaaatcatca-aatcgtg (SEQ ID NO: 29) Rev: caatcaatta-taggcctcgcagctt-taattaacgatcgagc-catggttttagagaccg-gaattattg (SEQ ID NO: 30)	Forw: ccatggctc-gatcgttaattaag-catggcaggcctataatt-gattgtttctcctcttagttg-taaataatctatc (SEQ ID NO: 31) Rev: taagcggccg-caatcggaccga-taccggtaggcgggat-tatctacctaacctaaacaacaaaag (SEQ ID NO: 32)	Forw: ataccggggatacctgcagggttaggcggc-cacaaaacgaaatcat-caaatcgtg (SEQ ID NO: 29) Rev: 'taagcggccg-caatcggaccga-taccggtaggcgggat-tatctacctaacctaaacaacaaaag (SEQ ID NO: 32)
p-BnPEF-var1_MCS_t-BnPEF-var1	Forw: ataccgggatacctgca-gggttaggcggccaaattt-attaaccatctattgttcac (SEQ ID NO: 33) Rev: caatcaattataggcctcg-catgctttaattaacgatcagccatgggacgagaaa-gaaaatggtcggag (SEQ ID NO: 34)	Forw: ccatggctcgcagcttaatt-aaagcatcggaggcctat-aattgattgtaaggaaatca-acttcaaatgcttttc (SEQ ID NO: 35) Rev: taagcggccgcaatcgg-accgataccggtaggcg-ccgacgttaagcgagagt-ggatag (SEQ ID NO: 36)	Forw: ataccgggatacctgca-gggttaggcggccaaattt-attaaccatctattgttcac (SEQ ID NO: 33) Rev: taagcggccgcaatcgg-accgataccggtaggcg-ccgacgttaagcgagagt-ggatag (SEQ ID NO: 36)
p-BnPEF-var2_MCS_t-BnPEF-var2	Forw: ataccgggatacctgca-gggttaggcggccagaaat-tacgtttgagttcaaatcag (SEQ ID NO: 37) Rev: caatcaattataggcctcg-catgctttaattaacgatcagccatgggacgagaaa-taaatggtcgag (SEQ ID NO: 38)	Forw: Ccatggctcgcagcttaatt-aaagcatcggaggcctat-taattgattgtaggaatca-acttcaaatgcttttc (SEQ ID NO: 39) Rev: taagcggccgcaatcgg-accgataccggtaggcg-cagaggtgaggaggag-ttgac (SEQ ID NO: 40)	Forw: ataccgggatacctgca-gggttaggcggccagaaat-tacgtttgagttcaaatcag (SEQ ID NO: 37) Rev: taagcggccgcaatcgg-accgataccggtaggcg-cagaggtgaggaggag-ttgac (SEQ ID NO: 40)
p-BnSCT2-var1_MCS_t-BnSCT2-var1	Forw: ataccgggatacctgca-gggttaggcggccagatg-caaaaacgtatagtcacac (SEQ ID NO: 41) Rev: caatcaattataggcctcg-catgctttaattaacgatcagccatgggtttctctgcttct	Forw: ccatggctcgcagcttaatt-aaagcatcggaggcctat-aattgattgAgttcctcact-cacttctctc (SEQ ID NO: 43) Rev: taagcggccgcaatcgg-accgataccggtaggcg	Forw: ataccgggatacctgca-gggttaggcggccagatg-caaaaacgtatagtcacac (SEQ ID NO: 41) Rev: taagcggccgcaatcgg-accgataccggtaggcg-cgccttatatggatgttctg

TABLE 15-continued

Primer pairs used for the generation of promoter-multiple cloning site-terminated-cassettes via Fusion-PCR using native <i>Brassica</i> terminator sequences.			
<i>Brassica napus</i> Promoter/Terminator cassette	Primer pair 1. PCR Promoter	Primer pair 1. PCR Terminator	Primer pair 2. PCR
	tggtgtcac (SEQ ID NO: 42)	ccgccttatatggattttgtg ttactgacc (SEQ ID NO: 44)	ttactgacc (SEQ ID NO: 44)
p-BnSCT2- var2_MCS_t- BnSCT2-var2	Forw: ataccgggatacctgca ggtaggcccggccagatg caaaaacgtatagtcaca c (SEQ ID NO: 45) Rev: caatcaattataggcctcg catgctttaattaacgatcg agccatggtttctctgcttct tggtgtcac (SEQ ID NO: 46)	Forw: ccatggctcgatcgtaatt aaagcatgaggcctat aattgattgAgttcctcact cacttctctc (SEQ ID NO: 47) Rev: taagcggccgcaatcgg accgataccggtaggcg ccgccttatatggattttgtg ttactgacc (SEQ ID NO: 48)	Forw: ataccgggatacctgca ggtaggcccggccagatg caaaaacgtatagtcaca c (SEQ ID NO: 45) Rev: taagcggccgcaatcgg accgataccggtaggcg ccgccttatatggattttgtg ttactgacc (SEQ ID NO: 48)
p-BnSETL- var1_MCS_t- BnSETL-var1	Forw: ataccgggatacctgca ggtaggcccggccagtag aagttattagcaactgtac acac (SEQ ID NO: 49) Rev: caatcaattataggcctcg catgctttaattaacgatcg agccatggtttgaccccttc ttgttctc (SEQ ID NO: 50)	Forw: ccatggctcgatcgtaatt aaagcatgaggcctat aattgattgtacatactatat ttttgtttaccttgtg (SEQ ID NO: 51) Rev: taagcggccgcaatcgg accgataccggtaggcg cccaaacacggctcaga gaagc (SEQ ID NO: 52)	Forw: ataccgggatacctgca ggtaggcccggccagtag aagttattagcaactgtac acac (SEQ ID NO: 49) Rev: taagcggccgcaatcgg accgataccggtaggcg cccaaacacggctcaga gaagc (SEQ ID NO: 52)
p-BnSETL- var2_MCS_t- BnSETL-var1	Forw: ataccgggatacctgca ggtaggcccggccatcgg ctacaaatccaactgg (SEQ ID NO: 53) Rev:- caatcaattataggcctcg catgctttaattaacgatcg agccatggtttgtcgttttc tcagcttc (SEQ ID NO: 54)	Forw: ccatggctcgatcgtaatt aaagcatgaggcctat aattgattgtacatactatat ttttgtttaccttgtg (SEQ ID NO: 51) Rev: taagcggccgcaatcgg accgataccggtaggcg cccaaacacggctcaga gaagc (SEQ ID NO: 52)	Forw: ataccgggatacctgca ggtaggcccggccatcgg ctacaaatccaactgg (SEQ ID NO: 53) Rev: taagcggccgcaatcgg accgataccggtaggcg cccaaacacggctcaga gaagc (SEQ ID NO: 52)
p-BnSCP_MCS_t- BnSCP	Forw: ataccgggatacctgca ggtaggcccggccaatca taagttgtatcagttcatc (SEQ-ID No: 73) Rev: caatcaattataggcctcg catgctttaattaacgatcg agccatggtgtttgactcat actggtgta (SEQ-ID No: 74)	Forw: ccatggctcgatcgtaatt aaagcatgaggcctat aattgattgggagaaaat atgggagaagatggaa (SEQ-ID No: 75) Rev: taagcggccgcaatcgg accgataccggtaggcg cctatagactgccaatc aaaccaac (SEQ-ID No: 76)	Forw: ataccgggatacctgca ggtaggcccggccaatca taagttgtatcagttcatc (SEQ-ID No: 73) Rev: taagcggccgcaatcgg accgataccggtaggcg cctatagactgccaatc aaaccaac (SEQ-ID No: 76)
p- BnCRU4_MCS_t- BnCRU4	Forw: ataccgggatacc- tgcaggttagg- ccggccaatgtacatg- gatgctatagatg (SEQ-ID No: 81) Rev: caatcaattatagg- cctcgcgatgcttaat- taacgatcgagccatg- gtagagcatg- tccgtgaacgacg (SEQ-ID No: 82)	Forw: ccatggctcgatcgtaat- taaagcatgagg- cctataaattgattgagcat- gagttagtgtatgtaa- cagcg (SEQ-ID No: 83) Rev: taagcggccgcaatc- ggaccgatacc- ggtaggcccgggaaga- gatggaagcttaca- gaatg (SEQ-ID No: 84)	Forw: ataccgggatacc- tgcaggttagg- ccggccaatgtacatg- gatgctatagatg (SEQ-ID No: 81) Rev: taagcggccgcaatc- ggaccgatacc- ggtaggcccgggaaga- gatggaagcttaca- gaatg (SEQ-ID No: 84)

TABLE 15-continued

Primer pairs used for the generation of promoter-multiple cloning site-terminated-cassettes via Fusion-PCR using native <i>Brassica</i> terminator sequences.			
<i>Brassica napus</i> Promoter/Terminator cassette	Primer pair 1. PCR Promoter	Primer pair 1. PCR Terminator	Primer pair 2. PCR
p-BnMYR_MCS_t- BnMYR	Forw: ataccgggatacctgca ggtaggcccggccacata aaaatatggtgagaaaat atc (SEQ-ID No: 89) Rev: caatcaattataggcctcg catgctttaattaacgatcg agccatgggttaaatgtg agattgtatatatg (SEQ-ID No: 90)	Forw: ccatggctcgatcgtaatt aaagcatgagaggcctat aattgattgaacactttatc cacatcaagatcgc (SEQ-ID No: 91) Rev: taagcggccgcaatcgg accgataccggtaggcg ccgatgtgtgctcgtaattg cactttt (SEQ-ID No: 92)	Forw: ataccgggatacctgca ggtaggcccggccacata aaaatatggtgagaaaat atc (SEQ-ID No: 89) Rev: taagcggccgcaatcgg accgataccggtaggcg ccgatgtgtgctcgtaattg cactttt (SEQ-ID No: 92)
p-BnMDP_MCS_t- BnMDP	Forw: ataccgggatacctgca ggtaggcccggccatgcg agagagaagaatgaa ataag (SEQ-ID No: 99) Rev: caatcaattataggcctcg catgctttaattaacgatcg agccatggcttttgagattg tatatatgaatg (SEQ- ID No: 100)	Forw: ccatggctcgatcgtaatt aaagcatgagaggcctat aattgattgatttctctaact aagaaactttgtag (SEQ-ID No: 101) Rev: taagcggccgcaatcgg accgataccggtaggcg cccgataaagatggtcta atgtccatc (SEQ-ID No: 102)	Forw: ataccgggatacctgca ggtaggcccggccatgcg agagagaagaatgaa ataag (SEQ-ID No: 99) Rev: taagcggccgcaatcgg accgataccggtaggcg cccgataaagatggtcta atgtccatc (SEQ-ID No: 102)
p-BnRTI- 4_MCS_t-BnRTI-4	Forw: ataccgggatacctgca ggtaggcccggccacttg cgccgaagatataccga c (SEQ-ID No: 107) Rev: caatcaattataggcctcg catgctttaattaacgatcg agccatggcttctctctata tatctcttac (SEQ-ID No: 108)	Forw: ccatggctcgatcgtaatt aaagcatgagaggcctat aattgattgatacttcacaa ctttgcataagcc (SEQ-ID No: 109) Rev: taagcggccgcaatcgg accgataccggtaggcg ccaccaaatccgaaacc gaatccgaac (SEQ- ID No: 110)	Forw: ataccgggatacctgca ggtaggcccggccacttg cgccgaagatataccga c (SEQ-ID No: 107) Rev: taagcggccgcaatcgg accgataccggtaggcg ccaccaaatccgaaacc gaatccgaac (SEQ- ID No: 110)
p- BnMTFL_MCS_t- BnMTFL	Forw: ataccgggatacctgca ggtaggcccggccatattc actacttatagagaacac (SEQ-ID No: 115) Rev: caatcaattataggcctcg catgctttaattaacgatcg agccatgggtgaaaaag tttggcgtatttc (SEQ- ID No: 116)	Forw: ccatggctcgatcgtaatt aaagcatgagaggcctat aattgattgacaagaag caacaaagcctaactat (SEQ-ID No: 117) Rev: taagcggccgcaatcgg accgataccggtaggcg ccgatttgagtttctgtgaa gttcaga (SEQ-ID No: 118)	Forw: ataccgggatacctgca ggtaggcccggccatattc actacttatagagaacac (SEQ-ID No: 115) Rev: taagcggccgcaatcgg accgataccggtaggcg ccgatttgagtttctgtgaa gttcaga (SEQ-ID No: 118)
p-BnSRP_MCS_t- BnSRP	Forw: ataccgggatacctgca ggtaggcccggccaaaac ggcaattgattctcgccct g (SEQ-ID No: 127) Rev: caatcaattataggcctcg catgctttaattaacgatcg agccatggagagaggtta ttgaaaccacgt (SEQ- ID No: 128)	Forw: ccatggctcgatcgtaatt aaagcatgagaggcctat aattgattgtttacatattg cccaagaggcataat (SEQ-ID No: 129) Rev: taagcggccgcaatcgg accgataccggtaggcg ccgttaataaaaacggta ccgaatttc (SEQ-ID No: 130)	Forw: ataccgggatacctgca ggtaggcccggccaaaac ggcaattgattctcgccct g (SEQ-ID No: 127) Rev: taagcggccgcaatcgg accgataccggtaggcg ccgttaataaaaacggta ccgaatttc (SEQ-ID No: 130)

TABLE 16

Primer pairs used for the generation of promoter-multiple cloning site-terminated-cassettes via Fusion-PCR using the OCS terminator sequence.

p-BnGRP_MCS_t-OCS	Forw: ataccggga-tacctgcaggttagg-cggccacaaaac-gaaatcatcaaactcgtg (SEQ ID NO: 29) Rev: caatcaatta-taggcctcgcctg-ctttaattaacgatc-gagccatggttttaga-gagccggaattattg (SEQ ID NO: 30)	Forw: ccatg-gctcgcgctgtaaat-taaagcatgagcagg-cctataattgatt-gctgctttaatgagatg-cgagacg (SEQ ID NO: 55) Rev: taagc-ggcccgaatcggacc-gataccggtagg-cgccacaatcag-taaattgaacggagaa-tattattc (SEQ ID NO: 56)	Forw: ataccggga-tacctgcaggttagg-cggccacaaaac-gaaatcatcaaactcgtg (SEQ ID NO: 29) Rev: taagc-ggcccgaatcggacc-gataccggtagg-cgccacaatcag-taaattgaacggagaa-tattattc (SEQ ID NO: 56)
p-BnPEF-var1_MCS_t-OCS	Forw: ataccggga-tacctgcaggttagg-cggccaaaatttat-taacccatctatttggttcac (SEQ ID NO: 33) Rev: caatcaatta-taggcctcgcctg-ctttaattaacgatc-gagccatgggacga-gaaagaaaatg-gtcggag (SEQ ID NO: 34)	Forw: ccatg-gctcgcgctgtaaat-taaagcatgagcagg-cctataattgatt-gctgctttaatgagatg-cgagacg (SEQ ID NO: 55) Rev: taagc-ggcccgaatcggacc-gataccggtagg-cgccacaatcag-taaattgaacggagaa-tattattc (SEQ ID NO: 56)	Forw: ataccggga-tacctgcaggttagg-cggccaaaatttat-taacccatctatttggttcac (SEQ ID NO: 33) Rev: taagc-ggcccgaatcggacc-gataccggtagg-cgccacaatcag-taaattgaacggagaa-tattattc (SEQ ID NO: 56)
p-BnPEF-var2_MCS_t-OCS	Forw: ataccggga-tacctgcaggttagg-cggccagaaattacg-tttgagttcaaattcag (SEQ ID NO: 37) Rev: caatcaatta-taggcctcgcctg-ctttaattaacgatc-gagccatgggacga-gaaataaattggtcgaag (SEQ ID NO: 38)	Forw: ccatg-gctcgcgctgtaaat-taaagcatgagcagg-cctataattgatt-gctgctttaatgagatg-cgagacg (SEQ ID NO: 55) Rev: taagc-ggcccgaatcggacc-gataccggtagg-cgccacaatcag-taaattgaacggagaa-tattattc (SEQ ID NO: 56)	Forw: ataccggga-tacctgcaggttagg-cggccagaaattacg-tttgagttcaaattcag (SEQ ID NO: 37) Rev: taagc-ggcccgaatcggacc-gataccggtagg-cgccacaatcag-taaattgaacggagaa-tattattc (SEQ ID NO: 56)
p-BnSCT2-var1_MCS_t-OCS	Forw: ataccgggatacctgca-gggttaggcggccagatg-caaaaacgtatagtcacac (SEQ ID NO: 41) Rev: caatcaattataggcctcgcctgcatgctttaattaacgatc-agccatggtttctctgcttcttggtgtcac (SEQ ID NO: 42)	Forw: ccatggctcgcgctgtaaat-aaagcatgagcaggcctat-aattgattgctgctttaatgagatgagcagc (SEQ ID NO: 55) Rev: taagcggcccgaatcggaccgataccggtaggcgccacaatcagtaaatgacggagaatattattc (SEQ ID NO: 56)	Forw: ataccgggatacctgca-gggttaggcggccagatg-caaaaacgtatagtcacac (SEQ ID NO: 41) Rev: taagcggcccgaatcggaccgataccggtaggcgccacaatcagtaaatgacggagaatattattc (SEQ ID NO: 56)
p-BnSCT2-var2_MCS_t-OCS	Forw: ataccgggatacctgca-gggttaggcggccagatg-caaaaacgtatagtcacac (SEQ ID NO: 45) Rev: caatcaattataggcctcgcctgcatgctttaattaacgatc-agccatggtttctctgcttcttggtgtcac (SEQ ID NO: 46)	Forw: ccatggctcgcgctgtaaat-aaagcatgagcaggcctat-aattgattgctgctttaatgagatgagcagc (SEQ ID NO: 55) Rev: taagcggcccgaatcggaccgataccggtaggcgccacaatcagtaaatgacggagaatattattc (SEQ ID NO: 56)	Forw: ataccgggatacctgca-gggttaggcggccagatg-caaaaacgtatagtcacac (SEQ ID NO: 45) Rev: taagcggcccgaatcggaccgataccggtaggcgccacaatcagtaaatgacggagaatattattc (SEQ ID NO: 56)
p-BnSETL-var1_MCS_t-OCS	Forw: ataccgggatacctgca-gggttaggcggccagtag-aagttattagcaactgtacacac (SEQ ID NO: 49)	Forw: ccatggctcgcgctgtaaat-aaagcatgagcaggcctat-aattgattgctgctttaatgagatgagcagc (SEQ ID NO: 55)	Forw: ataccgggatacctgca-gggttaggcggccagtag-aagttattagcaactgtacacac (SEQ ID NO: 49)

TABLE 16-continued

Primer pairs used for the generation of promoter-multiple cloning site-terminated-cassettes via Fusion-PCR using the OCS terminator sequence.			
	Rev: caatcaattataggcctcg catgctttaattaacgatcg agccatggtttgacccttc ttgtcttc (SEQ ID NO: 50)	Rev: taagcggccgcaatcgg accgataaccgtaggcg ccacaatcagtaaatga acggagaatattattc (SEQ ID NO: 56)	Rev: taagcggccgcaatcgg accgataaccgtaggcg ccacaatcagtaaatga acggagaatattattc (SEQ ID NO: 56)
p-BnSETL- var2_MCS_t-OCS	Forw: ataccgggataacctgca ggtagggccggccatcgg ctacaatccaactgg (SEQ ID NO: 53) Rev:- caatcaattataggcctcg catgctttaattaacgatcg agccatggtttgacccttc tcagcttc (SEQ ID NO: 54)	Forw: ccatggctcgatcgtaatt aaagcatgagggcctat aatgattgctgctttaatga gatatgcgagacg (SEQ ID NO: 55) Rev: taagcggccgcaatcgg accgataaccgtaggcg ccacaatcagtaaatga acggagaatattattc (SEQ ID NO: 56)	Forw: ataccgggataacctgca ggtagggccggccatcgg ctacaatccaactgg (SEQ ID NO: 53) Rev: taagcggccgcaatcgg accgataaccgtaggcg ccacaatcagtaaatga acggagaatattattc (SEQ ID NO: 56)
p-BnSCP_MCS_t- OCS	Forw: ataccgggataacctg- caggtagggccggc- caatcataagtgtgat- cagttcatc (SEQ ID No: 73) Rev: caatcaatta- taggcctcgcatgctt- taattaacgatcgagc- catgggtttgactca- tactggtgta (SEQ-ID No: 74)	Forw: ccatggctcgatcgtaat- taaagcatgagcagcc- tataattgattgctgctt- taatgagatgacga- gacg (SEQ-ID No: 55) Rev: taagcggccgcaatc- gaccgataccgg- taggcgccacaatcag- taaattgaacggagaa- tattattc (SEQ-ID No: 56)	Forw: ataccgggataacctg- caggtagggccggc- caatcataagtgtgat- cagttcatc (SEQ-ID No: 73) Rev: taagcggccgcaatc- gaccgataccgg- taggcgccacaatcag- taaattgaacggagaa- tattattc (SEQ-ID No: 56)
p- BnCRU4_MCS_t- OCS	Forw: ataccgggataacc- tgcaggttagg- ccggccaatgtacatg- gatgctgttagatg (SEQ-ID No: 81) Rev: caatcaattatagg- cctcgcatgctttaat- taacgatcgagccatg- gttagagcatg- tcctggaacgacg (SEQ-ID No: 82)	Forw: ccatggctcgatcgtaat- taaagcatgagcagc- cctataattgatt- cctataattgatt- gctgctttaatgagatg- cgagacg (SEQ-ID No: 55) Rev: taagcggccgcaatc- ggaccgatacc- ggtagggccacaat- cagtaaatgaacgga- gaattatttc (SEQ-ID No: 56)	Forw: ataccgggataacc- tgcaggttagg- ccggccaatgtacatg- gatgctgttagatg (SEQ-ID No: 81) Rev: taagcggccgcaatc- ggaccgatacc- ggtagggccacaat- cagtaaatgaacgga- gaattatttc (SEQ-ID No: 56)
p-BnMYR_MCS_t- OCS	Forw: ataccgggataacc- tgcaggttagg- ccggccacataaaaa- tatgttgagaaaatc (SEQ-ID No: 89) Rev: caatcaattatagg- cctcgcatgctttaat- taacgatcgagccatg- gggtaaatgttagatt- tgatatatg (SEQ-ID No: 90)	Forw: ccatggctcgatcgtaat- taaagcatgagcagc- cctataattgatt- gctgctttaatgagatg- cgagacg (SEQ-ID No: 55) Rev: taagcggccgcaatc- ggaccgatacc- ggtagggccacaat- cagtaaatgaacgga- gaattatttc (SEQ-ID No: 56)	Forw: ataccgggataacc- tgcaggttagg- ccggccacataaaaa- tatgttgagaaaatc (SEQ-ID No: 89) Rev: taagcggccgcaatc- ggaccgatacc- ggtagggccacaat- cagtaaatgaacgga- gaattatttc (SEQ-ID No: 56)
p-BnMDP_MCS_t- OCS	Forw: ataccgggataacctg- caggtagggccggc- catgagagagaaga- aatgaaataag (SEQ- ID No: 99) Rev: caatcaatta- taggcctcgcatgctt-	Forw: ccatggctcgatcgtaat- taaagcatgagcagc- tataattgattgctgctt- taatgagatgacga- gacg (SEQ-ID No: 55) Rev: taagcggccgcaatc- ggaccgatacc-	Forw: ataccgggataacctg- caggtagggccggc- catgagagagaaga- aatgaaataag (SEQ- ID No: 99) Rev: taagcggccgcaatc- gaccgataccg-

TABLE 16-continued

Primer pairs used for the generation of promoter-multiple cloning site-terminated-cassettes via Fusion-PCR using the OCS terminator sequence.			
	taattaacgatcgagc- catggcttttgagattgta- tatatgaatg (SEQ-ID No: 100)	gaccgataccgg- taggcgccacaatcag- taaattgaacggagaa- tattattc (SEQ-ID No: 56)	taggcgccacaatcag- taaattgaacggagaa- tattattc (SEQ-ID No: 56)
p-BnRTI- 4_MCS_t-OCS	Forw: ataccgggataacc- tgcagggttagg- ccggccact- tgcggccaagatatc- cgac (SEQ-ID No: 107) Rev: caatcaattatagg- cctcgcatgctttaat- taacgatcgagccatg- gcttctctatataatc- tcttac (SEQ-ID No: 108)	Forw: ccatggctcgatcgtaaat- taaagcatgcgagg- octataattgatt- gctgctttaatgagatg- cgagacg (SEQ-ID No: 55) Rev: taagcggccgcaatc- ggaccgataacc- ggtagcgccacaat- cagtaaattgaacgga- gaatattattc (SEQ-ID No: 56)	Forw: ataccgggataacc- tgcagggttagg- ccggccact- tgcggccaagatatc- cgac (SEQ-ID No: 107) Rev: taagcggccgcaatc- ggaccgataacc- ggtagcgccacaat- cagtaaattgaacgga- gaatattattc (SEQ-ID No: 56)
p- BnMTFL_MCS_t- OCS	Forw: ataccgggataacc- tgcagggttagg- ccggccatattcactact- tatagagaacac (SEQ- ID No: 115) Rev: caatcaattatagg- cctcgcatgctttaat- taacgatcgagccatg- gtgtgaaaaagt- ttggcgattttc (SEQ-ID No: 116)	Forw: ccatggctcgatcgtaaat- taaagcatgcgagg- cctataattgatt- gctgctttaatgagatg- cgagacg (SEQ-ID No: 55) Rev: taagcggccgcaatc- ggaccgataacc- ggtagcgccacaat- cagtaaattgaacgga- gaatattattc (SEQ-ID No: 56)	Forw: ataccgggataacc- tgcagggttagg- ccggccatattcactact- tatagagaacac (SEQ- ID No: 115) Rev: taagcggccgcaatc- ggaccgataacc- ggtagcgccacaat- cagtaaattgaacgga- gaatattattc (SEQ-ID No: 56)
p- BnGSTF_MCS_t- OCS	Forw: ataccgggataacc- tgcagggttagg- ccggccagagcattatg- cttccaagcggac (SEQ-ID No: 122) Rev: caatcaattatagg- cctcgcatgctttaat- taacgatcgagccatg- gttctactctaaact- tcgtaactcg (SEQ-ID No: 123)	Forw: ccatggctcgatcgtaaat- taaagcatgcgagg- cctataattgatt- gctgctttaatgagatg- cgagacg (SEQ-ID No: 55) Rev: taagcggccgcaatc- ggaccgataacc- ggtagcgccacaat- cagtaaattgaacgga- gaatattattc (SEQ-ID No: 56)	Forw: ataccgggataacc- tgcagggttagg- ccggccagagcattatg- cttccaagcggac (SEQ-ID No: 122) Rev: taagcggccgcaatc- ggaccgataacc- ggtagcgccacaat- cagtaaattgaacgga- gaatattattc (SEQ-ID No: 56)
p-BnSRP_MCS_t- OCS	Forw: ataccgggataacctg- cagggttagcggcca- aacggcaatt- gattctcgccctg (SEQ- ID No: 127) Rev: caatcaatta- taggcctcgcatgctt- taattaacgatcgagc- catggagagaggttatt- gaaaccacgt (SEQ- ID No: 128)	Forw: ccatggctcgatcgtaaat- taaagcatgcgaggcc- tataattgattgctgctt- taatgagatgcgga- gacg (SEQ-ID No: 55) Rev: taagcggccgcaatcg- gaccgataaccg- taggcgccacaatcag- taaattgaacggagaa- tattattc (SEQ-ID No: 56)	Forw: ataccgggataacctg- cagggttagcggcca- aacggcaatt- gattctcgccctg (SEQ- ID No: 127) Rev: taagcggccgcaatcg- gaccgataaccg- taggcgccacaatcag- taaattgaacggagaa- tattattc (SEQ-ID No: 56)
p-BnLSP_MCS_t- OCS	Forw: ataccgggataacctg- cagggttagcggcca- aatagtcagggttatgaat- cacag (SEQ-ID No: 134) Rev: caatcaatta- taggcctcgcatgctt-	Forw: ccatggctcgatcgtaaat- taaagcatgcgaggcc- tataattgattgctgctt- taatgagatgcgga- gacg (SEQ-ID No: 55) Rev: taagcggccgcaatcg- gaccgataaccg- taggcgccacaatcag- taaattgaacggagaa- tattattc (SEQ-ID No: 56)	Forw: ataccgggataacctg- cagggttagcggcca- aatagtcagggttatgaat- cacag (SEQ-ID No: 134) Rev: taagcggccgcaatcg- gaccgataaccg-

TABLE 16-continued

Primer pairs used for the generation of promoter-multiple cloning site-terminated-cassettes via Fusion-PCR using the OCS terminator sequence.			
	taattaacgatcgagc- catggtcttgaacttctt- gacattact (SEQ-ID No: 135)	gaccgataccgg- taggcgccacaatcag- taaattgaacggagaa- tattattc (SEQ-ID No: 56)	taggcgccacaatcag- taaattgaacggagaa- tattattc (SEQ-ID No: 56):
p-Napin_MCS_t- OCS	Forw: ataccgggataacc- tgcagggttagg- cggccataaggat- gacctaccattcttga (SEQ-ID No: 138) Rev: caatcaattatagg- cctcgcatgctttaat- taacgatcgagccatg- gtgttttaactctgtttgtatt (SEQ-ID No: 139)	Forw: ccatggctcgatcgtaaat- taaagcatgcgagg- cctataattgatt- gctgctttaatgagatg- cgagacg (SEQ-ID No: 55) Rev: taagcggccgcaatc- ggaccgataacc- ggtagcgccacaat- cagtaaatgaacgga- gaatattattc (SEQ-ID No: 56)	Forw: ataccgggataacc- tgcagggttagg- cggccataaggat- gacctaccattcttga (SEQ-ID No: 138) Rev: taagcggccgcaatc- ggaccgataacc- ggtagcgccacaat- cagtaaatgaacgga- gaatattattc (SEQ-ID No: 56)
p-LuPXR_MCS_t- OCS	Forw: ataccgggataacc- tgcagggttagg- cggccacacgggag- gacatagggactact (SEQ-ID No: 142) Rev: caatcaattatagg- cctcgcatgctttaat- taacgatcgagccatg- ggatttatgataaaaatg- tcggg (SEQ-ID No: 143)	Forw: ccatggctcgatcgtaaat- taaagcatgcgagg- cctataattgatt- gctgctttaatgagatg- cgagacg (SEQ-ID No: 55) Rev: taagcggccgcaatc- ggaccgataacc- ggtagcgccacaat- cagtaaatgaacgga- gaatattattc (SEQ-ID No: 56)	Forw: ataccgggataacc- tgcagggttagg- cggccacacgggag- gacatagggactact (SEQ-ID No: 142) Rev: taagcggccgcaatc- ggaccgataacc- ggtagcgccacaat- cagtaaatgaacgga- gaatattattc (SEQ-ID No: 56)

The promoter-terminator cassettes were cloned into the pCR2.1 (Invitrogen) vector according to the manufacturer's manual and subsequently sequenced. In a further step, the delta 6 Desaturase Gene (SEQ ID NO: 68) was introduced via the NcoI, PacI restrictions site between the promoter and terminator sequence.

Using the Multisite Gateway System (Invitrogen), a multiple cloning site (SEQ ID 57) was introduced into each of the three pENTR vectors pENTR/A pENTR/B and pENTR/C via HindIII and KpnI restrictions sites. Into the first position of this MCS, the promoter-delta 6 Desaturase-terminator cassette was cloned via FseI and KasI. Similarly, the DsRed gene was introduced into pENTR/C between the Napin promoter and the OCS terminator. By performing a site specific recombination (LR-reaction), the created pENTR/B, pENTR/C and an empty pENTR/A vector were combined with the pSUN destination vector according to the manufacturers (Invitrogen) Multisite Gateway manual to generate the final binary vectors SEQ ID: 3 pSUN-p-GRPL\_d6Des(Pir)\_t-OCS, SEQ ID: 8 pSUN-p-PEF-var1\_d6Des(Pir)\_t-OCS, SEQ ID: 11 pSUN-p-PEF-var2\_d6Des(Pir)\_t-OCS, SEQ ID: 18 pSUN-p-SCT2-var2\_d6Des(Pir)\_t-OCS, SEQ ID: 24 pSUN-p-SETL-vad\_t-OCS, SEQ ID: 79 pSUN-pBnCRU4\_d6Des(Pir)\_t-OCS, SEQ ID: 87 pSUN-pBnMYR\_d6Des(Pir)\_t-OCS, SEQ ID: 93 pSUN-pBnSETL-var2\_d6Des(Pir)\_t-OCS, SEQ ID: 94 pSUN-pBnSCT2-vad\_d6Des(Pir)\_t-OCS, SEQ ID: 97 pSUN-pBnMDP\_d6Des(Pir)\_t-OCS, SEQ ID: 105 pSUN-pBnRTI-4\_d6Des(Pir)\_t-OCS, SEQ ID: 113 pSUN-pBnMTFL\_d6Des(Pir)\_t-OCS, SEQ ID: 120 pSUN-pBnGSTF\_d6Des(Pir)\_t-OCS, SEQ ID: 132 pSUN-pBnLSP\_d6Des(Pir)\_t-OCS. Similarly, the two binary

vectors SEQ ID: 137 pSUN-pNapin\_d6Des(Pir)\_t-OCS and SEQ ID: 141 pSUN-pLuPXR\_d6Des(Pir)\_t-OCS were cloned as a positive control, that is, these two vectors are known to be capable to drive seed specific expression of PUFA genes, e.g. the delta-6-desaturase SEQ ID NO: 68.

The resulting vectors were subsequently used for the production of transgenic plants. The promoter activity in the transgenic plant seeds was measured based on the expression of delta 6 Desaturase and an observed modification in the lipid pattern of the seeds as described in example 5.

#### Example 4

##### Production of Transgenic Plants

a) Generation of Transgenic Rape Seed Plants (Amended Protocol According to Moloney et al. 1992, Plant Cell Reports, 8:238-242)

For the generation of transgenic rapeseed plants, the binary vectors were transformed into *Agrobacterium tumefaciens* C58C1:pGV2260 (Deblaere et al. 1984, Nucl. Acids. Res. 13: 4777-4788). For the transformation of rapeseed plants (cv. Kumily), a 1:50 dilution of an overnight culture of positive transformed acrobacteria colonies grown in Murashige-Skoog Medium (Murashige and Skoog 1962 Physiol. Plant. 15, 473) supplemented by 3% saccharose (3MS-Medium) was used. Petioles or Hypocotyledones of sterial rapeseed plants were incubated in a petri dish with a 1:50 acrobacterial dilution for 5-10 minutes. This was followed by a tree day cocubation in darkness at 25° C. on 3MS-Medium with 0.8% bacto-Agar. After three days the culture was put on to 16 hours light/8 hours darkness weekly on MS-medium contain-

ing 500 mg/l Claforan (Cefotaxime-Natrium), 100 nM Imazetapyr, 20 mikrom Benzylaminopurin (BAP) and 1.6 g/l Glucose. Growing sprouts were transferred to MS-Medium containing 2% saccharose, 250 mg/l Claforan and 0.8% Bacto-Agar. Even after three weeks no root formation was observed, a growth hormone 2-Indolbutyl acid was added to the medium for enhancing root formation.

Regenerated sprouts have been obtained on 2MS-Medium with Imazetapyr and Claforan and were transferred to the green house for sprouting. After flowering, the mature seeds were harvested and analysed for expression of the Desaturase gene via lipid analysis as described in Qui et al. 2001, J. Biol. Chem. 276, 31561-31566.

#### b) Production of Transgenic Flax Plants

The production of transgenic flax plants can be carried out according to the method of Bell et al., 1999, In Vitro Cell. Dev. Biol. Plant 35(6):456-465 using particle bombardment. Acrobacterial transformation could be carried out according to Mlynarova et al. (1994), Plant Cell Report 13: 282-285.

#### Example 5

##### Lipid Extraction

Lipids can be extracted as described in the standard literature including Ullman, Encyclopedia of Industrial Chemistry, Bd. A2, S. 89-90 and S. 443-613, VCH: Weinheim (1985); Fallon, A., et al., (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, Bd. 17; Rehm et al. (1993) Biotechnology, Bd. 3, Kapitel III: "Product recovery and purification", S. 469-714, VCH: Weinheim; Better, P. A., et al. (1988) Bio-separations: downstream processing for Biotechnology, John Wiley and Sons; Kennedy, J. F., und Cabral, J. M. S. (1992)

Recovery processes for biological Materials, John Wiley and Sons; Shaeiwitz, J. A., und Henry, J. D. (1988) Biochemical Separations, in: Ullmann's Encyclopedia of Industrial Chemistry, Bd. B3; Kapitel 11, S. 1-27, VCH: Weinheim; und Dechow, F. J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.

Alternatively, extraction will be carried out as described in Cahoon et al. (1999) Proc. Natl. Acad. Sci. USA 96 (22): 12935-12940, und Browse et al. (1986) Analytic Biochemistry 152:141-145. Quantitative and qualitative analysis of lipids or fatty acids are described in Christie, William W., Advances in Lipid Methodology, Ayr/Scotland: Oily Press (Oily Press Lipid Library; 2); Christie, William W., Gas Chromatography and Lipids. A Practical Guide—Ayr, Scotland: Oily Press, 1989, Repr. 1992, IX, 307 S. (Oily Press Lipid Library; 1); "Progress in Lipid Research, Oxford: Pergamon Press, 1 (1952)-16 (1977) u.d.T.: Progress in the Chemistry of Fats and Other Lipids CODEN.

Based on the analysed lipids, the expression of the Desaturase can be determined since the lipid pattern of successfully transformed plant seeds will differ from the pattern of control plant seeds. Seed specific expression of a delta-6-desaturase would result in formation of 18:3n-6 (GLA) and/or 18:4n-3 (SDA), depending on whether the delta 6 desaturase uses 18:2n-6 (LA) and/or 18:3n-3 (ALA) as substrate. Surprisingly, not only the two control promoters Napin and LuPXR harbored by the vectors SEQ ID: 137 pSUN-pNapin\_d6Des (Pir)\_t-OCS and SEQ ID: 141 pSUN-pLuPXR\_d6Des(Pir)\_t-OCS were capable to drive seed specific expression of the delta-6-desaturase as indicated by the formation of GLA, but also the promoters of the present invention (FIG. 2). Interestingly, the promoters influenced the ratio of the omega-3 fatty acid SDA to the omega-6 fatty acid GLA.

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<210> SEQ ID NO 4
<211> LENGTH: 174
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

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<400> SEQUENCE: 4

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<210> SEQ ID NO 5
<211> LENGTH: 360
<212> TYPE: DNA

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<213> ORGANISM: Brassica napus

<400> SEQUENCE: 5

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<213> ORGANISM: Brassica napus

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<210> SEQ ID NO 7
<211> LENGTH: 477
<212> TYPE: DNA
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<400> SEQUENCE: 7

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<210> SEQ ID NO 8
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<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
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<400> SEQUENCE: 8

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cgtaatcatg gcaactttt 15079

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<210> SEQ ID NO 12
<211> LENGTH: 121
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

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<400> SEQUENCE: 12

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a 121

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<210> SEQ ID NO 13
<211> LENGTH: 1083
<212> TYPE: DNA

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<213> ORGANISM: Brassica oleracea

<400> SEQUENCE: 13

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gaagatcaac accatcacca ccggaatgg gtgggtccct caggtcacia agtcatcacc    180
gtctcacttg acggccactc tcagtttcgc tccgtccaag acgctgtgga ctccatacca    240
aagaacaata acatgagtat cgttatcaag attgctccag gattttaccg agagaaagtg    300
gtggttccag cgacaaaacc gtacataacg tttaaaggag cgggtcggga cgtgacggtt    360
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caaacagctt ccgtcacagt ctccgctaata ttttctcgg ctagaaacat taccttcacg    480
aatactgcgc cggcaccaat gccgggaatg caagggtggc aggcgggtggc attaaggatc    540
tctggcgaca aagcttactt ttccggctgc ggattttacg gtgcacaaga cactttatgc    600
gacgatgcag gccgtcacta cttcaaggag tgttacattg aaggctctat cgactttatc    660
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cgcatcgtct acgcctacac ctacttcgat gctcttgttg ctcatggtgg ctgggacgat    900
tgggaccata aatccaataa aagcaagacg gcatttttgc gagtgtacaa ttgctatggg    960
ccaggagcag cagccacgac aggcgtatca tgggccagag ctttgacta tgagtcagct    1020
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<210> SEQ ID NO 14

<211> LENGTH: 1019

<212> TYPE: DNA

<213> ORGANISM: Brassica napus

<400> SEQUENCE: 14

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agcaatgctc ttagagagggc aaaagagtaa taaaagagag gagaaaagtt ttgtcaaac    180
atcattgtct ttgagaaagt aagatcctaac tttttttttg ttttgggatg ttaggctttt    240
gaaggctatg ttttttttgc tttcttttct ttgttcttag atcatgtcga aggtgttgaa    300
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tgcttcatga gatttatgta aaatccatcg ttcactgtat caatcttate cattttcttc    420
tgattaatct gcaacgtgca attagtttga tcaacaataa ttagccatgg ggtaaaagga    480
gaaacagagt tgcttatggt gacttggacg aagatttate aaacactctg agctgctgag    540
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ttgtacaaga gattaagggt tgaatgaacg tcgtaaaatg acggttatgc tcgtgagaga    660
atcgctgctt acgataagga cgaattgtaa tttgattggt atcaggttgt taaaagttga    720
gacaaaacgag aaaaaaacga agaacagact aaacaggtgt tacgtttcac attggtttgg    780
ttgtggagcc ttgaagttac tctatttaac cggccaacc ggtccaaccg gtcagggtta    840
caaacactg aagttagccg ccaacacgct tattacgtaa acggtagcca cgtttcgagc    900

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actgcgtttg ctaatttgc ttcactcaaa ttcgcagtct tctttcttcg catttgggct 960
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<210> SEQ ID NO 15
<211> LENGTH: 573
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

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<400> SEQUENCE: 15

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atggtgaaaa acaaaatctc atttacaaga caggaaaaaa aacaagaatg atgaaaggac 180
tctagtctga taattattct gagctcataa ttgagacact gcaagatatg aatttgttaa 240
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tgattcattt gtttcatgga ttatcttcaa tgcatagtcc tgtcaaaaa aaacaccaa 360
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cttactttgt tagctggctc gtctccaaga ccgaatctgt tagcaggctt cccatctggt 480
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<210> SEQ ID NO 16
<211> LENGTH: 996
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

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<400> SEQUENCE: 16

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ctcattgtct ttgagaaagt aagatctaac tttctttttt tttttttttt gggatgttag 240
gcttttgaag gctatgtttt ttttgcttcc ttttctttgt tcttagatca tgtcgaaggt 300
gttgaagtgt tggacgtaat aaatgttatt actcagctgc tacgtttaac tcttctctta 360
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<210> SEQ ID NO 17
<211> LENGTH: 576
<212> TYPE: DNA

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<213> ORGANISM: Brassica napus

<400> SEQUENCE: 17

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caacaagaa ctgttatagc ttctttcagt ttcattatca aacatgaagc agtaccacaca	420
agacctact ttgtagctg gtttgtctcc aagaccgaat ctgtagcag gcttcccatc	480
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<210> SEQ ID NO 18

<211> LENGTH: 15433

<212> TYPE: DNA

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Plasmid

<400> SEQUENCE: 18

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cagtgatcag attgtcggtt cccgccttca gtttaaaacta tcagtgtttg acaggatata	180
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gatgtttgat gttatggagc agcaacgatg ttacgcagca gggcagtcgc cctaaaacaa	480
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aaacttttct cctctctttt attactcttt tctctctcta agagcattgc ttgtgttgg 15060
agttcccaaa cgggttccaa caatgtcatt cacaccaggc ttcgatctat aaggaacaga 15120
tacacatagt caaaagcaca actacaaagt gtgactatac gtttttgcac ctggccggcc 15180
tagtagattt aaattggcct tagtggccaa gcttggcgta atcatggagc ctgctttttt 15240
gtacaaaact gggtaaccgc ctattaggcc acggtccgta cagtgtttaa acgattgacc 15300
tgcaggatac aagtgcgcac agactagcgg ccgctaacc cgggaattac cggtagtagg 15360
cgctactttt ggccgcctca gtagatttaa attggcctta gtggccaagc ttggcgtaat 15420
catggcaact ttt 15433

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&lt;210&gt; SEQ ID NO 19

&lt;211&gt; LENGTH: 172

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<212> TYPE: DNA
<213> ORGANISM: Brassica napus
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (113)..(113)
<223> OTHER INFORMATION: n is a, c, g, or t

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<400> SEQUENCE: 19
tcgagactgg gtatgtgagt gttggtgaat ctggagatgt tgagctcttt tactactttg      60
tgaatcaga gagaaatcca gataaagatc ctctcatgat ttggctaact ggngggcctg      120
gatgcagctc catttgtggt tttctgttg caaatggtcc tttggctttt aa                172

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<210> SEQ ID NO 20
<211> LENGTH: 1401
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

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<400> SEQUENCE: 20
atgagaaatc tttactttct agtcttattt cogttgagca tcttgatttt ggttgatgct      60
tctttgcatg tgaagtatct tcttggctct gaaggctctc ttccttttga gctcgagact      120
gggtatgtga gtggttggtga atctggagat gttgagctct tttactactt tgtgaaatca      180
gagagaaatc cagataaaga tcctctcatg atttggctaa ctggtgggcc tggatgcagc      240
tccatttgtg gtttactctt tgcaaatggt cccttggctt ttaaagggga tgagtataat      300
gggacactgc ctcttttaga gctaacatct ttttcttggc caaaggtggc taacatttta      360
tatttggaat ctctgctggt ttctggatat tcttatgcca aaactcggcg tgctgctgag      420
acgagcgaca ccaaacaaat tcaccaaact gaccagttcc ttaggagttg gtttgtggac      480
cacctgagat ttatatccaa ttcattttac gttggtggag attcatattc cggaagatt      540
gttcacggag ttgtgcaaca gatttcaact ggaaatgaaa aaggtctcgc accactcata      600
aatattcagg gatatgttct tggaaacctc gcagtagta caaacttaga accaaatcat      660
agagtttcat ttgcgcatcg gatgggactt atttcagatg agctccatga gtcacttgaa      720
agaaactgtg gaggcaaat ctttaacgta gatccaagta atgcaaatg tcaaatggg      780
cttctagctt atcatcgggt tatctcagag atatacatag agcagatttt gttaccaaac      840
tgcaaagtag attatgtctt atcagacata tcacaaacct taccaaataat cagaaccagt      900
cgaagaagag aactcaagga gttttcaaga aatgattcat catcgttgcc tcctcctagc      960
tgctttactt ataggtatct tctgtctgcc ttttgggcaa atgatgaaaa tgtacgcaga      1020
gctttaggcg tgaagaaggg ctctcgaaaa tggagtcgat gcaacactca aaacatacca      1080
tatacatatg atattcacia tgccattcca taccacgta ataatagccc taaaggcttc      1140
cgcgctctca tctacagtgg tgatcatgat atgatgatac ctttctcttc aactgaagca      1200
tggatcaaat ctctcaacta ttccattggt gatgactgga gaccttggat gatgagtagc      1260
aatcaagtcg ctggatatac aaggacttat gcaataaga tgacatttgc aacctcaag      1320
ggaggaggac acacagctga gtataatcca gaccaatgct cacttatggt caaaagatgg      1380
attgatggtg aatctctctg a                1401

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<210> SEQ ID NO 21
<211> LENGTH: 1401
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

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<400> SEQUENCE: 21

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atgagaaatc tttactttct agtcttattt ccgttgagca tcttgatttt ggttgatgct 60
tctttgcatg tgaagtatct tcttggctct gaaggtcctc ttccttttga gctcgagact 120
gggtatgtga gtgttggtga atctggagat gttgagctct tttactactt tgtgaaatca 180
gagagaaatc cagataaaga tcctctcatg atttggctaa ctggtgggccc tggatgcagc 240
tccatttgty gttttctggt tgcaaatggt cctttggctt ttaaagggaa tgagtataat 300
gggacactgc ctcttttaga gctaacatct ttttcttggg caaaggtggc taacatttta 360
tatttggaat ctctgctggt ttctggatat tcttatgcca aaactcggcg tgcctgctgag 420
acgagcgaca ccaaacaaat tcaccaaact gaccagttcc ttaggagttg gtttgggac 480
cacctgaggt ttatatccaa ttcattttac gttggtggag attcatattc cgggaagatt 540
gttccaggag ttgtgcaaca gatttcactt ggaaatgaaa aaggtctcac accactcata 600
aatattcagg gatattgtct tggaaacct gcagtagta caaacttaga accaaatcat 660
agagtttcat ttgcgcctcg gatgggactt atttcagatg agctccatga gtcacttgaa 720
agaaactgtg gaggcaaatt ctttaacgta gatccaagta atgcaaaatg tcaaatggg 780
cttctagctt atcatcagtg catctcagag atatacatag agcagatttt gttaccaaac 840
tgcaaatgag attatgtctt agcagacata tcacaaacct taccaaatat cagaaccagt 900
cgaagaagag aactcaagga gttttcaaga aatgattcat catcgttacc tctccaagc 960
tgctttactt ataggtattt tctgtctgcc ttttgggcaa atgatgaaa tgtacgcaga 1020
gctttaggcg tgaagaaggg ctctggaaaa tggagtcgat gcaacactca aaacatacca 1080
tatacatatg atattcacia tgccattcca tctcacgtca ataatagccg taaaggcttc 1140
cgcgctctca tctacagtgg tgatcatgat atgatgatac ctttctcttc aactgaagca 1200
tggatcaaat ctctcaacta ttccattggt gatgactgga gacctggat gatgactagc 1260
aatcaagtcg ctggatatac aaggacctat gcaataaga tgacatttgc aaccatcaag 1320
ggaggaggac aactgctgta gtataatcca gaccaatgct cacttatggt caaaagatgg 1380
attgatggtg aatctctctg a 1401

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&lt;210&gt; SEQ ID NO 22

&lt;211&gt; LENGTH: 1490

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Brassica napus

&lt;400&gt; SEQUENCE: 22

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gtagaagtta ttagcaactt gtacacactt acaactagcc aactgatatg tagaggtaa 60
acatgttaca aactcaaaaa taaaagaaac agtggagaaa atcgagtaac ctgaacaggt 120
gtttgatcaa aagtagaatg tgtgtcacta tctcttggtc gagcataaac acaataaag 180
accctggcct aaccaagctg ctgatccaat ccaagtcaca cacaccctca gctataaatg 240
aaacaaataa actttaacag atgaatacta gctgttgttc acagttctag tgtctcctca 300
ttacgtgaat tcaagctacg atcactatct caactcctac ataacatca gaatgctaca 360
aaactatgca caaaaacaaa agctacatct aatacgtgaa tcaattactc tcatcacaag 420
aaagaagatt tcaatcaccg tcgagaagga ggattcagtt aattgaaatca aagttccgat 480
caaaactgaa gactggtgag cacgaggagc acgaagaaga gtgtctcgaa gatacaacaa 540
gcaagaaate tactgagtga ctctctgaag ttattggcgc gattgagaga atcaatccga 600
attaatttcg gggaaaaaga taaattagat actaagcgat gggcttgggc tgggctaaga 660
aacaggtggc aattgggctg gaggaccocg cgattcatag cttccgatag cccaaaaaaa 720

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aacggataac atatttatcg ggtatttgaa tttcagtgaa ataagatatt ttctttttgt 780
taggaaaatt ttagaaaata atggaaatta aatagcgatt atgttacaag atacgatcag 840
catcgggcag tgcaaatgc tatagcttcc caagatttga tccttttggg ttatctccta 900
atgacaatta gtttaggatt ttgaaactta tattaatact attatccgac aacacttggt 960
tcagcttctt attttaacat tttttgtttt tttctattct tcttcccatc agcattttct 1020
ttttaaaaaa ttgaatactt taacttttta aaaatttcac aatgatcaga tgatattatg 1080
gaagatctca agagttaaat gtatccatct tggggcatta aaaccggtgt acgggatgat 1140
aaatacagac tttatatcat atgatagctc agtaattcat atttatcacg ttgctaaaaa 1200
aattataagg tactagtagt caacaaaatc aattaaagag aaagaaagaa acgcatgtga 1260
agagagttta caactggaaa agtaaaaata aaattaacgc atgttgaatg ctgacatgct 1320
agtatgtcca tgaatccacg tatcaagcgc cattcatcga tcgtcttctc ctttctaaat 1380
gaaaacaact tcacacatca caacaacaa tacacacaag acccctctc tctcgttgct 1440
tctctgccag cgaccaaatc gaagcttgag aagaacaaga aggggtcaaa 1490

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<210> SEQ ID NO 23
<211> LENGTH: 614
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

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<400> SEQUENCE: 23

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tacatactat attttttgtt taccttgtgt tagtttaatg ttcagtgctc tctctttatt 60
gtggcacgct tcttttgtgt atgttgtgct tatacaaagt tgaataaatg gaaagaaaag 120
gaagagtgta atttgttttg ttttaagtgt ttataaatat atatatatag gtcattttaga 180
tagttctagg tttctataaa actctctctc tggaagtaga atctgttttt gagaggatcc 240
agttgcctac taatctcccc caaaaacctt caagcttaac cttctctctc acaacaacag 300
aggaaacaca tctcttgagc tctgagttct cttctttgag catgtctatc gctaaactca 360
tctgccttat agcttccctc ttctctctat ctctctctct caccatttct ctgtaaaact 420
tattctctc cctcagctc tctatctctt ccttcagcat ctcacaatte ccaccataat 480
cgactgagga tgattcaccg tcatcaactt cagactcagc gttgtagtct tcatgagtct 540
cacaagcctt ggaccaagaa gactcatcat cgcaagttga tgatttatca tgatgcttct 600
ctgagccgtg tttg 614

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<210> SEQ ID NO 24
<211> LENGTH: 15920
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Plasmid

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<400> SEQUENCE: 24

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ctatacaaaag ttgatagctt ggcgtaatcg atgtaccgat atcaatttaa attggccggc 60
cgagctccct gcagggggcc cggcgcgct ctagattaat taaaggcctt agttactaat 120
cagtgatcag attgtcgttt cccgccttca gtttaaaacta tcagtgtttg acaggatata 180
ttggcgggta aacctaaag aaaagagcgt ttattagaat aatcggatat ttaaaagggc 240
gtgaaaaggt ttatccgttc gtccatttgt atgtcaatat ccatgataag tcgcgctgta 300
tgtgtttgtt tgaatattca tggaaacgcag tggcggtttt catggcttgt tatgactgtt 360

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t t t t t g g g g t	a c a g t c t a t g	c c t c g g g c a t	c c a a g c a g c a	a g c g c g t t a c	g c c g t g g g t c	420
g a t g t t t g a t	g t t a t g g a g c	a g c a a c a t g	t t a c g c a g c a	g g g c a g t c g c	c c t a a a a c a a	480
a g t t a a a c a t	c a t g g g t g a a	g c g g t c a t c g	c g a g g t g t c	c a c c c a g t g	t e g g a a g t e g	540
t g g g t g t c a t	c g a g c g c c a c	c t c g a a c c g a	c c c t c c t c g c	c g t g c a t c t g	t a t g g t a g c g	600
c c g t t g a c g g	c g g c c t t a a g	c c c c a t t c g g	a c a t c g a c c t	g c t t g t c a c c	g t t a c c g t c c	660
g t c t c g a c g a	g a c c a c g c g c	c g c g c g t t a	t c a a c g a c c t	t c t g g a a a c g	t e c g c c t c c c	720
c c g g c g a g a g	c g a a a t c c t g	c g c g c g g t t g	a g g t g a c g a t	t g t g g t g c a c	g a t g a c a t c a	780
t c c c c t g g c g	c t a t c c g g c c	a a a c g c g a a c	t c c a g t t c g g	c g a a t g g c a g	c g t a a t g a t a	840
t t c t g g c g g g	t a t c t t t g a a	c e g g c c a c c a	t e g a c a t t g a	t c t g g c g a t c	c t g c t c a c c a	900
a g g c c c g g g a	g c a t a g c g t g	g c c c t c g t c g	g c c c c g c g g c	c g a g g a a c t t	t t c g a c c c g g	960
t g c c g g a a c a	g g a t c t g t t c	g a a g c a c t g a	a c g a g a c g c t	g a c c c t g t g g	a a c t c c c c g c	1020
c g g a t t g g g c	g g g c g a t g a g	c g c a a t g t g g	t c c t t a c g c t	g a g c c g g a t t	t g g t a c t c g g	1080
c g g t t a c c g g	c a a g a t c g c g	c c g a a g g a t g	t e g c c g c c g a	c t g g g c g a t g	g a g c g c c t t c	1140
c g g c g c a a t a	c c a g c c c g t g	a t c c t c g a a g	c g c g c c a a g c	c t a t c t g g g c	c a a g a a g a a g	1200
a c c g t c t c g c	g t c c c g g g c c	g a c c a g c t c g	a a g a a t t t g t	c c a c t a t g t c	a a g g g c g a g a	1260
t c a c g a a g g t	c g t t g g c a a a	t a a t g t c t a g	c t a g a a a t t c	g t t c a a g c c g	a c g c c g c t t c	1320
g c g g c g c g g c	t t a a c t a a g	c g t t a g a t g c	a c t a a g c a c a	t a a t t g c t c a	c a g c c a a a c t	1380
a t c g a t g a g t	t g a a g g a c c c	c g t a g a a a a g	a t c a a a g g a t	c t t c t t g a g a	t c c t t t t t t t	1440
c t g c g c g t a a	t c t g c t g c t t	g c a a a c a a a a	a a a c c a c c g c	t a c c a g c g g t	g g t t t g t t t g	1500
c c g g a t c a a g	a g t a c c a a c	t c t t t t t c c g	a a g g t a a c t g	g c t t c a g c a g	a g c g c a g a t a	1560
c c a a a t a c t g	t c c t t c t a g t	g t a g c o g t a g	t t a g g c c a c c	a c t t c a a g a a	c t c t g t a g c a	1620
c c g c c t a c a t	a c c t c g c t c t	g c t a a t c c t g	t t a c c a g t g g	c t g c t g c c a g	t g g c g a t a a g	1680
t e g t g t c t t a	c e g g g t t g g a	c t c a a g a c g a	t a g t t a c c g g	a t a a g g c g c a	g c g g t c g g g c	1740
t g a a c g g g g g	g t t c g t g c a c	a c a g c c c a g c	t t g g a g c g a a	c g a c c t a c a c	c g a a c t g a g a	1800
t a c c t a c a g c	g t g a g c t a t g	a g a a a g c g c c	a c g c t t c c c g	a a g g g a g a a a	g g c g g a c a g g	1860
t a t c c g g t a a	g c g g c a g g t	c g g a a c a g g a	g a g c g c a c g a	g g g a g c t t c c	a g g g g g a a a c	1920
g c c t g g t a t c	t t t a t a g t c c	t g t c g g g t t t	c g c c a c c t c t	g a c t t g a g c g	t e g a t t t t t g	1980
t g a t g c t c g t	c a g g g g g g c g	g a g c c t a t g g	a a a a a c g c c a	g c a a c g c g g c	c t t t t t a c g g	2040
t t c c t g g c e t	t t t g t g g c c	t t t t g c t c a c	a t g t t c t t t c	c t g c g t t a t c	c c c t g a t t c t	2100
g t g g a t a a c c	g t a t t a c c g c	c t t t g a g t g a	g c t g a t a c c g	c t c g c c g c a g	c c g a a c g a c c	2160
g a g c g c a g c g	a g t c a g t g a g	c g a g g a a g c g	g a a g a g c g c c	t g a t g c g g t a	t t t t c t c c t t	2220
a c g c a t c t g t	g c g g t a t t t c	a c a c c g c a t a	g g c c g c g a t a	g g c c g a c g c g	a a g c g g c g g g	2280
g c g t a g g g a g	c g c a g c g a c c	g a a g g g t a g g	c g c t t t t t g c	a g c t c t t c g g	c t g t g c g c t g	2340
g c c a g a c a g t	t a t g c a c a g g	c c a g g c g g g t	t t t a a g a g t t	t t a a t a a g t t	t t a a a g a g t t	2400
t t a g g c g g a a	a a a t c g c c t t	t t t t c t c t t t	t a t a t c a g t c	a c t t a c a t g t	g t g a c c g g t t	2460
c c c a a t g t a c	g g c t t t g g g t	t c c c a a t g t a	c g g g t t c c g g	t t c c c a a t g t	a c g g c t t t g g	2520
g t t c c c a a t g	t a c g t g c t a t	c c a c a g g a a a	g a g a c c t t t t	c g a c c t t t t t	c c c c t g c t a g	2580
g g c a a t t t g c	c c t a g e a t c t	g c t c c g t a c a	t t a g g a a c c g	g c g g a t g c t t	c g c c c t e g a t	2640
c a g g t t g c g g	t a g c g c a t g a	c t a g g a t c g g	g c c a g c c t g c	c c c g c c t c c t	c c t t c a a a t c	2700
g t a c t c c g g c	a g g t c a t t t g	a c c c g a t c a g	c t t g c g c a c g	g t g a a a c a g a	a c t t c t t g a a	2760

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ctctccggcg	ctgccactgc	gttcgtagat	cgtcttgaac	aaccatctgg	cttctgcctt	2820
gcctgcggcg	cggcgtgcca	ggcggtagag	aaaacggccg	atgccggggg	cgatcaaaaa	2880
gtaatcgggg	tgaaccgtca	gcacgtcccg	gttcttgect	tctgtgatct	cgcggtacat	2940
ccaatcagca	agctcgatct	cgatgtactc	eggccgcccg	gtttcgctct	ttacgatctt	3000
gtagcggcta	atcaaggctt	caccctcgga	taccgtcacc	aggcggccgt	tcttgacctt	3060
cttggtagcg	tgcattggca	cgtgcgtggg	gtttaaccga	atgcaggttt	ctaccaggtc	3120
gtctttctgc	tttccgccat	cggtcgcg	gcagaacttg	agtacgtccg	caacgtgtgg	3180
acggaacacg	cgcccgggct	tgtctccctt	cccttcccgg	tatcgggtca	tggattcggg	3240
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gcctgcggaa	acctctacgt	gcccgtctgg	aaactcgtag	cggtacacct	cgccagctcg	3360
tcggtcacgc	ttcgacagac	ggaaaacggc	cacgtccatg	atgctgcgac	tatcgggggt	3420
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cctaategac	ggcgcaccgg	ctgccggcgg	ttgccgggat	tctttgcgga	ttcgatcagc	3540
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ctgcgcggcc	ttcaacttct	ccaccaggtc	atcaccacgc	gccgcgcgca	tttgtaaccg	3660
gcccgatggt	ttgcgaccgc	tcacgcgat	tcctcgggct	tgggggttcc	agtgcattg	3720
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gggcattcca	cggcgtcggt	gcctgggtgt	tcttgatttt	ccatgccgcc	tcctttagcc	3840
gctaaaaatc	atctactcat	ttattcattt	gctcatttac	tctggtagct	gcgcgatgta	3900
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ggccaacggt	gcagccttgc	tgctcgtgc	gctcggacgg	ccggcaacta	gcgtgtttgt	4080
gcttttgctc	atcttctctt	tacctcatta	actcaaatga	gttttgattt	aatttcagcg	4140
gccagcgctt	ggacctcgcg	ggcagcgtcg	ccctcggggt	ctgattcaag	aacggttgtg	4200
ccggcggcgg	cagtgctcgg	gtagctcacg	cgctcgtgga	tacgggactc	aagaatgggc	4260
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cgcgacacga	caaaggccgc	ttgtagcctt	ccatccgtga	cctcaatgcg	ctgcttaacc	4380
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gaccaaactc aagctgagga aaacgacaaa	2010

&lt;210&gt; SEQ ID NO 26

&lt;211&gt; LENGTH: 120

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Brassica napus

&lt;400&gt; SEQUENCE: 26

ttaagcgaga agacagctga ggagcctatg acgccaattg aatcaacctt ttccttggat	60
gtaaccacaa agttagactg ggaaacaatt gggaaaatac tatccaaagg ccatagtcga	120

&lt;210&gt; SEQ ID NO 27

&lt;211&gt; LENGTH: 1512

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Brassica napus

&lt;400&gt; SEQUENCE: 27

atggttgttc ttagcatggt ggcgttggtg aaaacagctt attctttgaa cagcttcgtc	60
tttgaggcgg aagacattgt attcggttcg ccttggtggt tcgccgtcgt cggcgtggcg	120
tgtctctcgc ttctctctgc cgggataatg tctggactca cgctcggact aatgtccctt	180
ggtctcgtcg agcttgagat tctccagcag agtggttctt ccgtggagaa aaagcaggcc	240
gctgctatct taccagtggg taagaagcag catcaacttc ttgtgactct gcttctatgc	300
aatgcagctg ccatggagge acttcctata tgtttggata agatatttca cccctttgtg	360
gctgttttac tctcagttac ttttgaactt gcctttggag agatcattcc acaagctata	420
tgctcgagat atggacttgc tgttggcgct aatttcttgt ggttggttcg cattttgatg	480

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ataatctgct atcccattgc ttaccctatt ggaaagggtc ttgatgccgt gatcgggcat	540
aataacacac tgtttaggcg agctcagctg aaagctctcg tctcaattca cagccaagag	600
gctggaag gaggtgaact gacacacgag gaaacaatga ttataagcgg agccttgat	660
ttgagcgaga agacggctga ggaggctatg acgccaattg aatcaacttt ttccttgat	720
gtaactacaa agttagactg ggaaacaatt ggaaaaatc tatccaaagg ccatagtcga	780
atccctgct acttagggaa tccaaaaaac atcattgggc ttttactggt gaagagtctt	840
ctaactgtac gagcggaagc agagaccccc ataagttctg tttccattag gaagatcca	900
agggttccat cagatatgcc attgtatgat attctcaacg agtttcaaaa ggggaacagt	960
cacatggcgc cggttgtcaa agtcaaagat aaagataaaa agaagaacat gcagttgatg	1020
agtaatgggg aaccacccaa ggaggaatat atgaactcat actcgagtcc tcttctaaca	1080
gctcctttgc ttaagcatgt ggatgaaagg catcatgatg ttgtggtggt tgatattgat	1140
aaagcaccia cacatgtgga aactaggggg agaaatttcc aacagaacgg ccttgtgaca	1200
aggtgggact tgccgcgctt gttggaagat aacgaggatg cagaagtat aggcacatc	1260
acgttagaag atgtctttga agaacttcta caagcagaga tcgtggatga aaccgacgtt	1320
tacattgatg tacataaaag ggtacgctg gctgctgcag cagcagcggc tgtatcatcc	1380
ataacacgag cttcgccagt ggagtatcaa agcaaggtag gagtaacggt gaagaagctt	1440
gtgggtaaag aagcacgaag taccaagaaa tcaaaaacca cggagcctct tttagcagaa	1500
tcatatagat aa	1512

&lt;210&gt; SEQ ID NO 28

&lt;211&gt; LENGTH: 1512

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Brassica napus

&lt;400&gt; SEQUENCE: 28

atgggtgttc tgagcatggt agtcctcgta aaagcagctt attcggtgaa cagctttgtc	60
ttcgaggcgg aagacatccg attcggttcc ccgtgggtgt tcgtcgtcgt cgggtgtagc	120
tgtctcctcg ttctcttcgc cgggataatg tctggcttaa cgctcggatt aatgtccctt	180
ggtctcgtcg agctcagat tctccagcag agtggttcct cctccgagaa aaaacaagcc	240
gctgctatct taccagtgtg taagaagcag catcaactgc ttgtgactct gcttctatgc	300
aatgcagctg ccatggagge acttcctata tgtcttgata agatcttcca tccctttgtg	360
gctgttttgc tctctgttac ttttgttctt gcttttgggg agataattcc acaagcgata	420
tgctcgaggt atgggcttgc tgttggggct aactttttgt ggctgggttcg cattttgatg	480
atactctgct atcctatcgc ttaccctata ggcaagggtc ttgatgcggt aatgggcat	540
aatgacacac tgtttaggcg agctcagctg aaagcacttg tctcaatgca cagccaggag	600
gctggaag gaggtgaact gacacacgag gaaacaatga ttataagcgg agccttgat	660
ctgagtgaga agacagctga ggaggctatg acgccaattg aatcaacatt ttccttgat	720
gtaactacaa agctaaactg ggaaacaatt ggaaaaatc tttccagagg acatagccgg	780
atcccagtat acttagggaa tccaaaaaac atcattgggc ttctattggt taagagtctt	840
ctaactgtac gagcgaaaac agaaacatca gtaagttctg tttccatcag gaagatcca	900
agggttccat cagatatgcc attgtatgat atcctcaacg agtttcaaaa ggggaacagt	960
cacatggcgc cggttgtcaa ggtcaaagat aaagataaaa agaagaacat gcagttgatg	1020
agtaatgggg aaccacccaa ggaggaatat atgaactcat actcgagtcc tcttctaaca	1080

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gctcctttgc ttaagcatgt ggatgaaagg catcatgatg ttgtggtggt tgatattgat 1140
aaagcaccaa cacatgtgga aactaggggg agaaatttcc aacagaacgg ccttgtgaca 1200
aggtagggact tgccgcgttt gttggaagat aacgaggatg cagaagtat aggcacatc 1260
acgttagaag atgtctttga agaacttcta caagcagaga tcgtggatga aaccgacgtt 1320
tacattgatg tacataaaag ggtacgcgtg gctgctgcag cagcagcggc tgtatcatcc 1380
ataaacacgag cttcgcagc ggagtatcaa agcaaggtag gagtaacggg gaagaagcct 1440
gtgggtaaag aagcacgaag taccaagaaa tcaaaaacca cggagcctct tttagcagaa 1500
tcatatagat aa 1512

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<210> SEQ ID NO 29
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

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<400> SEQUENCE: 29
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ataccggga tacctgcagg ttaggcggc cacaaaacga aatcatcaaa tcgtg 55
```

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<210> SEQ ID NO 30
<211> LENGTH: 69
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

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```
<400> SEQUENCE: 30
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caatcaatta taggcctcgc atgctttaat taacgatcga gccatggttt tagagagccg 60
gaattattg 69
```

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<210> SEQ ID NO 31
<211> LENGTH: 77
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

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<400> SEQUENCE: 31
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ccatggctcg atcgtaatt aaagcatgcg aggcctataa ttgattgttt ctctcttag 60
tttgtaaata atctatc 77
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<210> SEQ ID NO 32
<211> LENGTH: 65
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

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<400> SEQUENCE: 32
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taagcgccg caatcggacc gataccggta ggcgccgatt atctacctaa cctaacaac 60
aaaag 65
```

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<210> SEQ ID NO 33
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

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<400> SEQUENCE: 33  
ataccggga tacctgcagg ttaggccgcg caaatttatt aacctatcta tttgttcac 59

<210> SEQ ID NO 34  
<211> LENGTH: 70  
<212> TYPE: DNA  
<213> ORGANISM: Artificial sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 34  
caatcaatta taggcctcgc atgctttaat taacgatcga gccatgggac gagaaagaaa 60  
atggtcggag 70

<210> SEQ ID NO 35  
<211> LENGTH: 73  
<212> TYPE: DNA  
<213> ORGANISM: Artificial sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 35  
ccatggctcg atcgtaatt aaagcatgcg aggcctataa ttgattgtaa ggaatcaact 60  
tcaaatgctt ttc 73

<210> SEQ ID NO 36  
<211> LENGTH: 58  
<212> TYPE: DNA  
<213> ORGANISM: Artificial sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 36  
taagcggccg caatcggacc gataccgcta ggcgccgacg ttaagcgaga gtggatag 58

<210> SEQ ID NO 37  
<211> LENGTH: 57  
<212> TYPE: DNA  
<213> ORGANISM: Artificial sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 37  
ataccggga tacctgcagg ttaggccgcg cagaattacg tttgagttca aattcag 57

<210> SEQ ID NO 38  
<211> LENGTH: 69  
<212> TYPE: DNA  
<213> ORGANISM: Artificial sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 38  
caatcaatta taggcctcgc atgctttaat taacgatcga gccatgggac gagaaataaa 60  
tggtcgaag 69

<210> SEQ ID NO 39  
<211> LENGTH: 72  
<212> TYPE: DNA  
<213> ORGANISM: Artificial sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 39

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ccatggctcg atcgtaatt aaagcatgcg aggcctataa ttgattgtag gaatcaactt 60

caaatgcttt tc 72

<210> SEQ ID NO 40  
 <211> LENGTH: 57  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 40

taagcggcgc caatcggacc gataccggta ggcgccagag gtgaggagga gttgcac 57

<210> SEQ ID NO 41  
 <211> LENGTH: 55  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 41

ataccggga tacctgcagg ttagcggc cagatgcaaa aacgtatagt cacac 55

<210> SEQ ID NO 42  
 <211> LENGTH: 69  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 42

caatcaatta taggcctcgc atgcttaat taacgatcga gccatggttt ctctgcttct 60

tggtgtcac 69

<210> SEQ ID NO 43  
 <211> LENGTH: 68  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 43

ccatggctcg atcgtaatt aaagcatgcg aggcctataa ttgattgagt tcctcactca 60

cttctctc 68

<210> SEQ ID NO 44  
 <211> LENGTH: 64  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 44

taagcggcgc caatcggacc gataccggta ggcgccgect tatatggatt ttgtgttact 60

gacc 64

<210> SEQ ID NO 45  
 <211> LENGTH: 55  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

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<400> SEQUENCE: 45

ataccggga tacctgcagg ttaggccgcg cagatgcaa aacgtatagt cacac 55

<210> SEQ ID NO 46

<211> LENGTH: 69

<212> TYPE: DNA

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 46

caatcaatta taggcctcgc atgctttaat taacgatcga gccatggttt ctctgcttct 60

tggtgtcac 69

<210> SEQ ID NO 47

<211> LENGTH: 68

<212> TYPE: DNA

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 47

ccatggctcg atcgtaatt aaagcatgcg aggcotataa ttgattgagt tctcactca 60

cttctctc 68

<210> SEQ ID NO 48

<211> LENGTH: 64

<212> TYPE: DNA

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 48

taagcggccg caatcggacc gataccgcta ggcgccct tatatggatt ttgtgttact 60

gacc 64

<210> SEQ ID NO 49

<211> LENGTH: 60

<212> TYPE: DNA

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 49

ataccggga tacctgcagg ttaggccgcg cagtagaagt tattagcaac ttgtacacac 60

<210> SEQ ID NO 50

<211> LENGTH: 68

<212> TYPE: DNA

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 50

caatcaatta taggcctcgc atgctttaat taacgatcga gccatggttt gacccttct 60

tgcttctc 68

<210> SEQ ID NO 51

<211> LENGTH: 76

<212> TYPE: DNA

<213> ORGANISM: Artificial sequence

<220> FEATURE:

<223> OTHER INFORMATION: Primer

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<400> SEQUENCE: 51  
ccatggctcg atcgtaatt aaagcatgcg aggcctataa ttgattgtac atactatatt 60  
ttttgtttac cttgtg 76

<210> SEQ ID NO 52  
<211> LENGTH: 56  
<212> TYPE: DNA  
<213> ORGANISM: Artificial sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 52  
taagcggccg caatcggacc gataccggta ggcgccaaa cacggctcag agaagc 56

<210> SEQ ID NO 53  
<211> LENGTH: 52  
<212> TYPE: DNA  
<213> ORGANISM: Artificial sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 53  
ataccggga tacctgcagg ttaggccgcg catcggtac aaatccaact gg 52

<210> SEQ ID NO 54  
<211> LENGTH: 68  
<212> TYPE: DNA  
<213> ORGANISM: Artificial sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 54  
caatcaatta taggcctcgc atgcttaat taacgatcga gccatggtt gtcgtttcc 60  
tcagcttc 68

<210> SEQ ID NO 55  
<211> LENGTH: 72  
<212> TYPE: DNA  
<213> ORGANISM: Artificial sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 55  
ccatggctcg atcgtaatt aaagcatgcg aggcctataa ttgattgctg ctttaatgag 60  
atatcgaga cg 72

<210> SEQ ID NO 56  
<211> LENGTH: 68  
<212> TYPE: DNA  
<213> ORGANISM: Artificial sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 56  
taagcggccg caatcggacc gataccggta ggcgccaaa tcagtaaatt gaacggagaa 60  
tattattc 68

<210> SEQ ID NO 57  
<211> LENGTH: 161  
<212> TYPE: DNA  
<213> ORGANISM: Artificial sequence  
<220> FEATURE:

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<223> OTHER INFORMATION: Multiple cloning site assembled using long complementary primers

<400> SEQUENCE: 57

aagcttggcc actaaggcca atttaaatct actaggccgg ccaaagtagg cgcctactac 60

cggtaattcc cgggattagc ggccgctagt ctgtgcgcac ttgtatctcg cagggtcaatc 120

gtttaaacac tgtacggacc gtggcctaata aggccggtac c 161

<210> SEQ ID NO 58

<211> LENGTH: 157

<212> TYPE: DNA

<213> ORGANISM: Brassica napus

<400> SEQUENCE: 58

gaacagggga agagaaacga aaaaacacta ctaagaaaaa gaaaaaaacc gggcgtgcag 60

gtgtacagtg aggagaaaat atgggagaag atggaagagt tgaggaaggt agtaggatac 120

agtgttgcaa ggagtgtctac gtatgcagaa gagttaa 157

<210> SEQ ID NO 59

<211> LENGTH: 127

<212> TYPE: DNA

<213> ORGANISM: Brassica napus

<400> SEQUENCE: 59

tcgattcaag acaacgacaa cgccgagatc atttactcgc gggacgcacc tcagtcatga 60

gagggttacc acttgaagt atatacaacg ggtatcagat ctcaccccaa gaagctagaa 120

gtgttaa 127

<210> SEQ ID NO 60

<211> LENGTH: 101

<212> TYPE: DNA

<213> ORGANISM: Brassica napus

<400> SEQUENCE: 60

cttgatcgtt tttctattag ctgtggaag ttgcaacgct aataaggaaa ttacttgcca 60

agagaacgag ccatttcat gtaataaacac tgatcgttta a 101

<210> SEQ ID NO 61

<211> LENGTH: 273

<212> TYPE: DNA

<213> ORGANISM: Brassica napus

<400> SEQUENCE: 61

ttaaataaag atgatctaga gatctattca cgtgattata aaggctcacc ttcaaaactta 60

gtgacgggta tgagagaccg tcttccaatg tcttactctc tcagaatgga gtctttcaac 120

acgctccttc agtcaaatga gacagaaaga tacgaatctc gtccttttcc cgttggtgga 180

tacaactggt cacttattgt gtatcccaac gggaacaggc aggatagtgg ctcagggttc 240

atttcgcttt attagccata gacaactcgg tac 273

<210> SEQ ID NO 62

<211> LENGTH: 237

<212> TYPE: DNA

<213> ORGANISM: Brassica napus

<400> SEQUENCE: 62

ttaagtgcct atgcgacttc tgcagcgaca aagcttatga tcagattcta agtactggta 60

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ttgatcaat cctgcatgtg taaaaagaaa ggcgacgatg gtccaagtaa taatgtagtt 120
gtcgtaatga atatgtgaaa taaataaaaa aagccggaag tatccaaggc tatcatcgct 180
tgatcatatt atgtggtttg tctcgtgcat ggttagaagc gaataaaata gtatcga 237

```

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<210> SEQ ID NO 63
<211> LENGTH: 144
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

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<400> SEQUENCE: 63
ttaaagcagaa caaagccttt gagcgtgctc tagcaaccta tgaccaagac actcctgacc 60
gttggtataa tgttgctaga gctgttggtg gaacaacacc tgatgaagct aagagacaat 120
atgaccttct cgtacggaca tcga 144

```

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<210> SEQ ID NO 64
<211> LENGTH: 186
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

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```

<400> SEQUENCE: 64
tcgatgtgta cgaagagaag ctcgggaaga caaatacttg gccggagatt cttacacact 60
cgcggatctc caccacgttc cttacactta ctacttcctg aagacgggtc atgctggttt 120
ggccaacgac cgtcctaatt tcaaggcgtg gtgggaagac ctttgttctc gtcggttt 180
ccttaa 186

```

```

<210> SEQ ID NO 65
<211> LENGTH: 131
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

```

```

<400> SEQUENCE: 65
ttaaagcgtag agagaagaag caagctcaga ttagctggag tttctttatc agaaaagttt 60
tggcaaggcc cagctttcat ccccttgaag ctattcaccg gagttcactg taacgagcgg 120
agaagaatcg g 131

```

```

<210> SEQ ID NO 66
<211> LENGTH: 83
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

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```

<400> SEQUENCE: 66
tcgattatca tcatgttttg tgataatctt ccgtcagcaa tcgcaaggag tttcagtgac 60
ttttgcatgt tctgggttg agg 83

```

```

<210> SEQ ID NO 67
<211> LENGTH: 164
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

```

```

<400> SEQUENCE: 67
tcgagagcat ttgagcgtg ttcacagat acatagaga taaatggacc atgtgtacgc 60
cagatctgct atgtatatgt tcacaggtct ggccagatg gttgggttcc agagagtgtt 120
caaatattca gtcatagtct caaagcagtc actttcactt ttaa 164

```

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<210> SEQ ID NO 68
<211> LENGTH: 1380

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&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Pythium irregulare

&lt;400&gt; SEQUENCE: 68

```

atggtggacc tcaagcctgg agtgaagcgc ctggtgagct ggaaggagat ccgcgagcac    60
gcgacgcccc cgaccgctg gatcgtgatt caccacaagg tctacgacat ctccaagtgg    120
gactcgaccc cgggtggctc cgtgatgctc acgcaggccg gcgaggacgc cacggacgcc    180
ttcgcggtct tccaccctgc ctcgcgctc aagctgctcg agcagttcta cgtcgcgcac    240
gtggacgaaa cctccaagcg cgagatcgag ggggagccgg cgagcgacga ggagcgcgcg    300
cgcccgagcg gcatcaacga gttcatcgcg tccctaccctc gtctgcgctg caaggtcaag    360
ggcatggggc tctacgacgc cagcgcgctc tactacgctg ggaagctcgt gagcacgttc    420
ggcatcgcgg tgctctcgat ggcatctgc ttcttctca acagtctcgc catgtacatg    480
gtcgccggcg tgattatggg gctcttctac cagcagctcg gatggctggc gcacgacttc    540
ttgcacaacc aggtgtgcga gaaccgcacg ctcggaacc ttatcgctg cctcgtgggc    600
aacgcctggc agggcttcag catgcagtgg tggaagaaca agcacaacct gcaccacgcg    660
gtgcccgaacc tgcacagcgc caaggacgag ggcttcatcg gcgacccgga catcgacacc    720
atgccgctgc tggcgtggtc taaggagatg gcgcgcaagg cgttcgagtc ggcgcacggc    780
ccgttctca tccgcaacca ggcgttctca tacttccgcg tgctgctgct cgcgcgctg    840
agctggctcg cgcagctggt cttctacgtg ttcaccgagt tctcgttcgg catcttcgac    900
aaggctcgagt tgcacggacc ggagaaggcg ggtctgatcg tgcactacat ctggcagctc    960
gcgatcccg acttctgcaa catgagcctg tttgagggcg tggcatactt cctcatgggc   1020
caggcgtcct gcggcttgct cctggcgctg gtgttcagta ttggccacaa cggcatgtcg   1080
gtgtacgagc gcgaaaccaa gccggacttc tggcagctgc aggtgaccac gacgcgcaac   1140
atccgcgctg cggatttcat ggactggctc accggtggt tgaactacca gatcgacct   1200
cacctgttcc cgctcgtgcc gcgccacaac ttgccaaagg tcaacgtgct catcaagtcg   1260
ctatgcaagg agttcgacat cccgttccac gagaccgct tctgggaggg catctacgag   1320
gtcgtggacc acctggcgga catcagcaag gaattcatca ccgagttccc agcgatgtaa   1380

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&lt;210&gt; SEQ ID NO 69

&lt;211&gt; LENGTH: 705

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Discosoma

&lt;400&gt; SEQUENCE: 69

```

atggtgctgct cctccaagaa cgtcatcaag gagttcatgc gcttcaaggt gcgcatggag    60
ggcaccgtga acggccacga gttcgagatc gagggcgagg gcgagggccg cccctacgag    120
ggccacaaca ccgtgaagct gaaggtgacc aagggcggcc ccctgccctt cgcctgggac    180
atcctgtccc cccagttcca gtacggctcc aaggtgtacg tgaagacccc cgcgacatc    240
cccgactaca agaagctgct cttccccgag ggcttcaagt gggagcgctg gatgaacttc    300
gaggacggcg gcgtggtgac cgtgaaccag gactcctccc tgcaggacgg ctgcttcate    360
tacaaggtga agttcatcgg cgtgaacttc ccctccgacg gccccgtaat gcagaagaag    420
accatgggct gggaggcctc caccgagcgc ctgtaccccc gcgacggcgt gctgaagggc    480
gagatccaca aggccctgaa gctgaaggac ggcggccact acctggtgga gttcaagtcc    540
atctacatgg ccaagaagcc cgtgcagctg cccggctact actacgtgga ctccaagctg    600

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gacatcacct cccacaacga ggactacacc atcgtggagc agtacgagcg caccgagggc 660

cgccaccacc tgttcctgct cgagtctaga ggtaccgggt gttaa 705

&lt;210&gt; SEQ ID NO 70

&lt;211&gt; LENGTH: 2052

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Brassica napus

&lt;400&gt; SEQUENCE: 70

atcataagtt gtatcagttc atcaatcttg agaccctagc cctttccagt ctacaaggtc 60

catctgatat ttattcaatg attcactgcg atggattatt gctatgtaa tttaaatctg 120

ataatataga tagaaatctc gcagtttgga atccgttttt gagcctagtc aaatggatcg 180

aactctcgat ttcttacaca gggcattggg atatctatgg ttttgatagc gacaatctat 240

cccgtagaaa ctacaagatc ttgaggtttt gtaataaatt aggacatgaa gaggctgaga 300

tatatgagtt caagactaaa ctctggagaa gtgttgatta ctcttggtcg tattcttggt 360

atgcatggta tgacgaagct gtgtctatgg atggaaacat gtattggttt gttaaaaggg 420

acatagataa ctcccaaaat gaaaacttca tctctgtgtt tgatttttcc agagagatat 480

tcaaagaaac atgctgtctt cctttataa atcgtgatga tgtttggctt ttgccacgcc 540

tatcaggttt cagaggagat aggccttcta agttatctaa agataaatat gggaaatattc 600

agggtggtat tacaacaag gtgactgatg aagttgttcc gtggagcaag tattttaatg 660

tgactctcca atatccctcg agattatccc gtgaatatat caataatatg acattcttca 720

tccacaagac caataggatc atgttatggc gcaaggaaga agatgtcaaa aataaagata 780

tatacgtcaa tgtttacgaa atatgtgaag gtgtggctga gaaactagtt gagacaggac 840

gacatagacg tgggtataag ggttgcatca ctaagattgg ttatgtattt gtaccaagtc 900

tggttccggt tccagagtaa gaggaggctt ctgaggggtg ctcgatctct ttcatacatg 960

tttgcttatt atgttctaac gcactatgca tttcctttgg tgttgcttta aaatactaaa 1020

ccttaaaaca aagctggaaa gattgcagtc tctgattttc ttttttaaac ttttaattaa 1080

ttagcaaaaag aaaataaaag gaactggaac catgtttggt tcttggtaaa atcattttgtg 1140

accatatgag gttggtttgt atcactacta acacacaagt gaggtattta acacacaagt 1200

gaagtatcta ctaatcttga acggtccata tcttcggcat atagtttga tacttaaaac 1260

acaagtgaag tatctattta ctcttgcagc attcatcttc aaaattacat tttgtatttt 1320

ggtaacttaa tcttctatga gttttctgct tgaagttctt aaaacaattc ggttcacata 1380

gattctctgt tttctcttat agtagttgat aatctcatgg ttatagatgc tatgttacct 1440

gcgcatcact tagtggtgaa gttttgatcc taattaaatc aggtttcgaa cacaaccatt 1500

aattatagc tgacaaaaaa aaaaaaaaaa gaacacaacc atttcctttt tcatgactga 1560

ggattaattg aacaagtgga tgatgagaaa gcaaagaggc acgttgcgac ataaaaccat 1620

gcaatcttca gttctcgagc tgtgtcattt gtctttcttt gtgtgttttc tccattttgt 1680

ctctctctaa agaagttttg tgcctcttat tttctccgtc tctaccaacc attgttctct 1740

cctacttgct ctactgaatc taccataaac aggtttgtgt ttttcctttt tctgttttaa 1800

ttaaaccttt tcccacttca aattatagag ttttcatctc tttacattga ttttgtagt 1860

tgattatgga cttatactgg aagatgaaat gaacctaaccc attttatcag aatttggtta 1920

tgtgctcaaa catattagaa attgtgtttg catgaagttt cttctcaaat cacttgggat 1980

taaggcaatt tgtttaaccg ctttttctac tctctttttc tgtgtaaaga taccaccagt 2040

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atgagtcaaa ca 2052

<210> SEQ ID NO 71  
 <211> LENGTH: 587  
 <212> TYPE: DNA  
 <213> ORGANISM: Brassica napus

<400> SEQUENCE: 71

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 gagtgtctacg tatgcagagg agttaaaggc tctttatggt ttcacaggcg tggttgagcc 120  
 tcctcagtc aagtttgatga accaggatag tcatgatatt gcaaatgttt gtgttagact 180  
 tcgcttcctt atgtctgtta ttggaataaa ctagtgtgat ggtgtgcttg tgtgctaggg 240  
 tcagactcct tcaagctca aacatgtaat gtgtagtaaa tctcaacttt ctgtattttt 300  
 ttgtgacttt tgcctagtt ttattgattt ggattttcaa ataatctcct tctatccctt 360  
 tctttaagct gttttctata gcacatttca cctttcaact ttttttgagt gtatggactt 420  
 gttactcttg actcttaaga aagtttgacc caaatgcata agctcctcct tcatataaac 480  
 tagtcctggg atttttaacc aaatcgaacc gaaatgttg tatttttaac cgaatcgaac 540  
 aaaaatttca gttagttttt tggttgggtt gatttggcag gtctata 587

<210> SEQ ID NO 72  
 <211> LENGTH: 773  
 <212> TYPE: DNA  
 <213> ORGANISM: Brassica napus

<400> SEQUENCE: 72

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 tttctccac ttgttgcgc ctgtaaccac gccttcatat cctcagttcc tttttgtctc 180  
 ttcttgcaa actacgcttg tactcaaaag gtcagtagga ctcttcttcc tcctaataaa 240  
 gaaaacaagta gtggaataga gaaagatgaa tattcgtttg aggacgtcaa gcttggtcac 300  
 ggtgtaggca tggccgaatt tgacggggcg gaaccgggtc tcatacagag tgaggaagat 360  
 gaggagatgg cgaagaatc aacgaggatg atagagaaaa tcagggacga gggatatctt 420  
 gagaaagaag tacaagatgg tgaaaagtca ggaaatgcca agccagagaa ggttcaagat 480  
 cagactgcaa agcaagaagc acctaagact ggacatgaag gggagcttga gactactaca 540  
 actgaagctt ctactgaaa ggaagaggaa acatcttcca acgagccgat agaccaaggt 600  
 gtaagtgcgc caagtggaac aggggaagag aaacgaaaaa atactactaa gaaaaagaaa 660  
 aaaaaccggc gtgcaggtgt acagtgagga gaaaatatgg gagaagatgg aagtgttgag 720  
 gaaggtagta ggatacagtg ttgcaaggag tgctacgtat gcagaggagt taa 773

<210> SEQ ID NO 73  
 <211> LENGTH: 55  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 73

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<210> SEQ ID NO 74

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<211> LENGTH: 69  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 74  
  
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 ctggtggta 69  
  
 <210> SEQ ID NO 75  
 <211> LENGTH: 72  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 75  
  
 ccattgctcg atcgtaatt aaagcatgcg aggcctataa ttgattggga gaaaatatgg 60  
 gagaagatgg aa 72  
  
 <210> SEQ ID NO 76  
 <211> LENGTH: 61  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer  
  
 <400> SEQUENCE: 76  
  
 taagcggccg caatcggacc gataccgta ggcgctata gacctgcaa atcaaaccaa 60  
 c 61  
  
 <210> SEQ ID NO 77  
 <211> LENGTH: 1951  
 <212> TYPE: DNA  
 <213> ORGANISM: Brassica napus  
  
 <400> SEQUENCE: 77  
  
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 gttctgtttc tgtaaaaaag aacaaaatga gtggacaaac tgactaagtg acagctggga 120  
 agcacaaggt ggcatgtgga agattggaag aagaccata tatatattaa tattgcctca 180  
 tccttgcaat tatataaagt gaatacagtt tttattttag atgacggcac gcagttggaa 240  
 caagttagtt tccaccaga gttatattgg gcctcgaatg tgggtttagc tctggtctgt 300  
 gtggaatgct tataatggac tgatttataa atgtggccca gacattacca tctttaaattg 360  
 gatgaacaag tttcccctac taaaggagaa gaagacggaa caagttttag aaagaagcat 420  
 ccaagtggty gcacctgagc aagcatgcag ccatacactc gtcacgctcg gttcgtcgcg 480  
 tccgccacat catcacgtgg ctctcacgtg tttacttgag taaaataaaa atgttatgac 540  
 atcgaagctg atgtgtaaga acatgcactt tgatgtgcca tgcaactga aatgtgtcta 600  
 ctctctccat tcacaactca taagctcacc taattctcat cttcactcgt aataattatt 660  
 tcatatttct tcatccacga taaatgattt caaaagagag aatacataat ctgcagcgtc 720  
 agattttatt ttcagtgtaa gacattacat ggtgattaat cacctgattg gaataaccgt 780  
 aataatttgc aagttaacat aacatactaa ttaatctcaa caacgggaat tgcattactt 840  
 tatagaaata tgtgtgtgtg tgtgttataa aagctaattt gccagagtgt tataagggtat 900  
 tctactcgaa aaacaagttt aagagcattt ccaatgtaaa actccatatt ttcctttaa 960

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atggagtaaa aatgaaaata gagtaaaatt gctctaatac tattccattt tccactccat 1020
tatagagtaa tgaacaaaca aaaaataaac tactccattt atgaagtaaa tttcattata 1080
gagtgagata tgaagttgag ttggagcatt ccttactcta tatccacttt tactccattt 1140
tacaggaaaa agtggagttg ggatgaagat cccctaacta atgcataaac aaaaaaacat 1200
agtgcagtgt gaatgtcatt ccgattagcg gtacctattt tcattaattc gatccgtatt 1260
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taagacctca ctgaaagaaa atagaaaaca ctttccttg cgaatttaa ttaatattcc 1380
ctaaaaagca agatctaaac gaaaactttt ttttttgata agtatctaaa cgaaaactgt 1440
aaccaacca atcatattat taatttgtt tagccgaaac catttaatac ttttagaacc 1500
tcgttgattc ttctattttt aacagaatta ggataaataa attaggactg aattatgatg 1560
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tgtagaagcc ttaactcaca attaaagtaa aaaaaaaaag atgggtccaa cctctcttat 1680
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cgagtgccag ctgcaccaac tcaatgcact cgagccgagt cagatcatca agagtgaggg 1800
tggtcgcatt gaggtctggg accaccatgc acctcagctc cgttgctctg gcttcgcctt 1860
tgagcgttcc gtcattgagc ctcagggtct ttacttgecc actttcttga acgcccggaa 1920
actcacgttc gtcgttcacg gacatgctct a 1951

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&lt;210&gt; SEQ ID NO 78

&lt;211&gt; LENGTH: 514

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Brassica napus

&lt;400&gt; SEQUENCE: 78

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acgcctagtt tacaacaacg accgtcgtat agaagcgatc gttgacacag gcatgtaact 180
ctttgctgaa taaaatcata gttaatcttt ctcctttaat tatatatctt tgttaattag 240
aataaaatca taattagtct cttaagctta tatgcttctc atgatttagg tagatttttc 300
agagaaataa ataagaatgc aactagcaat agccaaactt tcacaaaaac attttagttt 360
atttccacca taagcgttgc gagtaaacag agacaaatgc aataaggttt cttcaggtta 420
aaatagtaaa acagaagaaa cgttttttca catgaaatcc ttcattgggt cctcatggtg 480
aactctcttc attctgtaag cttccatctc ttcc 514

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&lt;210&gt; SEQ ID NO 79

&lt;211&gt; LENGTH: 16397

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Plasmid

&lt;400&gt; SEQUENCE: 79

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ctatacaaaag ttgatagctt ggcgtaatcg atgtaccgat atcaatttaa attggccggc 60
cgagctccct gcagggggcc cggcgcgcct ctagattaat taaaggcctt agttactaat 120
cagtgatcag attgtcgttt cccgccttca gtttaaacata tcagtgtttg acaggatata 180
ttggcgggta aacctaaagag aaaagagcgt ttattagaat aatcggatat ttaaaagggc 240

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gtgaaaaggt ttatccgttc gtccatttgt atgtcaatat ccatgataag tgcgctgta	300
tgtgtttgtt tgaatattca tggaaacgcag tggcggtttt catggcttgt tatgactgtt	360
tttttgggtt acagtctatg cctcgggcat ccaagcagca agcgcgttac gccgtgggtc	420
gatgtttgat gttatggagc agcaacgatg ttacgcagca gggcagtcgc cctaaaaaa	480
agttaaacad catgggtgaa gcggctcatc cagaggtgtc caccagctg tcggaagtgc	540
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ccggcgagag cgaaatcctg cgcgcggttg aggtgacgat tgtgggtcac gatgacatca	780
tcccctggcg ctatccggcc aaacgcgaac tccagttcgg cgaatggcag cgtaatgata	840
ttctggcggg tatctttgaa ccggccacca tcgacattga tctggcgatc ctgctacca	900
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tgatgctcgt cagggggggc gagcctatgg aaaaacgcca gcaacgcggc ctttttacgg	2040
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<400> SEQUENCE: 83

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<210> SEQ ID NO 84
<211> LENGTH: 61
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 84

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g 61

<210> SEQ ID NO 85

<211> LENGTH: 1360

<212> TYPE: DNA

<213> ORGANISM: Brassica napus

<400> SEQUENCE: 85

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aactaaaatt ttattataaa acaagaaaat taaaatcata tactattttc tataaattct 180

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tcacccacc aaacctctcc taaaatatca aggctctaaa ccctagattg gcacaagaaa 1260

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<211> LENGTH: 652

<212> TYPE: DNA

<213> ORGANISM: Brassica napus

<400> SEQUENCE: 86

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tcaagtatat attaatgaat aatactttta tgccaagtca agggattgag agaaaaaaaa 180

aaactcaatt taacaggtag atttacatca tccaaccaac cacactgcat atattaatga 240

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<210> SEQ ID NO 87
<211> LENGTH: 14577
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Plasmid

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<400> SEQUENCE: 87

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&lt;211&gt; LENGTH: 1644

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Brassica napus

&lt;400&gt; SEQUENCE: 88

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<220> FEATURE:
<223> OTHER INFORMATION: Primer

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<400> SEQUENCE: 89

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<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
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<400> SEQUENCE: 90

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<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

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<400> SEQUENCE: 91

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<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

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<400> SEQUENCE: 92

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<210> SEQ ID NO 93
<211> LENGTH: 16452
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence

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&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Plasmid

&lt;400&gt; SEQUENCE: 93

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&lt;210&gt; SEQ ID NO 95

&lt;211&gt; LENGTH: 1428

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Brassica napus

&lt;400&gt; SEQUENCE: 95

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<210> SEQ ID NO 96
<211> LENGTH: 483
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

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<400> SEQUENCE: 96

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tcg 483

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<210> SEQ ID NO 97
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<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
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<400> SEQUENCE: 97

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 gtcaaatgac ctgccggagt acgattttaa ggaggaggcg ggcgagctg gcccgatcct 14520  
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gcagatgcta gggcaaatg ccctagcagg ggaaaaaggt cgaaaaggtc tctttcctgt 14640
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gcaagcagca gattacgcgc agaaaaaaag gatctcaaga agatcctttg atcttttcta 15780
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&lt;210&gt; SEQ ID NO 98

&lt;211&gt; LENGTH: 1152

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Brassica napus

&lt;400&gt; SEQUENCE: 98

```

atgaagagtc actacacaaa catcatttat gttgtttttc tcttattttg tcttttgatc 60
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cagcagaaga atggagcgca accaaactca atcctgggag aagcgcatta cttaaataaa 180
gatgatctag agatctatct acgtgattat aaaggctcac cttcaaattt agtgacgggt 240
atgagagacc gtctccaat gtcttactct ctcagaatgg agtctttcaa cagctcctt 300
cagtcaaag agacagagag atacgaatct cgtccttttc ccgttggtgg atacaactgg 360
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tatttagcca tagacaactc gactctcgtt tcttcgcatc aagaggtttt cgcagatctc 480
aggttttacg tattcaaaag gaccgagagg aatttcttca ccgtccaaga tacagatgta 540
tggcgatata atattttcaa aacgatgtgg ggattccctc gggtcctccc tcttgatacc 600
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gtgactgttc attctccctt tgaaagtcca gaacttttca ctgctgctag gaatttcct 720
aaccgaggt tcacctggac tattcagagg ttctccacgc tggctggaga tacgcatctc 780
tctaatacgt tctcggctcg aggaaggaat tggaatatac aagtgaatcc acgtggcct 840

```

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```
tcaacggggg cggaagagc catgtogatg tatcttatcc ttaatgcgaa cgagaaagt 900
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tcgctcttgt ggacaaccat cgaaaggcca atcgatcatt ggttcoactac tccgggatta 1020
ggttggggat acgatgagtt tatctctcta gatgatctca gagatttttg gaaaggttat 1080
gtcatgggtg atgtgttgat agttgaagtc gaaatggagg caatttcttc aaccaagtat 1140
ttccctagtt ag 1152
```

```
<210> SEQ ID NO 99
<211> LENGTH: 57
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer
```

```
<400> SEQUENCE: 99
```

```
ataccggga tacctgcagg ttaggccgcg catgcgagag agaagaaatg aaataag 57
```

```
<210> SEQ ID NO 100
<211> LENGTH: 71
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer
```

```
<400> SEQUENCE: 100
```

```
caatcaatta taggcctcgc atgctttaat taacgatcga gccatggctt ttgagattgt 60
atatatgaat g 71
```

```
<210> SEQ ID NO 101
<211> LENGTH: 73
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer
```

```
<400> SEQUENCE: 101
```

```
ccatggctcg atcgtaatt aaagcatgcg aggctataa ttgattgatt tctctaacta 60
agaaactttg tag 73
```

```
<210> SEQ ID NO 102
<211> LENGTH: 61
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer
```

```
<400> SEQUENCE: 102
```

```
taagcgccg caatcgacc gataccgta ggcgccgat aaagatggtc taatgtccat 60
c 61
```

```
<210> SEQ ID NO 103
<211> LENGTH: 1820
<212> TYPE: DNA
<213> ORGANISM: Brassica napus
```

```
<400> SEQUENCE: 103
```

```
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ctagggtgaa aatgcacttg ggaacatgac attaatgtaa agtgcctatg cgacttttgc 120
```

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```

aggcacgaat ctggtcagat tctaagtggc atttgatcaa tcctgcatgt gtgatgatgg 180
cttctgaaat aaaaatgggtg aaaatgggcc aagtataatg tagtaatgag tatgaaaaat 240
aaaaacgccg gaagcatcta aaatattgta tggtttgat cgtggtagag gtgactaaaa 300
taagtatcaa ctttcatatt tcacaacttt gcataagcca aagaaccoga gcaaatgaaa 360
tctaaaatcc tgcatttagc atccacgtga agatataatga ctgtgcttgg tgaagatata 420
tgactgtgct tgattgtcgg tcgactaatt tatgggtaat caaccgtcag aaatcgaatg 480
taactgtgac gtgttaacaa gagatttaaa tagatttttc catctctaga aagtgcgtat 540
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ttaactccaa agtaaaacaa agagagattg acaaaaaaaaa acaagagag tagtagagag 780
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acctgtgcag gtgtagatata ctgaggcaaa gaaataaatt aactaactac tacatatata 1500
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aagaatcttt cactttgcat cgacgtgtag atatctgact gtcgttcggt taatttatgt 1620
ttaattaacy gtcagaattt acatgtcact gacgtgtgaa caatgtagtt gtgtcttgac 1680
agctacatga gtctttcaaa ataatttggt tccccaacgt cgccaatgat aaagataaat 1740
aacatacata gtacgagttc atttacacct acgttgactc caaagtgaaa caaagagagt 1800
aagagatata tagagagaag 1820

```

&lt;210&gt; SEQ ID NO 104

&lt;211&gt; LENGTH: 572

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Brassica napus

&lt;400&gt; SEQUENCE: 104

```

atacttcaca actttgcata agccaaaaga atcctagggtg aaaaatatat acttggtttt 60
aaacttttaa gaaattcatt agcatccacg tgagatttca gctctatttg ggtatttcta 120
aattttattc atgtttagat tttttagagt tcggataacc catttagtta ttttaaaaat 180
tttaaaattt attatatatt ttaaaattct caaaatctat aaataaaata aaatattaca 240
tataaatcta actaacatata gtcaaaatc ataaatttaa catataaatt gatttggttc 300
agatatttgg atagagaatc aataaatatt tcaagtagtt ttagcgttct gagtatattt 360
taactatttt agataaatta aaggcatctt atatattttg gatgtttcta atatacagta 420

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aatctaaaaa ttatataata tatttcogta catttaggta cccaaaatat ttgggttcga 480
gtcgaattcg gttttagttt tgtaggtacc aaaattttga acccgtttga atatttaatc 540
aattttggtt cggattcggg ttccgatttg gt 572

```

```

<210> SEQ ID NO 105
<211> LENGTH: 16266
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Plasmid

```

```

<400> SEQUENCE: 105

```

```

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cagtgatcag attgtcgttt cccgccttca gtttaacta tcagtgtttg acaggatata 180
ttggcgggta aacctaaagag aaaagagcgt ttattagaat aatcggatat taaaaggggc 240
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tgtgtttgtt tgaatattca tggaaocgag tggcgggttt catggcttgt tatgactgtt 360
tttttggggt acagtctatg cctcgggcat ccaagcagca agcgcgttac gccgtgggtc 420
gatgtttgat gttatggagc agcaacgatg ttacgcagca gggcagtcgc cctaaaacaa 480
agttaaacat catgggtgaa gcggtcatcg ccgaggtgtc caccagctg tcggaagtcg 540
tgggtgtcat cgagccacc ctcgaaccga cctcctcgc cgtgcatctg tatggtagcg 600
ccgttgacgg cggccttaag cccattcgg acatcgacct gcttgcacc gttaccgtcc 660
gtctcgacga gaccacgcgc cgcgcgctta tcaacgacct tctggaaacg tccgcctccc 720
ccggcgagag cgaatcctg cgcgcggttg aggtgacgat tgtgggtcac gatgacatca 780
tcccctggcg ctatccggcc aaacgcgaac tccagttcgg cgaatggcag cgtaatgata 840
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gagcgcagcg	agtcagttag	cgaggaagcg	gaagagcgcc	tgatgcggta	ttttctcctt	2220
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ttaggcggaa	aaatcgccct	ttttctcttt	tatatcagtc	acttacatgt	gtgaccggtt	2460
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cttgggtacc ggctattag gccacggtcc gtacagtgtt taaacgattg acctgcagga 16140
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<210> SEQ ID NO 106
<211> LENGTH: 300
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

```

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<400> SEQUENCE: 106

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gaggttggct tcagttattg tgcgcctttg atacgtccga cgttttgttt tagacgatgc 180
cgtgaggaca agggagctaa aggtggagaa tgccgttggg gagatgagtt taatgttaag 240
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```

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<210> SEQ ID NO 107
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

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<400> SEQUENCE: 107

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```

<210> SEQ ID NO 108
<211> LENGTH: 69
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

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<400> SEQUENCE: 108

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```

<210> SEQ ID NO 109
<211> LENGTH: 71
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

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<400> SEQUENCE: 109

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ttgcataagc c 71

```

```

<210> SEQ ID NO 110
<211> LENGTH: 61
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

```

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<400> SEQUENCE: 110

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```

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c 61

```

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```

<210> SEQ ID NO 111
<211> LENGTH: 1335
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

<400> SEQUENCE: 111
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tgtaaaaatg accaaacttg tccaaagctt tcagttgcag aagagaagag aagacagttc    180
ataacatata tataagtctt aataacaaaa tgaaacacca aactccaatc gcagacaact    240
ctttcaccct ctttctctcg tttgtctcac aaatccttga ctctttgctt tgcaatattg    300
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gagtaagcta caaagctaca cttttgttt tgtggatata aattaattaa tcctcacaac    420
ctgagatfff tgataagaag aaatcttgat agtcaatgaa aatcgtagg taacatagac    480
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cgtgctgtga ctattgacta gagaccagac tgttctctgga agtagttgac tagaggcctg    600
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gcaaacacaa tcttttgagg tgattagttt ggatctttga tactcatttc cacaatattt   1140
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gcaaagatat ctttgccaac tggcactata ccttacctca aatcctcctt tataaagagc   1260
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ccaaactttt tcaca                                     1335

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```

<210> SEQ ID NO 112
<211> LENGTH: 521
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

<400> SEQUENCE: 112
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atfttctcca gccttagagc agcattatcg ataacaaact gctatagttt tttttaaaaa   180
attatgtagg tattataatt atctaagtac attctagctt tctagtatta attgaatcaa   240
taataaagtg acaggtgcta tatgaggttt tagaccgcat acaaaaagtg tttaaattgg   300
gttcttgact taatatatcc tcaactcttt aattttggca taattaagct ttacttttat   360
tttgccataa taaatattaa actctttcaa aaatctgctt aaatcctaaa atttctatft   420
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&lt;210&gt; SEQ ID NO 113

&lt;211&gt; LENGTH: 15776

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Plasmid

&lt;400&gt; SEQUENCE: 113

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&lt;210&gt; SEQ ID NO 114

&lt;211&gt; LENGTH: 303

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Brassica napus

&lt;400&gt; SEQUENCE: 114

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gctagagctg ttggtggaac aacacctgat gaagctaaga gacaatatga ccttctcgta 180
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<210> SEQ ID NO 115
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

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<400> SEQUENCE: 115

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<210> SEQ ID NO 116
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

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<400> SEQUENCE: 116

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<210> SEQ ID NO 117
<211> LENGTH: 74
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

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<400> SEQUENCE: 117

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aaagcctaaa ctat 74

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<210> SEQ ID NO 118
<211> LENGTH: 61
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

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<400> SEQUENCE: 118

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a 61

```

```

<210> SEQ ID NO 119
<211> LENGTH: 1565
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

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<400> SEQUENCE: 119

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cggatcttta atactgttga tggcaccttg cgacaagagg taactagtca tcgaaagcct 180
ttctctttaa gctgatttgg tggtttagta gtcactttct tgaggatgaa tgaattatta 240
tgttattatg ttaggaaatc tcaaagttag ttttgatcct ttatagtaat aatattttgc 300
gagtttggag tccatgggtt cagtaatggc aaaacgtgtg tatgtgaatg tacaggttag 360

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gtgaa 1565

```

```

<210> SEQ ID NO 120
<211> LENGTH: 16007
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Plasmid

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<400> SEQUENCE: 120

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tatgtaacga caactcatca tcacaaggat aagatcccag ccccatcaac gtactcggaa 15000
cagggatccc cgtaagctca acaaacctac ccaattcatc gctagaattc aaacaaccac 15060

```

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```

caccaacata caacacaggc ttcttagact cagaaatcaa cctaacaatc tgctccaaat 15120
gagaatcttc cggaggttta ggcatcctag acatataacc aggtaatctc atagcctggt 15180
cccaattagg aatcgcaagc tgttggtgaa tatctttagg aacatcaacc aaaacaggtc 15240
caggtctacc agaagtagct aaaaagaaag cttcctcaat aatcctaggg atatcttcaa 15300
catccatcac aagatagtta tgcttcgtaa tcgaacgcgt tacctcaaca atcggagtct 15360
cttgaaacgc atctgtacca atcatacgac gagggacttg tcctgtgatt gctacaagag 15420
gaacactatc taacaacgca tcggctaate cgctaacgag atttgtagct ccgggacctg 15480
aagtggctat acagatacct ggtttacctg aggatcgagc gtatccttct gctgcgaata 15540
cacctccttg ttcgtgacga ggaaggacgt tacggattga ggaagagcgg gttaaggctt 15600
ggtgaatctc cattgatgta cctccagggt aagcgaatac ggtttctacg ccttgacgtt 15660
ctaaagcttc gacgaggata tcagcgcctt tgcgggggtg atctggagcg aatcgggaga 15720
tgaatgttcc gggtttggtg ggtttgggtg gagagggagt ggttgtagaca ttggtgggtg 15780
tgttgagcac ggcggagatg gaggagggag agctggattt gataccgagg cggcgggagg 15840
aggagatga tttgttgggg tttagggaga atgggagggg gaatctggag attggtaatg 15900
gtgatttggg ggaggaagga gatggttggg tggagaagga gatcgaagaa gatggttggg 15960
ttggtgtgtg tgccgcccgc atggttcagc tgcacataca taacata 16007

```

```

<210> SEQ ID NO 121
<211> LENGTH: 660
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

```

```

<400> SEQUENCE: 121

```

```

atggcgatga aggtatatgg aaatgggatg tcagtgtgcg tggcacgtgt gcttctatgc 60
cttcacgaga aggagactga gttcgagctt gtcctcctcg atctctttgc ttgccaccac 120
aagctccctt ctttctctc catgaacccc tttggccaag ttcagttctt acaagacgac 180
gaccttacc tttttgagtc gagggcaatc acggcatata tagcagagaa acacaaagac 240
aaaggaacgg atctgacgag acatgcgacg gctaaagaag cagccattgt gaagctgtgg 300
tcggaagtgg agtcccacca cttcaacccc gcgatctccg ccgtcatcca ccagcttata 360
gttgtgcccg tcaaggcaa gactcctgat gcagccatcg tggaggagaa tctggagaag 420
ttagggaaag tgctcgatgt gtacgaagag aagctcggga agacaaaata cttggccgga 480
gattcttaca cactcgcgga tctccaccac gttccttaca cttactactt catgaagacg 540
ggctatgctg gtttgggtcaa cgaccgtcct aatgtcaagg cgtgggtggga agaccttgt 600
tctcgtccgg ctttctctaa agtctctcct ggcttgaccg ttgctccggc aacgaactga 660

```

```

<210> SEQ ID NO 122
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

```

```

<400> SEQUENCE: 122

```

```

ataccgggga tacctgcagg ttaggccggc cagagcatta tgcttccaag cggac 55

```

```

<210> SEQ ID NO 123
<211> LENGTH: 69
<212> TYPE: DNA

```

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<213> ORGANISM: Artificial sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Primer

<400> SEQUENCE: 123

caatcaatta taggcctcgc atgctttaat taacgatcga gccatgggttc actcctaactt 60  
 cgtaactcg 69

<210> SEQ ID NO 124  
 <211> LENGTH: 2447  
 <212> TYPE: DNA  
 <213> ORGANISM: Brassica napus

<400> SEQUENCE: 124

aacggcaatt gattctcggc ctgtgggtgga tacgtgtcctt tgtatgattt attttacatc 60  
 aaaactttga ttaattttaa ataaattaga aaattaagaa aatcagattt cttttttgca 120  
 aaagaaacat actattttgtg ataaatgggtt tagtttaaga ttttagttat ttatattcag 180  
 ttacgatggt actgttccac aaaatacaac aaaaatcaaa tgatctatct tgagtcatgc 240  
 agaaattatt tactatcttc ccacgaaaat taaagttatg aaattctata cgttcaaaat 300  
 atagaagttt ggtgtttcca atgaaagttt ttattttttt atcataaatt tattcatatt 360  
 aattaatata attattgaaa tagattaaac tcttttaaaa tatgatattg aaaggattaa 420  
 atttattttc aaatatataa atatccaaag ctcttgtcct gagagacaga aagagtatct 480  
 gattgtgtga cagaaactaa acagtatgag cttaattctc cataaacctg gatcatcgct 540  
 ttaaaacttt gtgtacatat caaacctaaa atggtactaa tttctttact cttattattg 600  
 actgccagag atgattataa aattacttag attacagtaa ttattgatca agatagttga 660  
 ctccocagtt cacatattag acattattgt tagtgtttgg aaatacaaat aaaatatgaa 720  
 attatattta tattctatta gcgaatatct tcaaatgta agagactctc accaaaaagt 780  
 tatttgaagg attttgaata attttctcac atttaaaata cttactaata caataataat 840  
 aacatttaag aaattgaata ttattatatt ttgtatttag aaacctgat gaaatagggt 900  
 ttttagtaat taacctcca actaaagatg aatcgtaaaa aaacctcaa ctaaaaatcc 960  
 tgtgaaataa accctcaact ttaatttcgt taacatatgt tacctcctg ctaaaaaacc 1020  
 gtgacggagg gtaacatatg ttaactgttt ataattaagt tgaaggttta taatgttgaa 1080  
 aacttagttg agggtttttt tacgattcaa aaatagttaa acggttttat cactaaaagt 1140  
 cattaaatgc tattaataa tttattatca tttatacatt gtttagatt gatttataag 1200  
 cctttaaaac taatttgtaa attttaatat attatttttt ataaattaat ttatacatcc 1260  
 aaaattaatt attttcaaca ctacttacia cttattataa cttcaaaata ttaaattatt 1320  
 tgatatttga aaatagtgat ataaaatatt tgtgtgttta ttcgctcatt gcaaaatc 1380  
 aaataattta aaatgtctaa gttatattaa gtcttaagta gtgtcgaaga taattcatca 1440  
 atgaagtcaa tctttctatt tagagcatga tgcacttttt cctattttca tgatttccgt 1500  
 catccagctc atactttcct cctatcccca aaaataatgc atgattattt gcattctcat 1560  
 taatttctaa ataaatagt tatatttttc ttttcttaat cagtagtata tttgatatat 1620  
 tgttcttgat ttattgtatt actttctggt tcaatataat gttggattat ttgatcctaa 1680  
 caagtagcag aaaatgtaaa aacttataaa atcattgtga aactgtatta atcatatgta 1740  
 aaagtattaa aatatttatg aagctttata aatcgggtat aaagtaatgt attaaaattt 1800  
 ataaattatt ttaagggtc tatatcaatc taaattaatg tataaatgat aataactttt 1860

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agtgataaaa ccctcaact atttttgaat cataaaaaaa acttcaacta agttttcaac 1920
attataaacc cgcaacttat aaactgttaa cgtatgtcac cctccgttgc ggttttttag 1980
atggacggta acatattgcta acagaattaa agttaagggt ttatttcaca aattttttag 2040
ttgacgtttt tttttacaat tcattcttat ttgatgggtt taattactaa aattccaatg 2100
aaatactagc aataactaatg cttttctctc caacatttta attttaattt ttattcactg 2160
tctaaaatgt tgaagatat agaacatcgt atattacttc tatacattga caaacagtca 2220
catattaaaa aaaatgtgat cacattttca aagtcatttg gaatataaaa taagtttate 2280
aagataaagg gatgggtaaa gaatagattc actggaatat gtctcgaata aaccaagaaa 2340
caaagttaa agtaaagaag ctttatcaaa agaaaaaaat taagaaaatt tattggcttt 2400
ttattggacg agtcatatta aatgacgtg gtttcaataa cctctct 2447

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```

<210> SEQ ID NO 125
<211> LENGTH: 865
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

```

```

<400> SEQUENCE: 125

```

```

ttacatatt ggccaagag gcataataaa aaatattgtg aaaaaaaaaa aaaaaatgac 60
gtggtttcac actaaactag agagtgcgat gaaccgggtc gaccgtcgat ttaagacaat 120
aactccctgc cgttggatct gtcacttttg gaagagacct ttccttgttt tcgccatatt 180
tctctaggag aaggggggtc gattattctg cttttgtcta tgcggaagta cgtatgtatt 240
tattcattgt caatgtatta aatccaacta atctgcttct tttttttata acaccatcca 300
acttatctgc ttattctgct tatttcttct gagtatttga accaaatcca actaatctcc 360
tttatcgtct aatgtcta atgaattact aatgaatcat ttcgtctgg ttaaagacca 420
ctagaacact gtaaccctta gaacatctca gtaaaccttt tgaacagtta tagtgaactt 480
ttttctttt tttttttgag aaccaacatt tatagtgaac ttcttcta at ggttaccaag 540
aacatttctc aatgcttata tttttctgaa agacactgca caaatatttg acgtaaatta 600
ttaggacatt tccaatagta tgggtctcat ttgtaatga aaatattttt aaaaattttt 660
attattaata tttattgtta aagatttttt aattaatata ttaaatcaat tcaatccaaa 720
aatgagacta aagttctact cactcgcaca ctcaaaattt ttaatttaa catttcttaa 780
ctagctttgt tcgaccaatc atcccagcca cgttccatta gtttgaatct gaaatctttg 840
gaaattcggc accgttttca ttaac 865

```

```

<210> SEQ ID NO 126
<211> LENGTH: 768
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

```

```

<400> SEQUENCE: 126

```

```

ctctctcttt gttttctcta acctctctct aagtctctgt taaaaaaaaa aaatcaatcc 60
tagtggccgg tgggttcacc accgcgggtc accaaccctt tttttgtttt tgtttgtaaa 120
tattttcgtt aggcgactct tttcttccgt ttatcggata aaaactttgc aagggtgactt 180
ttgttgtgtg ttttccaaac ccgatttctc tatcctttgc aaatcaatat cccgtttgat 240
ttgttagat tccagctctc tagttaatca cactttttcc ttcccatata tggattaat 300
cttagcgtgc agaattttat gacggagat ccattgtgtg ttagagatta agttgtttga 360

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```

ttaagcgtag agagaagaag caagctcaga ttagctggag tttctttatc agaaacgttt 420
tggcaaggcc cagctttcat ccctttgaag ctattcaccg gagttcactt gtaacgagcg 480
gatgaagaat cgagcataat tgacggcgaa cagcgatcag aggaacagtc aagtagattc 540
aactagtcga agaaagttaac tgaaagtcc cgttccggca tgtctccggc gagactgaca 600
gtgctatttc tttgactcta gaaacatcgt gaccatccta actgtacacg tgtcgttcat 660
gcttttagagt ttttatatta gcgaacacgt ggttttaatc ttatcttttg ttcggttggg 720
tttcgatatg gactgaatat atattaggat ggctggttga tctacttg 768

```

```

<210> SEQ ID NO 127
<211> LENGTH: 55
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

```

```
<400> SEQUENCE: 127
```

```
ataccggga tacctgcagg ttagccggc caaacggcaa ttgattctcg cctg 55
```

```

<210> SEQ ID NO 128
<211> LENGTH: 69
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

```

```
<400> SEQUENCE: 128
```

```
caatcaatta taggcctcgc atgctttaat taacgatcga gccatggaga gaggttattg 60
aaaccacgt 69
```

```

<210> SEQ ID NO 129
<211> LENGTH: 74
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

```

```
<400> SEQUENCE: 129
```

```
ccatggctcg atcgtaatt aaagcatcgc aggcctataa ttgattgttt acatattggc 60
ccaagaggca taat 74
```

```

<210> SEQ ID NO 130
<211> LENGTH: 61
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Primer

```

```
<400> SEQUENCE: 130
```

```
taagcggccg caatcggacc gataccggta ggcgccgtta atgaaaacgg taccgaattt 60
c 61
```

```

<210> SEQ ID NO 131
<211> LENGTH: 1593
<212> TYPE: DNA
<213> ORGANISM: Brassica napus

```

```
<400> SEQUENCE: 131
```

```
aatagtcaag tttatgaatc acagattagc catctagaat caaaggtgat gcaggtttca 60
tctccaaca agaactataa tccatgaaaa catagaacaa cataaactca tgaagctttt 120
```

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attcttatag gcatcaagaa aatttgggtga agcaatggaa attaaacatg aaaacaagtt 180
tccgagggtga agtcaactgat attgtatatg ttggttcttg aaactgaaac tattattatg 240
gaccatgtga tatatgtaga tggagaacca ccgttgtttt agttcaactga aggaatttga 300
agctccaaag gttacgaact cccaagatga acattctatt gaatctctca gaaaagtaag 360
tgagcatttt atcatattca gcttgtatta aatttgtggt ttcttatgaa attaacaata 420
ttaacttttt cctacagcta tgtctcactt ccgatactga tttagttgct ccttgtatct 480
catctacata gagaattttc aagatattat tttgcttga caaattagac atggctatga 540
agagatttga gagttttaat gcgcgggagg gatcatgcac aggtatttga aacctagtgc 600
cttgctctgt ctcatcattt acttgttata tttggaccaa acaacacatc tccatcaaat 660
catatttctt aaacgagttt gaatttgag gacattcatc aggaagtgc caatcgctcc 720
ttgagtttca cagttctctt aaagcatatt atatatgtgc tcttattaga tggtagaagt 780
ttcataaatt tgcaatgctt gtgtttgatc atcaatgaat aatgtaaaaa atttatacat 840
tgtgatagaa gtagagacct taatggatgt gtgtgcttta aagaggagac tgaataactt 900
ttatcagtgt tgcgaaaaaa aaaaagactt ttatctaact cgtgaaatgg gttgttttgg 960
aaagacattt tccacaattt tgacaatgaa cctccagaca tatctggttt cttacgtaaa 1020
acataaattg acctaactta attatttctg actgttattg aaatgttctt gagaattaa 1080
ataaatcatt catggagttt gtttggtagt agtaggtgga gctcatggga aaagtggcgc 1140
cacgtaactg actcatgttg ctatttttct gcttcaacttg tttactctcc ccttaataca 1200
aatttgtttt cttttgaagg ctctctactt gaacgtgtcc ttacactaga atcagcacca 1260
aacatattaa aacaccttca cggatagctt gtgaactgta tattcttttt gaaatattta 1320
ttatttatta gttttgaacg gggatattcat tgtattcttt tttttttttt tccaatgggg 1380
tattcattgt attcatatta gtttttcatc attatatttg acctaacctg gttaaccccg 1440
aagagaaaaa ctgtttattt aatttgtttt tgtaaaacat aaatgtgttt gtgacatgtg 1500
gcttatttca ttgatgcaag gtttgacacg ttgagttctt tgctatttat ctctcttgg 1560
atcccgagg cagtaatgtc aagaagtcca aga 1593

```

```

<210> SEQ ID NO 132
<211> LENGTH: 16034
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Plasmid

```

```

<400> SEQUENCE: 132

```

```

ctatacaaaag ttgatagctt ggcgtaatcg atgtaccgat atcaatttaa attggccggc 60
cgagctccct gcagggggcc cggcgcgcct ctagattaat taaaggcctt agttactaat 120
cagtgatcag attgtcgttt cccgccttca gtttaaaacta tcagtgtttg acaggatata 180
ttggcgggta aacctaaagag aaaagagcgt ttattagaat aatcggatat taaaagggc 240
gtgaaaagggt ttatccgttc gtccatttgt atgtcaatat ccatgataag tgcgctgta 300
tgtgtttgtt tgaatattca tggaaacgag tggcggtttt catggcttgt tatgactgtt 360
tttttggggg acagtctatg cctcgggcat ccaagcagca agcgcgttac gccgtgggtc 420
gatgtttgat gttatggagc agcaacgatg ttacgcagca gggcagtcgc cctaaaacaa 480
agttaaacad catgggtgaa gcggtcatcg ccgaggtgtc caccagctg tcggaagtgc 540

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tgggtgtcat	cgagcgccac	ctcgaaccga	cctcctcgc	cgtgcatctg	tatggtagcg	600
ccgttgacgg	cggccttaag	ccccattcgg	acatcgacct	gcttgteacc	gttaccgtcc	660
gtctcgacga	gaccacggcg	cgcgcgctta	tcaacgacct	tctggaaacg	tegcctccc	720
ccggcgagag	cgaaatcctg	cgcgcgggtg	aggtgacgat	tgtggtgcac	gatgacatca	780
tcccctggcg	ctatccggcc	aaacgcgaac	tccagttcgg	cgaatggcag	cgtaatgata	840
ttctggcggg	tatctttgaa	cgggccacca	tcgacattga	tctggcgatc	ctgctacca	900
aggcccggga	gcatagcgtg	gccctcgtcg	gccccgcggc	cgaggaactt	ttcgaccggg	960
tgccggaaca	ggatctgttc	gaagcactga	acgagacgct	gacctgtgg	aactccccgc	1020
cggattgggc	gggcgatgag	cgcaatgtgg	tccttacgct	gagccgatt	tggtactcgg	1080
cggttaccgg	caagatcggc	ccgaaggatg	tcgccgccga	ctggcgatg	gagcgccttc	1140
cggcgcaata	ccagcccgtg	atcctcgaag	cgcgccaaag	ctatctgggc	caagaagaag	1200
accgtctcgc	gtcccgggcc	gaccagctcg	aagaatttgt	ccactatgtc	aagggcgaga	1260
tcacgaaggt	cgttggcaaa	taatgtctag	ctagaaattc	gttcaagccg	acgccgcttc	1320
gcygcgcggc	ttaactcaag	cgttagatgc	actaagcaca	taattgctca	cagccaaact	1380
atcgatgagt	tgaaggacc	cgtagaaaag	atcaaaggat	cttcttgaga	tccttttttt	1440
ctgcgcgtaa	tctgctgctt	gcaaacaaaa	aaaccaccgc	taccagcggg	ggtttgtttg	1500
ccggatcaag	agctaccaac	tctttttccg	aaggttaactg	gcttcagcag	agcgcagata	1560
ccaaatactg	tccttctagt	gtagccgtag	ttaggccacc	acttcaagaa	ctctgtagca	1620
ccgctacat	acctcgcctc	gctaactcgt	ttaccagtgg	ctgctgccag	tgccgataag	1680
tcgtgtctta	ccgggttgga	ctcaagacga	tagttaccgg	ataaggcgca	gcygctgggc	1740
tgaacggggg	gttcgtgcac	acagcccagc	ttggagcgaa	cgacctacac	cgaactgaga	1800
tacctacagc	gtgagctatg	agaaagcgc	acgcttcccg	aagggagaaa	ggcggacagg	1860
tatccggtaa	gcygcagggt	cggaacacga	gagcgcaaga	gggagcttcc	agggggaaac	1920
gcctggtatc	tttatagtc	tgctgggttt	cgccacctct	gacttgagcg	tcgatttttg	1980
tgatgctcgt	cagggggcgc	gagcctatgg	aaaaacgcca	gcaacgcggc	ctttttacgg	2040
ttcctggcct	tttctggccc	ttttgctcac	atgttcttcc	ctgcgttatc	ccctgattct	2100
gtggataaac	gtattaccgc	ctttgagtga	gctgataccg	ctcggcgag	ccgaacgacc	2160
gagcgcagcg	agtcagttag	cgaggaagcg	gaagagcgc	tgatgcggta	ttttctcctt	2220
acgcacatct	gcygtatttc	acaccgcata	ggccgcgata	ggccgacgcg	aagcgcgggg	2280
gcgtaggagg	cgcagcgacc	gaagggtagg	cgttttttgc	agctcttcgg	ctgtgcgctg	2340
gccagacagt	tatgcacagg	ccagcgggtt	tttaagagtt	ttaataagtt	ttaaagagtt	2400
ttaggcggaa	aaatcgcctt	ttttctcttt	tatatcagtc	acttacatgt	gtgaccgggt	2460
cccaatgtac	ggctttgggt	tcccgaatga	cgggttccgg	ttcccgaatgt	acggctttgg	2520
gttcccgaatg	tacgtgctat	ccacagggaaa	gagacctttt	cgaccttttt	cccctgctag	2580
ggcaatttgc	cctagcatct	gctccgtaca	ttaggaaccg	gcygatgctt	cgcctcagat	2640
caggttgccg	tagcgcata	ctaggatcgg	gccagcctgc	cccgcctcct	ccttcaaatc	2700
gtactccggc	aggtcatttg	accgatcag	cttgccgacg	gtgaaacaga	acttcttgaa	2760
ctctccggcg	ctgccactgc	gttcgtagat	cgtcttgaac	aacctctgg	cttctgctt	2820
gcctcggcgc	cggcgtgcca	ggcggtagag	aaaacggccg	atgccggggt	cgatcaaaaa	2880
gtaatcgggg	tgaaccgtca	gcacgtccgg	gttcttgctt	tctgtgatct	cgcggtacat	2940

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ccaatcagca agctcgatct cgatgtactc eggcgcgccg gtttcgctct ttaogatctt	3000
gtagcggcta atcaaggctt caccctcgga taccgtcacc aggcggccgt tcttggcctt	3060
cttggtagcg tgcattggca cgtgcgtggt gtttaaccga atgcaggttt ctaccaggtc	3120
gtctttctgc tttccgccat cggctgcgcg gcagaacttg agtacgtccg caacgtgtgg	3180
acggaacacg cggccgggct tgtctccctt ccttcccgg tatcgggtca tggattcggg	3240
tagatgggaa accgccaatc gtaccaggtc gtaatcccac aactggcca tgcgcggcgg	3300
gcctgcggaa acctctactg gccctctctg aagctcgtag cggatcacct cgcagctcg	3360
tcggtcacgc ttcgacagac ggaaaacggc cacgtccatg atgctgcgac tatcgcgggt	3420
gcccacgtca tagagcatcg gaacgaaaa atctgggtgc tcgtcgcctt tgggcggctt	3480
cctaactgac gggcgcaccg ctgccggcgg ttgcccggat tctttgcgga ttcgatcagc	3540
ggccccttgc cagcattcac cggggcgtgc ttctgcctcg atgcgttgc gctgggcggc	3600
ctgcgcggcc ttcaacttct ccaccaggtc atcaccagc gccgcgcga tttgtaccgg	3660
gccggatggt ttgcgaccgc tcacgcgat tccctgggct tgggggttcc agtgcattg	3720
cagggccggc agacaacca gccgcttacg cctggccaac cgcctgtcc tccacacatg	3780
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The invention claimed is:

1. An expression cassette comprising an expression control sequence operatively linked to a nucleic acid of interest, wherein said expression control sequence is heterologous to and governs seed-specific expression of said nucleic acid of interest, and wherein said expression control sequence is at least 95% identical to the nucleic acid sequence SEQ ID NO: 22; wherein said expression control sequence governs seed-specific expression of said operatively linked nucleic acid of interest.

2. The expression cassette of claim 1, wherein said expression control sequence comprises the nucleic acid sequence SEQ ID NO: 22.

3. A vector comprising the expression cassette of claim 1.

4. The vector of claim 3, wherein said vector is an expression vector.

5. A non-human host cell comprising the expression cassette of claim 1 or a vector comprising said expression cassette.

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6. A non-human transgenic organism comprising the expression cassette of claim 1 or a vector comprising said polynucleotide.

7. A method of expressing a nucleic acid of interest in a host cell comprising:

(a) introducing an expression cassette comprising an expression control sequence operatively inked to a nucleic acid of interest, wherein said expression control sequence is heterologous to and governs seed-specific expression of said nucleic acid of interest, and wherein said expression control sequence is at least 95% identical to the nucleic acid sequence of SEQ ID NO: 22 or 25 or a vector comprising said expression control sequence, into a host cell; and

(b) expressing said nucleic acid of interest in said host cell.

8. The method of claim 7, wherein said host cell is a plant cell.

9. A method of expressing a nucleic acid of interest in a non-human organism comprising:

(a) introducing an expression cassette comprising an expression control sequence operatively inked to a nucleic acid of interest, wherein said expression control

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sequence is heterologous to and governs seed-specific expression of said nucleic acid of interest, and wherein said expression control sequence is at least 95% identical to the nucleic acid sequence of SEQ ID NO: 22 or 25 or a vector comprising said expression control sequence, into a non-human organism; and

(b) expressing said nucleic acid of interest in said non-human transgenic organism.

10. The method of claim 9, wherein said non-human transgenic organism is a plant or seed thereof.

11. The method of claim 9, wherein said nucleic acid of interest is expressed seed-specifically.

12. The method of claim 7, wherein said nucleic acid of interest is expressed seed-specifically.

13. The expression cassette of claim 1, wherein said expression control sequence is at least 98% identical to the nucleic acid sequence SEQ ID NO: 22.

14. The expression cassette of claim 1, wherein said expression control sequence is at least 99% identical to the nucleic acid sequence SEQ ID NO: 22.

\* \* \* \* \*

UNITED STATES PATENT AND TRADEMARK OFFICE  
**CERTIFICATE OF CORRECTION**

PATENT NO. : 8,853,383 B2  
APPLICATION NO. : 13/001742  
DATED : October 7, 2014  
INVENTOR(S) : Jörg Bauer et al.

Page 1 of 1

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

On the Title Page:

Item (75), Inventors: "Jörg Bauer, Durham, NC (US); Toralf Senger, Durham, NC (US)"

should read -- Jörg Bauer, Limburgerhof (DE); Toralf Senger, Heidelberg (DE) --

Signed and Sealed this  
Twenty-seventh Day of October, 2015



Michelle K. Lee  
*Director of the United States Patent and Trademark Office*