US 20120246763A1

(19) **United States**

(12) **Patent Application Publication**

Flasinski

(10) **Pub. No.: US 2012/0246763 A1**

(43) **Pub. Date: Sep. 27, 2012**

(54) **PLANT REGULATORY ELEMENTS AND USES THEREOF**

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(21) Appl. No.: **13/428,994**

(22) Filed: **Mar. 23, 2012**

Related U.S. Application Data

(60) Provisional application No. 61/467,875, filed on Mar. 25, 2011.

Publication Classification

(51) **Int. Cl.**

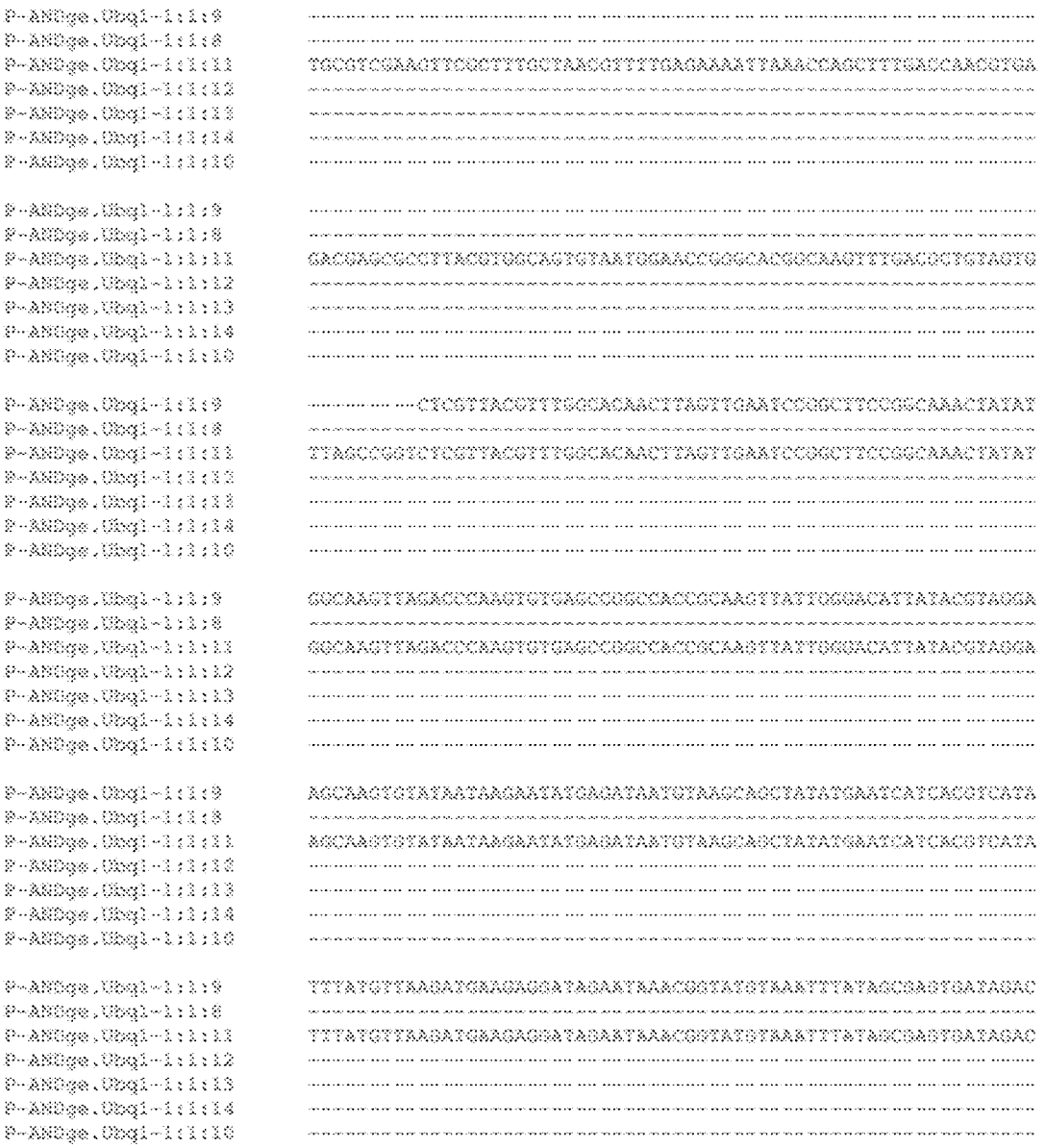
A01H 5/00	(2006.01)
C12N 5/10	(2006.01)
A01H 5/10	(2006.01)
A23L 1/10	(2006.01)
C07K 1/14	(2006.01)
C08B 30/00	(2006.01)
C07K 2/00	(2006.01)
C12N 15/29	(2006.01)
C11B 1/00	(2006.01)

(52) **U.S. Cl.** **800/298**; 536/23.6; 435/419; 554/9; 530/370; 536/102; 554/1; 426/443; 426/627; 426/622

(57) **ABSTRACT**

The present invention provides novel DNA molecules and constructs, including their nucleotide sequences, useful for modulating gene expression in plants and plant cells. The invention also provides transgenic plants, plant cells, plant parts, seeds, and commodity products comprising the DNA molecules operably linked to heterologous transcribable polynucleotides, along with methods of their use.

FIG. 1a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P-ANDge.Ubq1-1:1:8
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P-ANDge.Ubq1-1:1:9
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P-ANDge.Ubq1-1:1:11
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P-ANDge.Ubq1-1:1:10
P-ANDge.Ubq1-1:1:9
P-ANDge.Ubq1-1:1:8
P-ANDge.Ubq1-1:1:11
P-ANDge.Ubq1-1:1:12
P-ANDge.Ubq1-1:1:13
P-ANDge.Ubq1-1:1:14
P-ANDge.Ubq1-1:1:10

FIG. 1b

FIG. 1c

FIG. 1d

FIG. 1e

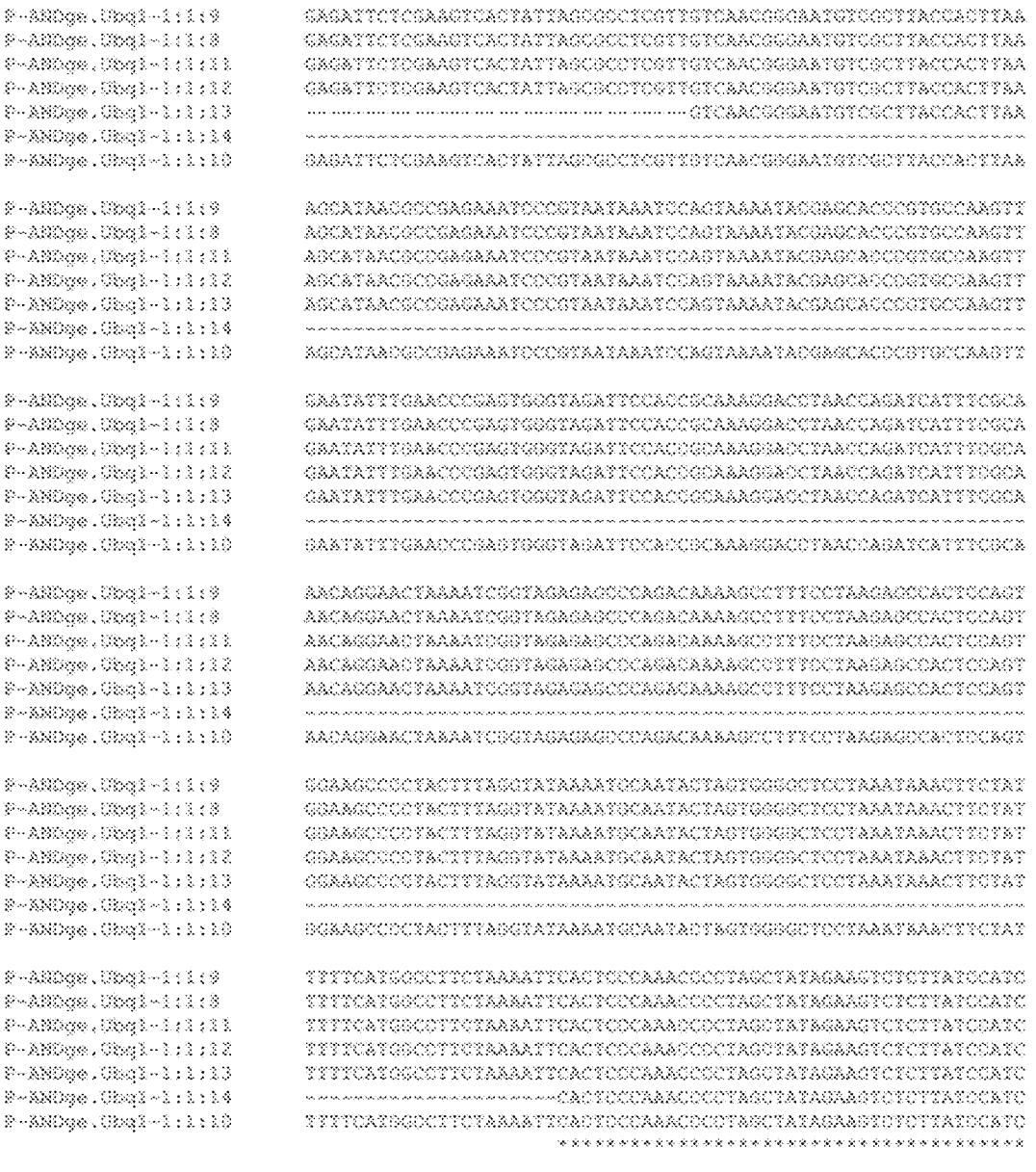

FIG. 1f

```
P~ANDge.Ubql~1;1;9      CTCTAAATAAAAATGDGAGTCTATTTTATTTCACCAGAGTTGATCGTAAATTTAGTCTCT
P~ANDge.Ubql~1;1;8      CTCTAAATAAAAATGGGAGTCTATTTTATTTCACCAGAGTTGATCGTAAATTTAGTCTCT
P~ANDge.Ubql~1;1;11     CTCTAAATAAAAATGGGAGTCTATTTTATTTCACCAGAGTTGATCGTAAATTTAGTCTCT
P~ANDge.Ubql~1;1;12     CTCTAAATAAAAATGGGAGTCTATTTTATTTCACCAGAGTTGATCGTAAATTTAGTCTCT
P~ANDge.Ubql~1;1;13     CTCTAAATAAAAATGGGAGTCTATTTTATTTCACCAGAGTTGATCGTAAATTTAGTCTCT
P~ANDge.Ubql~1;1;14     CTCTAAATAAAAATGGGAGTCTATTTTATTTCACCAGAGTTGATCGTAAATTTAGTCTCT
P~ANDge.Ubql~1;1;10     CTCTAAATAAAAATGGGAGTCTATTTTATTTCACCAGAGTTGATCGTAAATTTAGTCTCT
                        **********************************************************************

P~ANDge.Ubql~1;1;9      CAAATTTTATAAAGTTGAGGGTAGAGGATGACTGGAGTTGCTCTAAACGGACCTATCTTCA
P~ANDge.Ubql~1;1;8      CAAATTTTATAAAGTTGAGGGTAGAGGATGACTGGAGTTGCTCTAAACGGACCTATCTTCA
P~ANDge.Ubql~1;1;11     CAAATTTTATAAAGTTGAGGGTAGAGGATGACTGGAGTTGCTCTAAACGGACCTATCTTCA
P~ANDge.Ubql~1;1;12     CAAATTTTATAAAGTTGAGGGTAGAGGATGACTGGAGTTGCTCTAAACGGACCTATCTTCA
P~ANDge.Ubql~1;1;13     CAAATTTTATAAAGTTGAGGGTAGAGGATGACTGGAGTTGCTCTAAACGGACCTATCTTCA
P~ANDge.Ubql~1;1;14     CAAATTTTATAAAGTTGAGGGTAGAGGATGACTGGAGTTGCTCTAAACGGACCTATCTTCA
P~ANDge.Ubql~1;1;10     CAAATTTTATAAAGTTGAGGGTAGAGGATGACTGGAGTTGCTCTAAACGGACCTATCTTCA
                        **********************************************************************

P~ANDge.Ubql~1;1;9      AGTGACCTCAGTGAGCCCGTTTAACGGCGTCGACAAGTTTAATCTAACGGACACCAACCA
P~ANDge.Ubql~1;1;8      AGTGACCTCAGTGAGCCCGTTTAACGGCGTCGACAAGTTTAATCTAACGGACACCAACCA
P~ANDge.Ubql~1;1;11     AGTGACCTCAGTGAGCCCGTTTAACGGCGTCGACAAGTTTAATCTAACGGACACCAACCA
P~ANDge.Ubql~1;1;12     AGTGACCTCAGTGAGCCCGTTTAACGGCGTCGACAAGTTTAATCTAACGGACACCAACCA
P~ANDge.Ubql~1;1;13     AGTGACCTCAGTGAGCCCGTTTAACGGCGTCGACAAGTTTAATCTAACGGACACCAACCA
P~ANDge.Ubql~1;1;14     AGTGACCTCAGTGAGCCCGTTTAACGGCGTCGACAAGTTTAATCTAACGGACACCAACCA
P~ANDge.Ubql~1;1;10     AGTGACCTCAGTGAGCCCGTTTAACGGCGTCGACAAGTTTAATCTAACGGACACCAACCA
                        **********************************************************************

P~ANDge.Ubql~1;1;9      GAGAAGAGAACCACCGGCAGCCCGAGCCAAGCGACGTTGACATCTTGGCGGCGGCACGGC
P~ANDge.Ubql~1;1;8      GAGAAGAGAACCACCGCCAGCCCGAGCCAAGCGACGTTGACATCTTGGCGGCGGCACGGC
P~ANDge.Ubql~1;1;11     GAGAAGAGAACCACCGCCAGCCCGAGCCAAGCGACGTTGACATCTTGGCGGCGGCACGGC
P~ANDge.Ubql~1;1;12     GAGAAGAGAACCACCGCCAGCCCGAGCCAAGCGACGTTGACATCTTGGCGGCGGCACGGC
P~ANDge.Ubql~1;1;13     GAGAAGAGAACCACCGCCAGCCCCGAGCCAAGCGACGTTGACATCTTGGCGGCGGCACGGC
P~ANDge.Ubql~1;1;14     GAGAAGAGAACCACCGCCAGCCCGAGCCAAGCGACGTTGACATCTTGGCGGCGGCACGGC
P~ANDge.Ubql~1;1;10     GAGAAGAGAACCACCGCCAGCCCGAGCCAAGCGACGTTGACATCTTGGCGGCGGCACGGC
                        **********************************************************************

P~ANDge.Ubql~1;1;9      ATCTCCCTGGCGTCTGGCCCCCTCTCGAGACTTCCGCTCCACCTCCCACCGGTGGCGGTT
P~ANDge.Ubql~1;1;8      ATCTCCCTGGCGTCTGGCCCCCTCTCGAGACTTCCGCTCCACCTCCCACCGGTGGCGGTT
P~ANDge.Ubql~1;1;11     ATCTCCCTGGCGTCTGGCCCCCTCTCGAGACTTCCGCTCCACCTCCCACCGGTGGCGGTT
P~ANDge.Ubql~1;1;12     ATCTCCCTGGCGTCTGGCCCCCTCTCGAGACTTCCGCTCCACCTCCCACCGGTGGCGGTT
P~ANDge.Ubql~1;1;13     ATCTCCCTGGCGTCTGGCCCCCTCTCGAGACTTCCGCTCCACCTCCCACCGGTGGCGGTT
P~ANDge.Ubql~1;1;14     ATCTCCCTGGCGTCTGGCCCCCTCTCGAGACTTCCGCTCCACCTCCCACCGGTGGCGGTT
P~ANDge.Ubql~1;1;10     ATCTCCCTGGCGTCTGGCCCCCTCTCGAGACTTCCGCTCCACCTCCCACCGGTGGCGGTT
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FIG. 1g

```
P-ANOge.Obql-1:1:9      TCCAAGTCCGTTCCGCCTCCTCTCACACGGCACGAAACCGTGACGGCACCGGCAGCACG
P-ANOge.Obql-1:1:8      TCCAAGTCCGTTCCGCCTCCTCTCACACGGCACGAAACCGTGACGGCACCGGCAGCACG
P-ANOge.Obql-1:1:11     TCCAAGTCCGTTCCGCCTCCTCTCACACGGCACGAAACCGTGACGGCACCGGCAGCACG
P-ANOge.Obql-1:1:12     TCCAAGTCCGTTCCGCCTCCTCTCACACGGCACGAAACCGTGACGGCACCGGCAGCACG
P-ANOge.Obql-1:1:13     TCCAAGTCCGTTCCGCCTCCTCTCACACGGCACGAAACCGTGACGGCACCGGCAGCACG
P-ANOge.Obql-1:1:14     TCCAAGTCCGTTCCGCCTCCTCTCACACGGCACGAAACCGTGACGGCACCGGCAGCACG
P-ANOge.Obql-1:1:10     TCCAAGTCCGTTCCGCCTCCTCTCACACGGCACGAAACCGTGACGGCACCGGCAGCACG
                        ************************************************************

P-ANOge.Obql-1:1:9      GGGGGATTCGTTTCCCACCGTTCCTTCCGTTTCCCTTCCTCTCCCGCCGCTATAAATAGC
P-ANOge.Obql-1:1:8      GGGGGATTCGTTTCCCACCGCTCCTTCCGTTTCCCTTCCTCTCCCGCCGCTATAAATAGC
P-ANOge.Obql-1:1:11     GGGGGATTCGTTTCCCACCGCTCCTTCCGTTTCCCTTCCTCTCCCGCCGCTATAAATAGC
P-ANOge.Obql-1:1:12     GGGGGATTCGTTTCCCACCGCTCCTTCCGTTTCCCTTCCTCTCCCGCCGCTATAAATAGC
P-ANOge.Obql-1:1:13     GGGGGATTCGTTTCCCACCGCTCCTTCCGTTTCCCTTCCTCTCCCGCCGCTATAAATAGC
P-ANOge.Obql-1:1:14     GGGGGATTCGTTTCCCACCGCTCCTTCCGTTTCCCTTCCTCTCCCGCCGCTATAAATAGC
P-ANOge.Obql-1:1:10     GGNGGATTCGTTTCCCACCGCTCCTTCCGTTTCCCTTCCTCTCCCGCCGCTATAAATAGC
                        ************************************************************

P-ANOge.Obql-1:1:9      CAGCCCCATCCCCAGCTTCTTTC
P-ANOge.Obql-1:1:8      CAGCCCCATCCCCAGCTTCTTTC
P-ANOge.Obql-1:1:11     CAGCCCCATCCCCAGCTTCTTTC
P-ANOge.Obql-1:1:12     CAGCCCCATCCCCAGCTTCTTTC
P-ANOge.Obql-1:1:13     CAGCCCCATCCCCAGCTTCTTTC
P-ANOge.Obql-1:1:14     CAGCCCCATCCCCAGCTTCTTTC
P-ANOge.Obql-1:1:10     CAGCCCCATCCCCAGCTTCTTTC
                        ************************
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FIG. 1h

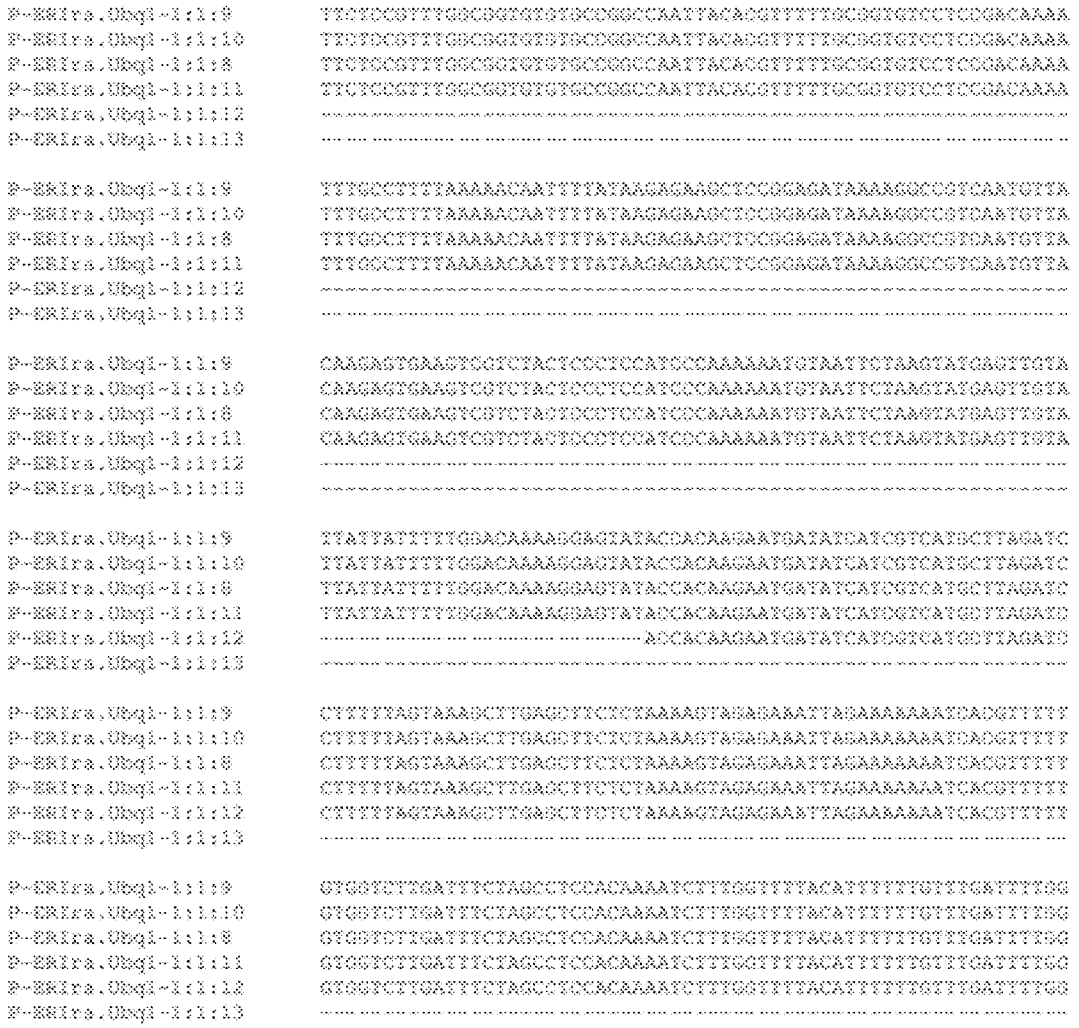
P-ERIra.Ubql-1:1:9
P-ERIra.Ubql-1:1:10 GTGGCCAGCTTTTGTTCTAGTTGAACGGCCCGGCCTTGCGGGCACCTAATACCCTAATT
P-ERIra.Ubql-1:1:8
P-ERIra.Ubql-1:1:11
P-ERIra.Ubql-1:1:12
P-ERIra.Ubql-1:1:13
P-ERIra.Ubql-1:1:9
P-ERIra.Ubql-1:1:10 AATCTATTGCAGCTAACCTCAAAAGAAATGCATTTGCAGTTGTCTGTGCCAATCAATCTA
P-ERIra.Ubql-1:1:8
P-ERIra.Ubql-1:1:11
P-ERIra.Ubql-1:1:12
P-ERIra.Ubql-1:1:13
P-ERIra.Ubql-1:1:9
P-ERIra.Ubql-1:1:10 CTAGCAGACTTACATTATAGATGGAGGAAATTAAATTCAGCCTTTGACGTGCATGCAACA
P-ERIra.Ubql-1:1:8
P-ERIra.Ubql-1:1:11
P-ERIra.Ubql-1:1:12
P-ERIra.Ubql-1:1:13
P-ERIra.Ubql-1:1:9
P-ERIra.Ubql-1:1:10 ACTGCACTGCACAGGATACCATCTTAGCCGTTGTGTCAAAGTTGCTTTGCTAAACGTTT
P-ERIra.Ubql-1:1:8
P-ERIra.Ubql-1:1:11
P-ERIra.Ubql-1:1:12
P-ERIra.Ubql-1:1:13
P-ERIra.Ubql-1:1:9
P-ERIra.Ubql-1:1:10 TGAGAAAACCAGCTTTGACCAAGCCGAGATGAGCGCCTTAGCTTTGCGACAATGTAATGT
P-ERIra.Ubql-1:1:8
P-ERIra.Ubql-1:1:11
P-ERIra.Ubql-1:1:12
P-ERIra.Ubql-1:1:13
P-ERIra.Ubql-1:1:9
P-ERIra.Ubql-1:1:10 AATGCGCCACGGCAAGTTAGACTCTGTAGTGTTAGCCGGCCTCTTTACGTTTGCCATAGT
P-ERIra.Ubql-1:1:8
P-ERIra.Ubql-1:1:11
P-ERIra.Ubql-1:1:12
P-ERIra.Ubql-1:1:13

FIG. 2a

FIG. 2b

FIG. 2c

FIG. 2d



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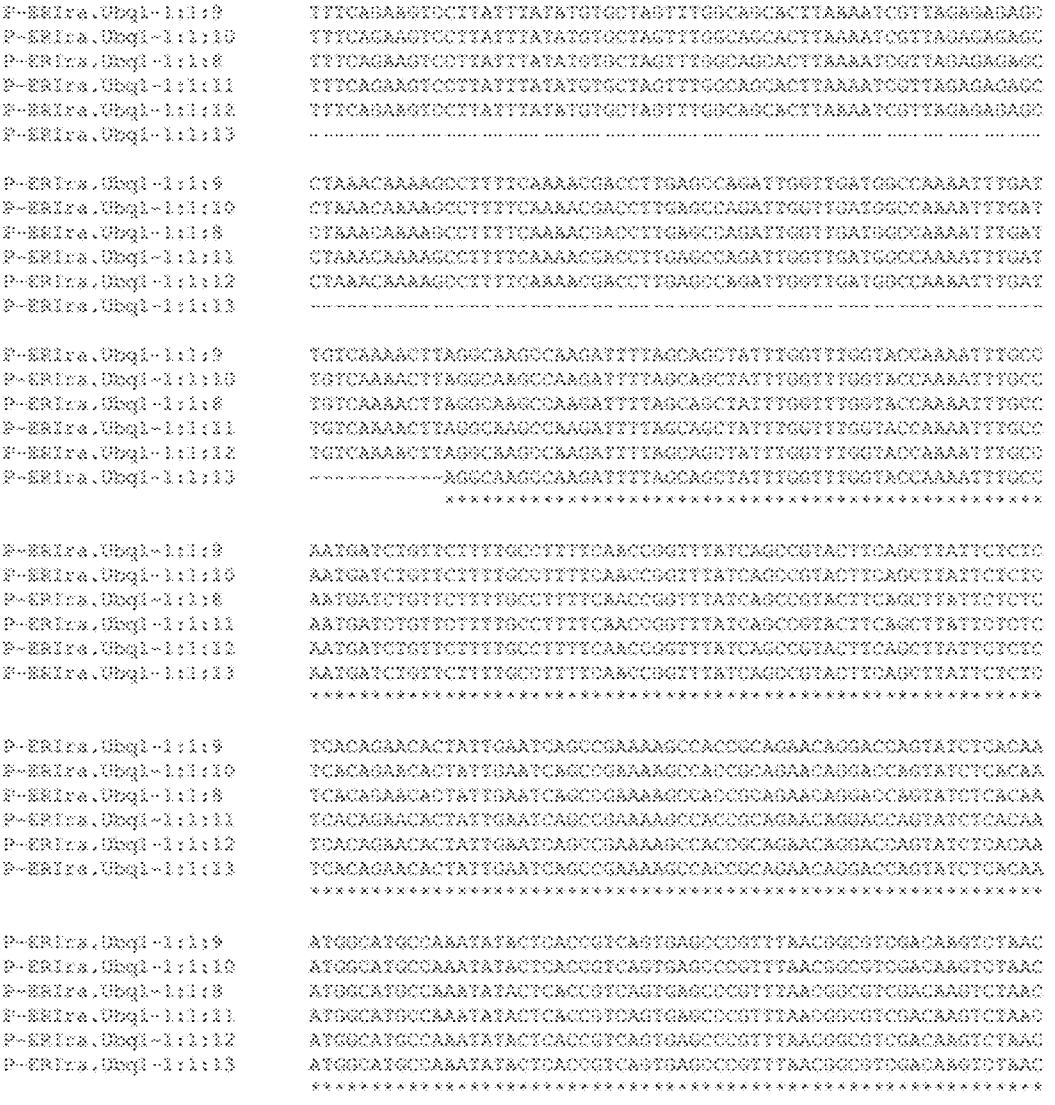

FIG. 2f

```
P-ERIra.Ubq1-1:1:9      GGDCACCAACDAGCGAACCACCAGCGTCAAGCTAGCCAAGCGAAGCAGACGGCCGAGACG
P-ERIra.Ubq1-1:1:10     GGCCACCAACCAGCGAACCACCAGCGTCAAGCTAGCCAAGCGAAGCAGACGGCCGAGACG
P-ERIra.Ubq1-1:1:8      GGCCACCAACCAGCGAACCACCAGCGTCAAGCTAGCCAAGCGAAGCAGACGGCCGAGACG
P-ERIra.Ubq1-1:1:11     GGCCACCAACCAGCGAACCACCAGCGTCAAGCTAGCCAAGCGAAGCAGACGGCCGAGACG
P-ERIra.Ubq1-1:1:12     GGCCACCAACCAGCGAACCACCAGCGTCAAGCTAGCCAAGCGAAGCAGACGGCCGAGACG
P-ERIra.Ubq1-1:1:13     GGCCACCAACCAGCGAACCACCAGCGTCAAGCTAGCCAAGCGAAGCAGACGGCCGAGACG
                        ************************************************************

P-ERIra.Ubq1-1:1:9      TTGACACGTTCGGCGCGGCATCTCTCTGGCCCCCTCTCGAGAGTTCCGCTCCACGTCGAC
P-ERIra.Ubq1-1:1:10     TTGACACGTTGGCGCGGCATCTCTCTGGCCCCCTCTCGAGAGTTCCGCTCCACGTCGAC
P-ERIra.Ubq1-1:1:8      TTGACACGTTGGCGCGGCATCTCTCTGGCCCCCTCTCGAGAGTTCCGCTCCACGTCGAC
P-ERIra.Ubq1-1:1:11     TTGACACGTTGGCGCGGCATCTCTCTGGCCCCCTCTCGAGAGTTCCGCTCCACGTCGAC
P-ERIra.Ubq1-1:1:12     TTGACACGTTCGGCGCGGCATCTCTCTGGCCCCCTCTCGAGAGTTCCGCTCCACGTCGAC
P-ERIra.Ubq1-1:1:13     TTGACACGTTGGCGCGGCATCTCTCTGGCCCCCTCTCGAGAGTTCCGCTCCACGTCGAC
                        ************************************************************

P-ERIra.Ubq1-1:1:9      TGGTGGCGGTTTCCAAGTCCGTTCCGCCTCCTGCTCGTCCTCACACGGCACGAAACCGTC
P-ERIra.Ubq1-1:1:10     TGGTGGCGGTTTCCAAGTCCGTTCCGCCTCCTGCTCGTCCTCACACGGCACGAAACCGTC
P-ERIra.Ubq1-1:1:8      TGGTGGCGGTTTCCAAGTCCGTTCCGCCTCCTGCTCGTCCTCACACGGCACGAAACCGTC
P-ERIra.Ubq1-1:1:11     TGGTGGCGGTTTCCAAGTCCGTTCCGCCTCCTGCTCGTCCTCACACGGCACGAAACCGTC
P-ERIra.Ubq1-1:1:12     TGGTGGCGGTTTCCAAGTCCGTTCCGCCTCCTGCTCGTCCTCACACGGCACGAAACCGTC
P-ERIra.Ubq1-1:1:13     TGGTGGCGGTTTCCAAGTCCGTTCCGCCTCCTGCTCGTCCTCACACGGCACGAAACCGTC
                        ************************************************************

P-ERIra.Ubq1-1:1:9      ACGGCACGGGCAGCACGGGGGATTCGTTTCCCACCGCTCCTTCCCTTTCCCTTCGTCGCC
P-ERIra.Ubq1-1:1:10     ACGCCACCGGCAGCACGGGGGATTCGTTTCCCACCGCTCCTTCCCTTTCCCTTCGTCGCC
P-ERIra.Ubq1-1:1:8      ACGCCACCGGCAGCACGGGGGATTCGTTTCCCACCGCTCCTTCCCTTTCCCTTCGTCGCC
P-ERIra.Ubq1-1:1:11     ACGCCACCGGCAGCACGGGGGATTCGTTTCCCACCGCTCCTTCCCTTTCCCTTCGTCGCC
P-ERIra.Ubq1-1:1:12     ACGGCACGGGCAGCACGGGGGATTCGTTTCCCACCGCTCCTTCCCTTTCCCTTCGTCGCC
P-ERIra.Ubq1-1:1:13     ACGCCACCGGCAGCACGGGGGATTCGTTTCCCACCGCTCCTTCCCTTTCCCTTCGTCGCC
                        ************************************************************

P-ERIra.Ubq1-1:1:9      CGCCGTTTTAAATAGCCAGCCCCATCCCCAGCTTCTCTCCCC
P-ERIra.Ubq1-1:1:10     CGCCGTTTTAAATAGCCAGCCCCATCCCCAGCTTCTCTCCCC
P-ERIra.Ubq1-1:1:8      CGCCGTTTTAAATAGCCAGCCCCATCCCCAGCTTCTCTCCCC
P-ERIra.Ubq1-1:1:11     CGCCGTTTTAAATAGCCAGCCCCATCCCCAGCTTCTCTCCCC
P-ERIra.Ubq1-1:1:12     CGCCGTTTTAAATAGCCAGCCCCATCCCCAGCTTCTCTCCCC
P-ERIra.Ubq1-1:1:13     CGCCGTTTTAAATAGCCAGCCCCATCCCCAGCTTCTCTCCCC
                        ******************************************
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FIG. 2g

FIG. 3a

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P~Sv.Ubql~1:1:2     CTTGTCATAATGCCATTACGTGGATTACAGGTAACTGGCCCTGTAACTACTCGTTCGGCC
P~Sv.Ubql~1:1:1     CTTGTCATAATGCCATTACGTGGATTACAGGTAACTGGCCCTGTAACTACTCGTTCGGCC
P~Sv.Ubql~1:1:3     ..............................................................

P~Sv.Ubql~1:1:2     ATCATCAAACGACGACGTTCCGCTAGCCGACGACACGGGTAATGCACGCAGCCACCCAGGC
P~Sv.Ubql~1:1:1     ATCATCAAACGACGACGTTCCGCTAGCCGACGACACGGGTAATGCACGCAGCCACCCAGGC
P~Sv.Ubql~1:1:3     ------------------------------CACGGGTAATGCACGCAGCCACCCAGGC
                                                  ****************************

P~Sv.Ubql~1:1:2     GCGCGCGCTAGCGGAGCACGGTCAGGTGACACGGGCGTCGTGACGCTTCCGAGTTGAAGG
P~Sv.Ubql~1:1:1     GCGCGCGCTAGCGGAGCACGGTCAGGTGACACGGGCGTCGTGACGCTTCCGAGTTGAAGG
P~Sv.Ubql~1:1:3     GCGCGCGCTAGCGGAGCACGGTCAGGTGACACGGGCGTCGTGACGCTTCCGAGTTGAAGG
                    ************************************************************

P~Sv.Ubql~1:1:2     GGTTAACGCCAGAACAGTGTTTGGCCAGGGTATGAACATAACAAAAAATATTCACACGA
P~Sv.Ubql~1:1:1     GGTTAACGCCAGAACAGTGTTTGGCCAGGGTATGAACATAACAAAAAATATTCACACGA
P~Sv.Ubql~1:1:3     GGTTAACGCCAGAACAGTGTTTGGCCAGGGTATGAACATAACAAAAAATATTCACACGA
                    ************************************************************

P~Sv.Ubql~1:1:2     AAGAATGGAAGTATGGAGCTGCTACTGTGTAAATGCCAAGCAGGAAACTCACGCCGGTA
P~Sv.Ubql~1:1:1     AAGAATGGAAGTATGGAGCTGCTACTGTGTAAATGCCAAGCAGGAAACTCACGCCGGTA
P~Sv.Ubql~1:1:3     AAGAATGGAAGTATGGAGCTGCTACTGTGTAAATGCCAAGCAGGAAACTCACGCCGGTA
                    ************************************************************

P~Sv.Ubql~1:1:2     ACATCCAACGGCCAACAGCTCGACGTGCCGTCAGCAGAGACATCGCAACACTGGTGATT
P~Sv.Ubql~1:1:1     ACATCCAACGGCCAACAGCTCGACGTGCCGTCAGCAGAGACATCGCAACACTGGTGATT
P~Sv.Ubql~1:1:3     ACATCCAACGGCCAACAGCTCGACGTGCCGTCAGCAGAGACATCGCAACACTGGTGATT
                    ************************************************************

P~Sv.Ubql~1:1:2     GGTGGAGCCGGCAGTATGCGCCCCAGCACGGCCGAGGTGGTGGTGGCCGTGGCCCTGCT
P~Sv.Ubql~1:1:1     GGTGGAGCTGGCAGTATGCGCCCCAGCACGGCCGAGGTGGTGGTGGCCGTGGCCCTGCT
P~Sv.Ubql~1:1:3     GGTGGAGCTGGCAGTATGCGCCCCAGCACGGCCGAGGTGGTGGTGGCCGTGGCCCTGCT
                    ************************************************************

P~Sv.Ubql~1:1:2     GTCTGCGCGGCTCGGCACAACTTGAAACTGGGCCACCGCCTCGTCGCAACTCGCAACCCG
P~Sv.Ubql~1:1:1     GTCTGCGCGGCTCGGCACAACTTGAAACTGGGCCACCGCCTCGTCGCAACTCGCAACCCG
P~Sv.Ubql~1:1:3     GTCTGCGCGGCTCGGCACAACTTGAAACTGGGCCACCGCCTCGTCGCAACTCGCAACCCG
                    ************************************************************

P~Sv.Ubql~1:1:2     TTGCCGGAAGAAAGCAATGGCTCGTAGGGCCCGGTAGAATCCAAGAATGTTGCGCTGG
P~Sv.Ubql~1:1:1     TTGCCGGAAGAAAGCAATGGCTCGTAGGGCCCGGTAGAATCCAAGAATGTTGCGCTGG
P~Sv.Ubql~1:1:3     TTGCCGGAAGAAAGCAATGGCTCGTAGGGCCCGGTAGAATCCAAGAATGTTGCGCTGG
                    ************************************************************

P~Sv.Ubql~1:1:2     GCTTCGATTCACATAACATGGGCCTGAAGCTCTAAAACGACGGCCCGGTCACCGGCGAT
P~Sv.Ubql~1:1:1     GCTTCGATTCACATAACATGGGCCTGAAGCTCTAAAACGACGGCCCGGTCACCGGCGAT
P~Sv.Ubql~1:1:3     GCTTCGATTCACATAACATGGGCCTGAAGCTCTAAAACGACGGCCCGGTCACCGGCGAT
                    ************************************************************
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FIG. 3b

```
P~Sv.Ubql~1:1:2     GGAAAGAGACCGGATCCTCCTCGTGAATTCTGGAAGGCCACACGAGAGCGACCCACCACC
P~Sv.Ubql~1:1:1     GGAAAGAGACCGGATCCTCCTCGTGAATTCTGGAAGGCCACACGAGAGCGACCCACCACC
P~Sv.Ubql~1:1:3     GGAAAGAGACCGGATCCTCCTTGTGAATTCTGGAAGGCCACACGAGAGCGACCCACCACC
                    ********************* ************************************

P~Sv.Ubql~1:1:2     GACGCGGAGGAGTCGTGCGTGGTCCAACACGGCCGGCCGGCTGGCTCGACCTTAACCA
P~Sv.Ubql~1:1:1     GACGCGGAGGAGTCGTGCGTGGTCCAACACGGCCGGCCGGCTGGCTCGACCTTAACCA
P~Sv.Ubql~1:1:3     GACGCGGAGGAGTCGTGCGTGGTCCAACACGGCCGGCCGGCTGGCTCGACCTTAACCA
                    ************************************************************

P~Sv.Ubql~1:1:2     GCAAGGCACGCCACGACCCGCCTCGCCCTCGAGGCATAAATACCCTCCCATCC
P~Sv.Ubql~1:1:1     GCAAGGCACGCCACGACCCGCCTCGCCCTCGAGGCATAAATACCCTCCCATCC
P~Sv.Ubql~1:1:3     GCAAGGCACGCCACGACCCGCCTCGCCCTCGAGGCATAAATACCCTCCCATCC
                    ***********************************************************
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FIG. 3c

FIG. 4a

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EXP-Zm.UbqM1:1:2    ATAAATTGACTACAAATAAAACAAATACCCTTTAAGAAA--TAAAAAAACTAAGCAAACAT
EXP-Zm.UbqM1:1:5    ATAAATTGACTACAAATAAAACAAATACCCTTTAAGAAA--TAAAAAAACTAAGCAAACAT
EXP-Zm.UbqM1:1:1    ATAAADTGACTAAAAAATAACTAAATACCTTTTAAGAAA--TAAAAAAACTAAGCAACCAT
EXP-Zm.UbqM1:1:4    ATAAADTGACTAAAAATTAAACAAATACCCTTTAAGAAATTAAAAAAACTAAGCAACCAT
                    ***** ****** *** ** ******* ********* ************* ** ***

EXP-Zm.UbqM1:1:2    TTTTCTTGTTTCGAGTAGATAATGACAGGCTGTTCAACGCCGTCGACGAGTCTAACGGAC
EXP-Zm.UbqM1:1:5    TTTTCTTGTTTCGAGTAGATAATGACAGGCTGTTCAACGCCGTCGACGAGTCTAACGGAC
EXP-Zm.UbqM1:1:1    TTTTCTTGTTTCGAGTAGATAATGACAGCCTGTTCAACGCCGTCGACGAGTCTAACGGAC
EXP-Zm.UbqM1:1:4    TTTTCTTGTTTCGAGTAGATAATGCCAGCCTGTTAAACGCCGTCGACGAGTCTAACGGAC
                    ********** ************** *** ***** ************************

EXP-Zm.UbqM1:1:2    ACCAACCAGCGAACCAGCAGCGTCGCGTCGGGCCAAGCGAAGCAGACGGCACGGCATCTC
EXP-Zm.UbqM1:1:5    ACCAACCAGCGAACCAGCAGCGTCGCGTCGGGCCAAGCGAAGCAGACGGCACGGCATCTC
EXP-Zm.UbqM1:1:1    ACCAACCAGCGAACCAGCAGCGTCGCGTCGGGCCAAGCGAAGCAGACGGCACGGCATCTC
EXP-Zm.UbqM1:1:4    ACCAACCAGCGAACCAGCAGCGTCGCGTCGGGCCAAGCGAAGCAGACGGCACGGCATCTC
                    ************************************************************

EXP-Zm.UbqM1:1:2    TGTAGCTGCCTCTGGACCGCTCTCGAGAGTTCCGCTCCAGCGTTGGACTTGCTCCGCTGT
EXP-Zm.UbqM1:1:5    TGTAGCTGCCTCTGGACCGCTCTCGAGAGTTCCGCTCCAGCGTTGGACTTGCTCCGCTGT
EXP-Zm.UbqM1:1:1    TGTAGCTGCCTCTGGACCGCTCTCGAGAGTTCCGCTCCAGCGTTGGACTTGCTCCGCTGT
EXP-Zm.UbqM1:1:4    TGTAGCTGCCTCTGGACCGCTCTCGAGAGTTCCGCTCCAGCGTTGGACTTGCTCCGCTGT
                    *** ********************************************************

EXP-Zm.UbqM1:1:2    CGGCATCCAGAAATTGCGTGGCGGAGCGGCAGACGTGAGCCGCCACGGCAGGCGGCCTCT
EXP-Zm.UbqM1:1:5    CGGCATCCAGAAATTGCGTGGCGGAGCGGCAGACGTGAGCCGCCACGGCAGGCGGCCTCT
EXP-Zm.UbqM1:1:1    CGGCATCCAGAAATTGCGTGGCGGAGCGGCAGACGTGAGCCGCCACGGCAGGCGG-----
EXP-Zm.UbqM1:1:4    CGGCATCCAGAAATTGCGTGGCGGAGCGGCAGACGTGAGCCGCCACGGCAGGCGGCCTCC
                    ****************************************** ***************

EXP-Zm.UbqM1:1:2    TCCTTCCTCTCACGGCACCGGCAGCTACGGGGGATTCCTTTCCCACCGCTCCTTCGCTTTC
EXP-Zm.UbqM1:1:5    TCCTTCCTCTCACGGCACCGGCAGCTACGGGGGATTCCTTTCCCACCGCTCCTTCGCTTTC
EXP-Zm.UbqM1:1:1    -CCTTCCTCTCACGGCACCGGCAGCTACGGGGGATTCCTTTCCCACCGCTCCTTCGCTTTC
EXP-Zm.UbqM1:1:4    TCCTTCCTCTCACGGCACCGGCAGCTACGGGGGATTCCTTTCCCACCGCTCCTTCGCTTTC
                     ************************************************************

EXP-Zm.UbqM1:1:2    CCTTCCTCGCCCGCCGTAATAAATAGACACCCCCTCCACACCCTCTTTCCCCAACCTCGT
EXP-Zm.UbqM1:1:5    CCTTCCTCGCCCGCCGTAATAAATAGACACCCCCTCCACACCCTCTTTCCCCAACCTCGT
EXP-Zm.UbqM1:1:1    CCTTCCTCGCCCGCCGTAATAAATAG--ACCCCCTCCACACCCTCTTTCCCCAACCTCGT
EXP-Zm.UbqM1:1:4    CCTTCCTCGCCCGCCGTAATAAATAGACACCCCCTCCACACCCTCTTTCCCCAACCTCGT
                    **************************  *************** ******************

EXP-Zm.UbqM1:1:2    GTTCGTTCGGAGCGCACACACACGCAACCAGATCTCCCCCAAATCCAGCCGTCGGCACCT
EXP-Zm.UbqM1:1:5    GTTCGTTCGGAGCGCACACACACGCAACCAGATCTCCCCCAAATCCAGCCGTCGGCACCT
EXP-Zm.UbqM1:1:1    GTTCGTTCGGAGCGCGCACACACACAACCAGATCTCCCCCAAATCCAGCCGTCGGCACCT
EXP-Zm.UbqM1:1:4    GTT-GTTCGGAGCGCACACACACACAACCAGATCTCCCCCAAATCCAGCCGTCGGCACCT
                    *** ************ ******** ************************ ************
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FIG. 4b

FIG. 4c

FIG. 4d

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EXP-Zm.UbqM1:1:2      CCTATCTATTATAATAAACAAGTATGTTTTATATAATTATTTTGATCTTGATATACTTGGAT
EXP-Zm.UbqM1:1:5      CCTATCTATTATAATAAACAAGTATGTTTTATATAATTATTTTGATCTTGATATACTTGGAT
EXP-Zm.UbqM1:1:1      CCTATCTATTATAATAAACAAGTATGTTTTATATAATTATTTTGATCTTGATATACTTGGAT
EXP-Zm.UbqM1:1:4      CCTATCTATTATAATAAACAAGTATGTTTTATATAATTATTTTGATCTTGATATACTTGGAT
                      ************************************************************

EXP-Zm.UbqM1:1:2      GATGGCATATGCAGCAGCTATATGTGGA-TTTTTTAGCCCTGCCTTCATACGCTATTTAT
EXP-Zm.UbqM1:1:5      GATGGCATATGCAGCAGCTATATGTGGA-TTTTTTAGCCCTGCCTTCATACGCTATTTAT
EXP-Zm.UbqM1:1:1      GATGGCATATGCAGCAGCTATATGTGGATTTTTTTAGCCCTGCCTTCATACGCTATTTAT
EXP-Zm.UbqM1:1:4      GATGGCATATGCAGCAGCTATATGTGGATTTTTTTAGCCCTGCCTTCATACGCTATTTAT
                      ***************************** ****************************

EXP-Zm.UbqM1:1:2      TTGCTTGGTACTGTTTCTTTTGTCCGATGCTCACCCTGTTGTTTGGTGATACTTCTGCAG
EXP-Zm.UbqM1:1:5      TTGCTTGGTACTGTTTCTTTTGTCCGATGCTCACCCTGTTGTTTGGTGATACTTCTGCAG
EXP-Zm.UbqM1:1:1      TTGCTTGGTACTGTTTCTTTTGT-CGATGCTCACCCTGTTGTTTGGTGATACTTCTGCAG
EXP-Zm.UbqM1:1:4      TTGCTTGGTACTGTTTCTTTTGT-CGATGCTCACCCTGTTGTTTGGTGATACTTCTGCAG
                      ************************ ******************* ****************
```

FIG. 4e

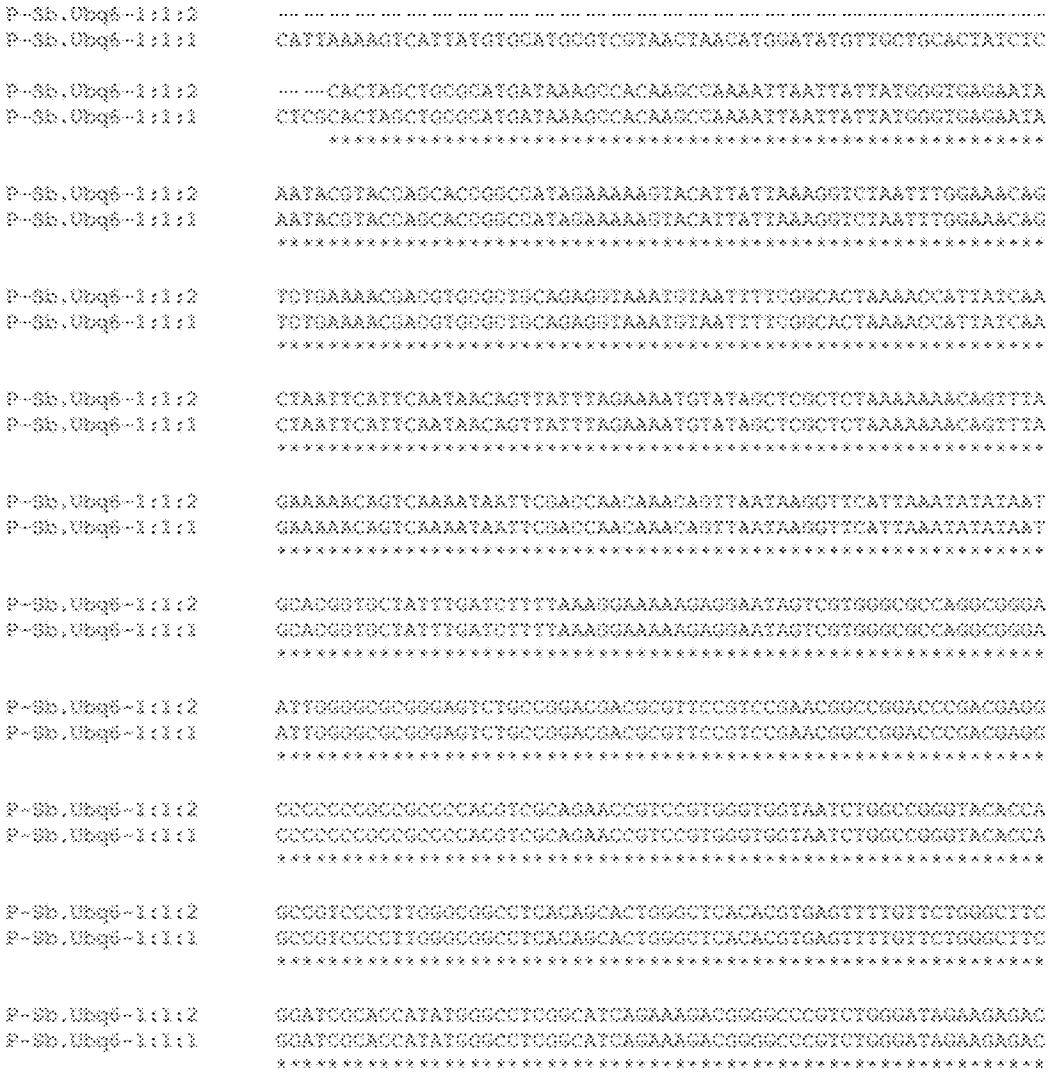

FIG. 5a

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P-Sb.Ubq6-1:1:2     AGGAACCTCCTCGTGGATTCCAGAAGCCAGCCACGAGCGACCACCGACGCGGAGGATACT
P-Sb.Ubq6-1:1:1     AGGAACCTCCTCGTGGATTCCAGAAGCCAGCCACGAGCGACCACCGACGCGGAGGATACT
                    ************************************************************

P-Sb.Ubq6-1:1:2     CGTCGTCCAAGTCCAACACGGCGGGCGGGCGGGCGGACGCGTGGGCTGGGCTAACTGCCT
P-Sb.Ubq6-1:1:1     CGTCGTCCAAGTCCAACACGGCGGGCGGGCGGGCGGACGCGTGGGCTGGGCTAACTGCCT
                    ************************************************************

P-Sb.Ubq6-1:1:2     AACCTTAACCTCCAAGGCACGCCAAGGCCCGCTTCTCCCACCCGACATAAATATCCCCCC
P-Sb.Ubq6-1:1:1     AACCTTAACCTCCAAGGCACGCCAAGGCCCGCTTCTCCCACCCGACATAAATATCCCCCC
                    ************************************************************

P-Sb.Ubq6-1:1:2     ATCCAGGCAAGGCGC
P-Sb.Ubq6-1:1:1     ATCCAGGCAAGGCGC
                    ***************
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FIG. 5b

FIG. 6a

FIG. 6b

FIG. 6c

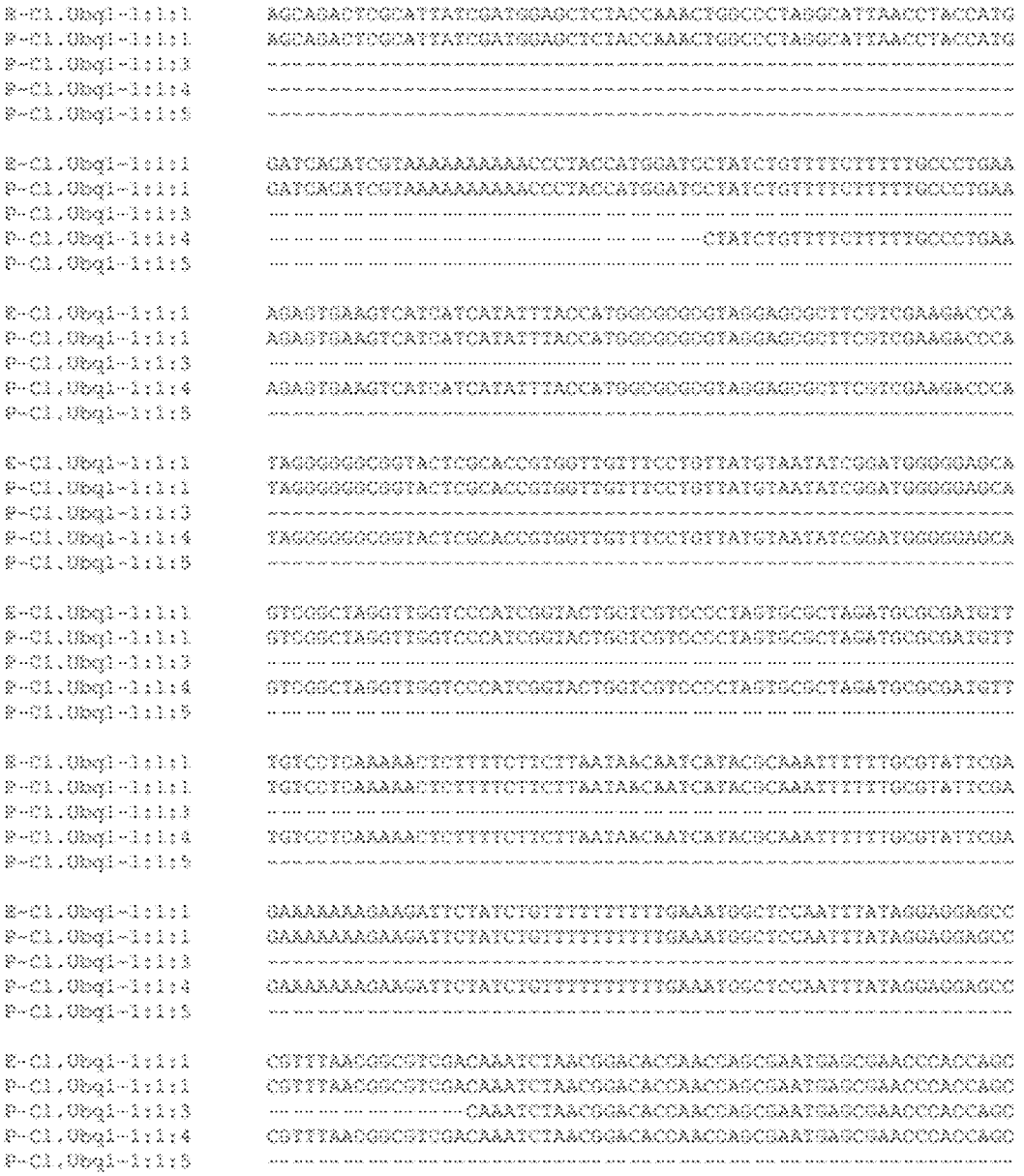

FIG. 7a

FIG. 7b

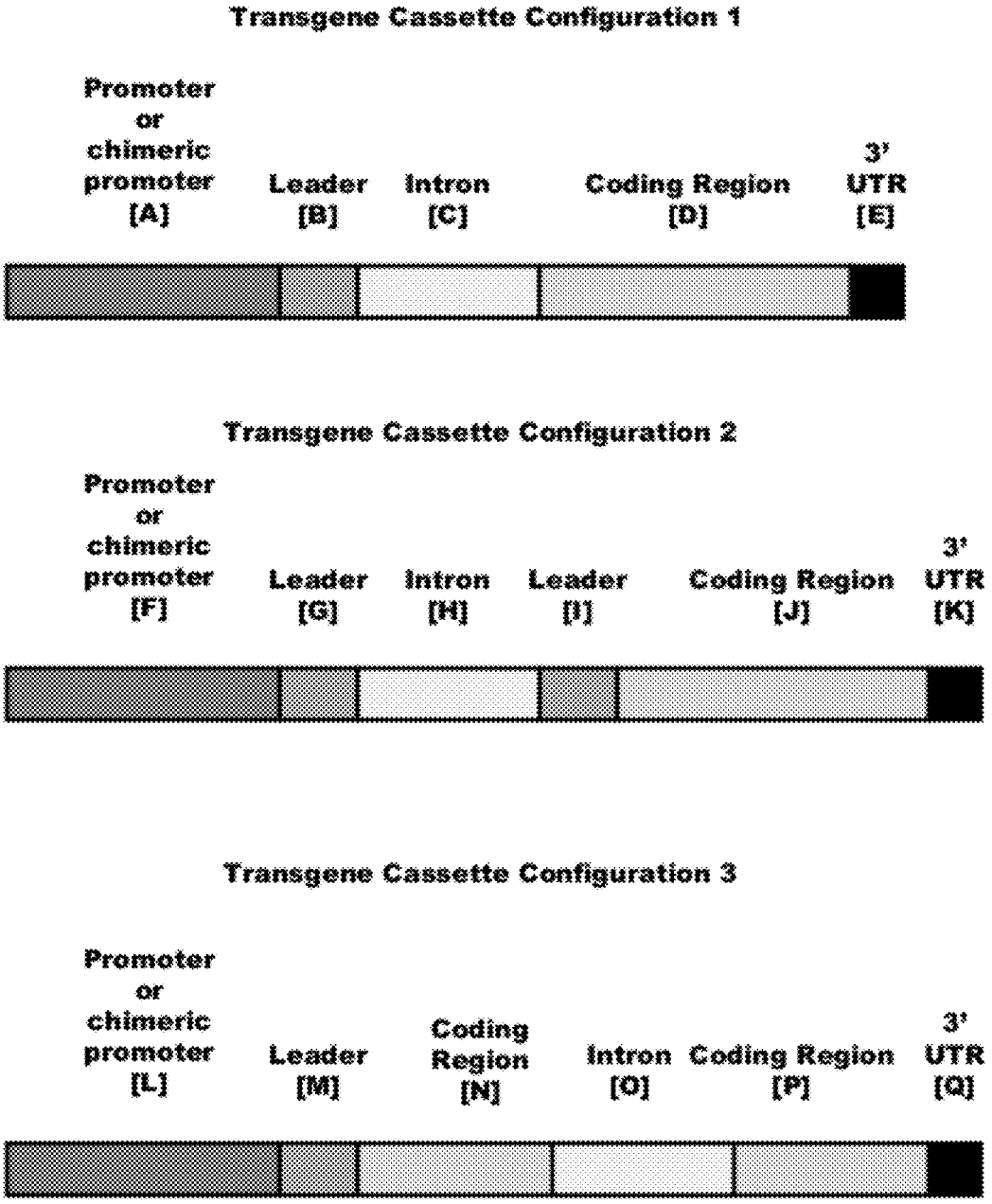
Transgene Cassette Configuration 1
Promoter or chimeric promoter [A]
Leader [B]
Intron [C]
Coding Region [D]
3' UTR [E]
Transgene Cassette Configuration 2
Promoter or chimeric promoter [F]
Leader [G]
Intron [H]
Leader [I]
Coding Region [J]
3' UTR [K]
Transgene Cassette Configuration 3
Promoter or chimeric promoter [L]
Leader [M]
Coding Region [N]
Intron [O]
Coding Region [P]
3' UTR [Q]

FIG. 8

PLANT REGULATORY ELEMENTS AND USES THEREOF

REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. provisional application No. 61/467,875 filed Mar. 25, 2011 which is herein incorporated by reference in its entirety.

INCORPORATION OF SEQUENCE LISTING

[0002] The sequence listing that is contained in the file named "MONS282US_seq.txt", which is 347 KB (as measured in Microsoft Windows®) and was created on Mar. 21, 2012, is filed herewith by electronic submission and is incorporated by reference herein.

FIELD OF THE INVENTION

[0003] The invention relates to the field of plant molecular biology and plant genetic engineering, and DNA molecules useful for modulating gene expression in plants.

BACKGROUND

[0004] Regulatory elements are genetic elements that regulate gene activity by modulating the transcription of an operably linked transcribable polynucleotide molecule. Such elements include promoters, leaders, introns, and 3' untranslated regions and are useful in the field of plant molecular biology and plant genetic engineering.

SUMMARY OF THE INVENTION

[0005] The present invention provides novel gene regulatory elements for use in plants. The present invention also provides DNA constructs comprising the regulatory elements. The present invention also provides transgenic plant cells, plants, and seeds comprising the regulatory elements. The sequences may be provided operably linked to a transcribable polynucleotide molecule. In one embodiment, the transcribable polynucleotide molecule may be heterologous with respect to a regulatory sequence provided herein. A regulatory element sequence provided by the invention thus may, in particular embodiments, be defined as operably linked to a heterologous transcribable polynucleotide molecule. The present invention also provides methods of making and using the regulatory elements, the DNA constructs comprising the regulatory elements, and the transgenic plant cells, plants, and seeds comprising the regulatory elements operably linked to a transcribable polynucleotide molecule.

[0006] Thus, in one aspect, the present invention provides a DNA molecule comprising a DNA sequence selected from the group consisting of: a) a sequence with at least about 85 percent sequence identity to any of SEQ ID NOs: 1-158 and 180-183; b) a sequence comprising any of SEQ ID NOs: 1-158 and 180-183; and c) a fragment of any of SEQ ID NOs: 1-158 and 180-183, wherein the fragment has gene-regulatory activity; wherein the sequence is operably linked to a heterologous transcribable polynucleotide molecule. In specific embodiments, the DNA molecule comprises at least about 90 percent, at least about 95 percent, at least about 98 percent, or at least about 99 percent sequence identity to the DNA sequence of any of SEQ ID NOs: 1-158 and 180-183. In certain embodiments of the DNA molecule, the DNA sequence comprises a regulatory element. In some embodiments the regulatory element comprises a promoter. In particular embodiments, the heterologous transcribable polynucleotide molecule comprises a gene of agronomic interest, such as a gene capable of providing herbicide resistance in plants, or a gene capable of providing plant pest resistance in plants.

[0007] The invention also provides a transgenic plant cell comprising a heterologous DNA construct provided by the invention, including a sequence of any of SEQ ID NOs: 1-158 and 180-183, or a fragment or variant thereof, wherein said sequence is operably linked to a heterologous transcribable polynucleotide molecule. In certain embodiments, the transgenic plant cell is a monocotyledonous plant cell. In other embodiments, the transgenic plant cell is a dicotyledonous plant cell.

[0008] Further provided by the invention is a transgenic plant, or part thereof, comprising a DNA molecule as provided herein, including a DNA sequence selected from the group consisting of: a) a sequence with at least 85 percent sequence identity to any of SEQ ID NOs: 1-158 and 180-183; b) a sequence comprising any of SEQ ID NOs: 1-158 and 180-183; and c) a fragment of any of SEQ ID NOs: 1-158 and 180-183, wherein the fragment has gene-regulatory activity; wherein the sequence is operably linked to a heterologous transcribable polynucleotide molecule. In specific embodiments, the transgenic plant may be a progeny plant of any generation that comprises the DNA molecule, relative to a starting transgenic plant comprising the DNA molecule. Still further provided is a transgenic seed comprising a DNA molecule according to the invention.

[0009] In yet another aspect, the invention provides a method of producing a commodity product comprising obtaining a transgenic plant or part thereof according to the invention and producing the commodity product therefrom. In one embodiment, a commodity product of the invention is protein concentrate, protein isolate, grain, starch, seeds, meal, flour, biomass, or seed oil. In another aspect, the invention provides a commodity produced using the above method. For instance, in one embodiment the invention provides a commodity product comprising a DNA molecule as provided herein, including a DNA sequence selected from the group consisting of: a) a sequence with at least 85 percent sequence identity to any of SEQ ID NOs: 1-158 and 180-183; b) a sequence comprising any of SEQ ID NOs: 1-158 and 180-183; and c) a fragment of any of SEQ ID NOs: 1-158 and 180-183, wherein the fragment has gene-regulatory activity; wherein the sequence is operably linked to a heterologous transcribable polynucleotide molecule.

[0010] In still yet another aspect, the invention provides a method of expressing a transcribable polynucleotide molecule that comprises obtaining a transgenic plant according to the invention, such as a plant comprising a DNA molecule as described herein, and cultivating plant, wherein a transcribable polynucleotide in the DNA molecule is expressed.

[0011] Throughout this specification and the claims, unless the context requires otherwise, the word "comprise" and its variations, such as "comprises" and "comprising," will be understood to imply the inclusion of a stated composition, step, and/or value, or group thereof, but not the exclusion of any other composition, step, and/or value, or group thereof.

BRIEF DESCRIPTION OF THE FIGURES

[0012] FIGS. **1***a*-**1***h* depict alignment of promoter size variants corresponding to promoter elements isolated from the grass species *Andropogon gerardii*. In particular, FIGS.

1*a*-**1***h* show alignment of the 2603 bp promoter sequence P-ANDge.Ubq1-1:1:11 (SEQ ID NO: 2), found in the transcriptional regulatory expression element group EXP-ANDge.Ubq1:1:9 (SEQ ID NO: 1), with promoter sequences derived via deletion analysis of P-ANDge.Ubq1-1:1:11. Deletion, for instance of the 5' end of P-ANDge.Ubq1-1:1:11, produced the promoter P-ANDge.Ubq1-1:1:9 (SEQ ID NO: 6), a 2114 bp sequence which is found within EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5). Other promoter sequences in FIG. **1** include P-ANDge.Ubq1-1:1:10 (SEQ ID NO: 9), a 1644 bp sequence comprised within EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8); P-ANDge.Ubq1-1:1:12 (SEQ ID NO: 11), a 1472 bp sequence comprised within EXP-ANDge.Ubq1:1:10 (SEQ ID NO: 10); P-ANDge.Ubq1-1:1:8 (SEQ ID NO: 13), a 1114 bp sequence comprised within EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12); P-ANDge.Ubq1-1:1:13 (SEQ ID NO: 15), a 771 bp sequence comprised within EXP-ANDge.Ubq1:1:11 (SEQ ID NO: 14); and P-ANDge.Ubq1-1:1:14 (SEQ ID NO: 17), a 482 bp sequence comprised within EXP-ANDge.Ubq1:1:12 (SEQ ID NO: 16).

[0013] FIGS. **2***a*-**2***g* depict alignment of promoter variants isolated from the grass *Saccharum ravennae* (*Erianthus ravennae*). In particular, FIGS. **2***a*-**2***g* show an alignment of the 2536 bp promoter sequence P-ERIra.Ubq1-1:1:10 (SEQ ID NO: 19) (found, for instance, within the transcriptional regulatory expression element group EXP-ERIra.Ubq1 (SEQ ID NO: 18)) with promoter sequences derived from deletion analysis of P-ERIra.Ubq1-1:1:10: a 2014 bp promoter sequence P-ERIra.Ubq1-1:1:9 (SEQ ID NO: 23); a 1525 bp promoter sequence P-ERIra.Ubq1-1:1:11 (SEQ ID NO: 26); a 1044 bp promoter sequence P-ERIra.Ubq1-1:1:8 (SEQ ID NO: 28); a 796 bp sequence P-ERIra.Ubq1-1:1:12 (SEQ ID NO: 30); and a 511 bp sequence P-ERIra.Ubq1-1:1:13 (SEQ ID NO: 32).

[0014] FIGS. **3***a*-**3***c* depict alignment of promoter size variants corresponding to promoter elements isolated from the grass species *Setaria viridis*. In particular, FIGS. **3***a*-**3***c* show an alignment of a 1493 bp promoter sequence, P-Sv.Ubq1-1:1:1 (SEQ ID NO: 34) with promoters derived from deletion analysis of the 5' end of P-Sv.Ubq1-1:1:1: a 1035 bp sized promoter P-Sv.Ubq1-1:1:2 (SEQ ID NO: 38); and a 681 bp promoter sequence P-Sv.Ubq1-1:1:3 (SEQ ID NO: 40).

[0015] FIGS. **4***a*-**4***e* depict alignment of transcriptional regulatory expression element group variants derived from the grass *Zea mays* subsp. *mexicana*. In particular, FIGS. **4***a*-**4***e* compare a 2005 bp transcriptional regulatory expression element group termed EXP-Zm.UbqM1:1:2 (SEQ ID NO: 49) with allelic variant EXP-Zm.UbqM1:1:5 (SEQ ID NO: 53), as well as with size variants EXP-Zm.UbqM1:1:1 (SEQ ID NO: 41), which is 1922 bps in length, and EXP-Zm.UbqM1:1:4 (SEQ ID NO: 45), which is 1971 bps in length.

[0016] FIGS. **5***a*-**5***b* depict alignment of promoter size variants isolated from the grass *Sorghum bicolor*. In particular, FIGS. **5***a*-**5***b* shows alignment of the 791 bp sized promoter element, P-Sb.Ubq6-1:1:2 (SEQ ID NO: 60) comprised within the transcriptional regulatory expression element group EXP-Sb.Ubq6 (SEQ ID NO: 59), with 855 bp promoter element P-Sb.Ubq6-1:1:1 (SEQ ID NO: 64) comprised within EXP-Sb.Ubq6:1:1 (SEQ ID NO: 63).

[0017] FIGS. **6***a*-**6***c* depict alignment of promoter size variants corresponding to promoter elements isolated from the grass *Setaria italica*. In particular, FIGS. **6***a*-**6***c* show an alignment of the 1492 bp promoter variant P-SETit.Ubq1-1:1:1 (SEQ ID NO: 70) with 1492 bp promoter variant P-SETit.Ubq1-1:1:4 (SEQ ID NO: 74), 1034 bp promoter element P-SETit.Ubq1-1:1:2 (SEQ ID NO: 76), and 680 bp promoter element P-SETit.Ubq1-1:1:3 (SEQ ID NO: 78).

[0018] FIGS. **7***a*-**7***b* depict alignment of promoter size variants and an enhancer element corresponding to promoter elements isolated from the grass species *Coix lachryma-jobi*. In particular, FIGS. **7***a* and **7***b* show an alignment of the 837 bp promoter variant, P-Cl.Ubq1-1:1:1 (SEQ ID NO: 80) found within transcriptional regulatory expression element group EXP-Cl.Ubq1:1:1 (SEQ ID NO: 79), with an enhancer fragment derived from P-Cl.Ubq1-1:1:1, termed E-Cl.Ubq1:1:1 (SEQ ID NO: 89) that is 798 bp in length, as well as with three 5' end deletion variants of P-Cl.Ubq1-1:1:1: a 742 bp element P-Cl.Ubq1-1:1:4 (SEQ ID NO: 84); a 401 bp element P-Cl.Ubq1-1:1:3 (SEQ ID NO: 86); and a 54 bp minimal promoter element P-Cl.Ubq1-1:1:5 (SEQ ID NO: 88).

[0019] FIG. **8** depicts transgene cassette configurations of the present invention.

BRIEF DESCRIPTION OF THE SEQUENCES

[0020] SEQ ID NOS: 1, 5, 8, 10, 12, 14, 16, 18, 22, 25, 27, 29, 31, 33, 37, 39, 41, 45, 49, 53, 55, 59, 63, 65, 69, 73, 75, 77, 79, 83, 85, 87, 90, 93, 95, 97, 98, 99, 100, 102, 104, 106, 108, 110, 112, 114, 115, 116, 117, 119, 121, 123, 124, 125, 126, 128, 130, 132, 133, 134, 136, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 180, 181 and 183 are sequences of transcriptional regulatory expression element groups or EXP sequences comprising a promoter sequence operably linked 5' to a leader sequence which is operably linked 5' to an intron sequence.

[0021] SEQ ID NOS: 2, 6, 9, 11, 13, 15, 17, 19, 23, 26, 28, 30, 32, 34, 38, 40, 42, 46, 50, 56, 60, 64, 66, 70, 74, 76, 78, 80, 84, 86, 88, 91, 96 and 135 are promoter sequences.

[0022] SEQ ID NOS: 3, 20, 35, 43, 47, 51, 57, 61, 67, 71 and 81 are leader sequences.

[0023] SEQ ID NOS: 4, 7, 21, 24, 36, 44, 48, 52, 54, 58, 62, 68, 72, 82, 92, 94, 101, 103, 105, 107, 109, 111, 113, 118, 120, 122, 127, 129, 131, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158 and 182 are intron sequences.

[0024] SEQ ID NO: 89 is the sequence of an enhancer.

DETAILED DESCRIPTION OF THE INVENTION

[0025] The invention disclosed herein provides polynucleotide molecules having beneficial gene regulatory activity from plant species. The design, construction, and use of these polynucleotide molecules are provided by the invention. The nucleotide sequences of these polynucleotide molecules are provided among SEQ ID NOs: 1-158 and 180-183. These polynucleotide molecules are, for instance, capable of affecting the expression of an operably linked transcribable polynucleotide molecule in plant tissues, and therefore selectively regulating gene expression, or activity of an encoded gene product, in transgenic plants. The present invention also provides methods of modifying, producing, and using the same. The invention also provides compositions, transformed host cells, transgenic plants, and seeds containing the promoters and/or other disclosed nucleotide sequences, and methods for preparing and using the same.

[0026] The following definitions and methods are provided to better define the present invention and to guide those of ordinary skill in the art in the practice of the present invention.

Unless otherwise noted, terms are to be understood according to conventional usage by those of ordinary skill in the relevant art.

DNA Molecules

[0027] As used herein, the term "DNA" or "DNA molecule" refers to a double-stranded DNA molecule of genomic or synthetic origin, i.e. a polymer of deoxyribonucleotide bases or a polynucleotide molecule, read from the 5' (upstream) end to the 3' (downstream) end. As used herein, the term "DNA sequence" refers to the nucleotide sequence of a DNA molecule. The nomenclature used herein corresponds to that of by Title 37 of the United States Code of Federal Regulations §1.822, and set forth in the tables in WIPO Standard ST.25 (1998), Appendix 2, Tables 1 and 3.

[0028] As used herein, the term "isolated DNA molecule" refers to a DNA molecule at least partially separated from other molecules normally associated with it in its native or natural state. In one embodiment, the term "isolated" refers to a DNA molecule that is at least partially separated from some of the nucleic acids which normally flank the DNA molecule in its native or natural state. Thus, DNA molecules fused to regulatory or coding sequences with which they are not normally associated, for example as the result of recombinant techniques, are considered isolated herein. Such molecules are considered isolated when integrated into the chromosome of a host cell or present in a nucleic acid solution with other DNA molecules, in that they are not in their native state.

[0029] Any number of methods well known to those skilled in the art can be used to isolate and manipulate a DNA molecule, or fragment thereof, disclosed in the present invention. For example, PCR (polymerase chain reaction) technology can be used to amplify a particular starting DNA molecule and/or to produce variants of the original molecule. DNA molecules, or fragment thereof, can also be obtained by other techniques such as by directly synthesizing the fragment by chemical means, as is commonly practiced by using an automated oligonucleotide synthesizer.

[0030] As used herein, the term "sequence identity" refers to the extent to which two optimally aligned polynucleotide sequences or two optimally aligned polypeptide sequences are identical. An optimal sequence alignment is created by manually aligning two sequences, e.g. a reference sequence and another sequence, to maximize the number of nucleotide matches in the sequence alignment with appropriate internal nucleotide insertions, deletions, or gaps. As used herein, the term "reference sequence" refers to a sequence provided as the polynucleotide sequences of SEQ ID NOs: 1-158 and 180-183.

[0031] As used herein, the term "percent sequence identity" or "percent identity" or "% identity" is the identity fraction times 100. The "identity fraction" for a sequence optimally aligned with a reference sequence is the number of nucleotide matches in the optimal alignment, divided by the total number of nucleotides in the reference sequence, e.g. the total number of nucleotides in the full length of the entire reference sequence. Thus, one embodiment of the invention is a DNA molecule comprising a sequence that when optimally aligned to a reference sequence, provided herein as SEQ ID NOs: 1-158 and 180-183, has at least about 85 percent identity, at least about 90 percent identity, at least about 95 percent identity, at least about 96 percent identity, at least about 97 percent identity, at least about 98 percent identity, or at least about 99 percent identity to the reference sequence. In particular embodiments such sequences may be defined as having gene-regulatory activity.

Regulatory Elements

[0032] A regulatory element is a DNA molecule having gene regulatory activity, i.e. one that has the ability to affect the transcription and/or translation of an operably linked transcribable polynucleotide molecule. The term "gene regulatory activity" thus refers to the ability to affect the expression pattern of an operably linked transcribable polynucleotide molecule by affecting the transcription and/or translation of that operably linked transcribable polynucleotide molecule. As used herein, a transcriptional regulatory expression element group or "EXP" sequence may be comprised of expression elements, such as enhancers, promoters, leaders and introns, operably linked. Thus a transcriptional regulatory expression element group may be comprised, for instance, of a promoter operably linked 5' to a leader sequence, which is in turn operably linked 5' to an intron sequence. The intron sequence may be comprised of a sequence beginning at the point of the first intron/exon splice junction of the native sequence and further may be comprised of a small leader fragment comprising the second intron/exon splice junction so as to provide for proper intron/exon processing to facilitate transcription and proper processing of the resulting transcript. Leaders and introns may positively affect transcription of an operably linked transcribable polynucleotide molecule as well as translation of the resulting transcribed RNA. The pre-processed RNA molecule comprises leaders and introns, which may affect the post-transcriptional processing of the transcribed RNA and/or the export of the transcribed RNA molecule from the cell nucleus into the cytoplasm. Following post-transcriptional processing of the transcribed RNA molecule, the leader sequence may be retained as part of the final messenger RNA and may positively affect the translation of the messenger RNA molecule.

[0033] Regulatory elements such as promoters, leaders, introns, and transcription termination regions (or 3' UTRs) are DNA molecules that have gene regulatory activity and play an integral part in the overall expression of genes in living cells. The term "regulatory element" refers to a DNA molecule having gene regulatory activity, i.e. one that has the ability to affect the transcription and/or translation of an operably linked transcribable polynucleotide molecule. Isolated regulatory elements, such as promoters and leaders that function in plants are therefore useful for modifying plant phenotypes through the methods of genetic engineering.

[0034] Regulatory elements may be characterized by their expression pattern effects (qualitatively and/or quantitatively), e.g. positive or negative effects and/or constitutive or other effects such as by their temporal, spatial, developmental, tissue, environmental, physiological, pathological, cell cycle, and/or chemically responsive expression pattern, and any combination thereof, as well as by quantitative or qualitative indications. A promoter is useful as a regulatory element for modulating the expression of an operably linked transcribable polynucleotide molecule.

[0035] As used herein, a "gene expression pattern" is any pattern of transcription of an operably linked DNA molecule into a transcribed RNA molecule. The transcribed RNA molecule may be translated to produce a protein molecule or may provide an antisense or other regulatory RNA molecule, such as a dsRNA, a tRNA, an rRNA, a miRNA, and the like.

[0036] As used herein, the term "protein expression" is any pattern of translation of a transcribed RNA molecule into a protein molecule. Protein expression may be characterized by its temporal, spatial, developmental, or morphological qualities as well as by quantitative or qualitative indications.

[0037] As used herein, the term "promoter" refers generally to a DNA molecule that is involved in recognition and binding of RNA polymerase II and other proteins (trans-acting transcription factors) to initiate transcription. A promoter may be initially isolated from the 5' untranslated region (5' UTR) of a genomic copy of a gene. Alternately, promoters may be synthetically produced or manipulated DNA molecules. Promoters may also be chimeric, that is a promoter produced through the fusion of two or more heterologous DNA molecules. Promoters useful in practicing the present invention include SEQ ID NOS: 2, 6, 9, 11, 13, 15, 17, 19, 23, 26, 28, 30, 32, 34, 38, 40, 42, 46, 50, 56, 60, 64, 66, 70, 74, 76, 78, 80, 84, 86, 88, 91, 96 and 135, or fragments or variants thereof. In specific embodiments of the invention, such molecules and any variants or derivatives thereof as described herein, are further defined as comprising promoter activity, i.e., are capable of acting as a promoter in a host cell, such as in a transgenic plant. In still further specific embodiments, a fragment may be defined as exhibiting promoter activity possessed by the starting promoter molecule from which it is derived, or a fragment may comprise a "minimal promoter" which provides a basal level of transcription and is comprised of a TATA box or equivalent sequence for recognition and binding of the RNA polymerase II complex for initiation of transcription.

[0038] In one embodiment, fragments are provided of a promoter sequence disclosed herein. Promoter fragments may comprise promoter activity, as described above, and may be useful alone or in combination with other promoters and promoter fragments, such as in constructing chimeric promoters. In specific embodiments, fragments of a promoter are provided comprising at least about 50, 95, 150, 250, 500, 750, or at least about 1000 contiguous nucleotides, or longer, of a polynucleotide molecule having promoter activity disclosed herein.

[0039] Compositions derived from any of the promoters presented as SEQ ID NOS: 2, 6, 9, 11, 13, 15, 17, 19, 23, 26, 28, 30, 32, 34, 38, 40, 42, 46, 50, 56, 60, 64, 66, 70, 74, 76, 78, 80, 84, 86, 88, 91, 96 and 135, such as internal or 5' deletions, for example, can be produced using methods known in the art to improve or alter expression, including by removing elements that have either positive or negative effects on expression; duplicating elements that have positive or negative effects on expression; and/or duplicating or removing elements that have tissue or cell specific effects on expression. Compositions derived from any of the promoters presented as SEQ ID NOS: 2, 6, 9, 11, 13, 15, 17, 19, 23, 26, 28, 30, 32, 34, 38, 40, 42, 46, 50, 56, 60, 64, 66, 70, 74, 76, 78, 80, 84, 86, 88, 91, 96 and 135 comprised of 3' deletions in which the TATA box element or equivalent sequence thereof and downstream sequence is removed can be used, for example, to make enhancer elements. Further deletions can be made to remove any elements that have positive or negative; tissue specific; cell specific; or timing specific (such as, but not limited to, circadian rhythms) effects on expression. Any of the promoters presented as SEQ ID NOS: 2, 6, 9, 11, 13, 15, 17, 19, 23, 26, 28, 30, 32, 34, 38, 40, 42, 46, 50, 56, 60, 64, 66, 70, 74, 76, 78, 80, 84, 86, 88, 91, 96 and 135 and fragments or enhancers derived there from can be used to make chimeric transcriptional regulatory element compositions comprised of any of the promoters presented as SEQ ID NOS: 2, 6, 9, 11, 13, 15, 17, 19, 23, 26, 28, 30, 32, 34, 38, 40, 42, 46, 50, 56, 60, 64, 66, 70, 74, 76, 78, 80, 84, 86, 88, 91, 96 and 135 and the fragments or enhancers derived therefrom operably linked to other enhancers and promoters. The efficacy of the modifications, duplications or deletions described herein on the desired expression aspects of a particular transgene may be tested empirically in stable and transient plant assays, such as those described in the working examples herein, so as to validate the results, which may vary depending upon the changes made and the goal of the change in the starting molecule.

[0040] As used herein, the term "leader" refers to a DNA molecule isolated from the untranslated 5' region (5' UTR) of a genomic copy of a gene and defined generally as a nucleotide segment between the transcription start site (TSS) and the protein coding sequence start site. Alternately, leaders may be synthetically produced or manipulated DNA elements. A leader can be used as a 5' regulatory element for modulating expression of an operably linked transcribable polynucleotide molecule. Leader molecules may be used with a heterologous promoter or with their native promoter. Promoter molecules of the present invention may thus be operably linked to their native leader or may be operably linked to a heterologous leader. Leaders useful in practicing the present invention include SEQ ID NOS: 3, 20, 35, 43, 47, 51, 57, 61, 67, 71 and 81 or fragments or variants thereof. In specific embodiments, such sequences may be provided defined as being capable of acting as a leader in a host cell, including, for example, a transgenic plant cell. In one embodiment such sequences are decoded as comprising leader activity.

[0041] The leader sequences (5' UTR) presented as SEQ ID NOS: 3, 20, 35, 43, 47, 51, 57, 61, 67, 71 and 81 may be comprised of regulatory elements or may adopt secondary structures that can have an effect on transcription or translation of a transgene. The leader sequences presented as SEQ ID NOS: 3, 20, 35, 43, 47, 51, 57, 61, 67, 71 and 81 can be used in accordance with the invention to make chimeric regulatory elements that affect transcription or translation of a transgene. In addition, the leader sequences presented as SEQ ID NOS: 3, 20, 35, 43, 47, 51, 57, 61, 67, 71 and 81 can be used to make chimeric leader sequences that affect transcription or translation of a transgene.

[0042] The introduction of a foreign gene into a new plant host does not always result in a high expression of the incoming gene. Furthermore, if dealing with complex traits, it is sometimes necessary to modulate several genes with spatially or temporarily different expression pattern. Introns can principally provide such modulation. However multiple use of the same intron in one plant has shown to exhibit disadvantages. In those cases it is necessary to have a collection of basic control elements for the construction of appropriate recombinant DNA elements. As the available collection of introns known in the art with expression enhancing properties is limited, alternatives are needed.

[0043] Compositions derived from any of the introns presented as SEQ ID NOS: 4, 7, 21, 24, 36, 44, 48, 52, 54, 58, 62, 68, 72, 82, 92, 94, 101, 103, 105, 107, 109, 111, 113, 118, 120, 122, 127, 129, 131, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158 and 182 can be comprised of internal deletions or duplications of cis regulatory elements; and/or alterations of the 5' and 3' sequences comprising the intron/exon splice junctions can be used to improve expression or specificity of

expression when operably linked to a promoter+leader or chimeric promoter+leader and coding sequence. Alterations of the 5' and 3' regions comprising the intron/exon splice junction can also be made to reduce the potential for introduction of false start and stop codons being produced in the resulting transcript after processing and splicing of the messenger RNA. The introns can be tested empirically as described in the working examples to determine the intron's effect on expression of a transgene.

[0044] In accordance with the invention a promoter or promoter fragment may be analyzed for the presence of known promoter elements, i.e. DNA sequence characteristics, such as a TATA-box and other known transcription factor binding site motifs. Identification of such known promoter elements may be used by one of skill in the art to design variants of the promoter having a similar expression pattern to the original promoter.

[0045] As used herein, the term "enhancer" or "enhancer element" refers to a cis-acting transcriptional regulatory element, a.k.a. cis-element, which confers an aspect of the overall expression pattern, but is usually insufficient alone to drive transcription, of an operably linked polynucleotide sequence. Unlike promoters, enhancer elements do not usually include a transcription start site (TSS) or TATA box or equivalent sequence. A promoter may naturally comprise one or more enhancer elements that affect the transcription of an operably linked polynucleotide sequence. An isolated enhancer element may also be fused to a promoter to produce a chimeric promoter cis-element, which confers an aspect of the overall modulation of gene expression. A promoter or promoter fragment may comprise one or more enhancer elements that effect the transcription of operably linked genes. Many promoter enhancer elements are believed to bind DNA-binding proteins and/or affect DNA topology, producing local conformations that selectively allow or restrict access of RNA polymerase to the DNA template or that facilitate selective opening of the double helix at the site of transcriptional initiation. An enhancer element may function to bind transcription factors that regulate transcription. Some enhancer elements bind more than one transcription factor, and transcription factors may interact with different affinities with more than one enhancer domain. Enhancer elements can be identified by a number of techniques, including deletion analysis, i.e. deleting one or more nucleotides from the 5' end or internal to a promoter; DNA binding protein analysis using DNase I footprinting, methylation interference, electrophoresis mobility-shift assays, in vivo genomic footprinting by ligation-mediated PCR, and other conventional assays; or by DNA sequence similarity analysis using known cis-element motifs or enhancer elements as a target sequence or target motif with conventional DNA sequence comparison methods, such as BLAST. The fine structure of an enhancer domain can be further studied by mutagenesis (or substitution) of one or more nucleotides or by other conventional methods. Enhancer elements can be obtained by chemical synthesis or by isolation from regulatory elements that include such elements, and they can be synthesized with additional flanking nucleotides that contain useful restriction enzyme sites to facilitate subsequence manipulation. Thus, the design, construction, and use of enhancer elements according to the methods disclosed herein for modulating the expression of operably linked transcribable polynucleotide molecules are encompassed by the present invention.

[0046] In plants, the inclusion of some introns in gene constructs leads to increased mRNA and protein accumulation relative to constructs lacking the intron.

[0047] This effect has been termed "intron mediated enhancement" (IME) of gene expression (Mascarenhas et al., (1990) *Plant Mol. Biol.* 15:913-920). Introns known to stimulate expression in plants have been identified in maize genes (e.g. tubA1, Adh1, Sh1, Ubi1 (Jeon et al. (2000) *Plant Physiol.* 123:1005-1014; Callis et al. (1987) *Genes Dev.* 1:1183-1200; Vasil et al. (1989) *Plant Physiol.* 91:1575-1579; Christiansen et al. (1992) *Plant Mol. Biol.* 18:675-689) and in rice genes (e.g. salt, tpi: McElroy et al., *Plant Cell* 2:163-171 (1990); Xu et al., *Plant Physiol.* 106:459-467 (1994)). Similarly, introns from dicotyledonous plant genes like those from petunia (e.g. rbcS), potato (e.g. st-ls1) and from *Arabidopsis thaliana* (e.g. ubq3 and pat1) have been found to elevate gene expression rates (Dean et al. (1989) *Plant Cell* 1:201-208; Leon et al. (1991) *Plant Physiol.* 95:968-972; Norris et al. (1993) *Plant Mol Biol* 21:895-906; Rose and Last (1997) *Plant J.* 11:455-464). It has been shown that deletions or mutations within the splice sites of an intron reduce gene expression, indicating that splicing might be needed for IME (Mascarenhas et al. (1990) *Plant Mol Biol.* 15:913-920; Clancy and Hannah (2002) *Plant Physiol.* 130: 918-929). However, that splicing per se is not required for a certain IME in dicotyledonous plants has been shown by point mutations within the splice sites of the pat1 gene from *A. thaliana* (Rose and Beliakoff (2000) *Plant Physiol.* 122: 535-542).

[0048] Enhancement of gene expression by introns is not a general phenomenon because some intron insertions into recombinant expression cassettes fail to enhance expression (e.g. introns from dicot genes (rbcS gene from pea, phaseolin gene from bean and the stls-1 gene from *Solanum tuberosum*) and introns from maize genes (adh1 gene the ninth intron, hsp81 gene the first intron)) (Chee et al. (1986) *Gene* 41:47-57; Kuhlemeier et al. (1988) *Mol Gen Genet* 212:405-411; Mascarenhas et al. (1990) *Plant Mol. Biol.* 15:913-920; Sinibaldi and Mettler (1992) In WE Cohn, K Moldave, eds, *Progress in Nucleic Acid Research and Molecular Biology*, Vol 42. Academic Press, New York, pp 229-257; Vancanneyt et al. 1990 *Mol. Gen. Genet.* 220:245-250). Therefore, not each intron can be employed in order to manipulate the gene expression level of non-endogenous genes or endogenous genes in transgenic plants. What characteristics or specific sequence features must be present in an intron sequence in order to enhance the expression rate of a given gene is not known in the prior art and therefore from the prior art it is not possible to predict whether a given plant intron, when used heterologously, will cause enhancement of expression at the DNA level or at the transcript level (IME).

[0049] As used herein, the term "chimeric" refers to a single DNA molecule produced by fusing a first DNA molecule to a second DNA molecule, where neither first nor second DNA molecule would normally be found in that configuration, i.e. fused to the other. The chimeric DNA molecule is thus a new DNA molecule not otherwise normally found in nature. As used herein, the term "chimeric promoter" refers to a promoter produced through such manipulation of DNA molecules. A chimeric promoter may combine two or more DNA fragments; an example would be the fusion of a promoter to an enhancer element. Thus, the design, construction, and use of chimeric promoters according to the methods disclosed herein for modulating the expression of operably

linked transcribable polynucleotide molecules are encompassed by the present invention.

[0050] As used herein, the term "variant" refers to a second DNA molecule that is in composition similar, but not identical to, a first DNA molecule and yet the second DNA molecule still maintains the general functionality, i.e. same or similar expression pattern, of the first DNA molecule. A variant may be a shorter or truncated version of the first DNA molecule and/or an altered version of the sequence of the first DNA molecule, such as one with different restriction enzyme sites and/or internal deletions, substitutions, and/or insertions. A "variant" can also encompass a regulatory element having a nucleotide sequence comprising a substitution, deletion and/or insertion of one or more nucleotides of a reference sequence, wherein the derivative regulatory element has more or less or equivalent transcriptional or translational activity than the corresponding parent regulatory molecule. The regulatory element "variants" will also encompass variants arising from mutations that naturally occur in bacterial and plant cell transformation. In the present invention, a polynucleotide sequence provided as SEQ ID NOs: 1-158 and 180-183 may be used to create variants that are in composition similar, but not identical to, the polynucleotide sequence of the original regulatory element, while still maintaining the general functionality, i.e. same or similar expression pattern, of the original regulatory element. Production of such variants of the present invention is well within the ordinary skill of the art in light of the disclosure and is encompassed within the scope of the present invention. Chimeric regulatory element "variants" comprise the same constituent elements as a reference sequence but the constituent elements comprising the chimeric regulatory element may be operatively linked by various methods known in the art such as, restriction enzyme digestion and ligation, ligation independent cloning, modular assembly of PCR products during amplification, or direct chemical synthesis of the regulatory element as well as other methods known in the art. The resulting chimeric regulatory element "variant" can be comprised of the same, or variants of the same, constituent elements of the reference sequence but differ in the sequence or sequences that comprise the linking sequence or sequences which allow the constituent parts to be operatively linked. In the present invention, a polynucleotide sequence provided as SEQ ID NOs: 1-158 and 180-183 provide a reference sequence wherein the constituent elements that comprise the reference sequence may be joined by methods known in the art and may comprise substitutions, deletions and/or insertions of one or more nucleotides or mutations that naturally occur in bacterial and plant cell transformation.

Constructs

[0051] As used herein, the term "construct" means any recombinant polynucleotide molecule such as a plasmid, cosmid, virus, autonomously replicating polynucleotide molecule, phage, or linear or circular single-stranded or double-stranded DNA or RNA polynucleotide molecule, derived from any source, capable of genomic integration or autonomous replication, comprising a polynucleotide molecule where one or more polynucleotide molecule has been linked in a functionally operative manner, i.e. operably linked. As used herein, the term "vector" means any recombinant polynucleotide construct that may be used for the purpose of transformation, i.e. the introduction of heterologous DNA into a host cell. The term includes an expression cassette isolated from any of the aforementioned molecules.

[0052] As used herein, the term "operably linked" refers to a first molecule joined to a second molecule, wherein the molecules are so arranged that the first molecule affects the function of the second molecule. The two molecules may or may not be part of a single contiguous molecule and may or may not be adjacent. For example, a promoter is operably linked to a transcribable polynucleotide molecule if the promoter modulates transcription of the transcribable polynucleotide molecule of interest in a cell. A leader, for example, is operably linked to coding sequence when it is capable of serving as a leader for the polypeptide encoded by the coding sequence.

[0053] The constructs of the present invention may be provided, in one embodiment, as double Ti plasmid border DNA constructs that have the right border (RB or AGRtu.RB) and left border (LB or AGRtu.LB) regions of the Ti plasmid isolated from *Agrobacterium tumefaciens* comprising a T-DNA, that along with transfer molecules provided by the *A. tumefaciens* cells, permit the integration of the T-DNA into the genome of a plant cell (see, for example, U.S. Pat. No. 6,603,061). The constructs may also contain the plasmid backbone DNA segments that provide replication function and antibiotic selection in bacterial cells, for example, an *Escherichia coli* origin of replication such as ori322, a broad host range origin of replication such as oriV or oriRi, and a coding region for a selectable marker such as Spec/Strp that encodes for Tn7 aminoglycoside adenyltransferase (aadA) conferring resistance to spectinomycin or streptomycin, or a gentamicin (Gm, Gent) selectable marker gene. For plant transformation, the host bacterial strain is often *A. tumefaciens* ABI, C58, or LBA4404; however, other strains known to those skilled in the art of plant transformation can function in the present invention.

[0054] Methods are known in the art for assembling and introducing constructs into a cell in such a manner that the transcribable polynucleotide molecule is transcribed into a functional mRNA molecule that is translated and expressed as a protein product. For the practice of the present invention, conventional compositions and methods for preparing and using constructs and host cells are well known to one skilled in the art, see, for example, *Molecular Cloning: A Laboratory Manual, 3rd edition Volumes* 1, 2, *and* 3 (2000) J. Sambrook, D. W. Russell, and N. Irwin, Cold Spring Harbor Laboratory Press. Methods for making recombinant vectors particularly suited to plant transformation include, without limitation, those described in U.S. Pat. Nos. 4,971,908; 4,940,835; 4,769,061; and 4,757,011 in their entirety. These types of vectors have also been reviewed in the scientific literature (see, for example, Rodriguez, et al., *Vectors: A Survey of Molecular Cloning Vectors and Their Uses*, Butterworths, Boston, (1988) and Glick, et al., *Methods in Plant Molecular Biology and Biotechnology*, CRC Press, Boca Raton, Fla. (1993)). Typical vectors useful for expression of nucleic acids in higher plants are well known in the art and include vectors derived from the tumor-inducing (Ti) plasmid of *Agrobacterium tumefaciens* (Rogers, et al., *Methods in Enzymology* 153: 253-277 (1987)). Other recombinant vectors useful for plant transformation, including the pCaMVCN transfer control vector, have also been described in the scientific literature (see, for example, Fromm, et al., *Proc. Natl. Acad. Sci. USA* 82: 5824-5828 (1985)).

[0055] Various regulatory elements may be included in a construct including any of those provided herein. Any such regulatory elements may be provided in combination with other regulatory elements. Such combinations can be designed or modified to produce desirable regulatory features. In one embodiment, constructs of the present invention comprise at least one regulatory element operably linked to a transcribable polynucleotide molecule operably linked to a 3' UTR.

[0056] Constructs of the present invention may include any promoter or leader provided herein or known in the art. For example, a promoter of the present invention may be operably linked to a heterologous non-translated 5' leader such as one derived from a heat shock protein gene (see, for example, U.S. Pat. Nos. 5,659,122 and 5,362,865). Alternatively, a leader of the present invention may be operably linked to a heterologous promoter such as the Cauliflower Mosaic Virus 35S transcript promoter (see, U.S. Pat. No. 5,352,605).

[0057] As used herein, the term "intron" refers to a DNA molecule that may be isolated or identified from the genomic copy of a gene and may be defined generally as a region spliced out during mRNA processing prior to translation. Alternately, an intron may be a synthetically produced or manipulated DNA element. An intron may contain enhancer elements that effect the transcription of operably linked genes. An intron may be used as a regulatory element for modulating expression of an operably linked transcribable polynucleotide molecule. A DNA construct may comprise an intron, and the intron may or may not be heterologous with respect to the transcribable polynucleotide molecule sequence. Examples of introns in the art include the rice actin intron (U.S. Pat. No. 5,641,876) and the corn HSP70 intron (U.S. Pat. No. 5,859,347). Introns useful in practicing the present invention include SEQ ID NOS: 4, 7, 21, 24, 36, 44, 48, 52, 54, 58, 62, 68, 72, 82, 92, 94, 101, 103, 105, 107, 109, 111, 113, 118, 120, 122, 127, 129, 131, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158 and 182. Further, when modifying intron/exon boundary sequences, it may be preferable to avoid using the nucleotide sequence AT or the nucleotide A just prior to the 5' end of the splice site (GT) and the nucleotide G or the nucleotide sequence TG, respectively just after 3' end of the splice site (AG) to eliminate the potential of unwanted start codons from being formed during processing of the messenger RNA into the final transcript. The sequence around the 5' or 3' end splice junction sites of the intron can thus be modified in this manner.

[0058] As used herein, the term "3' transcription termination molecule" or "3' UTR" refers to a DNA molecule that is used during transcription to produce the 3' untranslated region (3' UTR) of an mRNA molecule. The 3' untranslated region of an mRNA molecule may be generated by specific cleavage and 3' polyadenylation, a.k.a. polyA tail. A 3' UTR may be operably linked to and located downstream of a transcribable polynucleotide molecule and may include polynucleotides that provide a polyadenylation signal and other regulatory signals capable of affecting transcription, mRNA processing, or gene expression. PolyA tails are thought to function in mRNA stability and in initiation of translation. Examples of 3' transcription termination molecules in the art are the nopaline synthase 3' region (see, Fraley, et al., *Proc. Natl. Acad. Sci. USA,* 80: 4803-4807 (1983)); wheat hsp17 3' region; pea rubisco small subunit 3' region; cotton E6 3' region (U.S. Pat. No. 6,096,950); 3' regions disclosed in WO0011200A2; and the coixin 3' UTR (U.S. Pat. No. 6,635,806).

[0059] 3' UTRs typically find beneficial use for the recombinant expression of specific genes. In animal systems, a machinery of 3' UTRs has been well defined (e.g. Zhao et al., *Microbiol Mol Biol Rev* 63:405-445 (1999); Proudfoot, *Nature* 322:562-565 (1986); Kim et al., *Biotechnology Progress* 19:1620-1622 (2003); Yonaha and Proudfoot, *EMBO J.* 19:3770-3777 (2000); Cramer et al., *FEBS Letters* 498:179-182 (2001); Kuerstem and Goodwin, *Nature Reviews Genetics* 4:626-637 (2003)). Effective termination of RNA transcription is required to prevent unwanted transcription of trait-unrelated (downstream) sequences, which may interfere with trait performance. Arrangement of multiple gene expression cassettes in local proximity to one another (e.g. within one T-DNA) may cause suppression of gene expression of one or more genes in said construct in comparison to independent insertions (Padidam and Cao, *BioTechniques* 31:328-334 (2001). This may interfere with achieving adequate levels of expression, for instance in cases were strong gene expression from all cassettes is desired.

[0060] In plants, clearly defined polyadenylation signal sequences are not known. Hasegawa et al., *Plant J.* 33:1063-1072, (2003)) were not able to identify conserved polyadenylation signal sequences in both in vitro and in vivo systems in *Nicotiana sylvestris* and to determine the actual length of the primary (non-polyadenylated) transcript. A weak 3' UTR has the potential to generate read-through, which may affect the expression of the genes located in the neighboring expression cassettes (Padidam and Cao, *BioTechniques* 31:328-334 (2001)). Appropriate control of transcription termination can prevent read-through into sequences (e.g. other expression cassettes) localized downstream and can further allow efficient recycling of RNA polymerase, to improve gene expression. Efficient termination of transcription (release of RNA Polymerase II from the DNA) is pre-requisite for re-initiation of transcription and thereby directly affects the overall transcript level. Subsequent to transcription termination, the mature mRNA is released from the site of synthesis and template to the cytoplasm. Eukaryotic mRNAs are accumulated as poly(A) forms in vivo, so that it is difficult to detect transcriptional termination sites by conventional methods. However, prediction of functional and efficient 3' UTRs by bioinformatics methods is difficult in that there are no conserved sequences which would allow easy prediction of an effective 3' UTR.

[0061] From a practical standpoint, it is typically beneficial that a 3' UTR used in a transgene cassette possesses the following characteristics. The 3' UTR should be able to efficiently and effectively terminate transcription of the transgene and prevent read-through of the transcript into any neighboring DNA sequence which can be comprised of another transgene cassette as in the case of multiple cassettes residing in one T-DNA, or the neighboring chromosomal DNA into which the T-DNA has inserted. The 3' UTR should not cause a reduction in the transcriptional activity imparted by the promoter, leader and introns that are used to drive expression of the transgene. In plant biotechnology, the 3' UTR is often used for priming of amplification reactions of reverse transcribed RNA extracted from the transformed plant and used to (1) assess the transcriptional activity or expression of the transgene cassette once integrated into the plant chromosome; (2) assess the copy number of insertions

within the plant DNA; and (3) assess zygosity of the resulting seed after breeding. The 3' UTR is also used in amplification reactions of DNA extracted from the transformed plant to characterize the intactness of the inserted cassette.

[0062] 3' UTRs useful in providing expression of a transgene in plants may be identified based upon the expression of expressed sequence tags (ESTs) in cDNA libraries made from messenger RNA isolated from seed, flower and other tissues derived from Big bluestem (*Andropogon gerardii*), Plume grass (*Saccharum ravennae* (*Erianthus ravennae*)), Green bristlegrass (*Setaria viridis*), Teosinte (*Zea mays* subsp. *mexicana*), Foxtail millet (*Setaria italica*), or *Coix* (*Coix lacryma-jobi*). Libraries of cDNA are made from tissues isolated from selected plant species using methods known to those skilled in the art from flower tissue, seed, leaf and root. The resulting cDNAs are sequenced using various sequencing methods known in the art. The resulting ESTs are assembled into clusters using bioinformatics software such as clc_ref_assemble_complete version 2.01.37139 (CLC bio USA, Cambridge, Mass. 02142). Transcript abundance of each cluster is determined by counting the number of cDNA reads for each cluster. The identified 3' UTRs may be comprised of sequence derived from cDNA sequence as well as sequence derived from genomic DNA. The cDNA sequence is used to design primers, which are then used with GenomeWalker™ (Clontech Laboratories, Inc, Mountain View, Calif.) libraries constructed following the manufacturer's protocol to clone the 3' region of the corresponding genomic DNA sequence to provide a longer termination sequence. Analysis of relative transcript abundance either by direct counts or normalized counts of observed sequence reads for each tissue library can be used to infer properties about patters of expression. For example, some 3' UTRs may be found in transcripts seen in higher abundance in root tissue as opposed to leaf. This is suggestive that the transcript is highly expressed in root and that the properties of root expression may be attributable to the transcriptional regulation of the promoter, the lead, the introns or the 3' UTR. Empirical testing of 3' UTRs identified by the properties of expression within specific organs, tissues or cell types can result in the identification of 3' UTRs that enhance expression in those specific organs, tissues or cell types.

[0063] Constructs and vectors may also include a transit peptide coding sequence that expresses a linked peptide that is useful for targeting of a protein product, particularly to a chloroplast, leucoplast, or other plastid organelle; mitochondria; peroxisome; vacuole; or an extracellular location. For descriptions of the use of chloroplast transit peptides, see U.S. Pat. No. 5,188,642 and U.S. Pat. No. 5,728,925. Many chloroplast-localized proteins are expressed from nuclear genes as precursors and are targeted to the chloroplast by a chloroplast transit peptide (CTP). Examples of such isolated chloroplast proteins include, but are not limited to, those associated with the small subunit (SSU) of ribulose-1,5,-bisphosphate carboxylase, ferredoxin, ferredoxin oxidoreductase, the light-harvesting complex protein I and protein II, thioredoxin F, enolpyruvyl shikimate phosphate synthase (EPSPS), and transit peptides described in U.S. Pat. No. 7,193,133. It has been demonstrated in vivo and in vitro that non-chloroplast proteins may be targeted to the chloroplast by use of protein fusions with a heterologous CTP and that the CTP is sufficient to target a protein to the chloroplast. Incorporation of a suitable chloroplast transit peptide such as the *Arabidopsis thaliana* EPSPS CTP (CTP2) (See, Klee et al., *Mol. Gen. Genet.* 210:437-442 (1987)) or the *Petunia hybrida* EPSPS CTP (CTP4) (See, della-Cioppa et al., *Proc. Natl. Acad. Sci. USA* 83:6873-6877 (1986)) has been show to target heterologous EPSPS protein sequences to chloroplasts in transgenic plants (See, U.S. Pat. Nos. 5,627,061; 5,633,435; and 5,312,910 and EP 0218571; EP 189707; EP 508909; and EP 924299).

Transcribable Polynucleotide Molecules

[0064] As used herein, the term "transcribable polynucleotide molecule" refers to any DNA molecule capable of being transcribed into a RNA molecule, including, but not limited to, those having protein coding sequences and those producing RNA molecules having sequences useful for gene suppression. A "transgene" refers to a transcribable polynucleotide molecule heterologous to a host cell at least with respect to its location in the genome and/or a transcribable polynucleotide molecule artificially incorporated into a host cell's genome in the current or any prior generation of the cell.

[0065] A promoter of the present invention may be operably linked to a transcribable polynucleotide molecule that is heterologous with respect to the promoter molecule. As used herein, the term "heterologous" refers to the combination of two or more polynucleotide molecules when such a combination is not normally found in nature. For example, the two molecules may be derived from different species and/or the two molecules may be derived from different genes, e.g. different genes from the same species or the same genes from different species. A promoter is thus heterologous with respect to an operably linked transcribable polynucleotide molecule if such a combination is not normally found in nature, i.e. that transcribable polynucleotide molecule is not naturally occurring operably linked in combination with that promoter molecule.

[0066] The transcribable polynucleotide molecule may generally be any DNA molecule for which expression of a RNA transcript is desired. Such expression of an RNA transcript may result in translation of the resulting mRNA molecule and thus protein expression. Alternatively, for example, a transcribable polynucleotide molecule may be designed to ultimately cause decreased expression of a specific gene or protein. In one embodiment, this may be accomplished by using a transcribable polynucleotide molecule that is oriented in the antisense direction. One of ordinary skill in the art is familiar with using such antisense technology. Briefly, as the antisense transcribable polynucleotide molecule is transcribed, the RNA product hybridizes to and sequesters a complimentary RNA molecule inside the cell. This duplex RNA molecule cannot be translated into a protein by the cell's translational machinery and is degraded in the cell. Any gene may be negatively regulated in this manner.

[0067] Thus, one embodiment of the invention is a regulatory element of the present invention, such as those provided as SEQ ID NOs: 1-158 and 180-183, operably linked to a transcribable polynucleotide molecule so as to modulate transcription of the transcribable polynucleotide molecule at a desired level or in a desired pattern when the construct is integrated in the genome of a plant cell. In one embodiment, the transcribable polynucleotide molecule comprises a protein-coding region of a gene, and the promoter affects the transcription of an RNA molecule that is translated and expressed as a protein product. In another embodiment, the transcribable polynucleotide molecule comprises an antisense region of a gene, and the promoter affects the transcription of an antisense RNA molecule, double stranded RNA or

other similar inhibitory RNA molecule in order to inhibit expression of a specific RNA molecule of interest in a target host cell.

Genes of Agronomic Interest

[0068] Transcribable polynucleotide molecules may be genes of agronomic interest. As used herein, the term "gene of agronomic interest" refers to a transcribable polynucleotide molecule that when expressed in a particular plant tissue, cell, or cell type confers a desirable characteristic, such as associated with plant morphology, physiology, growth, development, yield, product, nutritional profile, disease or pest resistance, and/or environmental or chemical tolerance. Genes of agronomic interest include, but are not limited to, those encoding a yield protein, a stress resistance protein, a developmental control protein, a tissue differentiation protein, a meristem protein, an environmentally responsive protein, a senescence protein, a hormone responsive protein, an abscission protein, a source protein, a sink protein, a flower control protein, a seed protein, an herbicide resistance protein, a disease resistance protein, a fatty acid biosynthetic enzyme, a tocopherol biosynthetic enzyme, an amino acid biosynthetic enzyme, a pesticidal protein, or any other agent such as an antisense or RNAi molecule targeting a particular gene for suppression. The product of a gene of agronomic interest may act within the plant in order to cause an effect upon the plant physiology or metabolism or may be act as a pesticidal agent in the diet of a pest that feeds on the plant.

[0069] In one embodiment of the invention, a promoter of the present invention is incorporated into a construct such that the promoter is operably linked to a transcribable polynucleotide molecule that is a gene of agronomic interest. The expression of the gene of agronomic interest is desirable in order to confer an agronomically beneficial trait. A beneficial agronomic trait may be, for example, but is not limited to, herbicide tolerance, insect control, modified yield, fungal disease resistance, virus resistance, nematode resistance, bacterial disease resistance, plant growth and development, starch production, modified oils production, high oil production, modified fatty acid content, high protein production, fruit ripening, enhanced animal and human nutrition, biopolymers, environmental stress resistance, pharmaceutical peptides and secretable peptides, improved processing traits, improved digestibility, enzyme production, flavor, nitrogen fixation, hybrid seed production, fiber production, and biofuel production. Examples of genes of agronomic interest known in the art include those for herbicide resistance (U.S. Pat. Nos. 6,803,501; 6,448,476; 6,248,876; 6,225,114; 6,107,549; 5,866,775; 5,804,425; 5,633,435; and 5,463,175), increased yield (U.S. Pat. Nos. RE38,446; 6,716,474; 6,663,906; 6,476,295; 6,441,277; 6,423,828; 6,399,330; 6,372,211; 6,235,971; 6,222,098; and 5,716,837), insect control (U.S. Pat. Nos. 6,809,078; 6,713,063; 6,686,452; 6,657,046; 6,645,497; 6,642,030; 6,639,054; 6,620,988; 6,593,293; 6,555,655; 6,538,109; 6,537,756; 6,521,442; 6,501,009; 6,468,523; 6,326,351; 6,313,378; 6,284,949; 6,281,016; 6,248,536; 6,242,241; 6,221,649; 6,177,615; 6,156,573; 6,153,814; 6,110,464; 6,093,695; 6,063,756; 6,063,597; 6,023,013; 5,959,091; 5,942,664; 5,942,658, 5,880,275; 5,763,245; and 5,763,241), fungal disease resistance (U.S. Pat. Nos. 6,653,280; 6,573,361; 6,506,962; 6,316,407; 6,215,048; 5,516,671; 5,773,696; 6,121,436; 6,316,407; and 6,506,962), virus resistance (U.S. Pat. Nos. 6,617,496; 6,608,241; 6,015,940; 6,013,864; 5,850,023; and 5,304,730), nematode resistance (U.S. Pat. No. 6,228,992), bacterial disease resistance (U.S. Pat. No. 5,516,671), plant growth and development (U.S. Pat. Nos. 6,723,897 and 6,518,488), starch production (U.S. Pat. Nos. 6,538,181; 6,538,179; 6,538,178; 5,750,876; 6,476,295), modified oils production (U.S. Pat. Nos. 6,444,876; 6,426,447; and 6,380,462), high oil production (U.S. Pat. Nos. 6,495,739; 5,608,149; 6,483,008; and 6,476,295), modified fatty acid content (U.S. Pat. Nos. 6,828,475; 6,822,141; 6,770,465; 6,706,950; 6,660,849; 6,596,538; 6,589,767; 6,537,750; 6,489,461; and 6,459,018), high protein production (U.S. Pat. No. 6,380,466), fruit ripening (U.S. Pat. No. 5,512,466), enhanced animal and human nutrition (U.S. Pat. Nos. 6,723,837; 6,653,530; 6,541,259; 5,985,605; and 6,171,640), biopolymers (U.S. Pat. Nos. RE37,543; 6,228,623; and 5,958,745, and 6,946,588), environmental stress resistance (U.S. Pat. No. 6,072,103), pharmaceutical peptides and secretable peptides (U.S. Pat. Nos. 6,812,379; 6,774,283; 6,140,075; and 6,080,560), improved processing traits (U.S. Pat. No. 6,476,295), improved digestibility (U.S. Pat. No. 6,531,648) low raffinose (U.S. Pat. No. 6,166,292), industrial enzyme production (U.S. Pat. No. 5,543,576), improved flavor (U.S. Pat. No. 6,011,199), nitrogen fixation (U.S. Pat. No. 5,229,114), hybrid seed production (U.S. Pat. No. 5,689,041), fiber production (U.S. Pat. Nos. 6,576,818; 6,271,443; 5,981,834; and 5,869,720) and biofuel production (U.S. Pat. No. 5,998,700).

[0070] Alternatively, a gene of agronomic interest can affect the above mentioned plant characteristic or phenotype by encoding a RNA molecule that causes the targeted modulation of gene expression of an endogenous gene, for example via antisense (see e.g. U.S. Pat. No. 5,107,065); inhibitory RNA ("RNAi", including modulation of gene expression via miRNA-, siRNA-, trans-acting siRNA-, and phased sRNA-mediated mechanisms, e.g. as described in published applications US 2006/0200878 and US 2008/0066206, and in U.S. patent application Ser. No. 11/974,469); or cosuppression-mediated mechanisms. The RNA could also be a catalytic RNA molecule (e.g. a ribozyme or a riboswitch; see e.g. US 2006/0200878) engineered to cleave a desired endogenous mRNA product. Thus, any transcribable polynucleotide molecule that encodes a transcribed RNA molecule that affects an agronomically important phenotype or morphology change of interest may be useful for the practice of the present invention. Methods are known in the art for constructing and introducing constructs into a cell in such a manner that the transcribable polynucleotide molecule is transcribed into a molecule that is capable of causing gene suppression. For example, posttranscriptional gene suppression using a construct with an anti-sense oriented transcribable polynucleotide molecule to regulate gene expression in plant cells is disclosed in U.S. Pat. Nos. 5,107,065 and 5,759,829, and posttranscriptional gene suppression using a construct with a sense-oriented transcribable polynucleotide molecule to regulate gene expression in plants is disclosed in U.S. Pat. Nos. 5,283,184 and 5,231,020. Expression of a transcribable polynucleotide in a plant cell can also be used to suppress plant pests feeding on the plant cell, for example, compositions isolated from coleopteran pests (U.S. Patent Publication No. US20070124836) and compositions isolated from nematode pests (U.S. Patent Publication No. US20070250947). Plant pests include, but are not limited to arthropod pests, nematode pests, and fungal or microbial pests. Exemplary transcribable polynucleotide molecules for incorporation into constructs of the present invention include, for example,

DNA molecules or genes from a species other than the target species or genes that originate with or are present in the same species, but are incorporated into recipient cells by genetic engineering methods rather than classical reproduction or breeding techniques. The type of polynucleotide molecule can include, but is not limited to, a polynucleotide molecule that is already present in the plant cell, a polynucleotide molecule from another plant, a polynucleotide molecule from a different organism, or a polynucleotide molecule generated externally, such as a polynucleotide molecule containing an antisense message of a gene, or a polynucleotide molecule encoding an artificial, synthetic, or otherwise modified version of a transgene.

Selectable Markers

[0071] As used herein the term "marker" refers to any transcribable polynucleotide molecule whose expression, or lack thereof, can be screened for or scored in some way. Marker genes for use in the practice of the present invention include, but are not limited to transcribable polynucleotide molecules encoding β-glucuronidase (GUS described in U.S. Pat. No. 5,599,670), green fluorescent protein and variants thereof (GFP described in U.S. Pat. Nos. 5,491,084 and 6,146,826), proteins that confer antibiotic resistance, or proteins that confer herbicide tolerance. Useful antibiotic resistance markers, including those encoding proteins conferring resistance to kanamycin (nptII), hygromycin B (aph IV), streptomycin or spectinomycin (aad, spec/strep) and gentamycin (aac3 and aacC4) are known in the art. Herbicides for which transgenic plant tolerance has been demonstrated and the method of the present invention can be applied, include, but are not limited to: amino-methyl-phosphonic acid, glyphosate, glufosinate, sulfonylureas, imidazolinones, bromoxynil, dalapon, dicamba, cyclohexanedione, protoporphyrinogen oxidase inhibitors, and isoxasflutole herbicides. Transcribable polynucleotide molecules encoding proteins involved in herbicide tolerance are known in the art, and include, but are not limited to, a transcribable polynucleotide molecule encoding 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS for glyphosate tolerance described in U.S. Pat. Nos. 5,627,061; 5,633,435; 6,040,497; and 5,094,945); a transcribable polynucleotide molecule encoding a glyphosate oxidoreductase and a glyphosate-N-acetyl transferase (GOX described in U.S. Pat. No. 5,463,175; GAT described in U.S. Patent publication No. 20030083480, and dicamba monooxygenase U.S. Patent publication No. 20030135879); a transcribable polynucleotide molecule encoding bromoxynil nitrilase (Bxn for Bromoxynil tolerance described in U.S. Pat. No. 4,810,648); a transcribable polynucleotide molecule encoding phytoene desaturase (crtI) described in Misawa, et al., *Plant Journal* 4:833-840 (1993) and Misawa, et al., *Plant Journal* 6:481-489 (1994) for norflurazon tolerance; a transcribable polynucleotide molecule encoding acetohydroxyacid synthase (AHAS, aka ALS) described in Sathasiivan, et al., *Nucl. Acids Res.* 18:2188-2193 (1990) for tolerance to sulfonylurea herbicides; and the bar gene described in DeBlock, et al., *EMBO Journal* 6:2513-2519 (1987) for glufosinate and bialaphos tolerance. The promoter molecules of the present invention can express linked transcribable polynucleotide molecules that encode for phosphinothricin acetyltransferase, glyphosate resistant EPSPS, aminoglycoside phosphotransferase, hydroxyphenyl pyruvate dehydrogenase, hygromycin phosphotransferase, neomycin phosphotransferase, dalapon dehalogenase, bromoxynil resistant nitrilase, anthranilate synthase, aryloxyalkanoate dioxygenases, acetyl CoA carboxylase, glyphosate oxidoreductase, and glyphosate-N-acetyl transferase.

[0072] Included within the term "selectable markers" are also genes which encode a secretable marker whose secretion can be detected as a means of identifying or selecting for transformed cells. Examples include markers that encode a secretable antigen that can be identified by antibody interaction, or even secretable enzymes which can be detected catalytically. Selectable secreted marker proteins fall into a number of classes, including small, diffusible proteins which are detectable, (e.g. by ELISA), small active enzymes which are detectable in extracellular solution (e.g, alpha-amylase, beta-lactamase, phosphinothricin transferase), or proteins which are inserted or trapped in the cell wall (such as proteins which include a leader sequence such as that found in the expression unit of extension or tobacco pathogenesis related proteins also known as tobacco PR-S). Other possible selectable marker genes will be apparent to those of skill in the art and are encompassed by the present invention.

Cell Transformation

[0073] The invention is also directed to a method of producing transformed cells and plants which comprise a promoter operably linked to a transcribable polynucleotide molecule.

[0074] The term "transformation" refers to the introduction of nucleic acid into a recipient host. As used herein, the term "host" refers to bacteria, fungi, or plant, including any cells, tissue, organs, or progeny of the bacteria, fungi, or plant. Plant tissues and cells of particular interest include protoplasts, calli, roots, tubers, seeds, stems, leaves, seedlings, embryos, and pollen.

[0075] As used herein, the term "transformed" refers to a cell, tissue, organ, or organism into which a foreign polynucleotide molecule, such as a construct, has been introduced. The introduced polynucleotide molecule may be integrated into the genomic DNA of the recipient cell, tissue, organ, or organism such that the introduced polynucleotide molecule is inherited by subsequent progeny. A "transgenic" or "transformed" cell or organism also includes progeny of the cell or organism and progeny produced from a breeding program employing such a transgenic organism as a parent in a cross and exhibiting an altered phenotype resulting from the presence of a foreign polynucleotide molecule. The term "transgenic" refers to a bacteria, fungi, or plant containing one or more heterologous polynucleic acid molecules.

[0076] There are many methods for introducing polynucleic acid molecules into plant cells. The method generally comprises the steps of selecting a suitable host cell, transforming the host cell with a recombinant vector, and obtaining the transformed host cell. Suitable methods include bacterial infection (e.g. *Agrobacterium*), binary bacterial artificial chromosome vectors, direct delivery of DNA (e.g. via PEG-mediated transformation, desiccation/inhibition-mediated DNA uptake, electroporation, agitation with silicon carbide fibers, and acceleration of DNA coated particles, etc. (reviewed in Potrykus, et al., *Ann. Rev. Plant Physiol. Plant Mol. Biol.* 42: 205 (1991)).

[0077] Technology for introduction of a DNA molecule into cells is well known to those of skill in the art. Methods and materials for transforming plant cells by introducing a plant DNA construct into a plant genome in the practice of this invention can include any of the well-known and demon-

strated methods. Any transformation methods may be utilized to transform a host cell with one or more promoters and/or constructs of the present. Host cells may be any cell or organism such as a plant cell, algae cell, algae, fungal cell, fungi, bacterial cell, or insect cell. Preferred hosts and transformed cells include cells from: plants, *Aspergillus*, yeasts, insects, bacteria and algae.

[0078] Regenerated transgenic plants can be self-pollinated to provide homozygous transgenic plants. Alternatively, pollen obtained from the regenerated transgenic plants may be crossed with non-transgenic plants, preferably inbred lines of agronomically important species. Descriptions of breeding methods that are commonly used for different traits and crops can be found in one of several reference books, see, for example, Allard, *Principles of Plant Breeding*, John Wiley & Sons, NY, U. of CA, Davis, Calif., 50-98 (1960); Simmonds, *Principles of crop improvement*, Longman, Inc., NY, 369-399 (1979); Sneep and Hendriksen, Plant breeding perspectives, Wageningen (ed), Center for Agricultural Publishing and Documentation (1979); Fehr, *Soybeans: Improvement, Production and Uses,* 2nd Edition, Monograph, 16:249 (1987); Fehr, *Principles of variety development, Theory and Technique*, (Vol. 1) and *Crop Species Soybean* (Vol 2), Iowa State Univ., Macmillan Pub. Co., NY, 360-376 (1987). Conversely, pollen from non-transgenic plants may be used to pollinate the regenerated transgenic plants.

[0079] The transformed plants may be analyzed for the presence of the genes of interest and the expression level and/or profile conferred by the regulatory elements of the present invention. Those of skill in the art are aware of the numerous methods available for the analysis of transformed plants. For example, methods for plant analysis include, but are not limited to Southern blots or northern blots, PCR-based approaches, biochemical analyses, phenotypic screening methods, field evaluations, and immunodiagnostic assays. The expression of a transcribable polynucleotide molecule can be measured using TaqMan® (Applied Biosystems, Foster City, Calif.) reagents and methods as described by the manufacturer and PCR cycle times determined using the TaqMan® Testing Matrix. Alternatively, the Invader® (Third Wave Technologies, Madison, Wis.) reagents and methods as described by the manufacturer can be used transgene expression.

[0080] The seeds of the plants of this invention can be harvested from fertile transgenic plants and be used to grow progeny generations of transformed plants of this invention including hybrid plant lines comprising the construct of this invention and expressing a gene of agronomic interest.

[0081] The present invention also provides for parts of the plants of the present invention. Plant parts, without limitation, include leaves, stems, roots, tubers, seeds, endosperm, ovule, and pollen. The invention also includes and provides transformed plant cells which comprise a nucleic acid molecule of the present invention.

[0082] The transgenic plant may pass along the transgenic polynucleotide molecule to its progeny. Progeny includes any regenerable plant part or seed comprising the transgene derived from an ancestor plant. The transgenic plant is preferably homozygous for the transformed polynucleotide molecule and transmits that sequence to all offspring as a result of sexual reproduction. Progeny may be grown from seeds produced by the transgenic plant. These additional plants may then be self-pollinated to generate a true breeding line of plants. The progeny from these plants are evaluated, among other things, for gene expression. The gene expression may be detected by several common methods such as western blotting, northern blotting, immuno-precipitation, and ELISA.

Commodity Products

[0083] The present invention provides a commodity product comprising DNA molecules according to the invention. As used herein, a "commodity product" refers to any composition or product which is comprised of material derived from a plant, seed, plant cell or plant part comprising a DNA molecule of the invention. Commodity products may be sold to consumers and may be viable or nonviable. Nonviable commodity products include but are not limited to nonviable seeds and grains; processed seeds, seed parts, and plant parts; dehydrated plant tissue, frozen plant tissue, and processed plant tissue; seeds and plant parts processed for animal feed for terrestrial and/or aquatic animals consumption, oil, meal, flour, flakes, bran, fiber, milk, cheese, paper, cream, wine, and any other food for human consumption; and biomasses and fuel products. Viable commodity products include but are not limited to seeds and plant cells. Plants comprising a DNA molecule according to the invention can thus be used to manufacture any commodity product typically acquired from plants or parts thereof.

[0084] Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified. It should be appreciated by those of skill in the art that the techniques disclosed in the following examples represent techniques discovered by the inventors to function well in the practice of the invention. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments that are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention, therefore all matter set forth or shown in the accompanying drawings is to be interpreted as illustrative and not in a limiting sense.

EXAMPLES

Example 1

Identification and Cloning of Regulatory Elements

[0085] Novel ubiquitin transcriptional regulatory elements, or transcriptional regulatory expression element group (EXP) sequences were identified and isolated from genomic DNA of the monocot species Big bluestem (*Andropogon gerardii*), Plume Grass (*Saccharum ravennae* (*Erianthus ravennae*)), Green bristlegrass (*Setaria viridis*), Teosinte (*Zea mays* subsp. *mexicana*), Foxtail millet (*Setaria italica*), and *Coix* (*Coix lacryma-jobi*).

[0086] Ubiquitin 1 transcript sequences were identified from each of the above species. The 5' untranslated region (5' UTR) of each of the Ubiquitin 1 transcripts was used to design primers to amplify the corresponding transcriptional regulatory elements for the identified Ubiquitin gene, which comprises a promoter, leader (5' UTR) and first intron operably linked. The primers were used with GenomeWalker™ (Clontech Laboratories, Inc, Mountain View, Calif.) libraries constructed following the manufacturer's protocol to clone the 5' region of the corresponding genomic DNA sequence. Ubiq-

uitin transcriptional regulatory elements were also isolated from the monocot *Sorghum bicolor* using public sequences that are homologs to the Ubiquitin 4, 6 and 7 genes of *Zea mays*.

[0087] Using the identified sequences, a bioinformatic analysis was conducted to identify regulatory elements within the amplified DNA. Using the results of this analysis, regulatory elements were defined within the DNA sequences and primers designed to amplify the regulatory elements. The corresponding DNA molecule for each regulatory element was amplified using standard polymerase chain reaction conditions with primers containing unique restriction enzyme sites and genomic DNA isolated from *A. gerardii, S. ravennae, S. viridis, Z. mays* subsp. *mexicana, S. italica, C. lacryma-jobi*, and *S. bicolor*. The resulting DNA fragments were ligated into base plant expression vectors and sequenced. An analysis of the regulatory element TSS and intron/exon splice junctions was then done using transformed plant protoplasts. Briefly, the protoplasts were transformed with the plant expression vectors comprising the cloned DNA fragments operably linked to a heterologous transcribable polynucleotide molecule and the 5' RACE System for Rapid Amplification of cDNA Ends, Version 2.0 (Invitrogen, Carlsbad, Calif. 92008) was used to confirm the regulatory element TSS and intron/exon splice junctions by analyzing the sequence of the mRNA transcripts produced thereby.

[0088] Sequences of the identified transcriptional regulatory expression element groups ("EXP's") are provided herein as SEQ ID NOS: 1, 5, 8, 10, 12, 14, 16, 18, 22, 25, 27, 29, 31, 33, 37, 39, 41, 45, 49, 53, 55, 59, 63, 65, 69, 73, 75, 77, 79, 83, 85, 87, 90, 93, 95, 97, 98, 99, 100, 102, 104, 106, 108, 110, 112, 114, 115, 116, 117, 119, 121, 123, 124, 125, 126, 128, 130, 132, 133, 134, 136, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 180, 181 and 183, as listed in Table 1 below. Promoter sequences are provided herein as SEQ ID NOS: 2, 6, 9, 11, 13, 15, 17, 19, 23, 26, 28, 30, 32, 34, 38, 40, 42, 46, 50, 56, 60, 64, 66, 70, 74, 76, 78, 80, 84, 86, 88, 91, 96 and 135. Leader sequences are provided herein as SEQ ID NOS: 3, 20, 35, 43, 47, 51, 57, 61, 67, 71 and 81. Intron sequences are provided herein as SEQ ID NOS: 4, 7, 21, 24, 36, 44, 48, 52, 54, 58, 62, 68, 72, 82, 92, 94, 101, 103, 105, 107, 109, 111, 113, 118, 120, 122, 127, 129, 131, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158 and 182. An enhancer sequence is provided as SEQ ID NO: 89.

TABLE 1

Transcriptional regulatory expression element groups ("EXP's"), promoters, enhancers, leaders and introns isolated from various grass species.

Annotation	SEQ ID NO:	Size (bp)	Source Genus/species	Description and/or regulatory elements of EXP linked in 5' → 3' direction (SEQ ID NOs):	Plasmid Construct(s) and Amplicons comprising EXP
EXP-ANDge.Ubq1:1:9	1	3741	*A. gerardii*	EXP: P-ANDge.Ubq1-1:1:11 (SEQ ID NO: 2); L-ANDge.Ubq1-1:1:2 (SEQ ID NO: 3); I-ANDge.Ubq1-1:1:3 (SEQ ID NO: 4).	
P-ANDge.Ubq1-1:1:11	2	2603	*A. gerardii*	promoter	
L-ANDge.Ubq1-1:1:2	3	99	*A. gerardii*	leader	
I-ANDge.Ubq1-1:1:3	4	1039	*A. gerardii*	intron	
EXP-ANDge.Ubq1:1:7	5	3255	*A. gerardii*	EXP: P-ANDge.Ubq1-1:1:9 (SEQ ID NO: 6); L-ANDge.Ubq1-1:1:2 (SEQ ID NO: 3); I-ANDge.Ubq1-1:1:4 (SEQ ID NO: 7).	pMON136264, PCR0145892, pMON140896, PCR41
P-ANDge.Ubq1-1:1:9	6	2114	*A. gerardii*	promoter	
I-ANDge.Ubq1-1:1:4	7	1042	*A. gerardii*	intron	
EXP-ANDge.Ubq1:1:8	8	2785	*A. gerardii*	EXP: P-ANDge.Ubq1-1:1:10 (SEQ ID NO: 9); L-ANDge.Ubq1-1:1:2 (SEQ ID NO: 3); I-ANDge.Ubq1-1:1:4 (SEQ ID NO: 7).	pMON140917, PCR42
P-ANDge.Ubq1-1:1:10	9	1644	*A. gerardii*	promoter	
EXP-ANDge.Ubq1:1:10	10	2613	*A. gerardii*	EXP: P-ANDge.Ubq1-1:1:12 (SEQ ID NO: 11); L-ANDge.Ubq1-1:1:2 (SEQ ID NO: 3); I-ANDge.Ubq1-1:1:4 (SEQ ID NO: 7).	PCR0145815, PCR43
P-ANDge.Ubq1-1:1:12	11	1472	*A. gerardii*	promoter	
EXP-ANDge.Ubq1:1:6	12	2255	*A. gerardii*	EXP: P-ANDge.Ubq1-1:1:8 (SEQ ID NO: 13); L-ANDge.Ubq1-1:1:2 (SEQ ID NO: 3); I-ANDge.Ubq1-1:1:4 (SEQ ID NO: 7).	pMON136259, PCR0145893, pMON140898, PCR44
P-ANDge.Ubq1-1:1:8	13	1114	*A. gerardii*	promoter	
EXP-ANDge.Ubq1:1:11	14	1912	*A. gerardii*	EXP: P-ANDge.Ubq1-1:1:13 (SEQ ID NO: 15); L-ANDge.Ubq1-1:1:2 (SEQ ID NO: 3); I-ANDge.Ubq1-1:1:4 (SEQ ID NO: 7).	PCR0145817, pMON140899, PCR45
P-ANDge.Ubq1-1:1:13	15	771	*A. gerardii*	promoter	
EXP-ANDge.Ubq1:1:12	16	1623	*A. gerardii*	EXP: P-ANDge.Ubq1-1:1:14 (SEQ ID NO: 17); L-ANDge.Ubq1-1:1:2 (SEQ ID NO: 3); I-ANDge.Ubq1-1:1:4 (SEQ ID NO: 7).	PCR0145819, pMON140900, PCR46
P-ANDge.Ubq1-1:1:14	17	482	*A. gerardii*	promoter	
EXP-ERIra.Ubq1	18	3483	*E. ravennae*	EXP: P-ERIra.Ubq1-1:1:10 (SEQ ID NO: 19); L-ERIra.Ubq1-1:1:2 (SEQ ID NO: 20); I-ERIra.Ubq1-1:1:1 (SEQ ID NO: 21).	

TABLE 1-continued

Transcriptional regulatory expression element groups ("EXP's"), promoters, enhancers, leaders and introns isolated from various grass species.

Annotation	SEQ ID NO:	Size (bp)	Source Genus/species	Description and/or regulatory elements of EXP linked in 5' → 3' direction (SEQ ID NOs):	Plasmid Construct(s) and Amplicons comprising EXP
P-ERIra.Ubq1-1:1:10	19	2536	*E. ravennae*	promoter	
L-ERIra.Ubq1-1:1:2	20	94	*E. ravennae*	leader	
I-ERIra.Ubq1-1:1:1	21	1041	*E. ravennae*	intron	
EXP-ERIra.Ubq1:1:9	22	3152	*E. ravennae*	EXP: P-ERIra.Ubq1-1:1:9 (SEQ ID NO: 23); L-ERIra.Ubq1-1:1:2 (SEQ ID NO: 20); I-ERIra.Ubq1-1:1:2 (SEQ ID NO: 24).	pMON136263, PCR0145896, pMON140904, PCR50
P-ERIra.Ubq1-1:1:9	23	2014	*E. ravennae*	promoter	
I-ERIra.Ubq1-1:1:2	24	1044	*E. ravennae*	intron	
EXP-ERIra.Ubq1:1:10	25	2663	*E. ravennae*	EXP: P-ERIra.Ubq1-1:1:11 (SEQ ID NO: 26); L-ERIra.Ubq1-1:1:2 (SEQ ID NO: 20); I-ERIra.Ubq1-1:1:2 (SEQ ID NO: 24).	PCR0145820, pMON140905, PCR51
P-ERIra.Ubq1-1:1:11	26	1525	*E. ravennae*	promoter	
EXP-ERIra.Ubq1:1:8	27	2182	*E. ravennae*	EXP: P-ERIra.Ubq1-1:1:8 (SEQ ID NO: 28); L-ERIra.Ubq1-1:1:2 (SEQ ID NO: 20); I-ERIra.Ubq1-1:1:2 (SEQ ID NO: 24).	pMON136258, PCR0145897, PMON140906, PCR52, pMON142864, pMON142862
P-ERIra.Ubq1-1:1:8	28	1044	*E. ravennae*	promoter	
EXP-ERIra.Ubq1:1:11	29	1934	*E. ravennae*	EXP: P-ERIra.Ubq1-1:1:12 (SEQ ID NO: 30); L-ERIra.Ubq1-1:1:2 (SEQ ID NO: 20); I-ERIra.Ubq1-1:1:2 (SEQ ID NO: 24).	PCR0145821, pMON140907, PCR53
P-ERIra.Ubq1-1:1:12	30	796	*E. ravennae*	promoter	
EXP-ERIra.Ubq1:1:12	31	1649	*E. ravennae*	EXP: P-ERIra.Ubq1-1:1:13 (SEQ ID NO: 32); L-ERIra.Ubq1-1:1:2 (SEQ ID NO: 20); I-ERIra.Ubq1-1:1:2 (SEQ ID NO: 24).	PCR0145822, pMON140908, PCR54
P-ERIra.Ubq1-1:1:13	32	511	*E. ravennae*	promoter	
EXP-Sv.Ubq1:1:2	33	2631	*S. viridis*	EXP: P-Sv.Ubq1-1:1:1 (SEQ ID NO: 34); L-Sv.Ubq1-1:1:2 (SEQ ID NO: 35); I-Sv.Ubq1-1:1:1 (SEQ ID NO: 36).	pMON140878, PCR0145909, pMON129203, pMON131958
P-Sv.Ubq1-1:1:1	34	1493	*S. viridis*	promoter	
L-Sv.Ubq1-1:1:2	35	127	*S. viridis*	leader	
I-Sv.Ubq1-1:1:1	36	1011	*S. viridis*	intron	
EXP-Sv.Ubq1:1:3	37	2173	*S. viridis*	EXP: P-Sv.Ubq1-1:1:2 (SQ ID NO: 38); L-Sv.Ubq1-1:1:2 (SEQ ID NO: 35); I-Sv.Ubq1-1:1:1 (SEQ ID NO: 36).	PCR0145929, pMON129204
P-Sv.Ubq1-1:1:2	38	1035	*S. viridis*	promoter	
EXP-Sv.Ubq1:1:5	39	1819	*S. viridis*	EXP: P-Sv.Ubq1-1:1:3 (SEQ ID NO: 40); L-Sv.Ubq1-1:1:2 (SEQ ID NO: 35); I-Sv.Ubq1-1:1:1 (SEQ ID NO: 36).	pMON129205, pMON131959
P-Sv.Ubq1-1:1:3	40	681	*S. viridis*	promoter	
EXP-Zm.UbqM1:1:1 (Allele-1)	41	1922	*Z. mays* subsp. *mexicana*	EXP: P-Zm.UbqM1-1:1:1 (SEQ ID NO: 42); L-Zm.UbqM1-1:1:1 (SEQ ID NO: 43); I-Zm.UbqM1-1:1:5 (SEQ ID NO: 44).	pMON140881, PCR0145914, pMON129210, pMON131961
P-Zm.UbqM1-1:1:1 (Allele-1)	42	850	*Z. mays* subsp. *mexicana*	promoter	
L-Zm.UbqM1-1:1:1 (Allele-1)	43	78	*Z. mays* subsp. *mexicana*	leader	
I-Zm.UbqM1-1:1:5 (Allele-1)	44	994	*Z. mays* subsp. *mexicana*	intron	
EXP-Zm.UbqM1:1:4 (Allele-2)	45	1971	*Z. mays* subsp. *mexicana*	EXP: P-Zm.UbqM1-1:1:4 (SEQ ID NO: 46); L-Zm.UbqM1-1:1:5 (SEQ ID NO: 47); I-Zm.UbqM1-1:1:4 (SEQ ID NO: 48).	pMON140882, PCR0145915, pMON129212, pMON131963
P-Zm.UbqM1-1:1:4 (Allele-2)	46	887	*Z. mays* subsp. *mexicana*	promoter	
L-Zm.UbqM1-1:1:5 (Allele-2)	47	77	*Z. mays* subsp. *mexicana*	leader	
I-Zm.UbqM1-1:1:4 (Allele-2)	48	1007	*Z. mays* subsp. *mexicana*	intron	
EXP-Zm.UbqM1:1:2 (Allele-3)	49	2005	*Z. mays* subsp. *mexicana*	EXP: P-Zm.UbqM1-1:1:5 (SEQ ID NO: 50); L-Zm.UbqM1-1:1:4 (SEQ ID NO: 51); I-Zm.UbqM1-1:1:11 (SEQ ID NO: 52).	PCR0145916, pMON129211, pMON131962, pMON132047
P-Zm.UbqM1-1:1:5 (Allele-3)	50	877	*Z. mays* subsp. *mexicana*	promoter	

TABLE 1-continued

Transcriptional regulatory expression element groups ("EXP's"), promoters, enhancers, leaders and introns isolated from various grass species.

Annotation	SEQ ID NO:	Size (bp)	Source Genus/species	Description and/or regulatory elements of EXP linked in 5' → 3' direction (SEQ ID NOs):	Plasmid Construct(s) and Amplicons comprising EXP
L-Zm.UbqM1-1:1:4 (Allele-3)	51	78	*Z. mays* subsp. *mexicana*	leader	
I-Zm.UbqM1-1:1:11 (Allele-3)	52	1050	*Z. mays* subsp. *mexicana*	intron	
EXP-Zm.UbqM1:1:5 (Allele-3)	53	2005	*Z. mays* subsp. *mexicana*	EXP: P-Zm.UbqM1-1:1:5 (SEQ ID NO: 50); L-Zm.UbqM1-1:1:4 (SEQ ID NO: 51); I-Zm.UbqM1-1:1:12 (SEQ ID NO: 54).	
I-Zm.UbqM1-1:1:12 (Allele-3)	54	1050	*Z. mays* subsp. *mexicana*	intron	
EXP-Sb.Ubq4:1:1	55	1632	*S. bicolor*	EXP: P-Sb.Ubq4-1:1:1 (SEQ ID NO: 56); L-Sb.Ubq4-1:1:1 (SEQ ID NO: 57); I-Sb.Ubq4-1:1:1 (SEQ ID NO: 58).	pMON140886, PCR0145921, pMON129219, pMON132932
P-Sb.Ubq4-1:1:1	56	401	*S. bicolor*	promoter	
L-Sb.Ubq4-1:1:1	57	154	*S. bicolor*	leader	
I-Sb.Ubq4-1:1:1	58	1077	*S. bicolor*	intron	
EXP-Sb.Ubq6	59	2000	*S. bicolor*	EXP: P-Sb.Ubq6-1:1:2 (SEQ ID NO: 60); L-Sb.Ubq6-1:1:1 (SEQ ID NO: 61); I-Sb.Ubq6-1:1:1 (SEQ ID NO: 62).	
P-Sb.Ubq6-1:1:2	60	791	*S. bicolor*	promoter	
L-Sb.Ubq6-1:1:1	61	136	*S. bicolor*	leader	
I-Sb.Ubq6-1:1:1	62	1073	*S. bicolor*	intron	
EXP-Sb.Ubq6:1:1	63	2064	*S. bicolor*	EXP: P-Sb.Ubq6-1:1:1 (SEQ ID NO: 64); L-Sb.Ubq6-1:1:1 (SEQ ID NO: 61); I-Sb.Ubq6-1:1:1 (SEQ ID NO: 62).	pMON140887, PCR0145920, pMON129218
P-Sb.Ubq6-1:1:1	64	855	*S. bicolor*	promoter	
EXP-Sb.Ubq7:1:1	65	2000	*S. bicolor*	EXP: P-Sb.Ubq7-1:1:1 (SEQ ID NO: 66); L-Sb.Ubq7-1:1:1 (SEQ ID NO: 67); I-Sb.Ubq7-1:1:1 (SEQ ID NO: 68).	pMON132974
P-Sb.Ubq7-1:1:1	66	565	*S. bicolor*	promoter	
L-Sb.Ubq7-1:1:1	67	77	*S. bicolor*	leader	
I-Sb.Ubq7-1:1:1	68	1358	*S. bicolor*	intron	
EXP-SETit.Ubq1:1:1	69	2622	*S. italica*	EXP: P-SETit.Ubq1-1:1:1 (SEQ ID NO: 70); L-SETit.Ubq1-1:1:1 (SEQ ID NO: 71); I-SETit.Ubq1-1:1:1 (SEQ ID NO: 72).	pMON140877, PCR0145900, pMON129200
P-SETit.Ubq1-1:1:1	70	1492	*S. italica*	promoter	
L-SETit.Ubq1-1:1:1	71	127	*S. italica*	leader	
I-SETit.Ubq1-1:1:1	72	1003	*S. italica*	intron	
EXP-SETit.Ubq1:1:4	73	2622	*S. italica*	EXP: P-SETit.Ubq1-1:1:4 (SEQ ID NO: 74); L-SETit.Ubq1-1:1:1 (SEQ ID NO: 71); I-SETit.Ubq1-1:1:1 (SEQ ID NO: 72).	pMON132037
P-SETit.Ubq1-1:1:4	74	1492	*S. italica*	promoter	
EXP-SETit.Ubq1:1:2	75	2164	*S. italica*	EXP: P-SETit.Ubq1-1:1:2 (SEQ ID NO: 76); L-SETit.Ubq1-1:1:1 (SEQ ID NO: 71); I-SETit.Ubq1-1:1:1 (SEQ ID NO: 72).	
P-SETit.Ubq1-1:1:2	76	1034	*S. italica*	promoter	
EXP-SETit.Ubq1:1:3	77	1810	*S. italica*	EXP: P-SETit.Ubq1-1:1:3 (SEQ ID NO: 78); L-SETit.Ubq1-1:1:1 (SEQ ID NO: 71); I-SETit.Ubq1-1:1:1 (SEQ ID NO: 72).	PCR0145905, pMON129202, pMON131957
P-SETit.Ubq1-1:1:3	78	680	*S. italica*	promoter	
EXP-Cl.Ubq1:1:1	79	1940	C. lacryma-jobi	EXP: P-Cl.Ubq1-1:1:1 (SEQ ID NO: 80); L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81); I-Cl.Ubq1-1:1:1 (SEQ ID NO: 82).	pMON140889, PCR0145922, pMON140913, PCR19, pMON129221, pMON146795, pMON146796, pMON146797, pMON146798, pMON146799, pMON132047, pMON146800, pMON146801, pMON146802
P-Cl.Ubq1-1:1:1	80	837	C. lacryma-jobi	promoter	
L-Cl.Ubq1-1:1:1	81	86	C. lacryma-jobi	leader	
I-Cl.Ubq1-1:1:1	82	1017	C. lacryma-jobi	intron	
EXP-Cl.Ubq1:1:3	83	1845	C. lacryma-jobi	EXP: P-Cl.Ubq1-1:1:4 (SEQ ID NO: 84); L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81); I-Cl.Ubq1-1:1:1 (SEQ ID NO: 82).	PCR0145945, pMON140914, PCR20

TABLE 1-continued

Transcriptional regulatory expression element groups ("EXP's"), promoters, enhancers, leaders and introns isolated from various grass species.

Annotation	SEQ ID NO:	Size (bp)	Source Genus/species	Description and/or regulatory elements of EXP linked in 5' → 3' direction (SEQ ID NOs):	Plasmid Construct(s) and Amplicons comprising EXP
P-Cl.Ubq1-1:1:4	84	742	C. lacryma-jobi	promoter	
EXP-Cl.Ubq1:1:4	85	1504	C. lacryma-jobi	EXP: P-Cl.Ubq1-1:1:3 (SEQ ID NO: 86); L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81); I-Cl.Ubq1-1:1:1 (SEQ ID NO: 82).	PCR0145946, pMON140915, PCR21
P-Cl.Ubq1-1:1:3	86	401	C. lacryma-jobi	promoter	
EXP-Cl.Ubq1:1:5	87	1157	C. lacryma-jobi	EXP: P-Cl.Ubq1-1:1:5 (SEQ ID NO: 88); L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81); I-Cl.Ubq1-1:1:1 (SEQ ID NO: 82).	PCR0145947, pMON140916, PCR22
P-Cl.Ubq1-1:1:5	88	54	C. lacryma-jobi	promoter	
E-Cl.Ubq1-1:1:1	89	798	C. lacryma-jobi	enhancer	
EXP-Cl.Ubq1:1:12	90	3393	C. lacryma-jobi	EXP: P-Cl.Ubq1-1:1:9 (SEQ ID NO: 91); L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81); I-Cl.Ubq1-1:1:7 (SEQ ID NO: 92)	pMON142729
P-Cl.Ubq1-1:1:9	91	2287	C. lacryma-jobi	Promoter	
I-Cl.Ubq1-1:1:7	92	1020	C. lacryma-jobi	Intron	
EXP-Cl.Ubq1:1:16	93	3393	C. lacryma-jobi	EXP: P-Cl.Ubq1-1:1:9 (SEQ ID NO: 91); L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81); I-Cl.Ubq1-1:1:6 (SEQ ID NO: 94)	pMON146750, pMON142748
I-Cl.Ubq1-1:1:6	94	1020	C. lacryma-jobi	Intron	
EXP-Cl.Ubq1:1:11	95	2166	C. lacryma-jobi	EXP: P-Cl.Ubq1-1:1:10 (SEQ ID NO: 96); L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81); I-Cl.Ubq1-1:1:7 (SEQ ID NO: 92)	pMON142730
P-Cl.Ubq1-1:1:10	96	1060	C. lacryma-jobi	Promoter	
EXP-Cl.Ubq1:1:17	97	2166	C. lacryma-jobi	EXP: P-Cl.Ubq1-1:1:10 (SEQ ID NO: 96); L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81); I-Cl.Ubq1-1:1:6 (SEQ ID NO: 94)	pMON146751, pMON142749
EXP-Cl.Ubq1:1:10	98	1943	C. lacryma-jobi	EXP: P-Cl.Ubq1-1:1:1 (SEQ ID NO: 80); L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81); I-Cl.Ubq1-1:1:6 (SEQ ID NO: 94)	pMON140889, PCR0145922, pMON140913, PCR19, pMON129221
EXP-Cl.Ubq1:1:18	99	1943	C. lacryma-jobi	EXP: P-Cl.Ubq1-1:1:1 (SEQ ID NO: 80); L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81); I-Cl.Ubq1-1:1:7 (SEQ ID NO: 92)	pMON146795
EXP-Cl.Ubq1:1:19	100	1943	C. lacryma-jobi	EXP: P-Cl.Ubq1-1:1:1 (SEQ ID NO: 80); L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81); I-Cl.Ubq1-1:1:8 (SEQ ID NO: 101)	pMON146796
I-Cl.Ubq1-1:1:8	101	1020	C. lacryma-jobi	Intron	
EXP-Cl.Ubq1:1:20	102	1943	C. lacryma-jobi	EXP: P-Cl.Ubq1-1:1:1 (SEQ ID NO: 80); L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81); I-Cl.Ubq1-1:1:9 (SEQ ID NO: 103)	pMON146797
I-Cl.Ubq1-1:1:9	103	1020	C. lacryma-jobi	Intron	
EXP-Cl.Ubq1:1:21	104	1943	C. lacryma-jobi	EXP: P-Cl.Ubq1-1:1:1 (SEQ ID NO: 80); L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81); I-Cl.Ubq1-1:1:10 (SEQ ID NO: 105)	pMON146798
I-Cl.Ubq1-1:1:10	105	1020	C. lacryma-jobi	Intron	
EXP-Cl.Ubq1:1:22	106	1943	C. lacryma-jobi	EXP: P-Cl.Ubq1-1:1:1 (SEQ ID NO: 80); L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81); I-Cl.Ubq1-1:1:11 (SEQ ID NO: 107)	pMON146799
I-Cl.Ubq1-1:1:11	107	1020	C. lacryma-jobi	Intron	
EXP-Cl.Ubq1:1:23	108	1943	C. lacryma-jobi	EXP: P-Cl.Ubq1-1:1:1 (SEQ ID NO: 80); L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81); I-Cl.Ubq1-1:1:12 (SEQ ID NO: 109)	pMON132047, pMON146800
I-Cl.Ubq1-1:1:12	109	1020	C. lacryma-jobi	Intron	
EXP-Cl.Ubq1:1:24	110	1943	C. lacryma-jobi	EXP: P-Cl.Ubq1-1:1:1 (SEQ ID NO: 80); L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81); I-Cl.Ubq1-1:1:13 (SEQ ID NO: 111)	pMON146801
I-Cl.Ubq1-1:1:13	111	1020	C. lacryma-jobi	Intron	
EXP-Cl.Ubq1:1:25	112	1943	C. lacryma-jobi	EXP: P-Cl.Ubq1-1:1:1 (SEQ ID NO: 80); L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81); I-Cl.Ubq1-1:1:14 (SEQ ID NO: 113)	pMON146802
I-Cl.Ubq1-1:1:14	113	1020	C. lacryma-jobi	Intron	
EXP-Cl.Ubq1:1:13	114	1848	C. lacryma-jobi	EXP: P-Cl.Ubq1-1:1:4 (SEQ ID NO: 84); L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81); I-Cl.Ubq1-1:1:6 (SEQ ID NO: 94)	PCR0145945, pMON140914, PCR20
EXP-Cl.Ubq1:1:14	115	1507	C. lacryma-jobi	EXP: P-Cl.Ubq1-1:1:3 (SEQ ID NO: 86); L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81); I-Cl.Ubq1-1:1:6 (SEQ ID NO: 94)	PCR0145946, pMON140915, PCR21
EXP-Cl.Ubq1:1:15	116	1160	C. lacryma-jobi	EXP: P-Cl.Ubq1-1:1:5 (SEQ ID NO: 88); L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81); I-Cl.Ubq1-1:1:6 (SEQ ID NO: 94)	PCR0145947, pMON140916, PCR22
EXP-SETit.Ubq1:1:5	117	2625	*S. italica*	EXP: P-SETit.Ubq1-1:1:1 (SEQ ID NO: 70); L-SETit.Ubq1-1:1:1 (SEQ ID NO: 71); I-SETit.Ubq1-1:1:2 (SEQ ID NO: 118)	pMON140877, PCR0145900, pMON129200
I-SETit.Ubq1-1:1:2	118	1006	*S. italica*	Intron	
EXP-SETit.Ubq1:1:10	119	2625	*S. italica*	EXP: P-SETit.Ubq1-1:1:4 (SEQ ID NO: 64); L-SETit.Ubq1-1:1:1 (SEQ ID NO: 71); I-SETit.Ubq1-1:1:3 (SEQ ID NO: 120)	pMON132037

TABLE 1-continued

Transcriptional regulatory expression element groups ("EXP's"), promoters, enhancers, leaders and introns isolated from various grass species.

Annotation	SEQ ID NO:	Size (bp)	Source Genus/species	Description and/or regulatory elements of EXP linked in 5' → 3' direction (SEQ ID NOs):	Plasmid Construct(s) and Amplicons comprising EXP
I-SETit.Ubq1-1:1:3	120	1006	*S. italica*	Intron	
EXP-SETit.Ubq1:1:12	121	2625	*S. italica*	EXP: P-SETit.Ubq1-1:1:4 (SEQ ID NO: 64); L-SETit.Ubq1-1:1:1 (SEQ ID NO: 71); I-SETit.Ubq1-1:1:4 (SEQ ID NO: 122)	
I-SETit.Ubq1-1:1:4	122	1006	*S. italica*	Intron	
EXP-SETit.Ubq1:1:7	123	2167	*S. italica*	EXP: P-SETit.Ubq1-1:1:2 (SEQ ID NO: 71); L-SETit.Ubq1-1:1:1 (SEQ ID NO: 71); I-SETit.Ubq1-1:1:2 (SEQ ID NO: 118)	PCR0145928, pMON129201
EXP-SETit.Ubq1:1:6	124	1813	*S. italica*	EXP: P-SETit.Ubq1-1:1:3 (SEQ ID NO: 73); L-SETit.Ubq1-1:1:1 (SEQ ID NO: 71); I-SETit.Ubq1-1:1:2 (SEQ ID NO: 118)	PCR0145905, pMON129202
EXP-SETit.Ubq1:1:11	125	1813	*S. italica*	EXP: P-SETit.Ubq1-1:1:3 (SEQ ID NO: 73); L-SETit.Ubq1-1:1:1 (SEQ ID NO: 71); I-SETit.Ubq1-1:1:3 (SEQ ID NO: 120)	pMON131957
EXP-SETit.Ubq1:1:13	126	1813	*S. italica*	EXP: P-SETit.Ubq1-1:1:3 (SEQ ID NO: 73); L-SETit.Ubq1-1:1:1 (SEQ ID NO: 71); I-SETit.Ubq1-1:1:5 (SEQ ID NO: 127)	
I-SETit.Ubq1-1:1:5	127	1006	*S. italica*	Intron	
EXP-Sv.Ubq1:1:7	128	2634	*S. viridis*	EXP: P-Sv.Ubq1-1:1:1 (SEQ ID NO: 34); L-Sv.Ubq1-1:1:2 (SEQ ID NO: 35); I-Sv.Ubq1-1:1:2 (SEQ ID NO: 129)	pMON140878, PCR0145909, pMON129203
I-Sv.Ubq1-1:1:2	129	1014	*S. viridis*	Intron	
EXP-Sv.Ubq1:1:11	130	2634	*S. viridis*	EXP: P-Sv.Ubq1-1:1:1 (SEQ ID NO: 34); L-Sv.Ubq1-1:1:2 (SEQ ID NO: 35); I-Sv.Ubq1-1:1:3 (SEQ ID NO: 131)	pMON131958
I-Sv.Ubq1-1:1:3	131	1014	*S. viridis*	Intron	
EXP-Sv.Ubq1:1:8	132	2176	*S. viridis*	EXP: P-Sv.Ubq1-1:1:2 (SEQ ID NO: 38); L-Sv.Ubq1-1:1:2 (SEQ ID NO: 35); I-Sv.Ubq1-1:1:2 (SEQ ID NO: 129)	PCR0145929, pMON129204
EXP-Sv.Ubq1:1:9	133	1822	*S. viridis*	EXP: P-Sv.Ubq1-1:1:3 (SEQ ID NO: 40); L-Sv.Ubq1-1:1:2 (SEQ ID NO: 35); I-Sv.Ubq1-1:1:2 (SEQ ID NO: 129)	pMON129205
EXP-Sv.Ubq1:1:10	134	1822	*S. viridis*	EXP: P-Sv.Ubq1-1:1:4 (SEQ ID NO: 135); L-Sv.Ubq1-1:1:2 (SEQ ID NO: 35); I-Sv.Ubq1-1:1:2 (SEQ ID NO: 129)	PCR0145911
P-Sv.Ubq1-1:1:4	135	681	*S. viridis*	Promoter	
EXP-Sv.Ubq1:1:12	136	1822	*S. viridis*	EXP: P-Sv.Ubq1-1:1:3 (SEQ ID NO: 40); L-Sv.Ubq1-1:1:2 (SEQ ID NO: 35); I-Sv.Ubq1-1:1:3 (SEQ ID NO: 131)	pMON131959
EXP-Zm.UbqM1:1:6 (Allele-1)	137	1925	*Z. mays* subsp. *Mexicana*	EXP: P-Zm.UbqM1-1:1:1 (SEQ ID NO: 42); L-Zm.UbqM1-1:1:1 (SEQ ID NO: 43); I-Zm.UbqM1-1:1:13 (SEQ ID NO: 138)	pMON140881, PCR0145914, pMON129210
I-Zm.UbqM1-1:1:13 (Allele-1)	138	997	*Z. mays* subsp. *Mexicana*	Intron	
EXP-Zm.UbqM1:1:10 (Allele-1)	139	1925	*Z. mays* subsp. *Mexicana*	EXP: P-Zm.UbqM1-1:1:1 (SEQ ID NO: 42); L-Zm.UbqM1-1:1:1 (SEQ ID NO: 43); I-Zm.UbqM1-1:1:17 (SEQ ID NO: 140)	pMON131961
I-Zm.UbqM1-1:1:17 (Allele-1)	140	997	*Z. mays* subsp. *Mexicana*	Intron	
EXP-Zm.UbqM1:1:7 (Allele-2)	141	1974	*Z. mays* subsp. *Mexicana*	EXP: P-Zm.UbqM1-1:1:4 (SEQ ID NO: 46); L-Zm.UbqM1-1:1:5 (SEQ ID NO: 47); I-Zm.UbqM1-1:1:14 (SEQ ID NO: 142)	pMON140882, PCR0145915, pMON129212
I-Zm.UbqM1-1:1:14 (Allele-2)	142	1010	*Z. mays* subsp. *Mexicana*	Intron	
EXP-Zm.UbqM1:1:12 (Allele-2)	143	1974	*Z. mays* subsp. *Mexicana*	EXP: P-Zm.UbqM1-1:1:4 (SEQ ID NO: 46); L-Zm.UbqM1-1:1:5 (SEQ ID NO: 47); I-Zm.UbqM1-1:1:19 (SEQ ID NO: 144)	pMON131963
I-Zm.UbqM1-1:1:19 (Allele-2)	144	1010	*Z. mays* subsp. *Mexicana*	Intron	
EXP-Zm.UbqM1:1:8 (Allele-3)	145	2008	*Z. mays* subsp. *Mexicana*	EXP: P-Zm.UbqM1-1:1:5 (SEQ ID NO: 50); L-Zm.UbqM1-1:1:4 (SEQ ID NO: 51); I-Zm.UbqM1-1:1:15 (SEQ ID NO: 146)	PCR0145916, pMON129211
I-Zm.UbqM1-1:1:15 (Allele-3)	146	1053	*Z. mays* subsp. *Mexicana*	Intron	
EXP-Zm.UbqM1:1:9 (Allele-3)	147	2008	*Z. mays* subsp. *Mexicana*	EXP: P-Zm.UbqM1-1:1:5 (SEQ ID NO: 50); L-Zm.UbqM1-1:1:4 (SEQ ID NO: 51); I-Zm.UbqM1-1:1:16 (SEQ ID NO: 148)	
I-Zm.UbqM1-1:1:16 (Allele-3)	148	1053	*Z. mays* subsp. *Mexicana*	Intron	
EXP-Zm.UbqM1:1:11 (Allele-3)	149	2008	*Z. mays* subsp. *Mexicana*	EXP: P-Zm.UbqM1-1:1:5 (SEQ ID NO: 50); L-Zm.UbqM1-1:1:4 (SEQ ID NO: 51); I-Zm.UbqM1-1:1:18 (SEQ ID NO: 150)	pMON131962, pMON132047

TABLE 1-continued

Transcriptional regulatory expression element groups ("EXP's"), promoters, enhancers, leaders and introns isolated from various grass species.

Annotation	SEQ ID NO:	Size (bp)	Source Genus/species	Description and/or regulatory elements of EXP linked in 5' → 3' direction (SEQ ID NOs):	Plasmid Construct(s) and Amplicons comprising EXP
I-Zm.UbqM1-1:1:18 (Allele-3)	150	1053	*Z. mays* subsp. *Mexicana*	Intron	
EXP-Sb.Ubq4:1:2	151	1635	*S. bicolor*	EXP: P-Sb.Ubq4-1:1:1 (SEQ ID NO: 56); L-Sb.Ubq4-1:1:1 (SEQ ID NO: 57); I-Sb.Ubq4-1:1:2 (SEQ ID NO: 152)	pMON140886, PCR0145921, pMON129219, pMON132932
I-Sb.Ubq4-1:1:2	152	1080	*S. bicolor*	Intron	
EXP-Sb.Ubq6:1:2	153	2067	*S. bicolor*	EXP: P-Sb.Ubq6-1:1:1 (SEQ ID NO: 64); L-Sb.Ubq6-1:1:1 (SEQ ID NO: 57); I-Sb.Ubq6-1:1:2 (SEQ ID NO: 154)	pMON140887, PCR0145920, pMON129218, pMON132931
I-Sb.Ubq6-1:1:2	154	1076	*S. bicolor*	Intron	
EXP-Sb.Ubq6:1:3	155	2067	*S. bicolor*	EXP: P-Sb.Ubq6-1:1:1 (SEQ ID NO: 64); L-Sb.Ubq6-1:1:1 (SEQ ID NO: 57); I-Sb.Ubq6-1:1:3 (SEQ ID NO: 1569)	pMON132931
I-Sb.Ubq6-1:1:3	156	1076	*S. bicolor*	Intron	
EXP-Sb.Ubq7:1:2	157	2003	*S. bicolor*	EXP: P-Sb.Ubq7-1:1:1 (SEQ ID NO: 66); L-Sb.Ubq7-1:1:1 (SEQ ID NO: 67); I-Sb.Ubq7-1:1:A (SEQ ID NO: 158)	pMON132974
I-Sb.Ubq7-1:1:2	158	1361	*S. bicolor*	Intron	
EXP-SETit.Ubq1:1:E	180	2625	*S. italica*	EXP: P-SETit.Ubq1-1:1:4 (SEQ ID NO: 64); L-SETit.Ubq1-1:1:1 (SEQ ID NO: 71); I-SETit.Ubq1-1:1:5 (SEQ ID NO: 127)	
EXP-Zm.UbqM1:1:13 (Allele-3)	181	2008	*Z. mays* subsp. *Mexicana*	EXP: P-Zm.UbqM1-1:1:5 (SEQ ID NO: 50); L-Zm.UbqM1-1:1:4 (SEQ ID NO: 51); I-Zm.UbqM1-1:1:20 (SEQ ID NO: 182)	
I-Zm.UbqM1-1:1:20 (Allele-3)	182	1053	*Z. mays* subsp. *Mexicana*	Intron	
EXP-SETit.Ubq1:1:9	183	2625	*S. italica*	EXP: P-SETit.Ubq1-1:1:4 (SEQ ID NO: 64); L-SETit.Ubq1-1:1:1 (SEQ ID NO: 71); I-SETit.Ubq1-1:1:2 (SEQ ID NO: 118)	

[0089] As shown in Table 1, for example, the transcriptional regulatory EXP sequence designated EXP-ANDge.Ubq1:1:9 (SEQ ID NO: 1), with components isolated from *A. gerardii*, comprises a promoter element, P-ANDge.Ubq1-1:1:11 (SEQ ID NO: 2), operably linked 5' to a leader element, L-ANDge.Ubq1-1:1:2 (SEQ ID NO: 3), operably linked 5' to an intron element, I-ANDge.Ubq1-1:1:3 (SEQ ID NO: 4). Other EXP's are linked similarly, as outlined in Table 1.

[0090] As shown in Table 1, the sequence listing and FIGS. **1-7**, variants of promoter sequences from the species *A. gerardii, E. ravennae, Z. mays* subsp. *mexicana, S. bicolor, C. lacryma-jobi, S. italica*, and *S. viridis* were engineered which comprise shorter promoter fragments of, for instance, P-ANDge.Ubq1-1:1:11 (SEQ ID NO:2), P-ERIra.Ubq1-1:1:10 (SEQ ID NO:19) or other respective promoters from other species, and for instance resulting in P-ANDge.Ubq1-1:1:9 (SEQ ID NO: 6), P-ERIra.Ubq1-1:1:9 (SEQ ID NO: 23), P-Cl.Ubq1-1:1:10 (SEQ ID NO: 96), P-SETit.Ubq1-1:1:2 (SEQ ID NO: 76) and P-Sv.Ubq1-1:1:2 (SEQ ID NO: 38), as well as other promoter fragments. P-SETit.Ubq1-1:1:4 (SEQ ID NO: 74) comprises a single nucleotide change relative to P-SETit.Ubq1-1:1:1 (SEQ ID NO: 70). Likewise, P-Sv.Ubq1-1:1:3 (SEQ ID NO: 40) comprises a single nucleotide change relative to P-Sv.Ubq1-1:1:4 (SEQ ID NO: 135).

[0091] In some instances, variants of specific introns were created by altering the last 3' nucleotides of each respective intron following the sequence 5'-AG-3' of the 3' intron splice junction. These intron variants are shown in Table 2 below.

TABLE 2

3' end sequence of intron variants.

Annotation	SEQ ID NO:	Intron 3' end nucleotides immediately following 3' splice site AG
I-Cl.Ubq1-1:1:7	92	GTG
I-Cl.Ubq1-1:1:6	94	GTC
I-Cl.Ubq1-1:1:8	101	GCG
I-Cl.Ubq1-1:1:9	103	GAC
I-Cl.Ubq1-1:1:10	105	ACC
I-Cl.Ubq1-1:1:11	107	GGG
I-Cl.Ubq1-1:1:12	109	GGT
I-Cl.Ubq1-1:1:13	111	CGT
I-Cl.Ubq1-1:1:14	113	TGT
I-SETit.Ubq1-1:1:2	118	GTG
I-SETit.Ubq1-1:1:3	120	GGT
I-SETit.Ubq1-1:1:4	122	ACC

TABLE 2 -continued

3' end sequence of intron variants.

Annotation	SEQ ID NO:	Intron 3' end nucleotides immediately following 3' splice site AG
I-SETit.Ubq1-1:1:5	127	GGC
I-Sv.Ubq1-1:1:2	129	GTG
I-Sv.Ubq1-1:1:3	131	GGT
I-Zm.UbqM1-1:1:13 (Allele-1)	138	GTC
I-Zm.UbqM1-1:1:17 (Allele-1)	140	GGT
I-Zm.UbqM1-1:1:14 (Allele-2)	142	GTC
I-Zm.UbqM1-1:1:19 (Allele-2)	144	GGT
I-Zm.UbqM1-1:1:15 (Allele-3)	146	GTC
I-Zm.UbqM1-1:1:18 (Allele-3)	148	GGT
I-Sb.Ubq6-1:1:2	154	GTG
I-Sb.Ubq6-1:1:3	156	GGT
I-Zm.UbqM1-1:1:20 (Allele-3)	182	CGG

[0092] Also listed in Table 1 are three allelic variants isolated using the same primer sets designed for amplification of genomic DNA from *Z. mays* subsp. *mexicana*. Allelic variants of the EXP sequences are comprised of sequence that shares some identity within various regions of other sequences, but insertions, deletions and nucleotide mismatches may also be apparent within each promoter, leader and/or intron of each of the EXP sequences. The EXP sequence designated EXP-Zm.UbqM1:1:1 (SEQ ID NO: 41) represents a first allele (Allele-1) of the *Z. mays* subsp. *mexicana* Ubq1 gene transcriptional regulatory expression element group. The EXP sequences designated EXP-Zm.UbqM1:1:6 (SEQ ID NO: 137) and EXP-Zm.UbqM1:1:10 (SEQ ID NO: 139) represent a first allele (Allele-1), with the only difference between the two EXPs occurring in the last 3' nucleotides of each respective intron following the sequence 5'-AG-3' of the 3' intron splice junction. The EXP sequence designated EXP-Zm.UbqM1:1:4 (SEQ ID NO: 45) represents a second allele (Allele-2) of the *Z. mays* subsp. *mexicana* Ubq1 gene transcriptional regulatory expression element group. The EXP sequences designated EXP-Zm.UbqM1:1:7 (SEQ ID NO: 141) and EXP-Zm.UbqM1:1:12 (SEQ ID NO: 143) represent a second allele (Allele-2), with the only difference between the two EXPs occurring in the last 3' nucleotides of each respective intron following the sequence 5'-AG-3' of the 3' intron splice junction. The EXP sequences EXP-Zm.UbqM1:1:2 (SEQ ID NO: 49) and EXP-Zm.UbqM1:1:5 (SEQ ID NO: 53) represents a third allel (Allele-3) of the *Z. mays* subsp. *mexicana* Ubq1 gene transcriptional regulatory expression element group and comprise a single nucleotide difference at position 1034 within their respective introns (G for I-Zm.UbqM1-1:1:11, SEQ ID NO: 52 and T for I-Zm.UbqM1-1:1:12, SEQ ID NO: 54). The EXP sequences designated EXP-Zm.UbqM1:1:8 (SEQ ID NO: 145), EXP-Zm.UbqM1:1:9 (SEQ ID NO: 147), EXP-Zm.UbqM1:1:11 (SEQ ID NO: 149) and EXP-Zm.UbqM1:1:13 (SEQ ID NO: 181) also represent a third allele (Allele-3). The intron of EXP-Zm.UbqM1:1:9, I-Zm.UbqM1-1:1:16 (SEQ ID NO: 148) comprises a thymine residue at position 1034, while the introns of EXP-Zm.UbqM1:1:8, EXP-Zm.UbqM1:1:11 and EXP-Zm.UbqM1:1:13 (1-Zm.UbqM1-1:1:15, SEQ ID NO: 146; I-Zm.UbqM1-1:1:18, SEQ ID NO: 11 and; I-Zm.UbqM1-1:1:20, SEQ ID NO: 182) each comprise a guanine residue at position 1034. In addition, the last 3, 3' end nucleotides of EXP-Zm.UbqM1:1:8 (SEQ ID NO: 145) and EXP-Zm.UbqM1:1:9 (SEQ ID NO: 147) differ from those of EXP-Zm.UbqM1:1:11 (SEQ ID NO: 149) and EXP-Zm.UbqM1:1:13 (SEQ ID NO: 181).

Example 2

Analysis of Regulatory Elements Driving GUS in Corn Protoplasts

[0093] Corn leaf protoplasts were transformed with plant expression vectors containing an EXP sequence driving expression of the β-glucuronidase (GUS) transgene and compared to GUS expression in leaf protoplasts in which expression of GUS is driven by known constitutive promoters.

[0094] Expression of a transgene driven by EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ERIra.Ubq1:1:9 (SEQ ID NO: 22) or EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27) was compared with expression from known constitutive promoters. The foregoing EXP sequences were cloned into plant expression vectors as shown in Table 3 below to yield vectors in which an EXP sequence is operably linked 5' to a β-glucuronidase (GUS) reporter that contained a processable intron (referred to as GUS-2, SEQ ID NO: 160) derived from the potato light-inducible tissue-specific ST-LS1 gene (GenBank Accession: X04753) or a contiguous GUS coding sequence (GUS-1, SEQ ID NOS: 159), which was operably linked 5' to a 3' UTR derived from the *A. tumefaciens* Nopaline synthase gene (T-AGRtu.nos-1:1:13, SEQ ID NO: 161) or the wheat Hsp17 gene (T-Ta.Hsp17-1:1:1, SEQ ID NO: 162).

TABLE 3

GUS plant expression plasmid construct and corresponding EXP sequence, GUS coding sequence and 3' UTR used for transformation of corn leaf protoplasts. "SEQ ID NO:" refers to given EXP sequence.

Plasmid	EXP sequence	SEQ ID NO:	GUS	3' UTR
pMON19469	EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	GUS-1	T-AGRtu.nos-1:1:13

TABLE 3-continued

GUS plant expression plasmid construct and corresponding EXP sequence, GUS coding sequence and 3' UTR used for transformation of corn leaf protoplasts. "SEQ ID NO:" refers to given EXP sequence.

Plasmid	EXP sequence	SEQ ID NO:	GUS	3' UTR
pMON65328	EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1	163	GUS-2	T-Ta.Hsp17-1:1:1
pMON25455	EXP-Os.Act1:1:9	179	GUS-1	T-AGRtu.nos-1:1:13
pMON122605	EXP-Os.TubA-3:1:1	165	GUS-1	T-AGRtu.nos-1:1:13
pMON136264	EXP-ANDge.Ubq1:1:7	5	GUS-1	T-AGRtu.nos-1:1:13
pMON136259	EXP-ANDge.Ubq1:1:6	12	GUS-1	T-AGRtu.nos-1:1:13
pMON136263	EXP-ERIra.Ubq1:1:9	22	GUS-1	T-AGRtu.nos-1:1:13
pMON136258	EXP-ERIra.Ubq1:1:8	27	GUS-1	T-AGRtu.nos-1:1:13

[0095] Control plasmids (pMON19469, pMON65328, pMON25455 and pMON122605) used for comparison were constructed as described above and contain a known EXP sequence: EXP-CaMV.35S-enh+Zm.DnaK:1:1 (SEQ ID NO: 170), EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1 (SEQ ID NO: 163), EXP-Os.Act1:1:9 (SEQ ID NO: 179), or EXP-Os.TubA-3:1:1 (SEQ ID NO: 165), respectively, operably linked 5' to a GUS coding sequence and 3' UTR. Three additional controls were provided to assess background GUS and luciferase expression: a no DNA control, an empty vector which is not designed for transgene expression, and an expression vector used to express green fluorescent protein (GFP).

[0096] Two plasmids, for use in co-transformation and normalization of data, were also constructed using methods known in the art. Each plasmid contained a specific luciferase coding sequence that was driven by a constitutive EXP sequence. The plant vector pMON19437 comprises a transgene cassette with a constitutive promoter operably linked 5' to an intron, (EXP-CaMV.35S-enh+Zm.DnaK:1:1, SEQ ID NO: 170), operably linked 5' to a firefly (*Photinus pyralis*) luciferase coding sequence (LUCIFERASE:1:3, SEQ ID NO: 166), operably linked 5' to a 3' UTR from the *Agrobacterium tumefaciens* nopaline synthase gene (T-AGRtu.nos-1:1:13, SEQ ID NO: 161). The plant vector pMON63934 comprises a transgene cassette with a constitutive EXP sequence (EXP-CaMV.35S-enh-Lhcb1, SEQ ID NO: 168), operably linked 5' to a sea pansy (*Renilla reniformis*) luciferase coding sequence (CR-Ren.hRenilla Lucife-0:0:1, SEQ ID NO: 167), operably linked 5' to a 3' UTR from the *Agrobacterium tumefaciens* nopaline synthase gene (T-AGRtu.nos-1:1:13, SEQ ID NO: 161).

[0097] Corn leaf protoplasts were transformed using a PEG-based transformation method, as is well known in the art. Protoplast cells were transformed with pMON19437 plasmid DNA, pMON63934 plasmid DNA, and an equimolar quantity of one of the plasmids presented in Table 3 and incubated overnight in total darkness. Measurements of both GUS and luciferase were conducted by placing aliquots of a lysed preparation of cells transformed as above into two different small-well trays. One tray was used for GUS measurements, and a second tray was used to perform a dual luciferase assay using the dual luciferase reporter assay system (Promega Corp., Madison, Wis.; see for example, Promega Notes Magazine, No: 57, 1996, p. 02). One or two transformations for each EXP sequence were performed and the mean expression values for each EXP sequence determined from several samples from each transformation experiment. Sample measurements were made using four replicates of each EXP sequence construct transformation, or alternatively, three replicates of each EXP sequence construct per one of two transformation experiments. The mean GUS and luciferase expression levels are provided in Table 4. In this table, the firefly luciferase values (e.g. from expression of pMON19437) are provided in the column labeled "FLuc" and the *Renilla* luciferase values are provided as in the column labeled "RLuc."

TABLE 4

Mean GUS and Luciferase activity in transformed corn leaf protoplast cells.

Plasmid	EXP sequence	SEQ ID NO:	Gus	RLuc	FLuc
pMON19469	EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	789147	298899	36568
pMON65328	EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1	163	508327	158227	17193
pMON25455	EXP-Os.Act1:1:9	179	460579	183955	53813
pMON122605	EXP-Os.TubA-3:1:1	165	25082	25821	21004
pMON136264	EXP-ANDge.Ubq1:1:7	5	926083	101213	23704
pMON136259	EXP-ANDge.Ubq1:1:6	12	845274	193153	51479
pMON136263	EXP-ERIra.Ubq1:1:9	22	901985	132765	41313
pMON136258	EXP-ERIra.Ubq1:1:8	27	1011447	210635	66803

[0098] To compare the relative activity of each EXP sequence, GUS values were expressed as a ratio of GUS to luciferase activity and normalized with respect to the expression levels observed for the EXP sequence EXP-Os.TubA-3:1:1 (SEQ ID NO: 165). Table 5 below shows the GUS/RLuc ratios of expression normalized with respect to EXP-Os.TubA-3:1:1 expression in corn protoplasts.

[0099] As can be seen in Table 5, GUS expression, driven by EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ERIra.Ubq1:1:9 (SEQ ID NO: 22) or EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27) was 4.51 to 9.42 fold higher than GUS expression driven by EXP-Os.TubA-3:1:1 (SEQ ID NO: 165). GUS expression driven by EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ERIra.Ubq1:1:9 (SEQ ID NO: 22) or EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27) was also higher than that of EXP-CaMV.35S-enh+Zm.DnaK:1:1 (SEQ ID NO: 170), EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1 (SEQ ID NO: 163), or EXP-Os.Act1:1:9 (SEQ ID NO: 179).

TABLE 5

GUS/RLuc fold expression as relative to EXP-Os.TubA-3:1:1 expression in corn leaf protoplast cells.

Plasmid	EXP sequence	SEQ ID NO:	Gus/RLuc	Gus/RLuc Normalized with respect to EXP-Os.TubA-3:1:1
pMON19469	EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	2.640000	2.72
pMON65328	EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1	163	3.210000	3.31
pMON25455	EXP-Os.Act1:1:9	179	2.500000	2.57
pMON122605	EXP-Os.TubA-3:1:1	165	0.971000	1.00
pMON136264	EXP-ANDge.Ubq1:1:7	5	9.150000	9.42
pMON136259	EXP-ANDge.Ubq1:1:6	12	4.380000	4.51
pMON136263	EXP-ERIra.Ubq1:1:9	22	6.790000	6.99
pMON136258	EXP-ERIra.Ubq1:1:8	27	4.800000	4.94

[0100] Table 6 below show GUS/FLuc ratios of expression normalized with respect to EXP-Os.TubA-3:1:1 expression in corn protoplasts.

TABLE 6

GUS/FLuc fold expression as relative to EXP-Os.TubA-3:1:1 expression in corn leaf protoplast cells.

Plasmid	EXP sequence	SEQ ID NO:	Gus/FLuc	Normalized with respect to EXP-Os.TubA-3:1:1
pMON19469	EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	21.600000	18.15
pMON65328	EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1	163	29.600000	24.87
pMON25455	EXP-Os.Act1:1:9	179	8.560000	7.19
pMON122605	EXP-Os.TubA-3:1:1	165	1.190000	1.00
pMON136264	EXP-ANDge.Ubq1:1:7	5	39.100000	32.86
pMON136259	EXP-ANDge.Ubq1:1:6	12	16.400000	13.78
pMON136263	EXP-ERIra.Ubq1:1:9	22	21.800000	18.32
pMON136258	EXP-ERIra.Ubq1:1:8	27	15.100000	12.69

[0101] As can be seen in Table 6, GUS expression, driven by EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ERIra.Ubq1:1:9 (SEQ ID NO: 22) or EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27) demonstrated the same general trend when expressed as ratio of GUS/FLuc values and is normalized with respect to EXP-Os.TubA-3:1:1 (SEQ ID NO: 165). Expression was 12.69 to 32.86 fold higher than GUS expression driven by EXP-Os.TubA-3:1:1 (SEQ ID NO: 165). GUS expression driven by EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ERIra.Ubq1:1:9 (SEQ ID NO: 22) or EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27) was also higher in certain comparisons than that of EXP-CaMV.35S-enh+Zm.DnaK:1:1 (SEQ ID NO: 170), EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1 (SEQ ID NO: 163), or EXP-Os.Act1:1:9 (SEQ ID NO: 179).

Example 3

Analysis of Regulatory Elements Driving GUS in Corn Protoplasts Using GUS Transgene Cassette Amplicons

[0102] Corn leaf protoplasts were transformed with DNA amplicons derived from plant expression vectors containing an EXP sequence, driving expression of the β-glucuronidase (GUS) transgene, and compared to leaf protoplast in which expression of GUS is driven by known constitutive promoters in a series of experiments presented below.

[0103] In a first set of experiments, corn protoplast cells, derived from leaf tissue were transformed as above with amplicons produced from amplification of GUS transgene cassettes comprising plant expression vectors to compare expression of a transgene (GUS) driven by one of EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:10 (SEQ ID NO: 10), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ANDge.Ubq1:1:11 (SEQ ID NO: 14), EXP-ANDge.Ubq1:1:12 (SEQ ID NO: 16), EXP-ERIra.Ubq1:1:9 (SEQ ID NO: 22), EXP-ERIra.Ubq1:1:10 (SEQ ID NO: 25), EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27), EXP-ERIra.Ubq1:1:11 (SEQ ID NO: 29), EXP-ERIra.Ubq1:1:12 (SEQ ID NO: 31), EXP-SETit.Ubq1:1:5 (SEQ ID NO: 117), EXP-SETit.Ubq1:1:7 (SEQ ID NO: 123), EXP-SETit.Ubq1:1:6 (SEQ ID NO: 124), EXP-Sv.Ubq1:1:7 (SEQ ID NO: 128), EXP-Sv.Ubq1:1:8 (SEQ ID NO: 132), EXP-Sv.Ubq1:1:10 (SEQ ID NO: 134), EXP-Zm.UbqM1:1:6 (SEQ ID NO: 137), EXP-Zm.UbqM1:1:7 (SEQ ID NO: 141), EXP-Sb.Ubq4:1:2 (SEQ ID NO: 151), EXP-Sb.Ubq6:1:2 (SEQ ID NO: 153) and EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98) with that of known constitutive promoters. Each EXP sequence comprising the amplification template from which the transgene cassette amplicon is produced was cloned using methods known in the art into a plant expression vector shown in Table 7 below under the heading of "Amplicon Template." The resulting plant expression vectors comprise a transgene cassette comprised of a EXP sequence, operably linked 5' to a coding sequence for β-glucuronidase (GUS) that either contains a processable intron ("GUS-2" as discussed in Example 2 above), or a contiguous GUS coding sequence ("GUS-1", as discussed above), operably linked 5' to a 3' UTR T-AGRtu.nos-1:1:13 or T-Ta.Hsp17-1:1:1, as also noted above. Amplicons were produced using methods known to those skilled in the art using the plasmid construct templates presented in Table 7 below. Briefly, a 5' oligonucleotide primer was designed to anneal to the promoter sequence and a 3' oligonucleotide primer, which anneals at the 3' end of the 3' UTR was used for amplification of each transgene cassette. Successive 5' deletions were introduced into the promoter sequences comprising the transgene cassettes, giving rise to different EXP sequences, by the use of different oligonucleotide primers which were designed to anneal at different positions within the promoter sequence comprising each amplicon template.

TABLE 7

GUS plant expression amplicons and corresponding plasmid construct amplicon templates, EXP sequence, GUS coding sequence and 3' UTR used for transformation of corn leaf protoplasts.

Amplicon ID	Amplicon Template	EXP sequence	SEQ ID NO:	GUS Coding Sequence	3' UTR
PCR0145942	pMON25455	EXP-Os.Act1:1:9	179	GUS-1	T-AGRtu.nos-1:1:13
PCR0145941	pMON33449	P-CAMV.35S-ENH-1:1:102/L-CAMV.35S-1:1:2	169	GUS-1	T-AGRtu.nos-1:1:13
PCR0145943	pMON65328	EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1	163	GUS-2	T-Ta.Hsp17-1:1:1
PCR0145944	pMON81552	EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	GUS-1	T-AGRtu.nos-1:1:13
PCR0145892	pMON136264	EXP-ANDge.Ubq1:1:7	5	GUS-1	T-AGRtu.nos-1:1:13
PCR0145815	pMON136264	EXP-ANDge.Ubq1:1:10	10	GUS-1	T-AGRtu.nos-1:1:13
PCR0145893	pMON136259	EXP-ANDge.Ubq1:1:6	12	GUS-1	T-AGRtu.nos-1:1:13
PCR0145817	pMON136264	EXP-ANDge.Ubq1:1:11	14	GUS-1	T-AGRtu.nos-1:1:13
PCR0145819	pMON136264	EXP-ANDge.Ubq1:1:12	16	GUS-1	T-AGRtu.nos-1:1:13
PCR0145896	pMON136263	EXP-ERIra.Ubq1:1:9	22	GUS-1	T-AGRtu.nos-1:1:13
PCR0145820	pMON136263	EXP-ERIra.Ubq1:1:10	25	GUS-1	T-AGRtu.nos-1:1:13
PCR0145897	pMON136258	EXP-ERIra.Ubq1:1:8	27	GUS-1	T-AGRtu.nos-1:1:13
PCR0145821	pMON136263	EXP-ERIra.Ubq1:1:11	29	GUS-1	T-AGRtu.nos-1:1:13
PCR0145822	pMON136263	EXP-ERIra.Ubq1:1:12	31	GUS-1	T-AGRtu.nos-1:1:13
PCR0145900	pMON140877	EXP-SETit.Ubq1:1:5	117	GUS-1	T-AGRtu.nos-1:1:13
PCR0145928	pMON140877	EXP-SETit.Ubq1:1:7	123	GUS-1	T-AGRtu.nos-1:1:13
PCR0145905	pMON140877	EXP-SETit.Ubq1:1:6	124	GUS-1	T-AGRtu.nos-1:1:13
PCR0145909	pMON140878	EXP-Sv.Ubq1:1:7	128	GUS-1	T-AGRtu.nos-1:1:13
PCR0145929	pMON140878	EXP-Sv.Ubq1:1:8	132	GUS-1	T-AGRtu.nos-1:1:13
PCR0145911	pMON140878	EXP-Sv.Ubq1:1:10	134	GUS-1	T-AGRtu.nos-1:1:13
PCR0145914	pMON140881	EXP-Zm.UbqM1:1:6	137	GUS-1	T-AGRtu.nos-1:1:13

TABLE 7-continued

GUS plant expression amplicons and corresponding plasmid construct amplicon templates, EXP sequence, GUS coding sequence and 3' UTR used for transformation of corn leaf protoplasts.

Amplicon ID	Amplicon Template	EXP sequence	SEQ ID NO:	GUS Coding Sequence	3' UTR
PCR0145915	pMON140882	EXP-Zm.UbqM1:1:7	141	GUS-1	T-AGRtu.nos-1:1:13
PCR0145921	pMON140886	EXP-Sb.Ubq4:1:2	151	GUS-1	T-AGRtu.nos-1:1:13
PCR0145920	pMON140887	EXP-Sb.Ubq6:1:2	153	GUS-1	T-AGRtu.nos-1:1:13
PCR0145922	pMON140889	EXP-Cl.Ubq1:1:10	98	GUS-1	T-AGRtu.nos-1:1:13

[0104] Plasmid constructs listed as amplicon templates in Table 7 served as templates for amplification of transgene expression cassettes comprising the listed EXP sequences of Table 7. Control plasmids used to generate GUS transgene amplicons for comparison were constructed as previously described with known constitutive EXP sequences described in Example 2. Negative controls for determination of GUS and luciferase background, a no DNA control, and a control sample in which the two luciferase plasmids are used in transformation along with a plasmid DNA that does not express a coding sequence were also used. Plasmids pMON19437 and pMON63934, as discussed in Example 2, were also employed for co-transformation and normalization of data.

[0105] Corn leaf protoplasts were transformed using a PEG-based transformation method as described in Example 2, above. Table 8 below shows the average GUS and luciferase expression values determined for each transgene cassette.

TABLE 8

Mean GUS and Luciferase activity in transformed corn leaf protoplast cells.

EXP sequence	SEQ ID NO:	GUS	RLuc	FLuc
EXP-Os.Act1:1:9	179	1540.3	105416.8	2671.8
P-CAMV.35S-ENH-1:1:102/ L-CAMV.35S-1:1:2	169	10426.3	344088.6	8604.1
EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1	163	12530.8	137722.6	3067.1
EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	61036.1	208125.3	5787.6
EXP-ANDge.Ubq1:1:7	5	59447.4	84667.6	2578.4
EXP-ANDge.Ubq1:1:10	10	40123.3	76753.8	2419.8
EXP-ANDge.Ubq1:1:6	12	42621.0	121751.3	3974.8
EXP-ANDge.Ubq1:1:11	14	44358.5	87105.8	2687.1
EXP-ANDge.Ubq1:1:12	16	48219.0	107762.1	3279.6
EXP-ERIra.Ubq1:1:9	22	31253.0	171684.1	6476.1
EXP-ERIra.Ubq1:1:10	25	7905.8	21235.6	462.4
EXP-ERIra.Ubq1:1:8	27	39935.8	173766.6	5320.3
EXP-ERIra.Ubq1:1:11	29	34141.3	111626.8	3377.6
EXP-ERIra.Ubq1:1:12	31	11540.3	42362.1	1045.3
EXP-SETit.Ubq1:1:5	117	20496.5	88695.8	2358.8
EXP-SETit.Ubq1:1:7	123	75728.5	185223.8	4723.1

TABLE 8-continued

Mean GUS and Luciferase activity in transformed corn leaf protoplast cells.

EXP sequence	SEQ ID NO:	GUS	RLuc	FLuc
EXP-SETit.Ubq1:1:6	124	44148.3	161216.3	4962.1
EXP-Sv.Ubq1:1:7	128	15043.8	74670.6	1888.3
EXP-Sv.Ubq1:1:8	132	31997.8	113787.1	3219.8
EXP-Sv.Ubq1:1:10	134	38952.8	220208.6	7011.3
EXP-Zm.UbqM1:1:6	137	30528.3	90113.1	2453.6
EXP-Zm.UbqM1:1:7	141	34986.3	105724.7	2553.8
EXP-Sb.Ubq4:1:2	151	9982.3	72593.8	2171.6
EXP-Sb.Ubq6:1:2	153	33689.0	114709.6	3879.6
EXP-Cl.Ubq1:1:10	98	50622.3	107084.3	2621.3

[0106] To compare the relative activity of each EXP sequence GUS values were expressed as a ratio of GUS to luciferase activity and normalized with respect to the expression levels observed for EXP-Os.Act1:1:1 and EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1. Table 9 below shows the GUS/RLuc ratios of expression normalized with respect to EXP-Os.Act1:1:1 and EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1 driven expression in corn protoplasts. Table 10 below shows the GUS/FLuc ratios of expression normalized with respect to EXP-Os.Act1:1:1 and EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1 driven expression in corn protoplasts.

TABLE 9

GUS/RLuc and GUS/FLuc ratios of expression normalized with respect to EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1 (SEQ ID NO: 163) in corn protoplasts.

EXP sequence	SEQ ID NO:	GUS/RLuc Relative to EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1	GUS/FLuc Relative to EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1
EXP-Os.Act1:1:9	179	0.16	0.14
P-CAMV.35S-ENH-1:1:102/L-CAMV.35S-1:1:2	169	0.33	0.30

TABLE 9-continued

GUS/RLuc and GUS/FLuc ratios of expression normalized with respect to EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1 (SEQ ID NO: 163) in corn protoplasts.

EXP sequence	SEQ ID NO:	GUS/RLuc Relative to EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1	GUS/FLuc Relative to EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1
EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1	163	1.00	1.00
EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	3.22	2.58
EXP-ANDge.Ubq1:1:7	5	7.72	5.64
EXP-ANDge.Ubq1:1:10	10	5.75	4.06
EXP-ANDge.Ubq1:1:6	12	3.85	2.62
EXP-ANDge.Ubq1:1:11	14	5.60	4.04
EXP-ANDge.Ubq1:1:12	16	4.92	3.60
EXP-ERIra.Ubq1:1:9	22	2.00	1.18
EXP-ERIra.Ubq1:1:10	25	4.09	4.18
EXP-ERIra.Ubq1:1:8	27	2.53	1.84
EXP-ERIra.Ubq1:1:11	29	3.36	2.47
EXP-ERIra.Ubq1:1:12	31	2.99	2.70
EXP-SETit.Ubq1:1:5	117	2.54	2.13
EXP-SETit.Ubq1:1:7	123	4.49	3.92
EXP-SETit.Ubq1:1:6	124	3.01	2.18
EXP-Sv.Ubq1:1:7	128	2.21	1.95
EXP-Sv.Ubq1:1:8	132	3.09	2.43
EXP-Sv.Ubq1:1:10	134	1.94	1.36
EXP-Zm.UbqM1:1:6	137	3.72	3.05
EXP-Zm.UbqM1:1:7	141	3.64	3.35
EXP-Sb.Ubq4:1:2	151	1.51	1.13
EXP-Sb.Ubq6:1:2	153	3.23	2.13
EXP-Cl.Ubq1:1:10	98	5.20	4.73

TABLE 10

GUS/RLuc and GUS/FLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 (SEQ ID NO: 179) in corn leaf protoplasts.

EXP sequence	SEQ ID NO:	GUS/RLuc Relative to EXP-Os.Act1:1:9	GUS/FLuc Relative to EXP-Os.Act1:1:9
EXP-Os.Act1:1:9	179	1.00	1.00
P-CAMV.35S-ENH-1:1:102/L-CAMV.35S-1:1:2	169	2.07	2.10
EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1	163	6.23	7.09
EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	20.07	18.29
EXP-ANDge.Ubq1:1:7	5	48.05	39.99
EXP-ANDge.Ubq1:1:10	10	35.78	28.76
EXP-ANDge.Ubq1:1:6	12	23.96	18.60
EXP-ANDge.Ubq1:1:11	14	34.85	28.64
EXP-ANDge.Ubq1:1:12	16	30.62	25.50
EXP-ERIra.Ubq1:1:9	22	12.46	8.37
EXP-ERIra.Ubq1:1:10	25	25.48	29.66
EXP-ERIra.Ubq1:1:8	27	15.73	13.02
EXP-ERIra.Ubq1:1:11	29	20.93	17.53
EXP-ERIra.Ubq1:1:12	31	18.64	19.15
EXP-SETit.Ubq1:1:5	117	15.82	15.07
EXP-SETit.Ubq1:1:7	123	27.98	27.81
EXP-SETit.Ubq1:1:6	124	18.74	15.43
EXP-Sv.Ubq1:1:7	128	13.79	13.82
EXP-Sv.Ubq1:1:8	132	19.25	17.24
EXP-Sv.Ubq1:1:10	134	12.11	9.64
EXP-Zm.UbqM1:1:6	137	23.19	21.58
EXP-Zm.UbqM1:1:7	141	22.65	23.76

TABLE 10-continued

GUS/RLuc and GUS/FLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 (SEQ ID NO: 179) in corn leaf protoplasts.

EXP sequence	SEQ ID NO:	GUS/RLuc Relative to EXP-Os.Act1:1:9	GUS/FLuc Relative to EXP-Os.Act1:1:9
EXP-Sb.Ubq4:1:2	151	9.41	7.97
EXP-Sb.Ubq6:1:2	153	20.10	15.06
EXP-Cl.Ubq1:1:10	98	32.35	33.50

[0107] As can be seen in Tables 9 and 10, nearly all of the EXP sequences were capable of driving GUS transgene expression in corn cells. Average GUS expression was higher for EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:10 (SEQ ID NO: 10), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ANDge.Ubq1:1:11 (SEQ ID NO: 14), EXP-ANDge.Ubq1:1:12 (SEQ ID NO: 16), EXP-ERIra.Ubq1:1:9 (SEQ ID NO: 22), EXP-ERIra.Ubq1:1:10 (SEQ ID NO: 25), EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27), EXP-ERIra.Ubq1:1:11 (SEQ ID NO: 29), EXP-ERIra.Ubq1:1:12 (SEQ ID NO: 31), EXP-SETit.Ubq1:1:5 (SEQ ID NO: 117), EXP-SETit.Ubq1:1:7 (SEQ ID NO: 123), EXP-SETit.Ubq1:1:6 (SEQ ID NO: 124), EXP-Sv.Ubq1:1:7 (SEQ ID NO: 128), EXP-Sv.Ubq1:1:8 (SEQ ID NO: 132), EXP-Sv.Ubq1:1:10 (SEQ ID NO: 134), EXP-Zm.UbqM1:1:6 (SEQ ID NO: 137), EXP-Zm.UbqM1:1:7 (SEQ ID NO: 141), EXP-Sb.Ubq4:1:2 (SEQ ID NO: 151), EXP-Sb.Ubq6:1:2 (SEQ ID NO: 153) and EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98) when compared to GUS expression driven by EXP-Os.Act1:1:1 or EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1.

[0108] In a second set of experiments, a GUS cassette amplicon comprising the EXP sequence EXP-Zm.UbqM1:1:8 (SEQ ID NO: 145) was compared to the control amplicons, PCR0145942 (EXP-Os.Act1:1:9, SEQ ID NO: 179) and PCR0145944 (EXP-CaMV.35S-enh+Zm.DnaK:1:1, SEQ ID NO: 170) with respect to GUS expression. GUS expression driven by the EXP sequence EXP-Zm.UbqM1:1:8 was higher than that of the two controls. Table 11 below shows the mean GUS and luciferase values determined for each amplicon. Table 12 below shows the GUS/RLuc and GUS/FLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 and EXP-CaMV.35S-enh+Zm.DnaK:1:1 driven expression in corn protoplasts.

TABLE 11

Mean GUS and Luciferase activity in transformed corn leaf protoplast cells.

Amplicon	EXP sequence	SEQ ID NO:	GUS	RLuc	FLuc
PCR0145942	EXP-Os.Act1:1:9	179	1512.25	190461	11333.8
PCR0145944	EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	41176.5	330837	13885.8
PCR0145916	EXP-Zm.UbqM1:1:8	145	79581.5	330756	15262.5

TABLE 12

GUS/RLuc and GUS/FLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh + Zm.DnaK:1:1 (SEQ ID NO: 170) in corn leaf protoplasts.

EXP sequence	SEQ ID NO:	GUS/RLuc relative to EXP-Os.Act1:1:9	GUS/FLuc relative to EXP-Os.Act1:1:9	GUS/RLuc relative to EXP-CaMV.35S-enh + Zm.DnaK:1:1	GUS/FLuc relative to EXP-CaMV.35S-enh + Zm.DnaK:1:1
EXP-Os.Act1:1:9	179	1.00	1.00	0.06	0.04
EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	15.68	22.22	1.00	1.00
EXP-Zm.UbqM1:1:8	145	30.30	39.08	1.93	1.76

[0109] In a third set of experiments, amplicon GUS transgene cassettes were made as described above and assayed for expression driven by the EXP sequences, EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:13 (SEQ ID NO: 114), EXP-Cl.Ubq1:1:14 (SEQ ID NO: 115) and EXP-Cl.Ubq1:1:15 (SEQ ID NO: 116). The amplicons were comprised of an EXP sequence operably linked to the GUS-1 coding sequence which was operably linked to the T-AGRtu.nos-1:1:13 3' UTR. Expression was compared to the controls EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh+Zm.DnaK:1:1 (SEQ ID NO: 170). Table 13 below shows the mean GUS and luciferase values determined for each amplicon. Table 14 below shows the GUS/RLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 and EXP-CaMV.35S-enh+Zm.DnaK:1:1 driven expression in corn protoplasts.

TABLE 13

Mean GUS and Luciferase activity in transformed corn leaf protoplast cells.

Amplicon ID	EXP sequence	SEQ ID NO:	GUS	RLuc
PCR0145942	EXP-Os.Act1:1:9	179	9445.25	929755
PCR0145944	EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	78591.25	445127
PCR0146628	EXP-ANDge.Ubq1:1:8	8	192056.75	972642
PCR0145922	EXP-Cl.Ubq1:1:10	98	175295.25	395563
PCR0145945	EXP-Cl.Ubq1:1:13	114	173674.5	402966
PCR0145946	EXP-Cl.Ubq1:1:14	115	185987.5	390052
PCR0145947	EXP-Cl.Ubq1:1:15	116	9435	320749

TABLE 14

GUS/RLuc and GUS/FLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh + Zm.DnaK:1:1 (SEQ ID NO: 170) in corn leaf protoplasts.

EXP sequence	SEQ ID NO:	GUS/RLuc relative to EXP-Os.Act1:1:9	GUS/RLuc relative to EXP-CaMV.35S-enh + Zm.DnaK:1:1
EXP-Os.Act1:1:9	179	1.00	0.06
EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	17.38	1.00
EXP-ANDge.Ubq1:1:8	8	19.44	1.12
EXP-Cl.Ubq1:1:10	98	43.62	2.51

TABLE 14-continued

GUS/RLuc and GUS/FLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh + Zm.DnaK:1:1 (SEQ ID NO: 170) in corn leaf protoplasts.

EXP sequence	SEQ ID NO:	GUS/RLuc relative to EXP-Os.Act1:1:9	GUS/RLuc relative to EXP-CaMV.35S-enh + Zm.DnaK:1:1
EXP-Cl.Ubq1:1:13	114	42.43	2.44
EXP-Cl.Ubq1:1:14	115	46.94	2.70
EXP-Cl.Ubq1:1:15	116	2.90	0.17

[0110] As can be seen in Table 14 above, the EXP sequences EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:13 (SEQ ID NO: 114), EXP-Cl.Ubq1:1:14 (SEQ ID NO: 115) and EXP-Cl.Ubq1:1:15 (SEQ ID NO: 116) are capable of driving transgene expression. Expression driven by EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:13 (SEQ ID NO: 114) and EXP-Cl.Ubq1:1:14 (SEQ ID NO: 115) was higher than that of both controls. Expression driven by EXP-Cl.Ubq1:1:15 (SEQ ID NO: 116) was lower than EXP-CaMV.35S-enh+Zm.DnaK:1:1 (SEQ ID NO: 170) but higher than the control, EXP-Os.Act1:1:9 (SEQ ID NO: 179).

[0111] In a fourth set of experiments, amplicon GUS transgene cassettes were made as described above and assayed for expression driven by the EXP sequences, EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:16 (SEQ ID NO: 93) and EXP-Cl.Ubq1:1:17 (SEQ ID NO: 97). Expression was compared to the controls EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh+Zm.DnaK:1:1 (SEQ ID NO: 170). Table 15 below shows the mean GUS and luciferase values determined for each amplicon. Table 16 below shows the GUS/RLuc and GUS/FLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 and EXP-CaMV.35S-enh+Zm.DnaK:1:1 driven expression in corn protoplasts.

TABLE 15

Mean GUS and Luciferase activity in transformed corn leaf protoplast cells.

Amplicon ID	EXP sequence	SEQ ID NO:	GUS	RLuc	FLuc
PCR0145942	EXP-Os.Act1:1:9	179	5333.5	171941.75	77817.88
PCR0145944	EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	88517	177260.25	54207.38
PCR0145922	EXP-Cl.Ubq1:1:10	98	130125.75	194216	32055
pMON146750	EXP-Cl.Ubq1:1:16	93	134101.75	182317.5	32434.5
pMON146751	EXP-Cl.Ubq1:1:17	97	107122.5	151783.25	51354.38

TABLE 16

GUS/RLuc and GUS/FLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh + Zm.DnaK:1:1 (SEQ ID NO: 170) in corn leaf protoplasts.

Amplicon ID	EXP sequence	SEQ ID NO:	GUS/RLuc relative to EXP-Os.Act1:1:9	GUS/FLuc relative to EXP-Os.Act1:1:9	GUS/RLuc relative to EXP-CaMV.35S-enh + Zm.DnaK:1:1	GUS/FLuc relative to EXP-CaMV.35S-enh + Zm.DnaK:1:1
PCR0145942	EXP-Os.Act1:1:9	179	1.00	1.00	0.06	0.04
PCR0145944	EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	16.10	23.83	1.00	1.00
PCR0145922	EXP-Cl.Ubq1:1:10	98	21.60	59.23	1.34	2.49
pMON146750	EXP-Cl.Ubq1:1:16	93	23.71	60.32	1.47	2.53
pMON146751	EXP-Cl.Ubq1:1:17	97	22.75	30.43	1.41	1.28

[0112] As can be seen in Table 16, the EXP sequences EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:16 (SEQ ID NO: 93) and EXP-Cl.Ubq1:1:17 (SEQ ID NO: 97) were able to drive transgene expression. Expression driven by each of the EXP sequences was higher than that of both controls.

[0113] In a fifth set of experiments, amplicon GUS transgene cassettes were made as described above assay expression driven by the EXP sequences, EXP-Zm.UbqM1:1:11 (SEQ ID NO: 149) and EXP-Cl.Ubq1:1:23 (SEQ ID NO: 108). Expression was compared to the controls EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1 (SEQ ID NO: 163). Table 17 below shows the mean GUS and luciferase values determined for each amplicon. Table 18 below shows the GUS/RLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 and EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1 driven expression in corn protoplasts.

TABLE 18

GUS/RLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1 (SEQ ID NO: 163) in corn leaf protoplasts.

Amplicon	EXP sequence	SEQ ID NO:	GUS/RLuc relative to EXP-Os.Act1:1:9	GUS/RLuc relative to EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1
PCR0145943	EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1	163	2.48	1.00

TABLE 17

Mean GUS and Luciferase activity in transformed corn leaf protoplast cells.

Template	Amplicon	EXP sequence	SEQ ID NO:	GUS	RLuc
pMON65328	PCR0145943	EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1	163	70352.00	79028.75
pMON25455	PCR0145942	EXP-Os.Act1:1:9	179	33155.25	92337.00
pMON131962	pMON131962	EXP-Zm.UbqM1:1:11	149	18814.75	33663.00
pMON132047	pMON132047	EXP-Cl.Ubq1:1:23	108	15387.50	40995.50

TABLE 18-continued

GUS/RLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1 (SEQ ID NO: 163) in corn leaf protoplasts.

Amplicon	EXP sequence	SEQ ID NO:	GUS/RLuc relative to EXP-Os.Act1:1:9	GUS/RLuc relative to EXP-CaMV.35S-enh + Ta.Lhcb1 + Os. Act1:1:1
PCR0145942	EXP-Os.Act1:1:9	179	1.00	0.40
pMON131962	EXP-Zm.UbqM1:1:11	149	1.56	0.63
pMON132047	EXP-Cl.Ubq1:1:23	108	1.05	0.42

[0114] As can be seen in Table 18 above, the EXP sequences, EXP-Zm.UbqM1:1:11 (SEQ ID NO: 149) and EXP-Cl.Ubq1:1:23 (SEQ ID NO: 108) were able to drive GUS expression in corn leaf protoplasts. Expression was similar to that of the control, EXP-Os.Act1:1:9 (SEQ ID NO: 179) and lower than that of EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1 (SEQ ID NO: 163).

[0115] The efficacy of regulatory elements driving GUS expression from amplicons can be similarly studied in sugarcane leaf protoplasts. For instance, sugarcane protoplasts may be transformed with DNA amplicons derived from plant expression vectors containing an EXP sequence, driving expression of the β-glucuronidase (GUS) transgene, and compared to leaf protoplast in which expression of GUS is driven by known constitutive promoters. Likewise, regulatory elements driving CP4 expression from amplicons in corn or wheat protoplasts may be similarly studied.

Example 4

Analysis of Regulatory Elements Driving GUS in Wheat Protoplasts Using GUS Transgene Cassette Amplicons

[0116] Wheat leaf protoplasts were transformed with DNA amplicons derived from plant expression vectors containing an EXP sequence, driving expression of the β-glucuronidase (GUS) transgene, and compared to leaf protoplast in which expression of GUS was driven by known constitutive promoters.

[0117] Wheat protoplast cells derived from leaf tissue were transformed using methods known in the art with amplicons produced from amplification of GUS transgene cassettes comprising plant expression vectors to compare expression of a transgene (GUS) driven by the EXP sequences listed in Tables 10-11 with that of known constitutive promoters with methodology as described in a previous example (Example 3), using the same GUS cassette amplicons as that used for assay in Corn in Example 3 above. Control GUS cassette amplicons and Luciferase plasmids used for wheat protoplast transformation were also the same as those presented in the previous example and provided in Table 7 above in Example 3. Likewise, negative controls were used for the determination of GUS and luciferase background, as described above. Wheat leaf protoplasts were transformed using a PEG-based transformation method, as described in Example 3 above. Table 19 lists mean GUS and LUC activity seen in transformed wheat leaf protoplast cells, and Table 20 shows normalized GUS/RLuc ratios of expression in wheat protoplasts.

TABLE 19

Mean GUS and Luciferase activity in transformed wheat leaf protoplast cells.

EXP sequence	SEQ ID NO:	GUS	RLuc	GUS/RLuc
EXP-Os.Act1:1:9	179	2976.33	53334.8	0.0558047
P-CAMV.35S-ENH-1:1:102/ L-CAMV.35S-1:1:2	169	1431.33	55996.1	0.0255612
EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1	163	29299.3	50717.4	0.5776973
EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	34294.3	63307.9	0.5417066
EXP-ANDge.Ubq1:1:7	5	68444.3	60329.1	1.1345158
EXP-ANDge.Ubq1:1:10	10	60606.3	60659.4	0.9991245
EXP-ANDge.Ubq1:1:6	12	33386.3	56712.1	0.5886984
EXP-ANDge.Ubq1:1:11	14	43237.3	48263.4	0.8958609
EXP-ANDge.Ubq1:1:12	16	51712.7	64702.8	0.7992341
EXP-ERIra.Ubq1:1:9	22	20998.3	60273.4	0.3483845
EXP-ERIra.Ubq1:1:10	25	17268.3	25465.4	0.6781084
EXP-ERIra.Ubq1:1:8	27	34635.7	59467.1	0.5824341
EXP-ERIra.Ubq1:1:11	29	28979	56153.8	0.516065
EXP-ERIra.Ubq1:1:12	31	41409.7	55152.4	0.7508221
EXP-SETit.Ubq1:1:5	117	39427.7	57463.1	0.6861388
EXP-SETit.Ubq1:1:7	123	108091	49330.4	2.191169
EXP-SETit.Ubq1:1:6	124	58703	46110.1	1.2731047
EXP-Sv.Ubq1:1:7	128	29330	43367.1	0.676319
EXP-Sv.Ubq1:1:8	132	53359	40076.4	1.3314306
EXP-Sv.Ubq1:1:10	134	49122.7	53180.8	0.9236922
EXP-Zm.UbqM1:1:6	137	37268	54088.1	0.6890239
EXP-Zm.UbqM1:1:7	141	51408	47297.4	1.0869087
EXP-Sb.Ubq4:1:2	151	35660.3	62591.1	0.5697347
EXP-Sb.Ubq6:1:2	153	27543	57826.4	0.4763046
EXP-Cl.Ubq1:1:10	98	54493.3	41964.1	1.2985699

TABLE 20

GUS/RLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1 (SEQ ID NO: 163) in wheat leaf protoplasts.

EXP sequence	SEQ ID NO:	GUS/RLuc Relative to EXP-Os.Act1:1:9	GUS/RLuc Relative to EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1
EXP-Os.Act1:1:9	179	1.00	0.10
P-CAMV.35S-ENH-1:1:102/L-CAMV.35S-1:1:2	169	0.46	0.04
EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1	163	10.35	1.00
EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	9.71	0.94
EXP-ANDge.Ubq1:1:7	5	20.33	1.96
EXP-ANDge.Ubq1:1:10	10	17.90	1.73
EXP-ANDge.Ubq1:1:6	12	10.55	1.02
EXP-ANDge.Ubq1:1:11	14	16.05	1.55
EXP-ANDge.Ubq1:1:12	16	14.32	1.38
EXP-ERIra.Ubq1:1:9	22	6.24	0.60
EXP-ERIra.Ubq1:1:10	25	12.15	1.17
EXP-ERIra.Ubq1:1:8	27	10.44	1.01
EXP-ERIra.Ubq1:1:11	29	9.25	0.89
EXP-ERIra.Ubq1:1:12	31	13.45	1.30
EXP-SETit.Ubq1:1:5	117	12.30	1.19
EXP-SETit.Ubq1:1:7	123	39.26	3.79
EXP-SETit.Ubq1:1:6	124	22.81	2.20
EXP-Sv.Ubq1:1:7	128	12.12	1.17
EXP-Sv.Ubq1:1:8	132	23.86	2.30
EXP-Sv.Ubq1:1:10	134	16.55	1.60

TABLE 20-continued

GUS/RLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1 (SEQ ID NO: 163) in wheat leaf protoplasts.

EXP sequence	SEQ ID NO:	GUS/RLuc Relative to EXP-Os.Act1:1:9	GUS/RLuc Relative to EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1
EXP-Zm.UbqM1:1:6	137	12.35	1.19
EXP-Zm.UbqM1:1:7	141	19.48	1.88
EXP-Sb.Ubq4:1:2	151	10.21	0.99
EXP-Sb.Ubq6:1:2	153	8.54	0.82
EXP-Cl.Ubq1:1:10	98	23.27	2.25

[0118] As can be seen in Table 20 above, nearly all of the EXP sequences were capable of driving GUS transgene expression in wheat cells. GUS transgene expression driven by EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:10 (SEQ ID NO: 10), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ANDge.Ubq1:1:11 (SEQ ID NO: 14), EXP-ANDge.Ubq1:1:12 (SEQ ID NO: 16), EXP-ERIra.Ubq1:1:9 (SEQ ID NO: 22), EXP-ERIra.Ubq1:1:10 (SEQ ID NO: 25), EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27), EXP-ERIra.Ubq1:1:11 (SEQ ID NO: 29), EXP-ERIra.Ubq1:1:12 (SEQ ID NO: 31), EXP-SETit.Ubq1:1:5 (SEQ ID NO: 117), EXP-SETit.Ubq1:1:7 (SEQ ID NO: 123), EXP-SETit.Ubq1:1:6 (SEQ ID NO: 124), EXP-Sv.Ubq1:1:7 (SEQ ID NO: 128), EXP-Sv.Ubq1:1:8 (SEQ ID NO: 132), EXP-Sv.Ubq1:1:10 (SEQ ID NO: 134), EXP-Zm.UbqM1:1:6 (SEQ ID NO: 137), EXP-Zm.UbqM1:1:7 (SEQ ID NO: 141), EXP-Sb.Ubq4:1:2 (SEQ ID NO: 151), EXP-Sb.Ubq6:1:2 (SEQ ID NO: 153) and EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98) was much higher than GUS expression driven by EXP-Os.Act1:1:9. GUS expression of the amplicons in wheat leaf protoplast cells relative to EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1 was slightly different from the expression observed in corn protoplast cells. Each of EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:10 (SEQ ID NO: 10), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ANDge.Ubq1:1:11 (SEQ ID NO: 14), EXP-ANDge.Ubq1:1:12 (SEQ ID NO: 16), EXP-ERIra.Ubq1:1:10 (SEQ ID NO: 25), EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27), EXP-ERIra.Ubq1:1:12 (SEQ ID NO: 31), EXP-SETit.Ubq1:1:5 (SEQ ID NO: 117), EXP-SETit.Ubq1:1:7 (SEQ ID NO: 123), EXP-SETit.Ubq1:1:6 (SEQ ID NO: 124), EXP-Sv.Ubq1:1:7 (SEQ ID NO: 128), EXP-Sv.Ubq1:1:8 (SEQ ID NO: 132), EXP-Sv.Ubq1:1:10 (SEQ ID NO: 134), EXP-Zm.UbqM1:1:6 (SEQ ID NO: 137), EXP-Zm.UbqM1:1:7 (SEQ ID NO: 141) and EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98) demonstrated higher levels of GUS expression relative to EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1. The EXP sequences EXP-ERIra.Ubq1:1:9 (SEQ ID NO: 22), EXP-ERIra.Ubq1:1:11 (SEQ ID NO: 29), EXP-Sb.Ubq4:1:2 (SEQ ID NO: 151) and EXP-Sb.Ubq6:1:2 (SEQ ID NO: 153) demonstrated lower levels of GUS expression relative to EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1.

[0119] In a second set of experiments, amplicon GUS transgene cassettes were made as described above and assayed for expression driven by the EXP sequences, EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:13 (SEQ ID NO: 114), EXP-Cl.Ubq1:1:14 (SEQ ID NO: 115) and EXP-Cl.Ubq1:1:15 (SEQ ID NO: 116). The amplicons were comprised of an EXP sequence operably linked to the GUS-1 coding sequence which was operably linked to the T-AGRtu.nos-1:1:13 3' UTR. Expression was compared to the controls EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh+Zm.DnaK:1:1 (SEQ ID NO: 170). Table 21 below shows the mean GUS and luciferase values determined for each amplicon. Table 22 below shows the GUS/RLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 and EXP-CaMV.35S-enh+Zm.DnaK:1:1 driven expression in corn protoplasts.

TABLE 21

Mean GUS and Luciferase activity in transformed wheat leaf protoplast cells.

Amplicon ID	EXP sequence	SEQ ID NO:	GUS	RLuc
PCR0145942	EXP-Os.Act1:1:9	179	1234	176970.5
PCR0145944	EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	12883.5	119439
PCR0146628	EXP-ANDge.Ubq1:1:8	8	38353.3	171535.3
PCR0145922	EXP-Cl.Ubq1:1:10	98	34938	154245.8
PCR0145945	EXP-Cl.Ubq1:1:13	114	32121	122220.8
PCR0145946	EXP-Cl.Ubq1:1:14	115	56814	143318.3
PCR0145947	EXP-Cl.Ubq1:1:15	116	1890.5	167178.5

TABLE 22

GUS/RLuc and GUS/FLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh + Zm.DnaK:1:1 (SEQ ID NO: 170) in wheat leaf protoplasts.

EXP sequence	SEQ ID NO:	GUS/RLuc relative to EXP-Os.Act1:1:9	GUS/RLuc relative to EXP-CaMV.35S-enh + Zm.DnaK:1:1
EXP-Os.Act1:1:9	179	1.00	0.06
EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	15.47	1.00
EXP-ANDge.Ubq1:1:8	8	32.07	2.07
EXP-Cl.Ubq1:1:10	98	32.48	2.10
EXP-Cl.Ubq1:1:13	114	37.69	2.44
EXP-Cl.Ubq1:1:14	115	56.85	3.68
EXP-Cl.Ubq1:1:15	116	1.62	0.10

[0120] As can be seen in Table 22 above, the EXP sequences EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:13 (SEQ ID NO: 114), EXP-Cl.Ubq1:1:14 (SEQ ID NO: 115) and EXP-Cl.Ubq1:1:15 (SEQ ID NO: 116) are capable of driving transgene expression. Expression driven by EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:13 (SEQ ID NO: 114) and EXP-Cl.Ubq1:1:14 (SEQ ID NO: 115) was higher than that of both controls. Expression driven by EXP-Cl.Ubq1:1:15 (SEQ ID NO: 116) was lower than EXP-CaMV.35S-enh+Zm.DnaK:1:1 (SEQ ID NO: 170) but higher than the control, EXP-Os.Act1:1:9 (SEQ ID NO: 179).

[0121] In a third set of experiments, amplicon GUS transgene cassettes were made as described above to assay expression driven by the EXP sequences, EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:16 (SEQ ID NO: 93) and EXP-Cl.Ubq1:1:17 (SEQ ID NO: 97). Expression was compared to the controls EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh+Zm.DnaK:1:1 (SEQ ID NO: 170). Table 23 below shows the mean GUS and luciferase values determined

for each amplicon. Table 24 below shows the GUS/RLuc and GUS/FLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 and EXP-CaMV.35S-enh+Zm.DnaK:1:1 driven expression in corn protoplasts.

TABLE 23

Mean GUS and Luciferase activity in transformed wheat leaf protoplast cells.

Amplicon ID	EXP sequence	SEQ ID NO:	GUS	RLuc	FLuc
PCR0145942	EXP-Os.Act1:1:9	179	478	46584.5	2709.75
PCR0145944	EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	8178.5	43490.8	2927.25
PCR0145922	EXP-Cl.Ubq1:1:10	98	22068.3	47662.3	1289
pMON146750	EXP-Cl.Ubq1:1:16	93	34205	45064.5	1379.63
pMON146751	EXP-Cl.Ubq1:1:17	97	31758	45739.3	2820.75

[0122] As can be seen in Table 24 above, the EXP sequences EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:16 (SEQ ID NO: 93) and EXP-Cl.Ubq1:1:17 (SEQ ID NO: 97) were able to drive transgene expression. Expression driven by each of the EXP sequences was higher than that of both controls.

[0123] In a fourth set of experiments, amplicon GUS transgene cassettes were made as described above to assay expression driven by the EXP sequences, EXP-Zm.UbqM1:1:11 (SEQ ID NO: 149) and EXP-Cl.Ubq1:1:23 (SEQ ID NO: 108). Expression was compared to the controls EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1 (SEQ ID NO: 163). Table 25 below shows the mean GUS and luciferase values determined for each amplicon. Table 26 below shows the GUS/RLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 and EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1 driven expression in corn protoplasts.

TABLE 24

GUS/RLuc and GUS/FLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh + Zm.DnaK:1:1 (SEQ ID NO: 170) in wheat leaf protoplasts.

Amplicon ID	EXP sequence	SEQ ID NO:	GUS/RLuc relative to EXP-Os.Act1:1:9	GUS/FLuc relative to EXP-Os.Act1:1:9	GUS/RLuc relative to EXP-CaMV.35S-enh + Zm.DnaK:1:1	GUS/FLuc relative to EXP-CaMV.35S-enh + Zm.DnaK:1:1
PCR0145942	EXP-Os.Act1:1:9	179	1.00	1.00	0.05	0.06
PCR0145944	EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	18.33	15.84	1.00	1.00
PCR0145922	EXP-Cl.Ubq1:1:10	98	45.12	97.05	2.46	6.13
pMON146750	EXP-Cl.Ubq1:1:16	93	73.97	140.55	4.04	8.87
pMON146751	EXP-Cl.Ubq1:1:17	97	67.67	63.82	3.69	4.03

TABLE 25

Mean GUS and Luciferase activity in transformed wheat leaf protoplast cells.

Template	Amplicon ID	EXP sequence	SEQ ID NO:	GUS	RLuc
pMON65328	PCR0145943	EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1	163	67459.13	11682.00
pMON25455	PCR0145942	EXP-Os.Act1:1:9	179	56618.33	16654.83
pMON131962	pMON131962	EXP-Zm.UbqM1:1:11	149	53862.13	10313.75
pMON132047	pMON132047	EXP-Cl.Ubq1:1:23	108	38869.38	12279.00

TABLE 26

GUS/RLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1 (SEQ ID NO: 163) in wheat leaf protoplasts.

Amplicon ID	EXP sequence	SEQ ID NO:	GUS/RLuc relative to EXP-Os.Act1:1:9	GUS/RLuc relative to EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1
PCR0145943	EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1	163	1.70	1.00
PCR0145942	EXP-Os.Act1:1:9	179	1.00	0.59
pMON131962	EXP-Zm.UbqM1:1:11	149	1.54	0.90
pMON132047	EXP-Cl.Ubq1:1:23	108	0.93	0.55

[0124] As can be seen in Table 26 above, the EXP sequences, EXP-Zm.UbqM1:1:11 (SEQ ID NO: 149) and EXP-Cl.Ubq1:1:23 (SEQ ID NO: 108) were able to drive GUS expression in wheat leaf protoplasts. Expression was similar to that of the control, EXP-Os.Act1:1:9 (SEQ ID NO: 179) and lower than that of EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1 (SEQ ID NO: 163).

Example 5

Analysis of Regulatory Elements Driving GUS in Sugarcane Protoplasts Using GUS Transgene Cassette Amplicons

[0125] Sugarcane leaf protoplasts were transformed with DNA amplicons derived from plant expression vectors containing an EXP sequence, driving expression of the β-glucuronidase (GUS) transgene, and compared to leaf protoplast in which expression of GUS was driven by known constitutive promoters.

[0126] Sugarcane protoplast cells derived from leaf tissue were transformed using a PEG-based transformation method, as described in Example 3 above with amplicons produced from amplification of GUS transgene cassettes comprising plant expression vectors to compare expression of a transgene (GUS) driven by one of EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:10 (SEQ ID NO: 10), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ANDge.Ubq1:1:11 (SEQ ID NO: 14), EXP-ANDge.Ubq1:1:12 (SEQ ID NO: 16), EXP-ERIra.Ubq1:1:9 (SEQ ID NO: 22), EXP-ERIra.Ubq1:1:10 (SEQ ID NO: 25), EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27), EXP-ERIra.Ubq1:1:11 (SEQ ID NO: 29), EXP-ERIra.Ubq1:1:12 (SEQ ID NO: 31), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:13 (SEQ ID NO: 114), EXP-Cl.Ubq1:1:14 (SEQ ID NO: 115) and EXP-Cl.Ubq1:1:15 (SEQ ID NO: 116) and presented in Table 27 below, with that of known constitutive promoters.

TABLE 27

GUS plant expression amplicons and corresponding plasmid construct amplicon template and EXP sequence.

Amplicon ID	Amplicon Template	EXP sequence	SEQ ID NO:
PCR0145942	pMON25455	EXP-Os.Act1:1:9	179
PCR0145944	pMON81552	EXP-CaMV.35S-enh + Zm.DnaK:1:1	170
PCR0145892	pMON136264	EXP-ANDge.Ubq1:1:7	5
PCR0145815	pMON136264	EXP-ANDge.Ubq1:1:10	10
PCR0145893	pMON136259	EXP-ANDge.Ubq1:1:6	12
PCR0145817	pMON136264	EXP-ANDge.Ubq1:1:11	14
PCR0145819	pMON136264	EXP-ANDge.Ubq1:1:12	16
PCR0145896	pMON136263	EXP-ERIra.Ubq1:1:9	22
PCR0145820	pMON136263	EXP-ERIra.Ubq1:1:10	25
PCR0145897	pMON136258	EXP-ERIra.Ubq1:1:8	27
PCR0145821	pMON136263	EXP-ERIra.Ubq1:1:11	29
PCR0145822	pMON136263	EXP-ERIra.Ubq1:1:12	31
PCR0145922	pMON140889	EXP-Cl.Ubq1:1:10	98
PCR0145945	pMON140889	EXP-Cl.Ubq1:1:13	114
PCR0145946	pMON140889	EXP-Cl.Ubq1:1:14	115
PCR0145947	pMON140889	EXP-Cl.Ubq1:1:15	116

[0127] Control GUS cassette amplicons and Luciferase plasmids used for sugarcane protoplast transformation were also the same as those presented in Examples 2 through 4 and provided in Table 7 above in Example 3. Likewise, negative controls were used for the determination of GUS and luciferase background, as described above. Table 28 lists mean GUS and Luc activity seen in transformed sugarcane leaf protoplast cells, and Table 29 shows normalized GUS/RLuc ratios of expression in sugarcane leaf protoplasts.

TABLE 28

Mean GUS and Luciferase activity in transformed wheat leaf protoplast cells.

EXP sequence	SEQ ID NO:	GUS	RLuc	FLuc
EXP-Os.Act1:1:9	179	6667.5	3024.5	1129.25
EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	14872.8	5171	2019.5
EXP-ANDge.Ubq1:1:7	5	15225	4618.25	1775.75
EXP-ANDge.Ubq1:1:10	10	17275.3	4333	1678
EXP-ANDge.Ubq1:1:6	12	17236	5633.25	2240
EXP-ANDge.Ubq1:1:11	14	22487.8	6898.25	2878
EXP-ANDge.Ubq1:1:12	16	22145.3	6240.25	2676.5
EXP-ERIra.Ubq1:1:9	22	16796.5	7759.75	3179
EXP-ERIra.Ubq1:1:10	25	16267.5	5632.75	2436.75
EXP-ERIra.Ubq1:1:8	27	25351	9019.5	4313.5
EXP-ERIra.Ubq1:1:11	29	16652.3	3672.25	1534
EXP-ERIra.Ubq1:1:12	31	12654.5	3256.75	1261.5
EXP-Cl.Ubq1:1:10	98	22383.8	7097.5	3109.25
EXP-Cl.Ubq1:1:13	114	14532.3	2786.5	1198.25
EXP-Cl.Ubq1:1:14	115	19244.5	3455.25	1475
EXP-Cl.Ubq1:1:15	116	6676.5	3870.25	1497.75

TABLE 29

GUS/RLuc and GUS/FLuc ratios of expression normalized with respect to EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh + Zm.DnaK:1:1 (SEQ ID NO: 170) in sugarcane leaf protoplasts.

EXP sequence	SEQ ID NO:	GUS/RLuc relative to EXP-Os.Act1:1:9	GUS/FLuc relative to EXP-Os.Act1:1:9	GUS/RLuc relative to EXP-CaMV.35S-enh + Zm.DnaK:1:1	GUS/FLuc relative to EXP-CaMV.35S-enh + Zm.DnaK:1:1
EXP-Os.Act1:1:9	179	1.00	1.00	0.77	0.80
EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	1.30	1.25	1.00	1.00
EXP-ANDge.Ubq1:1:7	5	1.50	1.45	1.15	1.16
EXP-ANDge.Ubq1:1:10	10	1.81	1.74	1.39	1.40
EXP-ANDge.Ubq1:1:6	12	1.39	1.30	1.06	1.04
EXP-ANDge.Ubq1:1:11	14	1.48	1.32	1.13	1.06
EXP-ANDge.Ubq1:1:12	16	1.61	1.40	1.23	1.12
EXP-ERIra.Ubq1:1:9	22	0.98	0.89	0.75	0.72
EXP-ERIra.Ubq1:1:10	25	1.31	1.13	1.00	0.91
EXP-ERIra.Ubq1:1:8	27	1.27	1.00	0.98	0.80
EXP-ERIra.Ubq1:1:11	29	2.06	1.84	1.58	1.47
EXP-ERIra.Ubq1:1:12	31	1.76	1.70	1.35	1.36
EXP-Cl.Ubq1:1:10	98	1.43	1.22	1.10	0.98
EXP-Cl.Ubq1:1:13	114	2.37	2.05	1.81	1.65
EXP-Cl.Ubq1:1:14	115	2.53	2.21	1.94	1.77
EXP-Cl.Ubq1:1:15	116	0.78	0.75	0.60	0.61

[0128] As can be seen in Table 29 above, the EXP sequences EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:10 (SEQ ID NO: 10), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ANDge.Ubq1:1:11 (SEQ ID NO: 14), EXP-ANDge.Ubq1:1:12 (SEQ ID NO: 16), EXP-ERIra.Ubq1:1:9 (SEQ ID NO: 22), EXP-ERIra.Ubq1:1:10 (SEQ ID NO: 25), EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27), EXP-ERIra.Ubq1:1:11 (SEQ ID NO: 29), EXP-ERIra.Ubq1:1:12 (SEQ ID NO: 31), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:13 (SEQ ID NO: 114), EXP-Cl.Ubq1:1:14 (SEQ ID NO: 115) and EXP-Cl.Ubq1:1:15 (SEQ ID NO: 116) were all capable of driving transgene expression in sugarcane protoplasts. The EXP sequences, EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:10 (SEQ ID NO: 10), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ANDge.Ubq1:1:11 (SEQ ID NO: 14), EXP-ANDge.Ubq1:1:12 (SEQ ID NO: 16), EXP-ERIra.Ubq1:1:10 (SEQ ID NO: 25), EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27), EXP-ERIra.Ubq1:1:12 (SEQ ID NO: 31), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:13 (SEQ ID NO: 114) and EXP-Cl.Ubq1:1:14 (SEQ ID NO: 115) expressed GUS higher than EXP-CaMV.35S-enh+Zm.DnaK:1:1 (SEQ ID NO: 170) in this experiment.

Example 6

Analysis of Regulatory Elements Driving CP4 in Corn Protoplasts

[0129] This example illustrates the ability of EXP-Sv.Ubq1:1:7 (SEQ ID NO: 128), EXP-Sv.Ubq1:1:8 (SEQ ID NO: 132), EXP-Sv.Ubq1:1:9 (SEQ ID NO: 133), EXP-Zm.UbqM1:1:6 (SEQ ID NO: 137), EXP-Zm.UbqM1:1:8 (SEQ ID NO: 145), EXP-Zm.UbqM1:1:7 (SEQ ID NO: 141), EXP-SETit.Ubq1:1:5 (SEQ ID NO: 117), EXP-SETit.Ubq1:1:7 (SEQ ID NO: 123), EXP-SETit.Ubq1:1:6 (SEQ ID NO: 124), EXP-Sb.Ubq4:1:2 (SEQ ID NO: 151) and EXP-Sb.Ubq6:1:2 (SEQ ID NO: 153) in driving expression of glyphosate tolerance gene CP4 in corn protoplasts. These EXP sequences were cloned into plant binary transformation plasmid constructs using methods known in the art. The resulting plant expression vectors contained a right border region from *A. tumefaciens*, an ubiquitin EXP sequence operably linked 5' to a plastid targeted glyphosate tolerant EPSPS coding sequence (CP4, U.S. Pat. No. RE39247), operably linked 5' to the T-AGRtu.nos-1:1:13 3' UTR and a left border region from *A. tumefaciens* (B-AGRtu.left border). The resulting plasmid constructs were used to transform corn leaf protoplasts cells using methods known in the art.

[0130] Plasmid constructs listed in Table 30, with EXP sequences as defined in Table 1, were utilized. Three control plasmids (pMON30098, pMON42410, and pMON30167), with known constitutive regulatory elements driving either CP4 or GFP, were constructed and used to compare the relative CP4 expression levels driven by these EXP sequences with CP4 expression driven by known constitutive expression elements. Two other plasmids (pMON19437 and pMON63934) were also used as described above to evaluate transformation efficiency and viability. Each plasmid contains a specific luciferase coding sequence driven by a constitutive EXP sequence.

[0131] Corn leaf protoplasts were transformed using a PEG-based transformation method, as described in Example 2 above. Measurements of both CP4 and luciferase were conducted similarly to Example 2 above. The average levels of CP4 protein expression expressed as part per million (ppm) is shown in Table 30 below.

TABLE 30

Average CP4 protein expression in corn leaf protoplasts.

Plasmid	EXP sequence	SEQ ID NO:	CP4 Average ppm	CP4 STDEV ppm
No DNA	No DNA		0	0
pMON30098	GFP		0	0
pMON42410	EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1	163	34.1	15.6

TABLE 30-continued

Average CP4 protein expression in corn leaf protoplasts.

Plasmid	EXP sequence	SEQ ID NO:	CP4 Average ppm	CP4 STDEV ppm
pMON30167	EXP-Os.Act1:1:1	164	40.4	11.6
pMON129203	EXP-Sv.Ubq1:1:7	128	45.2	6.2
pMON129204	EXP-Sv.Ubq1:1:8	132	101.9	13.8
pMON129205	EXP-Sv.Ubq1:1:9	133	71.1	8.7
pMON129210	EXP-Zm.UbqM1:1:6	137	137.1	14.8
pMON129211	EXP-Zm.UbqM1:1:8	145	136.5	12.3
pMON129212	EXP-Zm.UbqM1:1:7	141	170.2	18.1
pMON129200	EXP-SETit.Ubq1:1:5	117	44.3	9.5
pMON129201	EXP-SETit.Ubq1:1:7	123	105.1	8.4
pMON129202	EXP-SETit.Ubq1:1:6	124	124.9	33.7
pMON129219	EXP-Sb.Ubq4:1:2	151	14.3	1
pMON129218	EXP-Sb.Ubq6:1:2	153	75.7	8.9

[0132] As can be seen in Table 30, EXP-Sv.Ubq1:1:7 (SEQ ID NO: 128), EXP-Sv.Ubq1:1:8 (SEQ ID NO: 132), EXP-Sv.Ubq1:1:9 (SEQ ID NO: 133), EXP-Zm.UbqM1:1:6 (SEQ ID NO: 137), EXP-Zm.UbqM1:1:8 (SEQ ID NO: 145), EXP-Zm.UbqM1:1:7 (SEQ ID NO: 141), EXP-SETit.Ubq1:1:5 (SEQ ID NO: 117), EXP-SETit.Ubq1:1:7 (SEQ ID NO: 123), EXP-SETit.Ubq1:1:6 (SEQ ID NO: 124) and EXP-Sb.Ubq6:1:2 (SEQ ID NO: 153) drove expression of the CP4 transgene at levels close to or higher than CP4 expression levels driven by EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1 and EXP-Os.Act1:1:1. The EXP sequence, EXP-Sb.Ubq4:1:2 (SEQ ID NO: 151) demonstrated the ability to drive expression of CP4, but the level of expression was lower than that of the constitutive controls.

[0133] Similar data to that above may also be obtained from plants stably transformed with plasmid constructs described above, for instance, plants of progeny generation(s) R_0, R_1 or F_1 or later. Likewise, expression from other plasmid constructs may be studied. For instance, pMON141619, comprises the EXP sequence EXP-ANDge.Ubq1:1:8, while pMON142862 is comprised of the EXP sequence EXP-ERIra.Ubq1:1:8. These and other constructs may be analyzed in this manner.

Example 7

Analysis of Regulatory Elements Driving CP4 in Corn Protoplasts Using CP4 Transgene Cassette Amplicons

[0134] This example illustrates the ability of EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8), EXP-ANDge.Ubq1:1:10 (SEQ ID NO: 10), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ANDge.Ubq1:1:11 (SEQ ID NO: 14), EXP-ANDge.Ubq1:1:12 (SEQ ID NO: 16), EXP-ERIra.Ubq1:1:9 (SEQ ID NO: 22), EXP-ERIra.Ubq1:1:10 (SEQ ID NO: 25), EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27), EXP-ERIra.Ubq1:1:11 (SEQ ID NO: 29), EXP-ERIra.Ubq1:1:12 (SEQ ID NO: 31), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:13 (SEQ ID NO: 114), EXP-Cl.Ubq1:1:14 (SEQ ID NO: 115), EXP-Cl.Ubq1:1:15 (SEQ ID NO: 116), EXP-Cl.Ubq1:1:16 (SEQ ID NO: 93) and EXP-Cl.Ubq1:1:17 (SEQ ID NO: 97) in driving expression of glyphosate tolerance gene CP4 in corn protoplasts. These EXP sequences were cloned into plant binary transformation plasmid constructs. The resulting plant expression vectors were used as amplification templates to produce a transgene cassette amplicon comprised of an ubiquitin EXP sequence operably linked 5' to a plastid targeted glyphosate tolerant EPSPS coding sequence (CP4, U.S. Pat. No. RE39247), operably linked 5' to the T-AGRtu.nos-1:1:13 3' UTR and a left border region from *A. tumefaciens*. The resulting amplicons were used to transform corn leaf protoplasts cells.

[0135] Corn leaf protoplasts were transformed using a PEG-based transformation method, as described in Example 2 above. Measurements of both CP4 were conducted using an ELISA-based assay. The average levels of CP4 protein expression expressed as part per million (ppm) is shown in Tables 31 and 32 below.

[0136] In a first series of experiments, expression of CP4 driven by amplicons comprised of the EXP sequences EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8), EXP-ANDge.Ubq1:1:10 (SEQ ID NO: 10), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ANDge.Ubq1:1:11 (SEQ ID NO: 14), EXP-ANDge.Ubq1:1:12 (SEQ ID NO: 16), EXP-ERIra.Ubq1:1:9 (SEQ ID NO: 22), EXP-ERIra.Ubq1:1:10 (SEQ ID NO: 25), EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27), EXP-ERIra.Ubq1:1:11 (SEQ ID NO: 29), EXP-ERIra.Ubq1:1:12 (SEQ ID NO: 31), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:13 (SEQ ID NO: 114), EXP-Cl.Ubq1:1:14 (SEQ ID NO: 115) and EXP-Cl.Ubq1:1:15 (SEQ ID NO: 116) were assayed in transformed corn leaf protoplasts and compared to CP4 expression levels driven by the constitutive controls, EXP-CaMV.35S-enh+Zm.DnaK:1:1 (SEQ ID NO: 170) and EXP-Os.Act1:1:1 (SEQ ID NO: 164). The average levels of CP4 protein expression expressed as part per million (ppm) is shown in Tables 31 below.

TABLE 31

Average CP4 protein expression in corn leaf protoplasts.

Amplicon Template	Amplicon ID	EXP sequence	SEQ ID NO:	CP4 ng/mg total protein Average	CP4 ng/mg total protein STDEV
		no DNA		0.0	0.0
pMON30098		GFP (negative control)		0.0	0.0
pMON19469	PCR24	EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	605.5	27.6
pMON30167	PCR25	EXP-Os.Act1:1:1	164	50.6	14.2
pMON140896	PCR41	EXP-ANDge.Ubq1:1:7	5	459.0	60.9
pMON140917	PCR42	EXP-ANDge.Ubq1:1:8	8	258.2	38.4
pMON140897	PCR43	EXP-ANDge.Ubq1:1:10	10	324.8	21.6
pMON140898	PCR44	EXP-ANDge.Ubq1:1:6	12	394.9	66.4
pMON140899	PCR45	EXP-ANDge.Ubq1:1:11	14	508.7	89.6
pMON140900	PCR46	EXP-ANDge.Ubq1:1:12	16	329.3	14.5
pMON140904	PCR50	EXP-ERIra.Ubq1:1:9	22	148.6	24.4
pMON140905	PCR51	EXP-ERIra.Ubq1:1:10	25	215.8	22.6
pMON140906	PCR52	EXP-ERIra.Ubq1:1:8	27	376.6	44.1
pMON140907	PCR53	EXP-ERIra.Ubq1:1:11	29	459.9	104.7

TABLE 31-continued

Average CP4 protein expression in corn leaf protoplasts.

Amplicon Template	Amplicon ID	EXP sequence	SEQ ID NO:	CP4 ng/mg total protein Average	CP4 ng/mg total protein STDEV
pMON140908	PCR54	EXP-ERIra.Ubq1:1:12	31	221.6	15.9
pMON140913	PCR19	EXP-Cl.Ubq1:1:10	98	287.8	50.9
pMON140914	PCR20	EXP-Cl.Ubq1:1:13	114	585.8	47.9
pMON140915	PCR21	EXP-Cl.Ubq1:1:14	115	557.5	76.6
pMON140916	PCR22	EXP-Cl.Ubq1:1:15	116	33.2	9.5

[0137] As can be seen in Table 31 above, the EXP sequences EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8), EXP-ANDge.Ubq1:1:10 (SEQ ID NO: 10), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ANDge.Ubq1:1:11 (SEQ ID NO: 14), EXP-ANDge.Ubq1:1:12 (SEQ ID NO: 16), EXP-ERIra.Ubq1:1:9 (SEQ ID NO: 22), EXP-ERIra.Ubq1:1:10 (SEQ ID NO: 25), EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27), EXP-ERIra.Ubq1:1:11 (SEQ ID NO: 29), EXP-ERIra.Ubq1:1:12 (SEQ ID NO: 31), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:13 (SEQ ID NO: 114), EXP-Cl.Ubq1:1:14 (SEQ ID NO: 115) and EXP-Cl.Ubq1:1:15 (SEQ ID NO: 116) were able to drive CP4 expression. All of the EXP sequences with the exception of one EXP-Cl.Ubq1:1:15 (SEQ ID NO: 116) drove CP4 expression levels at a much higher level than the constitutive control, EXP-Os.Act1:1:1 (SEQ ID NO: 164). Expression levels were lower than that of EXP-CaMV.35S-enh+Zm.DnaK:1:1 (SEQ ID NO: 170).

[0138] In a second series of experiments, expression of CP4 driven by amplicons comprised of the EXP sequences EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:16 (SEQ ID NO: 93) and EXP-Cl.Ubq1:1:17 (SEQ ID NO: 97) were assayed in transformed corn leaf protoplasts and compared to CP4 expression levels driven by the constitutive control, EXP-Os.Act1:1:1 (SEQ ID NO: 164). The average levels of CP4 protein expression expressed as part per million (ppm) is shown in Tables 32 below.

TABLE 32

Average CP4 protein expression in corn leaf protoplasts.

Amplicon Template	Amplicon ID	EXP sequence	SEQ ID NO:	Maize Leaf CP4 mg/total protein Avg	Maize Leaf CP4 mg/total protein StdDev
pMON30167	PCR25	EXP-Os.Act1:1:1	164	12.2	1.69
pMON140913	PCR19	EXP-Cl.Ubq1:1:10	98	307.5	24.21
pMON142748	pMON142748	EXP-Cl.Ubq1:1:16	93	245.95	30.14
pMON142749	pMON142749	EXP-Cl.Ubq1:1:17	97	302.85	25.32

[0139] As can be seen in Table 32 above, the EXP sequences EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:16 (SEQ ID NO: 93) and EXP-Cl.Ubq1:1:17 (SEQ ID NO: 97) were able to drive CP4 expression. Expression levels driven by all three EXP sequences were higher than that of the constitutive control, EXP-Os.Act1:1:1 (SEQ ID NO: 164).

Example 8

Analysis of Regulatory Elements Driving CP4 in Wheat Protoplasts

[0140] This example illustrates the ability of EXP-Sv.Ubq1:1:7 (SEQ ID NO: 128), EXP-Sv.Ubq1:1:8 (SEQ ID NO: 132), EXP-Sv.Ubq1:1:9 (SEQ ID NO: 133), EXP-Zm.UbqM1:1:6 (SEQ ID NO: 137), EXP-Zm.UbqM1:1:8 (SEQ ID NO: 145), EXP-Zm.UbqM1:1:7 (SEQ ID NO: 141), EXP-SETit.Ubq1:1:5 (SEQ ID NO: 117), EXP-SETit.Ubq1:1:7 (SEQ ID NO: 123), EXP-SETit.Ubq1:1:6 (SEQ ID NO: 124), EXP-Sb.Ubq4:1:2 (SEQ ID NO: 151) and EXP-Sb.Ubq6:1:2 (SEQ ID NO: 153) to drive CP4 expression in wheat leaf protoplasts. These EXP sequences were cloned into plant binary transformation plasmid constructs using methods known in the art, and as described in Examples 2 and 5 above.

[0141] Three control plasmids (pMON30098, pMON42410, as previously described, and pMON43647 comprising a right border region from *Agrobacterium tumefaciens* with EXP-Os.Act1+CaMV.35S.2xA1-B3+Os.Act1:1:1 (SEQ ID NO: 138) operably linked 5' to a plastid targeted glyphosate tolerance coding sequence (CP4, U.S. Pat. No. RE39247), operably linked 5' to T-AGRtu.nos-1:1:13, and a left border region (B-AGRtu.left border) with known constitutive regulatory elements driving either CP4 or GFP were constructed as outlined in Example 5.

[0142] Wheat leaf protoplasts were transformed using a PEG-based transformation method as described in the previous examples with the exception that 1.5×10^5 protoplast cells per assay were used. Assays of luciferase and CP4 transgene expression were performed as described in Example 6 above. The mean CP4 expression levels determined by CP4 ELISA are presented in Table 34 below.

TABLE 34

Mean CP4 Protein Expression in Wheat Leaf Protoplast Cells.

Plasmid	EXP sequence	SEQ ID NO:	CP4 Average ppm	CP4 STDEV ppm
No DNA	No DNA		0	0
pMON30098	GFP		0	0
pMON43647	EXP-Os.Act1 + CaMV.35S.2xA1-B3 + Os.Act1:1:1	172	656.2	124.5
pMON42410	EXP-CaMV.35S-enh + Ta.Lhcb1 + Os.Act1:1:1	163	438.3	78.9
pMON30167	EXP-Os.Act1:1:1	164	583	107.4
pMON129203	EXP-Sv.Ubq1:1:7	128	156.9	25.1
pMON129204	EXP-Sv.Ubq1:1:8	132	39.5	7
pMON129205	EXP-Sv.Ubq1:1:9	133	154.5	56.5
pMON129210	EXP-Zm.UbqM1:1:6	137	1500	0
pMON129211	EXP-Zm.UbqM1:1:8	145	199.7	64.9
pMON129212	EXP-Zm.UbqM1:1:7	141	234.6	66.9
pMON129200	EXP-SETit.Ubq1:1:5	117	725.7	149.7
pMON129201	EXP-SETit.Ubq1:1:7	123	64.9	14.5
pMON129202	EXP-SETit.Ubq1:1:6	124	122.9	48.7
pMON129219	EXP-Sb.Ubq4:1:2	151	113.1	32.8

[0143] The total amount of CP4 expression in wheat protoplasts driven by the EXP sequences and the known constitutive EXP sequence EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1 demonstrated different levels of CP4 expression in wheat protoplasts when compared to corn protoplasts.

[0144] Several EXP sequences drove CP4 expression at lower levels in wheat protoplasts than the known constitutive EXP sequences EXP-Os.Act1+CaMV.35S.2xA1-B3+Os.Act1:1:1 and EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1. Two EXP sequences, EXP-Zm.UbqM1:1:6 (SEQ ID NO: 137), and EXP-SETit.Ubq1:1:5 (SEQ ID NO: 117), provide higher levels of CP4 expression in wheat protoplasts than the known constitutive, EXP sequences in this assay. EXP-Zm.UbqM1:1:2 drove expression of CP4 at the highest level, with expression levels being 2.2 to 3.4 fold higher than EXP-Os.Act1+CaMV.35S.2×A1-B3+Os.Act1:1:1 and EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1, respectively. All EXP sequences assayed demonstrated the capacity to drive expression of CP4 in wheat cells.

Example 9

Analysis of Regulatory Elements Driving CP4 in Wheat Protoplasts Using CP4 Transgene Cassette Amplicons

[0145] This example illustrates the ability of EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8), EXP-ANDge.Ubq1:1:10 (SEQ ID NO: 10), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ANDge.Ubq1:1:11 (SEQ ID NO: 14), EXP-ANDge.Ubq1:1:12 (SEQ ID NO: 16), EXP-ERIra.Ubq1:1:9 (SEQ ID NO: 22), EXP-ERIra.Ubq1:1:10 (SEQ ID NO: 25), EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27), EXP-ERIra.Ubq1:1:11 (SEQ ID NO: 29), EXP-ERIra.Ubq1:1:12 (SEQ ID NO: 31), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:13 (SEQ ID NO: 114), EXP-Cl.Ubq1:1:14 (SEQ ID NO: 115), EXP-Cl.Ubq1:1:15 (SEQ ID NO: 116), EXP-Cl.Ubq1:1:16 (SEQ ID NO: 93) and EXP-Cl.Ubq1:1:17 (SEQ ID NO: 97) in driving expression of glyphosate tolerance gene CP4 in wheat protoplasts. These EXP sequences were cloned into plant binary transformation plasmid constructs. The resulting plant expression vectors were used as amplification templates to produce a transgene cassette amplicon comprised of an ubiquitin EXP sequence operably linked 5' to a plastid targeted glyphosate tolerant EPSPS coding sequence (CP4, U.S. Pat. No. RE39247), operably linked 5' to the T-AGRtu.nos-1:1:13 3' UTR and a left border region from *A. tumefaciens*. The resulting amplicons were used to transform corn leaf protoplasts cells.

[0146] Wheat leaf protoplasts were transformed using a PEG-based transformation method, as described in Example 2 above. Measurements of both CP4 were conducted using an ELISA-based assay. The average levels of CP4 protein expression expressed as part per million (ppm) is shown in Tables 35 and 36 below.

[0147] In a first series of experiments, expression of CP4 driven by amplicons comprised of the EXP sequences EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8), EXP-ANDge.Ubq1:1:10 (SEQ ID NO: 10), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ANDge.Ubq1:1:11 (SEQ ID NO: 14), EXP-ANDge.Ubq1:1:12 (SEQ ID NO: 16), EXP-ERIra.Ubq1:1:9 (SEQ ID NO: 22), EXP-ERIra.Ubq1:1:10 (SEQ ID NO: 25), EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27), EXP-ERIra.Ubq1:1:11 (SEQ ID NO: 29), EXP-ERIra.Ubq1:1:12 (SEQ ID NO: 31), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:13 (SEQ ID NO: 114), EXP-Cl.Ubq1:1:14 (SEQ ID NO: 115) and EXP-Cl.Ubq1:1:15 (SEQ ID NO: 116) were assayed in transformed wheat leaf protoplasts and compared to CP4 expression levels driven by the constitutive controls, EXP-CaMV.35S-enh+Zm.DnaK:1:1 (SEQ ID NO: 170) and EXP-Os.Act1:1:1 (SEQ ID NO: 164). The average levels of CP4 protein expression expressed as part per million (ppm) is shown in Tables 35 below.

TABLE 35

Average CP4 protein expression in wheat leaf protoplasts.

Amplicon Template	Amplicon ID	EXP sequence	SEQ ID NO:	CP4 ng/mg total protein Average	CP4 ng/mg total protein STDEV
		no DNA		0.00	0.00
pMON30098		GFP (negative control)		0.00	0.00
pMON19469	PCR24	EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	76.11	18.65

TABLE 35-continued

Average CP4 protein expression in wheat leaf protoplasts.

Amplicon Template	Amplicon ID	EXP sequence	SEQ ID NO:	CP4 ng/mg total protein Average	CP4 ng/mg total protein STDEV
pMON30167	PCR25	EXP-Os.Act1:1:1	164	3.83	0.73
pMON140896	PCR41	EXP-ANDge.Ubq1:1:7	5	103.46	16.31
pMON140917	PCR42	EXP-ANDge.Ubq1:1:8	8	61.48	1.99
pMON140897	PCR43	EXP-ANDge.Ubq1:1:10	10	62.65	4.58
pMON140898	PCR44	EXP-ANDge.Ubq1:1:6	12	48.74	3.09
pMON140899	PCR45	EXP-ANDge.Ubq1:1:11	14	54.91	3.50
pMON140900	PCR46	EXP-ANDge.Ubq1:1:12	16	42.81	5.97
pMON140904	PCR50	EXP-ERIra.Ubq1:1:9	22	31.26	1.69
pMON140905	PCR51	EXP-ERIra.Ubq1:1:10	25	49.82	5.96
pMON140906	PCR52	EXP-ERIra.Ubq1:1:8	27	37.43	4.52
pMON140907	PCR53	EXP-ERIra.Ubq1:1:11	29	27.17	0.96
pMON140908	PCR54	EXP-ERIra.Ubq1:1:12	31	17.41	4.13
pMON140913	PCR19	EXP-Cl.Ubq1:1:10	98	66.66	13.45
pMON140914	PCR20	EXP-Cl.Ubq1:1:13	114	79.42	10.74
pMON140915	PCR21	EXP-Cl.Ubq1:1:14	115	75.53	9.32
pMON140916	PCR22	EXP-Cl.Ubq1:1:15	116	0.00	0.00

[0148] As can be seen in Table 31 above, the EXP sequences EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8), EXP-ANDge.Ubq1:1:10 (SEQ ID NO: 10), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ANDge.Ubq1:1:11 (SEQ ID NO: 14), EXP-ANDge.Ubq1:1:12 (SEQ ID NO: 16), EXP-ERIra.Ubq1:1:9 (SEQ ID NO: 22), EXP-ERIra.Ubq1:1:10 (SEQ ID NO: 25), EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27), EXP-ERIra.Ubq1:1:11 (SEQ ID NO: 29), EXP-ERIra.Ubq1:1:12 (SEQ ID NO: 31), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:13 (SEQ ID NO: 114), EXP-Cl.Ubq1:1:14 (SEQ ID NO: 115) and EXP-Cl.Ubq1:1:15 (SEQ ID NO: 116) were able to drive CP4 expression. All of the EXP sequences with the exception of one EXP-Cl.Ubq1:1:15 (SEQ ID NO: 116) drove CP4 expression levels at a much higher level than the constitutive control, EXP-Os.Act1:1:1 (SEQ ID NO: 164). Expression levels were around the same level or lower than that of EXP-CaMV.35S-enh+Zm.DnaK:1:1 (SEQ ID NO: 170) for most of the EXP sequences.

[0149] In a second series of experiments, expression of CP4 driven by amplicons comprised of the EXP sequences EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:16 (SEQ ID NO: 93) and EXP-Cl.Ubq1:1:17 (SEQ ID NO: 97) were assayed in transformed wheat leaf protoplasts and compared to CP4 expression levels driven by the constitutive control, EXP-Os.Act1:1:1 (SEQ ID NO: 164). The average levels of CP4 protein expression expressed as part per million (ppm) is shown in Tables 32 below.

TABLE 36

Average CP4 protein expression in wheat leaf protoplasts.

Amplicon Template	Amplicon ID	EXP sequence	SEQ ID NO:	Maize Leaf CP4 mg/total protein Avg	Maize Leaf CP4 mg/total protein StdDev
pMON30167	PCR25	EXP-Os.Act1:1:1	164	15.84	2.12
pMON140913	PCR19	EXP-Cl.Ubq1:1:10	98	736.32	79.56
pMON142748	pMON142748	EXP-Cl.Ubq1:1:16	93	593.72	80.22
pMON142749	pMON142749	EXP-Cl.Ubq1:1:17	97	763.95	86.94

[0150] As can be seen in Table 36 above, the EXP sequences EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:16 (SEQ ID NO: 93) and EXP-Cl.Ubq1:1:17 (SEQ ID NO: 97) were able to drive CP4 expression. Expression levels driven by all three EXP sequences were higher than that of the constitutive control, EXP-Os.Act1:1:1 (SEQ ID NO: 164).

Example 10

Analysis of Regulatory Elements Driving CP4 in Sugarcane Protoplasts

[0151] This example illustrates the ability of EXP-Sv.Ubq1:1:7 (SEQ ID NO: 128), EXP-Sv.Ubq1:1:8 (SEQ ID NO: 132), EXP-Sv.Ubq1:1:9 (SEQ ID NO: 133), EXP-Zm.UbqM1:1:6 (SEQ ID NO: 137), EXP-Zm.UbqM1:1:8 (SEQ ID NO: 145), EXP-Zm.UbqM1:1:7 (SEQ ID NO: 141), EXP-SETit.Ubq1:1:5 (SEQ ID NO: 117), EXP-SETit.Ubq1:1:7 (SEQ ID NO: 123), EXP-SETit.Ubq1:1:6 (SEQ ID NO: 124), EXP-Sb.Ubq4:1:2 (SEQ ID NO: 151), EXP-Sb.Ubq6:1:2

(SEQ ID NO: 153) and EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98) in driving expression of CP4 in sugar cane leaf protoplasts. The EXP sequences were cloned into plant binary transformation plasmid constructs. The resulting vectors contained a right border region from *Agrobacterium tumefaciens*, an ubiquitin EXP sequence operably linked 5' to a plastid targeted glyphosate tolerant EPSPS coding sequence (CP4, U.S. Pat. No. RE39247), operably linked 5' to the T-AGRtu.nos-1:1:13 (SEQ ID NO: 127) or T-CaMV.35S-1:1:1 (SEQ ID NO: 140) 3' UTR and a left border region from *A. tumefaciens* (B-AGRtu.left border). The resulting plasmid constructs were used to transform sugarcane leaf protoplasts cells using PEG transformation method.

[0152] Plasmid constructs pMON129203, pMON12904, pMON12905, pMON129210, pMON129211, pMON129212, pMON129200, pMON129201, pMON129202, pMON129219, and pMON129218 are as described in Table 12 above.

[0153] Three control plasmids (pMON30167 described above; pMON130803 also comprising EXP-Os.Act1:1:1 (SEQ ID NO: 164); and pMON132804 comprising EXP-P-CaMV.35S-enh-1:1:13/L-CaMV.35S-1:1:2/I-Os.Act1-1:1:19 (SEQ ID NO: 139), with known constitutive regulatory elements driving CP4 were constructed and used to compare the relative CP4 expression levels driven by the ubiquitin EXP sequences listed in Table 37 below.

[0154] Sugarcane leaf protoplasts were transformed using a PEG-based transformation method. The mean CP4 expression levels determined by CP4 ELISA are presented in Table 37 below.

TABLE 37

Mean CP4 Protein Expression in Sugarcane Leaf Protoplast Cells.

			Experiment 1		Experiment 2	
Plasmid Construct	EXP sequence	SEQ ID NO:	CP4 Average ppm	CP4 STDEV ppm	CP4 Average ppm	CP4 STDEV ppm
pMON132804	EXP-P-CaMV.35S-enh-1:1:13/L-CaMV.35S-1:1:2/I-Os.Act1-1:1:19	173	557.97	194.05	283.63	95.8
pMON30167	EXP-Os.Act1:1:1	164	57.15	20.99	18.36	5.41
pMON130803	EXP-Os.Act1:1:1	164	34.26	1.61	16.57	3.71
pMON129203	EXP-Sv.Ubq1:1:7	128	89.2	32.46	56.86	9.55
pMON129204	EXP-Sv.Ubq1:1:8	132	87.2	45.87	98.46	12.93
pMON129205	EXP-Sv.Ubq1:1:9	133	263.57	70.14	72.53	9.25
pMON129210	EXP-Zm.UbqM1:1:6	137	353.08	29.16	199.31	41.7
pMON129211	EXP-Zm.UbqM1:1:8	145	748.18	15.1	411.24	17.12
pMON129212	EXP-Zm.UbqM1:1:7	141	454.88	75.77	215.06	23.22
pMON129200	EXP-SETit.Ubq1:1:5	117	150.74	63.21	91.71	41.35
pMON129201	EXP-SETit.Ubq1:1:7	123	119.57	58.1	102.72	31.12
pMON129202	EXP-SETit.Ubq1:1:6	124	43.79	25.77	97.63	46.07
pMON129219	EXP-Sb.Ubq4:1:2	151	95.63	38.69		
pMON129218	EXP-Sb.Ubq6:1:2	153	343.34	119.2	179.75	51.16
pMON129221	EXP-Cl.Ubq1:1:10	98	374.8	205.28	258.93	38.03

[0155] As can be seen in Table 37 above, the EXP sequences demonstrated the ability to drive expression CP4 expression in sugarcane protoplasts. The levels of expression were similar to or greater than that of CP4 expression driven by EXP-Os.Act1:1:1 (SEQ ID NO: 164). One EXP sequence, EXP-Zm.UbqM1:1:8 (SEQ ID NO: 145), demonstrated higher levels of expression when compared to EXP-P-CaMV.35S-enh-1:1:13/L-CaMV.35S-1:1:2/1-Os.Act1-1:1:19 (SEQ ID NO: 139) in sugarcane protoplasts.

Example 11

Analysis of Regulatory Elements Driving CP4 in Sugarcane Protoplasts Using CP4 Transgene Cassette Amplicons

[0156] This example illustrates the ability of EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8), EXP-ANDge.Ubq1:1:10 (SEQ ID NO: 10), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ANDge.Ubq1:1:11 (SEQ ID NO: 14), EXP-ANDge.Ubq1:1:12 (SEQ ID NO: 16), EXP-ERIra.Ubq1:1:9 (SEQ ID NO: 22), EXP-ERIra.Ubq1:1:10 (SEQ ID NO: 25), EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27), EXP-ERIra.Ubq1:1:11 (SEQ ID NO: 29), EXP-ERIra.Ubq1:1:12 (SEQ ID NO: 31), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:13 (SEQ ID NO: 114), EXP-Cl.Ubq1:1:14 (SEQ ID NO: 115) and EXP-Cl.Ubq1:1:15 (SEQ ID NO: 116) in driving expression of the glyphosate tolerance gene CP4 in sugarcane protoplasts. These EXP sequences were cloned into plant binary transformation plasmid constructs. The resulting plant expression vectors were used as amplification templates to produce a transgene cassette amplicon comprised of an ubiquitin EXP sequence operably linked 5' to a plastid targeted glyphosate tolerant EPSPS coding sequence (CP4, U.S. Pat. No. RE39247), operably linked 5' to the T-AGRtu.nos-1:1:13 3' UTR and a left border region from *A. tumefaciens*. The resulting amplicons were used to transform sugarcane leaf protoplasts cells.

[0157] Sugarcane leaf protoplasts were transformed using a PEG-based transformation method, as described in Example 2 above. Measurements of both CP4 were conducted using an ELISA-based assay.

[0158] Expression of CP4 driven by amplicons comprised of the EXP sequences EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8), EXP-ANDge.Ubq1:1:10 (SEQ ID NO: 10), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ANDge.Ubq1:1:11 (SEQ ID NO: 14), EXP-ANDge.Ubq1:1:12 (SEQ ID NO: 16), EXP-ERIra.Ubq1:1:9 (SEQ ID NO: 22), EXP-ERIra.Ubq1:1:10 (SEQ ID NO: 25), EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27), EXP-ERIra.Ubq1:1:11 (SEQ ID NO: 29), EXP-ERIra.Ubq1:1:12

(SEQ ID NO: 31), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:13 (SEQ ID NO: 114), EXP-Cl.Ubq1:1:14 (SEQ ID NO: 115) and EXP-Cl.Ubq1:1:15 (SEQ ID NO: 116) were assayed in transformed wheat leaf protoplasts and compared to CP4 expression levels driven by the constitutive controls, EXP-CaMV.35S-enh+Zm.DnaK:1:1 (SEQ ID NO: 170) and EXP-Os.Act1:1:1 (SEQ ID NO: 164). The average levels of CP4 protein expression expressed as part per million (ppm) is shown in Table 38 below.

TABLE 38

Average CP4 protein expression in sugarcane leaf protoplasts.

Amplicon Template	Amplicon ID	EXP sequence	SEQ ID NO:	CP4 ng/mg total protein Average	CP4 ng/mg total protein STDEV
pMON19469	PCR24	EXP-CaMV.35S-enh + Zm.DnaK:1:1	170	99.6	7.2
pMON30167	PCR25	EXP-Os.Act1:1:1	164	0.0	0.0
pMON140896	PCR41	EXP-ANDge.Ubq1:1:7	5	21.9	3.3
pMON140917	PCR42	EXP-ANDge.Ubq1:1:8	8	15.4	1.9
pMON140897	PCR43	EXP-ANDge.Ubq1:1:10	10	20.7	2.2
pMON140898	PCR44	EXP-ANDge.Ubq1:1:6	12	21.8	2.8
pMON140899	PCR45	EXP-ANDge.Ubq1:1:11	14	36.9	7.2
pMON140900	PCR46	EXP-ANDge.Ubq1:1:12	16	51.7	5.6
pMON140904	PCR50	EXP-ERIra.Ubq1:1:9	22	10.3	1.1
pMON140905	PCR51	EXP-ERIra.Ubq1:1:10	25	25.3	4.7
pMON140906	PCR52	EXP-ERIra.Ubq1:1:8	27	29.9	4.6
pMON140907	PCR53	EXP-ERIra.Ubq1:1:11	29	44.0	7.1
pMON140908	PCR54	EXP-ERIra.Ubq1:1:12	31	37.0	5.4
pMON140913	PCR19	EXP-Cl.Ubq1:1:10	98	19.2	1.3
pMON140914	PCR20	EXP-Cl.Ubq1:1:13	114	20.5	2.1
pMON140915	PCR21	EXP-Cl.Ubq1:1:14	115	23.2	1.6
pMON140916	PCR22	EXP-Cl.Ubq1:1:15	116	0.0	0.0

[0159] As can be seen in Table 38 above, the EXP sequences EXP-ANDge.Ubq1:1:7 (SEQ ID NO: 5), EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8), EXP-ANDge.Ubq1:1:10 (SEQ ID NO: 10), EXP-ANDge.Ubq1:1:6 (SEQ ID NO: 12), EXP-ANDge.Ubq1:1:11 (SEQ ID NO: 14), EXP-ANDge.Ubq1:1:12 (SEQ ID NO: 16), EXP-ERIra.Ubq1:1:9 (SEQ ID NO: 22), EXP-ERIra.Ubq1:1:10 (SEQ ID NO: 25), EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27), EXP-ERIra.Ubq1:1:11 (SEQ ID NO: 29), EXP-ERIra.Ubq1:1:12 (SEQ ID NO: 31), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Cl.Ubq1:1:13 (SEQ ID NO: 114) and EXP-Cl.Ubq1:1:14 (SEQ ID NO: 115) were able to drive CP4 expression. EXP-Cl.Ubq1:1:15 (SEQ ID NO: 116) did not appear to express CP4 expression in this assay.

Example 12

Analysis of Regulatory Elements Driving GUS in Transgenic Corn

[0160] Corn plants were transformed with plant expression vectors containing a EXP sequences driving expression of the β-glucuronidase (GUS) transgene, and the resulting plants were analyzed for GUS protein expression. The ubiquitin EXP sequences were cloned into plant binary transformation plasmid constructs using methods known in the art.

[0161] The resulting plant expression vectors contain a right border region from *A. tumefaciens*, a first transgene cassette to assay the EXP sequence operably linked to a coding sequence for β-glucuronidase (GUS) that possesses the processable intron GUS-2, described above, operably linked 5' to the 3' UTR from the rice lipid transfer protein gene (T-Os.LTP-1:1:1, SEQ ID NO: 141); a second transgene selection cassette used for selection of transformed plant cells that confers resistance to the herbicide glyphosate (driven by the rice Actin 1 promoter), and a left border region from *A. tumefaciens*. The resulting plasmids were used to transform corn plants. Table 39 lists the plasmid designations, the EXP sequences and the SEQ ID NOs, which are also described in Table 1.

TABLE 39

Binary plant transformation plasmids and the associated EXP sequences.

Plasmid Construct	EXP sequence	SEQ ID NO:	Data
pMON142865	EXP-ANDge.Ubq1:1:8	8	R_0 and R_1
pMON142864	EXP-ERIra.Ubq1:1:8	27	R_0 and R_1
pMON142729	EXP-Cl.Ubq1:1:12	90	R_0
pMON142730	EXP-Cl.Ubq1:1:11	95	R_0
pMON132047	EXP-Cl.Ubq1:1:23	108	R_0
pMON132037	EXP-SETit.Ubq1:1:10	119	R_0 and F_1
pMON131957	EXP-SETit.Ubq1:1:11	125	F1
pMON131958	EXP-Sv.Ubq1:1:11	130	R_0 and F_1
pMON131959	EXP-Sv.Ubq1:1:12	136	R_0
pMON131961	EXP-Zm.UbqM1:1:10	139	R_0
pMON131963	EXP-Zm.UbqM1:1:12	143	R_0
pMON131962	EXP-Zm.UbqM1:1:11	149	R_0
pMON132932	EXP-Sb.Ubq4:1:2	151	R_0
pMON132931	EXP-Sb.Ubq6:1:3	155	R_0
pMON132974	EXP-Sb.Ubq7:1:2	157	R_0 and F_1

[0162] Plants were transformed using *Agrobacterium*-mediated transformations, for instance as described in U.S. Patent Application Publication 20090138985.

[0163] Histochemical GUS analysis was used for qualitative expression analysis of transformed plants. Whole tissue

sections were incubated with GUS staining solution X-Gluc (5-bromo-4-chloro-3-indolyl-b-glucuronide) (1 milligram/milliliter) for an appropriate length of time, rinsed, and visually inspected for blue coloration. GUS activity was qualitatively determined by direct visual inspection or inspection under a microscope using selected plant organs and tissues. The R_0 plants are inspected for expression in the roots and leaves as well as the anther, silk and developing seed and embryo 21 days after pollination (21 DAP).

[0164] For quantitative analysis, total protein was extracted from selected tissues of transformed corn plants. One microgram of total protein was used with the fluorogenic substrate 4-methyleumbelliferyl-β-D-glucuronide (MUG) in a total reaction volume of 50 microliters. The reaction product, 4-methlyumbelliferone (4-MU), is maximally fluorescent at high pH, where the hydroxyl group is ionized. Addition of a basic solution of sodium carbonate simultaneously stops the assay and adjusts the pH for quantifying the fluorescent product. Fluorescence was measured with excitation at 365 nm, emission at 445 nm using a Fluoromax-3 (Horiba; Kyoto, Japan) with Micromax Reader, with slit width set at excitation 2 nm and emission 3 nm.

[0165] The average R_0 GUS expression observed for each transformation is presented in Tables 40 and 41 below. The R_0 GUS assay performed on transformants transformed with pMON131957 (EXP-SETit.Ubq1:1:11, SEQ ID NO:125) did not pass quality standards. These transformants were assayed at F1 generation and are presented further below in this example.

TABLE 40

Average R_0 GUS expression in root and leaf tissue.

EXP sequence	SEQ ID NO:	V3 Root	V4 Root	V7 Root	VT Root	V3 Leaf	V4 Leaf	V7 Leaf	VT Leaf
EXP-ANDge.Ubq1:1:8	8	nd	255	199	70	nd	638	168	130
EXP-ERIra.Ubq1:1:8	27	nd	477	246	62	nd	888	305	242
EXP-Cl.Ubq1:1:12	90	nd	27	147	52	nd	75	189	199
EXP-Cl.Ubq1:1:11	95	nd	28	77	50	nd	101	177	223
EXP-Cl.Ubq1:1:23	108	0	nd	75	34	201	nd	194	200
EXP-SETit.Ubq1:1:10	119	0	nd	29	57	58	nd	37	46
EXP-Sv.Ubq1:1:11	130	nd	nd	nd	9	20	nd	55	29
EXP-Sv.Ubq1:1:12	136	63	nd	0	28	184	nd	27	16
EXP-Zm.UbqM1:1:10	139	0	nd	237	18	221	nd	272	272
EXP-Zm.UbqM1:1:12	143	0	nd	21	43	234	nd	231	196
EXP-Zm.UbqM1:1:11	149	124	nd	103	112	311	nd	369	297
EXP-Sb.Ubq4:1:2	151	125	nd	0	95	233	nd	150	88
EXP-Sb.Ubq6:1:3	155	154	nd	13	128	53	nd	39	55
EXP-Sb.Ubq7:1:2	157	37	nd	22	18	165	nd	89	177

TABLE 41

Average R_0 GUS expression in corn reproductive organs (anther, silk) and developing seed (embryo and endosperm).

EXP sequence	SEQ ID NO:	VT Anther	VT/R1 Silk	21 DAP Embryo	21 DAP Endosperm
EXP-ANDge.Ubq1:1:8	8	247	256	24	54
EXP-ERIra.Ubq1:1:8	27	246	237	36	61
EXP-Cl.Ubq1:1:12	90	420	121	26	220
EXP-Cl.Ubq1:1:11	95	326	227	41	221
EXP-Cl.Ubq1:1:23	108	598	416	212	234

TABLE 41-continued

Average R_0 GUS expression in corn reproductive organs (anther, silk) and developing seed (embryo and endosperm).

EXP sequence	SEQ ID NO:	VT Anther	VT/R1 Silk	21 DAP Embryo	21 DAP Endosperm
EXP-SETit.Ubq1:1:10	119	132	85	50	63
EXP-Sv.Ubq1:1:11	130	217	3	45	92
EXP-Sv.Ubq1:1:12	136	120	21	49	112
EXP-Zm.UbqM1:1:10	139	261	506	403	376
EXP-Zm.UbqM1:1:12	143	775	362	253	247
EXP-Zm.UbqM1:1:11	149	551	452	234	302
EXP-Sb.Ubq4:1:2	151	213	0	25	79
EXP-Sb.Ubq6:1:3	155	295	87	51	61
EXP-Sb.Ubq7:1:2	157	423	229	274	90

[0166] In R_0 corn plants, GUS expression levels in the leaf and root differed amongst the ubiquitin EXP sequences. While all of the EXP sequences demonstrated the ability to drive GUS transgene expression in stably transformed plants, each EXP sequence demonstrated a unique pattern of expression relative to the others. For example, high levels of GUS expression were observed in early stages of root development (V4 and V7) for EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8) and EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27) and declined by VT stage. Root expression driven by EXP-Zm.UbqM1:1:10 (SEQ ID NO: 139) demonstrated no expression at V3 but was high at V7 and then dropped by VT stage. Root expression driven by EXP-Zm.UbqM1:1:11 (SEQ ID NO: 149) was maintained to a similar level throughout development from stages V3, V7 through VT. Root expression was observed to increase from early development (V3/V4) to V7 stage and then drop from V7 to V8 stage in plants transformed with EXP-Cl.Ubq1:1:12 (SEQ ID NO: 90), EXP-Cl.Ubq1:1:11 (SEQ ID NO: 95) and EXP-Cl.Ubq1:1:23 (SEQ ID NO: 108). GUS expression levels showed dramatic differences in leaf tissue as well. The highest levels of leaf expression were conferred in early development (V3/V4) with EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8) and EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27) which decline at V7 through VT stage. GUS expression is retained from V3 through VT stage using EXP-Zm.UbqM1:1:10 (SEQ ID NO: 139), EXP-Zm.UbqM1:1:11

(SEQ ID NO: 149), EXP-Zm.UbqM1:1:12 (SEQ ID NO: 143) and EXP-Cl.Ubq1:1:23 (SEQ ID NO: 108); and to a lower extent using EXP-SETit.Ubq1:1:10 (SEQ ID NO: 119) and EXP-Sb.Ubq6:1:3 (SEQ ID NO: 155). Expression in the leaf increased from V3 to V7 to VT stage using EXP-Cl. Ubq1:1:12 (SEQ ID NO: 90), EXP-Cl.Ubq1:1:11 (SEQ ID NO: 95) and EXP-Cl.Ubq1:1:23 (SEQ ID NO: 108) while expression declined from V3 to VT stage using EXP-Sv. Ubq1:1:12 (SEQ ID NO: 136) and EXP-Sb.Ubq4:1:2 (SEQ ID NO: 151).

[0167] Likewise, with respect to reproductive tissue (anther and silk) and developing seed (21DAP embryo and endosperm) different patterns of expression were observed unique to each EXP sequence. For example, High levels of expression were observed in anther and silk as well as the developing seed using EXP-Zm.UbqM1:1:10 (SEQ ID NO: 139), EXP-Zm.UbqM1:1:11 (SEQ ID NO: 149), EXP-Zm. UbqM1:1:12 (SEQ ID NO: 143) and EXP-Cl.Ubq1:1:23 (SEQ ID NO: 108). Expression was high in the anther and silk but low in the developing seed using EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8) and EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27). Expression driven by EXP-Sb.Ubq7:1:2 (SEQ ID NO: 157) was high in reproductive tissue and high in the developing embryo but was lower in the developing endosperm. The EXP sequence, EXP-Sb.Ubq4:1:2 (SEQ ID NO: 151) only demonstrated expression in the anther but not in the silk and expressed much lower in the developing seed. EXP-Sv.Ubq1: 1:11 (SEQ ID NO: 130) demonstrated a similar pattern as EXP-Sb.Ubq4:1:2 (SEQ ID NO: 151) with respect to reproductive tissue and developing seed, but whereas EXP-Sb. Ubq4:1:2 (SEQ ID NO: 151) showed expression in root and leaf tissues, EXP-Sv.Ubq1:1:11 (SEQ ID NO: 130) expressed much lower in these same tissues.

[0168] R_0 generation transformants, selected for single copy insertions were crossed with a non-transgenic LH244 line (resulting in F_1) or were self-pollinated (resulting in R_1) in order to produce an F_1 or R_1 population of seeds. In either case, heterozygous F_1 or R_1 plants were selected for study. GUS expression levels were measured in selected tissues over the course of development as previously described. The F_1 or R_1 tissues used for this study included: imbibed seed embryo, imbibed seed endosperm, root and coleoptide at 4 days after germination (DAG); leaf and root at V3 stage; root and mature leaf at V8 stage; root, mature leaves, VT stage (at tasseling, prior to reproduction) anther, pollen, leaf and senescing leaf; R1 cob, silk, root and internode; kernel 12 days after pollination (DAP) and; embryo and endosperm 21 and 38 DAP. Selected tissue samples were also analyzed for F_1 plants exposed to conditions of drought and cold stress for transformants comprising pMON132037 (EXP-SETit.Ubq1:1:10, SEQ ID NO: 119), pMON131957 (EXP-SETit.Ubq1:1:11, SEQ ID NO: 125), pMON131958 (EXP-Sv.Ubq1:1:11, SEQ ID NO: 130) and pMON132974 (EXP-Sb.Ubq7:1:2, SEQ ID NO: 157). V3 root and leaf tissue was sampled after cold and drought exposure.

[0169] Drought stress was induced in F_1, V3 plants transformed with pMON132037 (EXP-SETit.Ubq1:1:10, SEQ ID NO: 119), pMON131957 (EXP-SETit.Ubq1:1:11, SEQ ID NO: 125), pMON131958 (EXP-Sv.Ubq1:1:11, SEQ ID NO: 130) and pMON132974 (EXP-Sb.Ubq7:1:2, SEQ ID NO: 157) by withholding watering for 4 days allowing the water content to be reduced by at least 50% of the original water content of the fully watered plant. The drought protocol was comprised essentially of the following steps. V3 stage plants were deprived of water. As a corn plant experiences drought, the shape of the leaf will change from the usual healthy and unfolded appearance to a leaf demonstrating folding at the mid-rib vascular bundle and appearing V-shaped when viewed from the leaf tip to the stem. This change in morphology usually began to occur by about 2 days after the cessation of watering and was shown in earlier experiments to be associated with water loss of around 50% as measured by weight of pots prior to cessation of watering and weight of pots when the leaf curl morphology was observed in un-watered plants. Plants were considered to be under drought conditions, when the leaves showed wilting as evidenced by an inward curling (V-shape) of the leaf. This level of stress is considered to be a form of sub-lethal stress. Once each plant demonstrated drought induction as defined above, the plant was destroyed to acquire both root and leaf samples.

[0170] In addition to drought, F_1 V3 stage plants transformed with pMON132037 (EXP-SETit.Ubq1:1:10, SEQ ID NO: 119), pMON131957 (EXP-SETit.Ubq1:1:11, SEQ ID NO: 125), pMON131958 (EXP-Sv.Ubq1:1:11, SEQ ID NO: 130) and pMON132974 (EXP-Sb.Ubq7:1:2, SEQ ID NO: 157) were also exposed to conditions of cold to determine if the regulatory elements demonstrated cold-induced expression of GUS. Whole plants were assayed for induction of GUS expression under cold stress at V3 stage. V3 stage corn plants were exposed to a temperature of 12° C. in a growth chamber for 24 hours. Plants in the growth chamber were grown under a white light fluence of 800 micro moles per meter squared per second with a light cycle of ten hours of white light and fourteen hours of darkness. After cold exposure, leaf and root tissues were sampled for quantitative GUS expression.

[0171] GUS expression was measured as described above. The average F_1 GUS expression determined for each tissue sample is presented in Tables 42 and 43 below.

TABLE 42

Average F_1 GUS expression in plants transformed with pMON142864 and pMON142865.

Organ	pMON142864	pMON142865
V3 Leaf	86	74
V3 Root	41	52
V8 Leaf	109	123
V8 Root	241	252
VT Flower, anthers	168	208
VT Leaf	158	104
R1 Cob	171	224
R1 silk	314	274
R1 Root	721	308
R1 internode	428	364
R2 Seed-12DAP	109	72
R3 Seed-21DAP-Embryo	45	32
R3 Seed-21DAP-Endosperm	175	196
R5 Seed-38DAP-Embryo	163	58
R5 Seed-38DAP-Endosperm	90	69

TABLE 43

Average F_1 GUS expression in plants transformed with pMON132037, pMON131957, pMON131958 and pMON132974.

Organ	pMON132037	pMON131957	pMON131958	pMON132974
Imbibed Seed Embryo	536	285	288	1190
Imbibed Seed Endosperm	95	71	73	316
Coleoptile-4 DAG	218	60	143	136
Root-4 DAG	74	33	101	48
V3 Leaf	104	120	66	52
V3 Root	74	71	81	194
V3 Leaf-cold	73	15	72	N/A
V3 Root-cold	113	44	89	49
V3 Leaf-drought	97	344	103	157
V3 Root-drought	205	153	129	236
V8 Leaf	185	142	77	282
V8 Root	33	16	61	28
VT Flower-anthers	968	625	619	888
VT Leaf	138	89	132	268
VT Leaf-senescing	121	100	156	345
VT Pollen	610	1119	332	4249
R1 Cob	291	70	168	127
R1 silk	164	124	167	101
R1 Root	36	39	39	21
R1 internode	255	89	232	141
R2 Seed-12DAP	138	170	165	169
R3 Seed-21 DAP-Embryo	94	97	489	389
R3 Seed-21 DAP-Endosperm	57	118	52	217
R5 Seed-38 DAP-Embryo	600	147	377	527
R5 Seed-38 DAP-Endosperm	58	36	57	106

[0172] In F_1 corn plants, GUS expression levels in the various tissues sampled differed amongst the ubiquitin EXP sequences. While all of the EXP sequences demonstrated the ability to drive GUS transgene expression in stably transformed F_1 corn plants, each EXP sequence demonstrated a unique pattern of expression relative to the others. For example, R1 root expression is about twice that for EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27) than

[0173] EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8). GUS expression in the developing seed embryo at 38 DAP is almost three fold higher for EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27) than EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8). In contrast leaf and root expression at V3 and V8 stage is about the same for EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27) than EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8).

[0174] The F_1 GUS expression in imbided seeds (embryo and endosperm tissues) was much higher in plants transformed with EXP-Sb.Ubq7:1:2 (SEQ ID NO: 157) than in those transformed with EXP-SETit.Ubq1:1:10 (SEQ ID NO: 119), EXP-SETit.Ubq1:1:11 (SEQ ID NO: 125) and EXP-Sv.Ubq1:1:11 (SEQ ID NO: 130). Drought caused an increase in V3 root expression in plants transformed with EXP-SETit.Ubq1:1:10 (SEQ ID NO: 119), EXP-SETit.Ubq1:1:11 (SEQ ID NO: 125), EXP-Sv.Ubq1:1:11 (SEQ ID NO: 130) and EXP-Sb.Ubq7:1:2 (SEQ ID NO: 157), but only increased leaf expression in plants transformed with EXP-SETit.Ubq1:1:11 (SEQ ID NO: 125), EXP-Sv.Ubq1:1:11 (SEQ ID NO: 130) and EXP-Sb.Ubq7:1:2 (SEQ ID NO: 157). The drought enhanced V3 expression was greatest using EXP-SETit.Ubq1:1:11 (SEQ ID NO: 125). Pollen expression was also much higher in plants transformed with EXP-Sb.Ubq7:1:2 (SEQ ID NO: 157) than in those transformed with EXP-SETit.Ubq1:1:10 (SEQ ID NO: 119), EXP-SETit.Ubq1:1:11 (SEQ ID NO: 125) and EXP-Sv.Ubq1:1:11 (SEQ ID NO: 130). Expression in the R1 internode was greatest with EXP-SETit.Ubq1:1:10 (SEQ ID NO: 119) and EXP-Sv.Ubq1:1:11 (SEQ ID NO: 130) and least in plants transformed with EXP-SETit.Ubq1:1:11 (SEQ ID NO: 125).

[0175] Each EXP sequence demonstrated the ability to drive transgene expression in stably transformed corn plants. However, each EXP sequence had a pattern of expression for each tissue that was unique and offers an opportunity to select the EXP sequence which will best provide expression of a specific transgene depending upon the tissue expression strategy needed to achieve the desired results. This example demonstrates EXP sequences isolated from homologous genes do not necessarily behave equivalently in the transformed plant and that expression can only be determined through empirical

investigation of the properties for each EXP sequence and cannot be predicted based upon the gene homology from which the promoter was derived.

Example 13

Analysis of Regulatory Elements Driving CP4 in Transgenic Corn

[0176] Corn plants were transformed with plant expression vectors containing EXP sequences driving expression of the CP4 transgene, and the resulting plants were analyzed for CP4 protein expression.

[0177] The EXP sequences EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8), EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Sv.Ubq1:1:9 (SEQ ID NO: 133) and EXP-Zm.UbqM1:1:7 (SEQ ID NO: 141) were cloned into plant binary transformation plasmid constructs. The resulting vectors contained a right border region from *Agrobacterium tumefaciens*, an ubiquitin EXP sequence operably linked 5' to a plastid targeted glyphosate tolerant EPSPS coding sequence (CP4, U.S. Pat. No. RE39247), operably linked 5' to the T-AGRtu.nos-1:1:13 (SEQ ID NO: 127) 3' UTR and a left border region from *A. tumefaciens*. Table 44 below shows the plasmid constructs used to transform corn and the corresponding EXP sequences.

TABLE 44

CP4 plasmid constructs and corresponding EXP sequences used to transform corn.

Plasmid Construct	EXP sequence	SEQ ID NO:	Data
pMON141619	EXP-ANDge.Ubq1:1:8	8	R_0 and F_1
pMON142862	EXP-ERIra.Ubq1:1:8	27	R_0 and F_1
pMON129221	EXP-Cl.Ubq1:1:10	98	R_0 and F_1
pMON129205	EXP-Sv.Ubq1:1:9	133	R_0 and F_1
pMON129212	EXP-Zm.UbqM1:1:7	141	R_0

[0178] The resulting plasmids were used to transform corn plants. Transformed plants were selected for one or two copies of the inserted T-DNA and grown in the greenhouse. Selected tissues were sampled from the R_0 transformed plants at specific stages of development and CP4 protein levels were measured in those tissues using an CP4 ELISA assay. The average CP4 expression observed for each transformation is presented in Tables 45 and 46 below and graphically in FIG. 7.

TABLE 45

Average leaf and root CP4 expression in R_0 transformed corn plants.

EXP sequence	SEQ ID NO:	V4 Leaf	V7 Leaf	VT Leaf	V4 Root	V7 Root	VT Root
EXP-ANDge.Ubq1:1:8	8	20.90	18.53	25.49	11.50	26.54	17.20
EXP-ERIra.Ubq1:1:8	27	19.92	16.60	25.58	9.92	26.31	13.33
EXP-Cl.Ubq1:1:10	98	10.70	12.49	17.42	7.56	13.95	6.68
EXP-Sv.Ubq1:1:9	133	3.72	4.34	4.48	2.90	6.99	2.78
EXP-Zm.UbqM1:1:7	141	13.42	21.89	38.78	9.56	16.69	11.15

TABLE 46

Average CP4 expression in reproductive tissue and developing seed in R_0 transformed corn plants.

EXP sequence	SEQ ID NO:	VT Tassel	R1 Silk	R3 Embryo	R3 Endosperm
EXP-ANDge.Ubq1:1:8	8	24.14	5.55	7.29	4.91
EXP-ERIra.Ubq1:1:8	27	19.20	10.27	12.60	4.70
EXP-Cl.Ubq1:1:10	98	18.70	16.21	8.26	8.82
EXP-Sv.Ubq1:1:9	133	7.10	4.72	3.13	1.74
EXP-Zm.UbqM1:1:7	141	67.25	11.21	7.85	10.69

[0179] As can be seen in Tables 45 and 46, each of the EXP sequences EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8), EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Sv.Ubq1:1:9 (SEQ ID NO: 133) and EXP-Zm.UbqM1:1:7 (SEQ ID NO: 141) was able to drive CP4 expression in all tissues sampled from the R_0 transformed plants. Higher expression of CP4 in the root and leaf of transformants comprising EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8) and EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27) driving CP4 than EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98) driving CP4 may be related to the level of vegetative tolerance to glyphosate application as observed for these populations of transformants (see Example 14 below).

[0180] Each EXP sequence exhibited a unique expression pattern with respect to the level of expression for each tissue sampled. For example, while CP4 expression in leaf, root and tassel were similar for the EXP sequences, EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8) and EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27), expression in silk using EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8) was half that of expression driven by ERIra.Ubq1:1:8 (SEQ ID NO: 21). This might be advantageous for expression of transgenes in which constitutive expression is desired but less expression in silk tissue would be preferred. The EXP sequences demonstrate unique patterns of CP4 constitutive expression in R_0 transformed corn plants.

[0181] The R_0 transformed corn plants were crossed with a non-transgenic LH244 variety to produce F_1 seed. The resulting F_1 generation seed was analyzed for segregation of the transgene cassette and plants heterozygous for the CP4 cassette were selected for analysis of CP4 expression. Seed was grown in the greenhouse and two groups of plants were produced, one group was sprayed with glyphosate while the other was left unsprayed. Expression of CP4 was analyzed in selected tissues using a standard ELISA based assay. The average CP4 expression is shown in Tables 47 and 48 below.

TABLE 47

Average CP4 expression in F_1 transformed corn plants.

Organ	pMON141619	pMON142862	pMON129221
V4 Leaf	11.50	13.51	7.68
V4 Root	12.48	12.60	10.29
V7 Leaf	16.59	20.21	12.01
V7 Root	11.00	13.62	8.15
VT Leaf	39.88	44.85	29.42
VT Root	17.43	21.83	13.43
VT Flower, anthers	52.74	55.72	53.62
R1 Silk	16.01	23.81	14.42
R3 Seed-21 DAP-Embryo	33.29	57.96	51.64
R3 Seed-21 DAP-Endosperm	2.99	3.20	6.44

[0182] As can be seen in Table 47 above, CP4 expression in leaf and root was higher in F_1 transformants transformed with

pMON141619 (EXP-ANDge.Ubq1:1:8, SEQ ID NO: 5) and pMON142862 (EXP-ERIra.Ubq1:1:8, SEQ ID NO: 27) than in those transformed with pMON129221 (EXP-Cl.Ubq1:1:10, SEQ ID NO: 98). Expression in the anther tissue was similar for all three EXP sequences while expression in the silk was highest using EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27). Expression in the developing embryo (21 DAP) was highest in transformants comprising EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27) and EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98) driving CP4. Expression in the developing endosperm was higher in transformants comprising EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98) driving CP4.

TABLE 48

Average CP4 expression in F_1 transformed corn plants.

Organ	pMON129205
V4 Leaf	1.73
V4 Root	2.44
V7 Leaf	2.84
V7 Root	1.51
VT Leaf	3.29
VT Root	2.63
VT Flower, anthers	7.52
R1 Silk	1.99
R3 Seed-21 DAP-Embryo	3.40
R3 Seed-21 DAP-Endosperm	1.79

[0183] As can be seen in Tables 47-48 above, CP4 expression was lower in all tissues of F_1 transformants transformed with pMON129205 (EXP-Sv.Ubq1:1:9, SEQ ID NO: 133) than those transformed with pMON141619 (EXP-ANDge.Ubq1:1:8, SEQ ID NO: 8), pMON142862 (EXP-ERIra.Ubq1:1:8, SEQ ID NO: 27) and pMON129221 (EXP-Cl.Ubq1:1:10, SEQ ID NO: 98).

[0184] The unique patterns of expression conferred by each of the EXP sequences assayed provide an opportunity to produce a transgenic plant in which expression can be fine-tuned to make small adjustments in transgene expression for optimal performance or effectiveness. In addition, empirical testing of these EXP sequences driving different transgene expression may produce results in which one particular EXP sequence is most suitable for expression of a specific transgene or class of transgenes while another EXP sequence is found to be best for a different transgene or class of transgenes.

Example 14

Analysis of Vegetative Glyphosate Tolerance in R_0 Transgenic Corn Plants

[0185] Corn plants were transformed with plant expression vectors containing EXP sequences driving expression of the CP4 transgene, and the resulting plants were assessed for vegetative and reproductive tolerance to glyphosate application.

[0186] F_1 transformed corn plants described in Example 13 above transformed with pMON141619, pMON142862, pMON129221, pMON129205 and pMON129212 and comprised of the EXP sequences EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8), EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27), EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98), EXP-Sv.Ubq1:1:9 (SEQ ID NO: 133) and EXP-Zm.UbqM1:1:7 (SEQ ID NO: 141), respectively driving CP4 were assessed for both vegetative and reproductive tolerance when sprayed with glyphosate. Ten F_1 plants for each event were divided into two groups, the first group consisting of five plants that received glyphosate spray and V4 and V8 stage of development; and a second group of five plants that were left unsprayed (i.e. control). Glyphosate was applied by broadcast foliar spray application using Roundup WeatherMax® at an application rate of 1.5 a.e./acre (a.e. acid equivalent). After seven to ten days, the leaves of each plant were assessed for damage. Vegetative tolerance (Veg Tol in Table 49) was assessed comparing the unsprayed and sprayed plants for each event and a damage rating scale was used to provide a final rating for vegetative tolerance (T=tolerant, NT=not tolerant). In addition seed set was assayed for all of the plants in each event. Seed set measures between control plants and sprayed plants was compared and an assignment of reproductive tolerance (Repro Tol in Table 49) was given for each event based upon the percent seed set of sprayed plants relative to the controls (T=tolerant, NT=not tolerant). Table 49 below shows the vegetative and reproductive tolerance ratings for each event sprayed at V4 and V8 stage. The letter "T" denotes tolerant and "NT" denotes not tolerant.

TABLE 49

Leaf damage ratings of individual transformed corn events at V4 and V8 stage.

Plasmid Construct	EXP sequence	SEQ ID NO:	Event	Veg Tol V4	Veg Tol V8	Repro Tol
pMON141619	EXP-ANDge.Ubq1:1:8	8	Event 1	T	T	NT
			Event 2	T	T	T
			Event 3	T	T	NT
			Event 4	T	T	NT
			Event 5	T	T	T
			Event 6	T	T	NT
			Event 7	T	T	T
			Event 8	T	T	T
			Event 9	T	T	NT
pMON142862	EXP-ERIra.Ubq1:1:8	27	Event 1	T	T	T
			Event 2	T	T	NT
			Event 3	T	T	T
			Event 4	T	T	T
			Event 5	T	T	NT
			Event 6	T	T	T
			Event 7	T	T	NT
			Event 8	T	T	T
			Event 9	T	T	T

TABLE 49-continued

Leaf damage ratings of individual transformed corn events at V4 and V8 stage.

Plasmid Construct	EXP sequence	SEQ ID NO:	Event	Veg Tol V4	Veg Tol V8	Repro Tol
pMON129221	EXP-Cl.Ubq1:1:10	98	Event 1	T	T	NT
			Event 2	T	T	NT
			Event 3	NT	NT	T
			Event 4	NT	NT	T
			Event 5	T	T	NT
			Event 6	NT	NT	T
			Event 7	T	T	T
pMON129205	EXP-Sv.Ubq1:1:9	133	Event 1	NT	NT	
			Event 2	NT	NT	NT
			Event 3	T	T	NT
			Event 4	NT	NT	
			Event 5	NT	NT	NT
			Event 6	NT	NT	NT
			Event 7	NT	NT	NT
pMON129212	EXP-Zm.UbqM1:1:7	141	Event 1	T	T	
			Event 2	T	T	
			Event 3	T	T	
			Event 4	T	T	
			Event 5	T	T	
			Event 6	T	T	
			Event 7	T	T	
			Event 8	T	T	
			Event 9	T	T	
			Event 10	T	T	

[0187] From Table 49 above, all transformed events assayed comprising CP4 transgene cassettes comprising the EXP sequences EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8), EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27) and EXP-Zm.UbqM1:1:7 (SEQ ID NO: 141) demonstrated full vegetative tolerance based upon damage ratings that did not exceed a score of ten. Four events of nine comprising EXP-ANDge.Ubq1:1:8 (SEQ ID NO: 8) and six events of nine comprising EXP-ERIra.Ubq1:1:8 (SEQ ID NO: 27) were both vegetatively and reproductively tolerant to glyphosate application. In contrast, events comprising EXP-Cl.Ubq1:1:10 (SEQ ID NO: 98) were either vegetatively tolerant or reproductively tolerant but not both. Only one event comprising EXP-Sv.Ubq1:1:9 (SEQ ID NO: 133) demonstrated vegetative tolerance and none of the events tested were reproductive tolerant. All events comprising EXP-Zm.UbqM1:1:7 (SEQ ID NO: 141) demonstrated vegetative tolerance but and assessment of reproductive tolerance is still in progress.

Example 15

Analysis of Expression Using Different 3' End Intron/Exon Splice Junction Sequences

[0188] Corn and Wheat leaf protoplast cells were transformed with plant expression constructs comprising EXP sequences driving GUS expression that comprise the same promoter and leader but have different 3' end nucleotides following the intron/exon splice junction sequence, 5'-AG-3' to see if expression is affected by the slight change in sequence. Expression was also compared to that of two constitutive control plasmids.

[0189] Plant expression constructs are built comprising a GUS expression cassette. The resulting vectors are comprised of the *Coix lacryma-jobi* ubiquitin promoter, P-Cl.Ubq1-1:1:1 (SEQ ID NO: 80) operably linked 5' to the leader sequence, L-Cl.Ubq1-1:1:1 (SEQ ID NO: 81), operably linked 5' to an intron element shown in Table 50 below which each comprise different nucleotides at the very 3' end just after the intron/exon splice junction 5'-AG-3' sequence, operably linked 5' to a GUS coding sequence which is operably linked 5' to T-AGRtu.nos-1:1:13 (SEQ ID NO: 127) 3' UTR. Table 50 below shows the plant expression constructs and the corresponding 3' end sequence.

TABLE 50

Plant expression constructs, introns and 3' end sequence following the intron/exon splice junction sequence 5'-AG-3'.

Plasmid construct	EXP sequence	SEQ ID NO:	Intron Variant	Intron 3' end nucleotides immediately following 3' splice site AG
pMON140889	EXP-Cl.Ubq1:1:10	98	I-Cl.Ubq1-1:1:6 (SEQ ID NO: 94)	GTC

TABLE 50 -continued

Plant expression constructs, introns and 3' end sequence following the intron/exon splice junction sequence 5'-AG-3'.

Plasmid construct	EXP sequence	SEQ ID NO:	Intron Variant	Intron 3' end nucleotides immediately following 3' splice site AG
pMON146795	EXP-Cl.Ubq1:1:18	99	I-Cl.Ubq1-1:1:7 (SEQ ID NO: 92)	GTG
pMON146796	EXP-Cl.Ubq1:1:19	100	I-Cl.Ubq1-1:1:8 (SEQ ID NO: 101)	GCG
pMON146797	EXP-Cl.Ubq1:1:20	102	I-Cl.Ubq1-1:1:9 (SEQ ID NO: 103)	GAC
pMON146798	EXP-Cl.Ubq1:1:21	104	I-Cl.Ubq1-1:1:10 (SEQ ID NO: 105)	ACC
pMON146799	EXP-Cl.Ubq1:1:22	106	I-Cl.Ubq1-1:1:11 (SEQ ID NO: 107)	GGG
pMON146800	EXP-Cl.Ubq1:1:23	108	I-Cl.Ubq1-1:1:12 (SEQ ID NO: 109)	GGT
pMON146801	EXP-Cl.Ubq1:1:24	110	I-Cl.Ubq1-1:1:13 (SEQ ID NO: 111)	CGT
pMON146802	EXP-Cl.Ubq1:1:25	112	I-Cl.Ubq1-1:1:14 (SEQ ID NO: 113)	TGT
pMON25455	EXP-Os.Act1:1:9	179		Constitutive Control
pMON65328	EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1	163		Constitutive Control

[0190] Corn and Wheat protoplasts were transformed as previously described and assayed for GUS and luciferase expression. Table 51 below shows the average GUS and RLuc values for both corn and wheat protoplast expression.

TABLE 51

Average GUS and RLuc values for corn and wheat protoplast cells.

EXP sequence	Intron 3' end nucleotides immed. following 3' splice site AG	Corn Average GUS	Corn Average RLuc	Corn GUS/RLuc	Wheat Ave. GUS	Wheat Ave. RLuc	Wheat GUS/RLuc
EXP-Cl.Ubq1:1:10	GTC	140343.0	93870.75	1.50	40906.25	17381.75	2.35
EXP-Cl.Ubq1:1:18	GTG	143106.25	60565.25	2.36	56709.00	17898.75	3.17
EXP-Cl.Ubq1:1:19	GCG	136326.83	88589.75	1.54	43211.00	17352.50	2.49
EXP-Cl.Ubq1:1:20	GAC	138110.83	104751.42	1.32	31711.50	17953.57	1.77
EXP-Cl.Ubq1:1:21	ACC	137906.75	72519.50	1.90	54164.17	17772.83	3.05

TABLE 51 -continued

Average GUS and RLuc values for corn and wheat protoplast cells.

EXP sequence	Intron 3' end nucleotides immed. following 3' splice site AG	Corn Average GUS	Corn Average RLuc	Corn GUS/ RLuc	Wheat Ave. GUS	Wheat Ave. RLuc	Wheat GUS/ RLuc
EXP-Cl.Ubq1:1:22	GGG	137306.83	92643.42	1.48	55198.25	14476.75	3.81
EXP-Cl.Ubq1:1:23	GGT	144085.50	64351.25	2.24	43008.83	13911.50	3.09
EXP-Cl.Ubq1:1:24	CGT	142061.50	65884.00	2.16	51210.50	15041.00	3.40
EXP-Cl.Ubq1:1:25	TGT	140353.00	61249.50	2.29	49577.75	15348.25	3.23
EXP-Os.Act1:1:9	Constitutive Control	37665.25	65835.50	0.57	10830.25	17716.50	0.61
EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1	Constitutive Control	49833.75	41268.75	1.21	15598.83	14877.50	1.05

[0191] The GUS/RLuc values for each *Coix lacryma-jobi* ubiquitin EXP sequence from Table 46 above were used to normalize the expression relative to the two constitutive controls EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1 (SEQ ID NO: 163) and are presented in Table 52 below.

TABLE 52

Normalized expression values of the *Coix lacryma-jobi* ubiquitin EXP sequences relative to EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1 (SEQ ID NO: 163).

EXP sequence	Intron 3' end nucleotides immediately following 3' splice site AG	Corn GUS/RLuc Normalized with respect to EXP-Os.Act1:1:9	Corn GUS/RLuc Normalized with respect to EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1	Wheat GUS/Rluc Normalized with respect to EXP-Os.Act1:1:9	Wheat GUS/Rluc Normalized with respect to EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1
EXP-Cl.Ubq1:1:10	GTC	2.61	1.24	3.85	2.24
EXP-Cl.Ubq1:1:18	GTG	4.13	1.96	5.18	3.02
EXP-Cl.Ubq1:1:19	GCG	2.69	1.27	4.07	2.38
EXP-Cl.Ubq1:1:20	GAC	2.30	1.09	2.89	1.68
EXP-Cl.Ubq1:1:21	ACC	3.32	1.57	4.99	2.91
EXP-Cl.Ubq1:1:22	GGG	2.59	1.23	6.24	3.64
EXP-Cl.Ubq1:1:23	GGT	3.91	1.85	5.06	2.95
EXP-Cl.Ubq1:1:24	CGT	3.77	1.79	5.57	3.25
EXP-Cl.Ubq1:1:25	TGT	4.01	1.90	5.28	3.08
EXP-Os.Act1:1:9	Constitutive Control	1.00	0.47	1.00	0.58

TABLE 52 -continued

Normalized expression values of the *Coix lacryma-jobi* ubiquitin EXP sequences relative to EXP-Os.Act1:1:9 (SEQ ID NO: 179) and EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1 (SEQ ID NO: 163).

		Corn		Wheat	
EXP sequence	Intron 3' end nucleotides immediately following 3' splice site AG	GUS/RLuc Normalized with respect to EXP-Os.Act1:1:9	GUS/RLuc Normalized with respect to EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1	GUS/Rluc Normalized with respect to EXP-Os.Act1:1:9	GUS/Rluc Normalized with respect to EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1
EXP-CaMV.35S-enh+Ta.Lhcb1+Os.Act1:1:1	Constitutive Control	2.11	1.00	1.72	1.00

[0192] As is shown in Table 52 above, each of the *Coix lacryma-jobi* ubiquitin EXP sequences provided expression that was greater than either constitutive control in both corn and wheat. Expression in corn protoplasts was relatively similar for all of the *Coix* ubiquitin EXP sequences. Expression in wheat was a little more variable. The use of different 3' end nucleotides following the intron/exon splice junction sequence, 5'-AG-3' did not appear to dramatically affect expression of GUS with the exception of GUS driven by EXP-Cl.Ubq1:1:20 (SEQ ID NO: 102). EXP-Cl.Ubq1:1:20 comprises the 3' end nucleotide sequences, 5'-GAC-3' following the intron/exon splice junction 5'-AG-3' sequence and caused expression to drop slightly relative to the other *Coix* ubiquitin EXP sequences. Assessment of the resulting spliced messenger RNA showed that approximately 10% of the mRNA expressed using EXP-Cl.Ubq1:1:20 (SEQ ID NO: 102) to drive GUS expression was improperly spliced. The mRNA resulting from GUS expression using the other *Coix* ubiquitin EXP sequences appeared to process properly. This experiment provides evidence that any of the 3' end nucleotides for any of the intron variants presented in Table 2 of Example 1 with the exception of the 3' end sequence 5'-GAC-3' which is found associated only with the intron element, I-Cl.Ubq1-1:1:9 (SEQ ID NO: 103) should be suitable for use in transgene expression cassettes without significant loss of activity and processing.

Example 16

Enhancers Derived from the Regulatory Elements

[0193] Enhancers are derived from the promoter elements provided herein, such as those presented as SEQ ID NOS: 2, 6, 9, 11, 13, 15, 17, 19, 23, 26, 28, 30, 32, 34, 38, 40, 42, 46, 50, 56, 60, 64, 66, 70, 74, 76, 78, 80, 84, 86, 88, 91, 96 and 135. The enhancer element may be comprised of one or more cis regulatory elements that, when operably linked 5' or 3' to a promoter element, or operably linked 5' or 3' to additional enhancer elements that are operably linked to a promoter, can enhance or modulate expression of a transgene, or provide expression of a transgene in a specific cell type or plant organ or at a particular time point in development or circadian rhythm. Enhancers are made by removing the TATA box or functionally similar elements and any downstream sequence from the promoters that allow transcription to be initiated from the promoters provided herein as described above, including fragments thereof, in which the TATA box or functionally similar elements and sequence downstream of the TATA box are removed. The enhancer element, E-Cl.Ubq1-1:1:1 (SEQ ID NO: 89) which is derived from the promoter element, P-Cl.Ubq1-1:1:1 is provided herein to demonstrate enhancers derived from a promoter element.

[0194] Enhancer elements may be derived from the promoter elements provided herein and cloned using methods known in the art to be operably linked 5' or 3' to a promoter element, or operably linked 5' or 3' to additional enhancer elements that are operably linked to a promoter. Alternatively, enhancer elements are cloned, using methods known in the art, to be operably linked to one or more copies of the enhancer element which are operably linked 5' or 3' to a promoter element, or operably linked 5' or 3' to additional enhancer elements that are operably linked to a promoter. Enhancer elements can also be cloned to be operably linked 5' or 3' to a promoter element derived from a different genus organism, or operably linked 5' or 3' to additional enhancer elements derived from other genus organisms or the same genus organism that are operably linked to a promoter derived from either the same or different genus organism, resulting in a chimeric regulatory element. A GUS expression plant transformation vector is constructed using methods known in the art similar to the constructs described in the previous examples in which the resulting plant expression vectors contain a right border region from *A. tumefaciens*, a first transgene cassette to test the regulatory or a chimeric regulatory element comprised of, a regulatory or chimeric regulatory element, operably linked to an intron derived from the HSP70 heat shock protein of *Z. mays* (1-Zm.DnaK-1:1:1 SEQ ID NO: 144) or any of the introns presented herein or any other intron, operably linked to a coding sequence for β-glucuronidase (GUS) that either possesses a processable intron (GUS-2, SEQ ID NO: 160) or no intron (GUS-1, SEQ ID NO: 159), operably linked to the Nopaline synthase 3' UTR from *A. tumefaciens* (T-AGRtu.nos-1:1:13, SEQ ID NO: 161) or the 3' UTR from the rice lipid transfer protein gene (T-Os.LTP-1:1:1, SEQ ID NO: 175); a second transgene selection cassette used for selection of transformed plant cells that confers resistance to the herbicide glyphosate (driven by the rice Actin 1 promoter), or alternatively, the antibiotic kanamycin (driven by the rice Actin 1 promoter) and a left border region from *A. tumefaciens*. The resulting plasmids are used to transform corn plants or other genus plants by the methods described above or by other *Agrobacterium*-mediated or par-

ticle bombardment methods known in the art. Alternatively, protoplast cells derived from corn or other genus plants are transformed using methods known in the art to perform transient assays

[0195] GUS expression driven by the regulatory element comprising one or more enhancers is evaluated in stable or transient plant assays to determine the effects of the enhancer element on expression of a transgene. Modifications to one or more enhancer elements or duplication of one or more enhancer elements is performed based upon empirical experimentation and the resulting gene expression regulation that is observed using each regulatory element composition. Altering the relative positions of one or more enhancers in the resulting regulatory or chimeric regulatory element may affect the transcriptional activity or specificity of the regulatory or chimeric regulatory element and is determined empirically to identify the best enhancers for the desired transgene expression profile within the corn plant or other genus plant.

Example 17

Analysis of Intron Enhancement of GUS Activity Using Plant Derived Protoplasts

[0196] An intron is selected based upon experimentation and comparison with an intronless expression vector control to empirically select an intron and configuration within the vector T-DNA element arrangement for optimal expression of a transgene. For example, in the expression of an herbicide resistance gene, such as CP4 which confers tolerance to glyphosate, it is desirable to have transgene expression within the reproductive tissues as well as the vegetative tissues, to prevent the loss of yield when applying the herbicide. An intron in this instance would be selected upon its ability when operably linked to a constitutive promoter, to enhance expression of the herbicide resistance conferring transgene, particularly within the reproductive cells and tissues of the transgenic plant and thus providing both vegetative and reproductive tolerance to the transgenic plant, when sprayed with the herbicide. In most ubiquitin genes, the 5' UTR is comprised of a leader, which has an intron sequence embedded within it. The expression elements derived from such genes are therefore assayed using the entire 5' UTR comprising the promoter, leader, and intron. To achieve different expression profiles or to modulate the level of transgene expression, the intron from such an expression element may be removed or substituted with a heterologous intron.

[0197] Introns presented herein as SEQ ID NOS: 4, 7, 21, 24, 36, 44, 48, 52, 54, 58, 62, 68, 72, 82, 92, 94, 101, 103, 105, 107, 109, 111, 113, 118, 120, 122, 127, 129, 131, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158 and 182 are identified using genomic DNA contigs in comparison to expressed sequence tag clusters or cDNA contigs to identify exon and intron sequences within the genomic DNA. In addition, 5' UTR or leader sequences are also used to define the intron/exon splice junction of one or more introns under conditions when the gene sequence encodes a leader sequence that is interrupted by one or more introns. Introns are cloned using methods known in the art into a plant transformation vector to be operably linked 3' to a transcriptional regulatory element and leader fragment and operably linked 5' to either a second leader fragment or to coding sequences, for instance as depicted in the two transgene cassettes presented in FIG. **1**.

[0198] Thus, for instance, a first possible transgene cassette (Transgene Cassette Configuration 1 in FIG. **8**) is comprised of a promoter or chimeric promoter element [A], operably linked 5' to a leader element [B], operably linked 5' to a test intron element [C], operably linked to a coding region [D], which is operably linked to a 3' UTR element [E]. Alternatively, a second possible transgene cassette (Transgene Cassette Configuration 2 in FIG. **8**) is comprised of a promoter or chimeric promoter element [F], operably linked 5' to a first leader element or first leader element fragment [G], operably linked 5' to a test intron element [H], operably linked 5' to a second leader element or first leader element second fragment [I], operably linked to a coding region [J], which is operably linked to a 3' UTR element [K]. Further, a third possible transgene cassette (Transgene Cassette Configuration 3 in FIG. **8**) is comprised of a promoter or chimeric promoter element [L], operably linked 5' to a leader element [M], operably linked 5' to a first fragment of the coding sequence element [N], operably linked 5' to an intron element [O] element, operably linked 5' to a second fragment of the coding sequence element [P], which is operably linked to a 3' UTR element [Q]. Transgene Cassette Configuration 3 is designed to allow splicing of the intron in such a manner as to produce a complete open reading frame without a frame shift between the first and second fragment of the coding sequence.

[0199] The first 6 nucleotides on the 5' end and the last 6 nucleotides on the 3' end of the introns presented as SEQ ID NOS: 4, 7, 21, 24, 36, 44, 48, 52, 54, 58, 62, 68, 72, 82, 92, 94, 101, 103, 105, 107, 109, 111, 113, 118, 120, 122, 127, 129, 131, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158 and 182 represent nucleotides before and after the intron/exon splice junction, respectively. These short 6 nucleotide sequences, for example, can be modified by having additional sequence appended (i.e. native or artificial) to facilitate cloning of the intron into a plant transformation vector, so long as the first and second nucleotides from the 5' end (GT) and the fourth and fifth nucleotide from the 3' end (AG) of SEQ ID NOS: 4, 7, 21, 24, 36, 44, 48, 52, 54, 58, 62, 68, 72, 82, 92, 94, 101, 103, 105, 107, 109, 111, 113, 118, 120, 122, 127, 129, 131, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158 and 182 are preserved, thus preserving the intron/exon splice junction of the intron. As discussed above, it may be preferable to avoid using the nucleotide sequence AT or the nucleotide A just prior to the 5' end of the splice site (GT) and the nucleotide G or the nucleotide sequence TG, respectively just after 3' end of the splice site (AG) to eliminate the potential of unwanted start codons from being formed during processing of the messenger RNA into the final transcript. The sequence around the 5' or 3' end splice junction sites of the intron can thus be modified.

[0200] The introns are assayed for an enhancement effect through the ability to enhance expression in transient assay or stable plant assay. For transient assay of intron enhancement, a base plant vector is constructed using methods known in the art. The intron is cloned into a base plant vector which comprises an expression cassette comprised of a constitutive promoter such as the Cauliflower mosaic virus promoter, P-CaMV.35S-enh-1:1:9 (SEQ ID NO: 176), operably linked 5' to a leader element, L-CaMV.35S-1:1:15 (SEQ ID NO: 177), operably linked 5' to a test intron element (e.g. one of SEQ ID NOS: 4, 7, 21, 24, 36, 44, 48, 52, 54, 58, 62, 68, 72, 82, 92, 94, 101, 103, 105, 107, 109, 111, 113, 118, 120, 122, 127, 129, 131, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158 and 182), operably linked to a coding sequence for

β-glucuronidase (GUS) that either possesses a processable intron (GUS-2, SEQ ID NO: 160) or no intron (GUS-1, SEQ ID NO: 159), operably linked to the Nopaline synthase 3' UTR from *A. tumefaciens* (T-AGRtu.nos-1:1:13, SEQ ID NO: 161). Protoplast cells derived from corn or other genus plant tissue are transformed with the base plant vector and luciferase control vectors as described previously in Example 2 above and assayed for activity. To compare the relative ability of the intron to enhance expression, GUS values are expressed as a ratio of GUS to luciferase activity and compared with those levels imparted by a construct comprising the constitutive promoter operably linked to a known intron standard such as that as the intron derived from the HSP70 heat shock protein of *Zea mays*, I-Zm.DnaK-1:1:1 (SEQ ID NO: 178) as well as a construct comprising the constitutive promoter but without an intron operably linked to the promoter.

[0201] For stable plant assay of the introns presented as SEQ ID NOS: 4, 7, 21, 24, 36, 44, 48, 52, 54, 58, 62, 68, 72, 82, 92, 94, 101, 103, 105, 107, 109, 111, 113, 118, 120, 122, 127, 129, 131, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158 and 182, a GUS expression plant transformation vector is constructed similar to the constructs described in the previous examples in which the resulting plant expression vectors contains a right border region from *A. tumefaciens*, a first transgene cassette to test the intron comprised of a constitutive promoter such as the Cauliflower mosaic virus promoter, P-CaMV.35S-enh-1:1:9 (SEQ ID NO: 176), operably linked 5' to a leader element, L-CaMV.35S-1:1:15 (SEQ ID NO: 177), operably linked 5' to a test intron element provided herein, operably linked to a coding sequence for β-glucuronidase (GUS) that either possesses a processable intron (GUS-2, SEQ ID NO: 160) or no intron (GUS-1, SEQ ID NO: 158), operably linked to the Nopaline synthase 3' UTR from *A. tumefaciens* (T-AGRtu.nos-1:1:13, SEQ ID NO: 161); a second transgene selection cassette used for selection of transformed plant cells that confers resistance to glyphosate (driven by the rice Actin 1 promoter), or alternatively, the antibiotic kanamycin (driven by the rice Actin 1 promoter) and a left border region from *A. tumefaciens*. The resulting plasmids are used to transform corn plants or other genus plants by the methods described above or by *Agrobacterium*-mediated methods known in the art. Single-copy or low copy number transformants are selected for comparison to single-copy or low copy number transformed plants, transformed with a plant transformation vector identical to the test vector but without the test intron to determine if the test intron provides an intron mediated enhancement effect.

[0202] Any of the introns presented as SEQ ID NOS: 4, 7, 21, 24, 36, 44, 48, 52, 54, 58, 62, 68, 72, 82, 92, 94, 101, 103, 105, 107, 109, 111, 113, 118, 120, 122, 127, 129, 131, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158 and 182 can be modified in a number of ways, such as deleting fragments within the intron sequence, which may reduce expression or duplication of fragments with the intron that may enhance expression. In addition, sequences within the intron that may affect the specificity of expression to either particular cells types or tissues and organs can be duplicated or altered or deleted to affect expression and patterns of expression of the transgene. In addition, the introns provided herein can be modified to remove any potential start codons (ATG) that may cause unintentional transcripts from being expressed from improperly spliced introns as different, longer or truncated proteins. Once the intron has been empirically tested, or it has been altered based upon experimentation, the intron is used to enhance expression of a transgene in stably transformed plants that can be of any genus monocot or dicot plant, so long as the intron provides enhancement of the transgene. The intron can also be used to enhance expression in other organisms, such as algae, fungi or animal cells, so long as the intron provides enhancement or attenuation or specificity of expression of the transgene to which it is operably linked.

[0203] Having illustrated and described the principles of the present invention, it should be apparent to persons skilled in the art that the invention can be modified in arrangement and detail without departing from such principles. We claim all modifications that are within the spirit and scope of the claims. All publications and published patent documents cited herein are hereby incorporated by reference to the same extent as if each individual publication or patent application is specifically and individually indicated to be incorporated by reference.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 183

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<213> ORGANISM: Andropogon gerardii

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<212> TYPE: DNA
<213> ORGANISM: Andropogon gerardii

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<211> LENGTH: 99
<212> TYPE: DNA
<213> ORGANISM: Andropogon gerardii

<400> SEQUENCE: 3

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<212> TYPE: DNA
<213> ORGANISM: Andropogon gerardii

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<212> TYPE: DNA
<213> ORGANISM: Andropogon gerardii

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<212> TYPE: DNA
<213> ORGANISM: Andropogon gerardii

<400> SEQUENCE: 6

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<210> SEQ ID NO 7
<211> LENGTH: 1042
<212> TYPE: DNA
<213> ORGANISM: Andropogon gerardii

<400> SEQUENCE: 7

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ccgtgctgtt atggttcgta gatggattct gattgctcag taactgggaa tcctgggatg 360

gttctagctg gttcgcagat aagatcgatt tcatgatatg ctatatcttg tttggttgcc 420

gtggttccgt taaatctgtc tgttatgatc ttagtctttg ataaggttcg gtcgtgctag 480

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taattatttc gatatacttg aatgatgtca tatgcagcat ctgtgtgaat ttttggccct 960

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<210> SEQ ID NO 8
<211> LENGTH: 2785
<212> TYPE: DNA
<213> ORGANISM: Andropogon gerardii

<400> SEQUENCE: 8

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atcgtgcaaa tttctctcta ggtgtgtgtg tgactgtgtg agtaacaatt tctctagttg 180

tgcgcgactg ctgcttactt tggagattac aatatctttc taaaatgctt cgattactta 240

tttataaacc gtctctaagg ccaattgctc aagattcatt caacaattga aacgtctcac 300

atgattaaat catataaagt ttctaagtct tgtttgacaa gatttttta gattttcatc 360

taaattggat gaaactatca aacactaatt ttaaaaaata taagagaagc tccggagata 420

aaaggtcgtc tatgttatta taagagtaaa gtcgtctatt ctcttcgtcc caacatatat 480

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aattctaagc atgaattgct ttctttttgg acaaaaggag catgccacaa cacaagaatg 540

atgtcaccgt catgcttgga tcctttttatg gtaaagcttc accttctata atctaacaat 600

agagaaatca gggaaaaatc atgttttggt tgtttttatt tctaacctcc acaataactt 660

tggtttacca ttttttgttt gattttagtt ttagagaagc gtttataaca ggacctaaaa 720

tctttttttca gtacacagta caacgcagac gctcatacac gcacgcacac tcacctctat 780

gaacacacgt aagaaaaccc tacaccttga gcaccttcga aggactgagc cggtaaatat 840

agagattctc gaagtcacta ttagcgcctc gttgtcaacg ggaatgtcgc ttaccactta 900

aagcataacg ccgagaaatc ccgtaataaa tccagtaaaa tacgagcacc cgtgccaagt 960

tgaatatttg aacccgagtg ggtagattcc accgcaaagg acctaaccag atcatttcgc 1020

aaacaggaac taaaatcggt agagagccca gacaaaagcc tttcctaaga gccactccag 1080

tggaagcccc tactttaggt ataaaatgca atactagtgg ggctcctaaa taaacttcta 1140

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tcaaatttta taagttgagg gtagaggatg actggagttg ctctaaacgg acctatcttc 1320

aagtgacctc agtgagcccg tttaacggcg tcgacaagtt taatctaacg gacaccaacc 1380

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<210> SEQ ID NO 9
<211> LENGTH: 1644
<212> TYPE: DNA
<213> ORGANISM: Andropogon gerardii

<400> SEQUENCE: 9

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atcgtgcaaa tttctctcta ggtgtgtgtg tgactgtgtg agtaacaatt tctctagttg 180

tgcgcgactg ctgcttactt tggagattac aatatctttc taaaatgctt cgattactta 240

tttataaacc gtctctaagg ccaattgctc aagattcatt caacaattga aacgtctcac 300

atgattaaat catataaagt ttctaagtct tgtttgacaa gatttttta gattttcatc 360

taaattggat gaaactatca aacactaatt ttaaaaaata taagagaagc tccggagata 420

aaaggtcgtc tatgttatta taagagtaaa gtcgtctatt ctcttcgtcc caacatatat 480

aattctaagc atgaattgct ttctttttgg acaaaaggag catgccacaa cacaagaatg 540

atgtcaccgt catgcttgga tccttttatg gtaaagcttc accttctata atctaacaat 600

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tggtttacca ttttttgttt gattttagtt ttagagaagc gtttataaca ggacctaaaa 720

tctttttca gtacacagta caacgcagac gctcatacac gcacgcacac tcacctctat 780

gaacacacgt aagaaaaccc tacaccttga gcaccttcga aggactgagc cggtaaatat 840

agagattctc gaagtcacta ttagcgcctc gttgtcaacg ggaatgtcgc ttaccactta 900

aagcataacg ccgagaaatc ccgtaataaa tccagtaaaa tacgagcacc cgtgccaagt 960

tgaatatttg aacccgagtg ggtagattcc accgcaaagg acctaaccag atcatttcgc 1020

aaacaggaac taaaatcggt agagagccca gacaaaagcc tttcctaaga gccactccag 1080

tggaagcccc tactttaggt ataaaatgca atactagtgg ggctcctaaa taaacttcta 1140

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tcaaatttta taagttgagg gtagaggatg actggagttg ctctaaacgg acctatcttc 1320

aagtgacctc agtgagcccg tttaacggcg tcgacaagtt taatctaacg gacaccaacc 1380

agagaagaga accaccgcca gcgccgagcc aagcgacgtt gacatcttgg cgcggcacgg 1440

catctccctg gcgtctggcc ccctctcgag acttccgctc cacctcccac cggtggcggt 1500

ttccaagtcc gttccgcctc ctctcacacg gcacgaaacc gtgacgggca ccggcagcac 1560

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ccagccccat ccccagcttc tttc 1644

<210> SEQ ID NO 10
<211> LENGTH: 2613
<212> TYPE: DNA
<213> ORGANISM: Andropogon gerardii

<400> SEQUENCE: 10

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cgtctcacat gattaaatca tataaagttt ctaagtcttg tttgacaaga ttttttttaga 180

ttttcatcta aattggatga aactatcaaa cactaatttt aaaaaatata agagaagctc 240

cggagataaa aggtcgtcta tgttattata agagtaaagt cgtctattct cttcgtccca 300

acatatataa ttctaagcat gaattgcttt ctttttggac aaaaggagca tgccacaaca 360

caagaatgat gtcaccgtca tgcttggatc cttttatggt aaagcttcac cttctataat 420

ctaacaatag agaaatcagg gaaaaatcat gttttggttg tttttatttc taacctccac 480

aataactttg gtttaccatt ttttgtttga ttttagtttt agagaagcgt ttataacagg 540

acctaaaatc ttttttcagt acacagtaca acgcagacgc tcatacacgc acgcacactc 600

acctctatga acacacgtaa gaaaacccta caccttgagc accttcgaag gactgagccg 660

gtaaatatag agattctcga agtcactatt agcgcctcgt tgtcaacggg aatgtcgctt 720

accacttaaa gcataacgcc gagaaatccc gtaataaatc cagtaaaata cgagcacccg 780

tgccaagttg aatatttgaa cccgagtggg tagattccac cgcaaaggac ctaaccagat 840

catttcgcaa acaggaacta aaatcggtag agagcccaga caaaagcctt tcctaagagc 900

cactccagtg gaagccccta ctttaggtat aaaatgcaat actagtgggg ctcctaaata 960

aacttctatt tttcatggcc ttctaaaatt cactcccaaa cccctagcta tagaagtctc 1020

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ctatcttcaa gtgacctcag tgagcccgtt taacggcgtc gacaagttta atctaacgga 1200

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ttactggtac ttttttttgac atgaacctac ggcttaataa ttagtcttca tcaaataaaa 2460

agcatatttt ttaattattt cgatatactt gaatgatgtc atatgcagca tctgtgtgaa 2520

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tcatcctgtt gtttggtgat ccttttgcag gtg 2613

<210> SEQ ID NO 11
<211> LENGTH: 1472
<212> TYPE: DNA
<213> ORGANISM: Andropogon gerardii

<400> SEQUENCE: 11

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cgtctcacat gattaaatca tataaagttt ctaagtcttg tttgacaaga tttttttaga 180

ttttcatcta aattggatga aactatcaaa cactaatttt aaaaaatata agagaagctc 240

cggagataaa aggtcgtcta tgttattata agagtaaagt cgtctattct cttcgtccca 300

acatatataa ttctaagcat gaattgcttt ctttttggac aaaaggagca tgccacaaca 360

caagaatgat gtcaccgtca tgcttggatc cttttatggt aaagcttcac cttctataat 420

ctaacaatag agaaatcagg gaaaaatcat gttttggttg tttttatttc taacctccac 480

aataactttg gtttaccatt ttttgtttga ttttagtttt agagaagcgt ttataacagg 540

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acctctatga acacacgtaa gaaaacccta caccttgagc accttcgaag gactgagccg 660

gtaaatatag agattctcga agtcactatt agcgcctcgt tgtcaacggg aatgtcgctt 720

accacttaaa gcataacgcc gagaaatccc gtaataaatc cagtaaaata cgagcacccg 780

tgccaagttg aatatttgaa cccgagtggg tagattccac cgcaaaggac ctaaccagat 840

catttcgcaa acaggaacta aaatcggtag agagcccaga caaaagcctt tcctaagagc 900

cactccagtg gaagccccta ctttaggtat aaaatgcaat actagtgggg ctcctaaata 960

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ataaatagcc agccccatcc ccagcttctt tc 1472

<210> SEQ ID NO 12
<211> LENGTH: 2255
<212> TYPE: DNA
<213> ORGANISM: Andropogon gerardii

<400> SEQUENCE: 12

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ggacctaaaa tctttttttca gtacacagta caacgcagac gctcatacac gcacgcacac 240

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cggtaaatat agagattctc gaagtcacta ttagcgcctc gttgtcaacg ggaatgtcgc 360

ttaccactta aagcataacg ccgagaaatc ccgtaataaa tccagtaaaa tacgagcacc 420

cgtgccaagt tgaatatttg aacccgagtg ggtagattcc accgcaaagg acctaaccag 480

atcatttcgc aaacaggaac taaaatcggt agagagccca gacaaaagcc tttcctaaga 540

gccactccag tggaagcccc tactttaggt ataaaatgca atactagtgg ggctcctaaa 600

taaacttcta tttttcatgg ccttctaaaa ttcactccca aacccctagc tatagaagtc 660

tcttatccat cctctaaata aaaatgggag tctattttat ttcaccagag ttgatcgtaa 720

atttagtctc tcaaatttta taagttgagg gtagaggatg actggagttg ctctaaacgg 780

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gacaccaacc agagaagaga accaccgcca gcgccgagcc aagcgacgtt gacatcttgg 900

cgcggcacgg catctccctg gcgtctggcc ccctctcgag acttccgctc cacctcccac 960

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<210> SEQ ID NO 13
<211> LENGTH: 1114
<212> TYPE: DNA
<213> ORGANISM: Andropogon gerardii

<400> SEQUENCE: 13

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tcacctctat gaacacacgt aagaaaaccc tacaccttga gcaccttcga aggactgagc 300

cggtaaatat agagattctc gaagtcacta ttagcgcctc gttgtcaacg ggaatgtcgc 360

ttaccactta aagcataacg ccgagaaatc ccgtaataaa tccagtaaaa tacgagcacc 420

cgtgccaagt tgaatatttg aacccgagtg ggtagattcc accgcaaagg acctaaccag 480

atcatttcgc aaacaggaac taaaatcggt agagagccca gacaaaagcc tttcctaaga 540

gccactccag tggaagcccc tactttaggt ataaaatgca atactagtgg ggctcctaaa 600

taaacttcta tttttcatgg ccttctaaaa ttcactccca aacccctagc tatagaagtc 660

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atttagtctc tcaaatttta taagttgagg gtagaggatg actggagttg ctctaaacgg 780

acctatcttc aagtgacctc agtgagcccg tttaacggcg tcgacaagtt taatctaacg 840

gacaccaacc agagaagaga accaccgcca gcgccgagcc aagcgacgtt gacatcttgg 900

cgcggcacgg catctccctg gcgtctggcc ccctctcgag acttccgctc cacctcccac 960

cggtggcggt ttccaagtcc gttccgcctc ctctcacacg gcacgaaacc gtgacgggca 1020

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ctataaatag ccagccccat ccccagcttc tttc 1114

<210> SEQ ID NO 14
<211> LENGTH: 1912
<212> TYPE: DNA
<213> ORGANISM: Andropogon gerardii

<400> SEQUENCE: 14

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gcaaaggacc taaccagatc atttcgcaaa caggaactaa aatcggtaga gagcccagac 180

aaaagccttt cctaagagcc actccagtgg aagcccctac tttaggtata aaatgcaata 240

ctagtggggc tcctaaataa acttctattt ttcatggcct tctaaaattc actcccaaac 300

ccctagctat agaagtctct tatccatcct ctaaataaaa atgggagtct attttatttc 360

accagagttg atcgtaaatt tagtctctca aattttataa gttgagggta gaggatgact 420

ggagttgctc taaacggacc tatcttcaag tgacctcagt gagcccgttt aacggcgtcg 480

acaagtttaa tctaacggac accaaccaga gaagagaacc accgccagcg ccgagccaag 540

cgacgttgac atcttggcgc ggcacggcat ctccctggcg tctggccccc tctcgagact 600

tccgctccac ctcccaccgg tggcggtttc caagtccgtt ccgcctcctc tcacacggca 660

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cccttcctct cccgccgcta taaatagcca gccccatccc cagcttcttt ccccaacctc 780

atcttctctc gtgttgttcg gcacaacccg atcgatcccc aactccctcg tcgtctctcc 840

tcgcgagcct cgtcgatccc ccgcttcaag gtacggcgat cgattatctt ccctctctct 900

accttctctc tcttataggg cctgctagct ctgttcctgt ttttccatgg ctgcgaggta 960

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gtatatgctg cagttagttt tactggtact ttttttgaca tgaacctacg gcttaataat 1740

tagtcttcat caaataaaaa gcatattttt taattatttc gatatacttg aatgatgtca 1800

tatgcagcat ctgtgtgaat ttttggccct gtcttcatat gctgtttatt tgtttgggac 1860

tgtttctttg gttgataact catcctgttg tttggtgatc cttttgcagg tg 1912

<210> SEQ ID NO 15
<211> LENGTH: 771
<212> TYPE: DNA
<213> ORGANISM: Andropogon gerardii

<400> SEQUENCE: 15

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gcaaaggacc taaccagatc atttcgcaaa caggaactaa aatcggtaga gagcccagac 180

aaaagccttt cctaagagcc actccagtgg aagcccctac tttaggtata aaatgcaata 240

ctagtggggc tcctaaataa acttctattt ttcatggcct tctaaaattc actcccaaac 300

ccctagctat agaagtctct tatccatcct ctaaataaaa atgggagtct attttatttc 360

accagagttg atcgtaaatt tagtctctca aattttataa gttgagggta gaggatgact 420

ggagttgctc taaacggacc tatcttcaag tgacctcagt gagcccgttt aacggcgtcg 480

acaagtttaa tctaacggac accaaccaga gaagagaacc accgccagcg ccgagccaag 540

cgacgttgac atcttggcgc ggcacggcat ctccctggcg tctggccccc tctcgagact 600

tccgctccac ctcccaccgg tggcggtttc caagtccgtt ccgcctcctc tcacacggca 660

cgaaaccgtg acgggcaccg gcagcacggg gggattcctt tcccaccgct ccttcccttt 720

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<210> SEQ ID NO 16
<211> LENGTH: 1623
<212> TYPE: DNA
<213> ORGANISM: Andropogon gerardii

<400> SEQUENCE: 16

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agaggatgac tggagttgct ctaaacggac ctatcttcaa gtgacctcag tgagcccgtt 180

taacggcgtc gacaagttta atctaacgga caccaaccag agaagagaac caccgccagc 240

gccgagccaa gcgacgttga catcttggcg cggcacggca tctccctggc gtctggcccc 300

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gaatgatgtc atatgcagca tctgtgtgaa tttttggccc tgtcttcata tgctgtttat 1560

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gtg 1623

<210> SEQ ID NO 17
<211> LENGTH: 482
<212> TYPE: DNA
<213> ORGANISM: Andropogon gerardii

<400> SEQUENCE: 17

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tattttattt caccagagtt gatcgtaaat ttagtctctc aaattttata agttgagggt 120

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agaggatgac tggagttgct ctaaacggac ctatcttcaa gtgacctcag tgagcccgtt 180

taacggcgtc gacaagttta atctaacgga caccaaccag agaagagaac caccgccagc 240

gccgagccaa gcgacgttga catcttggcg cggcacggca tctccctggc gtctggcccc 300

ctctcgagac ttccgctcca cctcccaccg gtggcggttt ccaagtccgt tccgcctcct 360

ctcacacggc acgaaaccgt gacgggcacc ggcagcacgg ggggattcct ttcccaccgc 420

tccttccctt tcccttcctc tcccgccgct ataaatagcc agccccatcc ccagcttctt 480

tc 482

<210> SEQ ID NO 18
<211> LENGTH: 3483
<212> TYPE: DNA
<213> ORGANISM: Saccharum ravennae

<400> SEQUENCE: 18

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ctagcagact tacattatag atggaggaaa ttaaattcag cctttgacgt ggatgcaaca 180

actgcactgc acaggatacc atcttagccg ttgtgtcaaa gtttgctttg ctaaacgttt 240

tgagaaaacc agctttgacc aacgcgagat gagcgcctta cgtttggcac aatgtaatgt 300

aatccggcac ggcaagttag actctgtagt gttagccggc ctctttacgt ttggcatagt 360

ttaattgaat ccggcatggc aagttagacc gtagtgtgag ccggccaacg caagttatta 420

tgacatatgt ataagagcaa gtgtattgtc acgtgatatt tatgttgaga tgaagaagag 480

aaaataaaca gcctgcaaat ttatagcgag tgatagatgg gcacaaggct tcctatttct 540

taaatcagac tttgtaagaa caaaaaaagg acttataaga gaatgggata aaccatatat 600

caatggtgta gtatgttagt atgcattaag atctgactat tatatgagtg agttgttaaa 660

ttcattttag gtgacatggc ccggttaaat tattagccat accctaacag ctctaaaaaa 720

gatatattcg ttgaggcact tttatgcaac cacatagtca acttgaatgc cgcttgagtg 780

cgttctcaag ttttttttct tgcaaattac gctttttttaa gaaagtataa tttggatcgt 840

gcgatttttt ttctctaggt gtgcgtgact gtgtgagtaa caattttgga tctcagaaag 900

gtaataaaag aataatactg ctgcctactt tgaggattac aatatctttc tctaaaatgt 960

tttggtttgt tatttaaacc gtctttaagg ccaattgctc aagattcatt caacaattga 1020

aacgtctcac atgattaaat catataaggt tgctaaggtc ttgtttgaca aggttttttt 1080

tgtggaaatt tcatctaaat ttttgagtga aactatcaaa tactaattta aaaaaggcaa 1140

attttgctgg aggacactgc agaaacgtgt aattggccgg cacaaaccgc caaacggaga 1200

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caaaggggca tcaatagtca ttttagaaag tttctctctc ccgagcagtg gaaatgatta 1380

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tttgcctttt aaaaacaatt ttataagaga agctccggag ataaaaggcc gtcaatgtta 1560

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tttcagaagt ccttatttat atgtgctagt ttggcagcac ttaaaatcgt tagagagagc 1860

ctaaacaaaa gccttttcaa aacgaccttg agccagattg gttgatggcc aaaatttgat 1920

tgtcaaaact taggcaagcc aagattttag cagctatttg gtttggtacc aaaatttgcc 1980

aatgatctgt tcttttgcct tttcaaccgg tttatcagcc gtacttcagc ttattctctc 2040

tcacagaaca ctattgaatc agccgaaaag ccaccgcaga acaggaccag tatctcacaa 2100

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cgccgtttta aatagccagc cccatcccca gcttctctcc ccgtacggcg atcatcctcc 2460

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tatgcttaga tatatgaagc aacatcctgc tacggtttaa taattattgt ttatatctaa 3300

tagacaagcc tgctttttaa ttattttgat atacttggat gatggcatac agcagctatg 3360

tgtggatttt taaataccca gcatcatgag catgcatgac cctgccttag tatgctgttt 3420

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cag 3483

<210> SEQ ID NO 19
<211> LENGTH: 2536
<212> TYPE: DNA
<213> ORGANISM: Saccharum ravennae

<400> SEQUENCE: 19

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aatctattgc agctaacctc aaaagaaatg catttgcagt tgtctgtccc aatcaatcta 120

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ctagcagact tacattatag atggaggaaa ttaaattcag cctttgacgt ggatgcaaca 180

actgcactgc acaggatacc atcttagccg ttgtgtcaaa gtttgctttg ctaaacgttt 240

tgagaaaacc agctttgacc aacgcgagat gagcgcctta cgtttggcac aatgtaatgt 300

aatccggcac ggcaagttag actctgtagt gttagccggc ctctttacgt ttggcatagt 360

ttaattgaat ccggcatggc aagttagacc gtagtgtgag ccggccaacg caagttatta 420

tgacatatgt ataagagcaa gtgtattgtc acgtgatatt tatgttgaga tgaagaagag 480

aaaataaaca gcctgcaaat ttatagcgag tgatagatgg gcacaaggct tcctatttct 540

taaatcagac tttgtaagaa caaaaaaagg acttataaga gaatgggata aaccatatat 600

caatggtgta gtatgttagt atgcattaag atctgactat tatatgagtg agttgttaaa 660

ttcattttag gtgacatggc ccggttaaat tattagccat accctaacag ctctaaaaaa 720

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gtaataaaag aataatactg ctgcctactt tgaggattac aatatctttc tctaaaatgt 960

tttggtttgt tatttaaacc gtctttaagg ccaattgctc aagattcatt caacaattga 1020

aacgtctcac atgattaaat catataaggt tgctaaggtc ttgtttgaca aggttttttt 1080

tgtggaaatt tcatctaaat ttttgagtga aactatcaaa tactaattta aaaaaggcaa 1140

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tttgcctttt aaaaacaatt ttataagaga agctccggag ataaaaggcc gtcaatgtta 1560

caagagtgaa gtcgtctact ccctccatcc caaaaaatgt aattctaagt atgagttgta 1620

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tttcagaagt ccttatttat atgtgctagt ttggcagcac ttaaaatcgt tagagagagc 1860

ctaaacaaaa gccttttcaa aacgaccttg agccagattg gttgatggcc aaaatttgat 1920

tgtcaaaact taggcaagcc aagattttag cagctatttg gtttggtacc aaaatttgcc 1980

aatgatctgt tcttttgcct tttcaaccgg tttatcagcc gtacttcagc ttattctctc 2040

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acggcaccgg cagcacgggg gattcctttc ccaccgctcc ttcccttccc cttcctcgcc 2400

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cgccgtttta aatagccagc cccatcccca gcttctctcc ccaacctcag cttctctcgt 2460

tgttcggagc gcacacacaa cccgatcccc aatcccctcg tctctcctcg cgagcctcgt 2520

cgatccccgc ttcaag 2536

<210> SEQ ID NO 20
<211> LENGTH: 94
<212> TYPE: DNA
<213> ORGANISM: Saccharum ravennae

<400> SEQUENCE: 20

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tctcctcgcg agcctcgtcg atccccgctt caag 94

<210> SEQ ID NO 21
<211> LENGTH: 1041
<212> TYPE: DNA
<213> ORGANISM: Saccharum ravennae

<400> SEQUENCE: 21

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gtggtattat gctaacctat gatatggttc gatcgtgcta gctacgtcct gtgtcataat 480

ttttagcatg ccctttttg tttggttttg tctgattggg ctgtagatca gagtatactg 540

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cttcataatt aaaatggatg gaaagatata tggataggta catgtgttgc tgtgggtttt 660

actggtactt tgttagatat acatgcttag atacatgaag caacatgatg ttacagttca 720

ataattcttg tttacctaat aaacaaataa ggataggtgt atgttgctgt gggttttgct 780

ggtactttgt tagatatata tgcttagata tatgaagcaa catcctgcta cggtttaata 840

attattgttt atatctaata gacaagcctg ctttttaatt attttgatat acttggatga 900

tggcatacag cagctatgtg tggatttta aatacccagc atcatgagca tgcatgaccc 960

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<210> SEQ ID NO 22
<211> LENGTH: 3152
<212> TYPE: DNA
<213> ORGANISM: Saccharum ravennae

<400> SEQUENCE: 22

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cagcctgcaa atttatagcg agtgatagat gggcacaagg cttcctattt cttaaatcag 120

actttgtaag aacaaaaaaa ggacttataa gagaatggga taaaccatat atcaatggtg 180

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tagtatgtta gtatgcatta agatctgact attatatgag tgagttgtta aattcatttt 240

aggtgacatg gcccggttaa attattagcc ataccctaac agctctaaaa aagatatatt 300

cgttgaggca cttttatgca accacatagt caacttgaat gccgcttgag tgcgttctca 360

agttttttt cttgcaaatt acgcttttt aagaaagtat aatttggatc gtgcgatttt 420

ttttctctag gtgtgcgtga ctgtgtgagt aacaattttg gatctcagaa aggtaataaa 480

agaataatac tgctgcctac tttgaggatt acaatatctt tctctaaaat gttttggttt 540

gttatttaaa ccgtctttaa ggccaattgc tcaagattca ttcaacaatt gaaacgtctc 600

acatgattaa atcatataag gttgctaagg tcttgtttga caaggttttt tttgtggaaa 660

tttcatctaa atttttgagt gaaactatca aatactaatt taaaaaaggc aaattttgct 720

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ttaaaaacaa ttttataaga gaagctccgg agataaaagg ccgtcaatgt tacaagagtg 1140

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tttggacaaa aggagtatac cacaagaatg atatcatcgt catgcttaga tccttttag 1260

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ttggcgcggg catctctctg gccccctctc gagagttccg ctccacctcc actggtggcg 1860

gtttccaagt ccgttccgcc tcctgctcct cctcacacgg cacgaaaccg tcacggcacc 1920

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gcgcacacac aacccgatcc ccaatccccc cgtctctcct cgcgagcctc gtcgatcccc 2100

gcttcaaggt acggcgatca tcctcccttt ctctaccttc tcttctctag actaggtcgg 2160

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acatatatct tcataattaa aatggatgga aagatatatg gataggtaca tgtgttgctg 2760

tgggttttac tggtactttg ttagatatac atgcttagat acatgaagca acatgatgtt 2820

acagttcaat aattcttgtt tacctaataa acaaataagg ataggtgtat gttgctgtgg 2880

gttttgctgg tactttgtta gatatatatg cttagatata tgaagcaaca tcctgctacg 2940

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<210> SEQ ID NO 23
<211> LENGTH: 2014
<212> TYPE: DNA
<213> ORGANISM: Saccharum ravennae

<400> SEQUENCE: 23

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actttgtaag aacaaaaaaa ggacttataa gagaatggga taaaccatat atcaatggtg 180

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aggtgacatg gcccggttaa attattagcc ataccctaac agctctaaaa aagatatatt 300

cgttgaggca cttttatgca accacatagt caacttgaat gccgcttgag tgcgttctca 360

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agaataatac tgctgcctac tttgaggatt acaatatctt tctctaaaat gttttggttt 540

gttatttaaa ccgtctttaa ggccaattgc tcaagattca ttcaacaatt gaaacgtctc 600

acatgattaa atcatataag gttgctaagg tcttgtttga caaggttttt tttgtggaaa 660

tttcatctaa atttttgagt gaaactatca aatactaatt taaaaaaggc aaattttgct 720

ggaggacact gcagaaacgt gtaattggcc ggcacaaacc gccaaacgga gaatttgccc 780

agtaccatta taaattcatg ataaattcat ggttgtttgc cagtggggct agggttcctc 840

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catcaatagt cattttagaa agtttctctc tcccgagcag tggaaatgat tattctattt 960

ggcgcgatgt ccaccggcaa acaaccacga atttgtaatg gtactaggca aattctccgt 1020

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aagtcgtcta ctccctccat cccaaaaaat gtaattctaa gtatgagttg tattattatt 1200

tttggacaaa aggagtatac cacaagaatg atatcatcgt catgcttaga tccttttag 1260

taaagcttga gcttctctaa aagtagagaa attagaaaaa aatcacgttt ttgtggtctt 1320

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gatttctagc ctccacaaaa tctttggttt tacatttttt gtttgatttt ggtttcagaa 1380

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aagccttttc aaaacgacct tgagccagat tggttgatgg ccaaaatttg attgtcaaaa 1500

cttaggcaag ccaagatttt agcagctatt tggtttggta ccaaaatttg ccaatgatct 1560

gttcttttgc cttttcaacc ggtttatcag ccgtacttca gcttattctc tctcacagaa 1620

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ccaaatatac tcaccgtcag tgagcccgtt taacggcgtc gacaagtcta acggccacca 1740

accagcgaac caccagcgtc aagctagcca agcgaagcag acggccgaga cgttgacacc 1800

ttggcgcggg catctctctg gccccctctc gagagttccg ctccacctcc actggtggcg 1860

gtttccaagt ccgttccgcc tcctgctcct cctcacacgg cacgaaaccg tcacggcacc 1920

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taaatagcca gccccatccc cagcttctct cccc 2014

<210> SEQ ID NO 24
<211> LENGTH: 1044
<212> TYPE: DNA
<213> ORGANISM: Saccharum ravennae

<400> SEQUENCE: 24

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tggcgttatg atggttaact tgtcatactc ctgcggtgtg cggtctatag tgcttttagg 180

acatcaattt gacctggctc gttcgagatc ggcgatccat ggttaggacc ctaggcggtg 240

gagtcgggtt agatccgcgc tgtttgtgtt agtagatgga tgcgaccttt acttcagaca 300

cgttctgatt gttaacttgt cagcacctgg gagtcctggg atggttctag ctggttcgca 360

gatgagatcg atttcatgat ctgctgtatc ttgtttcgtt aggttccttt taatctatcc 420

gtggtattat gctaacctat gatatggttc gatcgtgcta gctacgtcct gtgtcataat 480

ttttagcatg ccctttttg tttggttttg tctgattggg ctgtagatca gagtatactg 540

tttcaaacta cctactggat atatttatta aatttgaatc tgtatgtgtg tcacatatat 600

cttcataatt aaaatggatg gaaagatata tggataggta catgtgttgc tgtgggtttt 660

actggtactt tgttagatat acatgcttag atacatgaag caacatgatg ttacagttca 720

ataattcttg tttacctaat aaacaaataa ggataggtgt atgttgctgt gggttttgct 780

ggtactttgt tagatatata tgcttagata tatgaagcaa catcctgcta cggtttaata 840

attattgttt atatctaata gacaagcctg ctttttaatt attttgatat acttggatga 900

tggcatacag cagctatgtg tggattttta aatacccagc atcatgagca tgcatgaccc 960

tgccttagta tgctgtttat ttgcttgaga cttctttttt tgttggtact caccttttgt 1020

agtttggtga ctcttctgca ggtg 1044

<210> SEQ ID NO 25
<211> LENGTH: 2663
<212> TYPE: DNA
<213> ORGANISM: Saccharum ravennae

<400> SEQUENCE: 25

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aatcatataa ggttgctaag gtcttgtttg acaaggtttt ttttgtggaa atttcatcta 180

aatttttgag tgaaactatc aaatactaat ttaaaaaagg caaattttgc tggaggacac 240

tgcagaaacg tgtaattggc cggcacaaac cgccaaacgg agaatttgcc cagtaccatt 300

ataaattcat gataaattca tggttgtttg ccagtggggc tagggttcct cgcgtatggt 360

gcggaatgtg gtttggttcg accaactcga actcaatccg atccaaaggg gcatcaatag 420

tcattttaga aagtttctct ctcccgagca gtggaaatga ttattctatt tggcgcgatg 480

tccaccggca aacaaccacg aatttgtaat ggtactaggc aaattctccg tttggcggtg 540

tgtgccggcc aattacacgt ttttgcggtg tcctccgaca aaatttgcct tttaaaaaca 600

attttataag agaagctccg gagataaaag gccgtcaatg ttacaagagt gaagtcgtct 660

actccctcca tcccaaaaaa tgtaattcta agtatgagtt gtattattat ttttggacaa 720

aaggagtata ccacaagaat gatatcatcg tcatgcttag atccttttta gtaaagcttg 780

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ccttttcaac cggtttatca gccgtacttc agcttattct ctctcacaga acactattga 1140

atcagccgaa aagccaccgc agaacaggac cagtatctca caaatggcat gccaaatata 1200

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ccaccagcgt caagctagcc aagcgaagca gacggccgag acgttgacac cttggcgcgg 1320

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agtcgggtta gatccgcgct gtttgtgtta gtagatggat gcgaccttta cttcagacac 1920

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tggtattatg ctaacctatg atatggttcg atcgtgctag ctacgtcctg tgtcataatt 2100

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ctggtacttt gttagatata catgcttaga tacatgaagc aacatgatgt tacagttcaa 2340

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ttattgttta tatctaatag acaagcctgc tttttaatta ttttgatata cttggatgat 2520

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gtttggtgac tcttctgcag gtg 2663

<210> SEQ ID NO 26
<211> LENGTH: 1525
<212> TYPE: DNA
<213> ORGANISM: Saccharum ravennae

<400> SEQUENCE: 26

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gcggaatgtg gtttggttcg accaactcga actcaatccg atccaaaggg gcatcaatag 420

tcattttaga aagtttctct ctcccgagca gtggaaatga ttattctatt tggcgcgatg 480

tccaccggca aacaaccacg aatttgtaat ggtactaggc aaattctccg tttggcggtg 540

tgtgccggcc aattacacgt ttttgcggtg tcctccgaca aaatttgcct tttaaaaaca 600

attttataag agaagctccg gagataaaag gccgtcaatg ttacaagagt gaagtcgtct 660

actccctcca tcccaaaaaa tgtaattcta agtatgagtt gtattattat ttttggacaa 720

aaggagtata ccacaagaat gatatcatcg tcatgcttag atccttttta gtaaagcttg 780

agcttctcta aaagtagaga aattagaaaa aaatcacgtt tttgtggtct tgatttctag 840

cctccacaaa atctttggtt ttacattttt tgtttgattt tggtttcaga agtccttatt 900

tatatgtgct agtttggcag cacttaaaat cgttagagag agcctaaaca aaagcctttt 960

caaaacgacc ttgagccaga ttggttgatg gccaaaattt gattgtcaaa acttaggcaa 1020

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ccttttcaac cggtttatca gccgtacttc agcttattct ctctcacaga acactattga 1140

atcagccgaa aagccaccgc agaacaggac cagtatctca caaatggcat gccaaatata 1200

ctcaccgtca gtgagcccgt ttaacggcgt cgacaagtct aacggccacc aaccagcgaa 1260

ccaccagcgt caagctagcc aagcgaagca gacggccgag acgttgacac cttggcgcgg 1320

gcatctctct ggcccccctct cgagagttcc gctccacctc cactggtggc ggtttccaag 1380

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agccccatcc ccagcttctc tcccc 1525

<210> SEQ ID NO 27

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<211> LENGTH: 2182
<212> TYPE: DNA
<213> ORGANISM: Saccharum ravennae

<400> SEQUENCE: 27

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gtgccggcca attacacgtt tttgcggtgt cctccgacaa aatttgcctt ttaaaaacaa 120

ttttataaga gaagctccgg agataaaagg ccgtcaatgt tacaagagtg aagtcgtcta 180

ctccctccat cccaaaaaat gtaattctaa gtatgagttg tattattatt tttggacaaa 240

aggagtatac cacaagaatg atatcatcgt catgcttaga tccttttag taaagcttga 300

gcttctctaa aagtagagaa attagaaaaa aatcacgttt ttgtggtctt gatttctagc 360

ctccacaaaa tctttggttt tacatttttt gtttgatttt ggtttcagaa gtccttattt 420

atatgtgcta gtttggcagc acttaaaatc gttagagaga gcctaaacaa aagccttttc 480

aaaacgacct tgagccagat tggttgatgg ccaaaatttg attgtcaaaa cttaggcaag 540

ccaagatttt agcagctatt tggtttggta ccaaaatttg ccaatgatct gttcttttgc 600

cttttcaacc ggtttatcag ccgtacttca gcttattctc tctcacagaa cactattgaa 660

tcagccgaaa agccaccgca gaacaggacc agtatctcac aaatggcatg ccaaatatac 720

tcaccgtcag tgagcccgtt taacggcgtc gacaagtcta acggccacca accagcgaac 780

caccagcgtc aagctagcca agcgaagcag acggccgaga cgttgacacc ttggcgcggg 840

catctctctg gccccctctc gagagttccg ctccacctcc actggtggcg gtttccaagt 900

ccgttccgcc tcctgctcct cctcacacgg cacgaaaccg tcacggcacc ggcagcacgg 960

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aattcttgtt tacctaataa acaaataagg ataggtgtat gttgctgtgg gttttgctgg 1920

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<210> SEQ ID NO 28
<211> LENGTH: 1044
<212> TYPE: DNA
<213> ORGANISM: Saccharum ravennae

<400> SEQUENCE: 28

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ttttataaga gaagctccgg agataaaagg ccgtcaatgt tacaagagtg aagtcgtcta 180

ctccctccat cccaaaaaat gtaattctaa gtatgagttg tattattatt tttggacaaa 240

aggagtatac cacaagaatg atatcatcgt catgcttaga tccttttttag taaagcttga 300

gcttctctaa aagtagagaa attagaaaaa aatcacgttt ttgtggtctt gatttctagc 360

ctccacaaaa tctttggttt tacatttttt gtttgatttt ggtttcagaa gtccttattt 420

atatgtgcta gtttggcagc acttaaaatc gttagagaga gcctaaacaa aagccttttc 480

aaaacgacct tgagccagat tggttgatgg ccaaaatttg attgtcaaaa cttaggcaag 540

ccaagatttt agcagctatt tggtttggta ccaaaatttg ccaatgatct gttcttttgc 600

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tcaccgtcag tgagcccgtt taacggcgtc gacaagtcta acggccacca accagcgaac 780

caccagcgtc aagctagcca agcgaagcag acggccgaga cgttgacacc ttggcgcggg 840

catctctctg gccccctctc gagagttccg ctccacctcc actggtggcg gtttccaagt 900

ccgttccgcc tcctgctcct cctcacacgg cacgaaaccg tcacggcacc ggcagcacgg 960

gggattcctt tcccaccgct ccttcccttt cccttcctcg cccgccgttt taaatagcca 1020

gccccatccc cagcttctct cccc 1044

<210> SEQ ID NO 29
<211> LENGTH: 1934
<212> TYPE: DNA
<213> ORGANISM: Saccharum ravennae

<400> SEQUENCE: 29

accacaagaa tgatatcatc gtcatgctta gatccttttt agtaaagctt gagcttctct 60

aaaagtagag aaattagaaa aaaatcacgt ttttgtggtc ttgatttcta gcctccacaa 120

aatctttggt tttacatttt ttgtttgatt ttggtttcag aagtccttat ttatatgtgc 180

tagtttggca gcacttaaaa tcgttagaga gagcctaaac aaaagccttt tcaaaacgac 240

cttgagccag attggttgat ggccaaaatt tgattgtcaa aacttaggca agccaagatt 300

ttagcagcta tttggtttgg taccaaaatt tgccaatgat ctgttctttt gccttttcaa 360

ccggtttatc agccgtactt cagcttattc tctctcacag aacactattg aatcagccga 420

aaagccaccg cagaacagga ccagtatctc acaaatggca tgccaaatat actcaccgtc 480

agtgagcccg tttaacggcg tcgacaagtc taacggccac caaccagcga accaccagcg 540

tcaagctagc caagcgaagc agacggccga gacgttgaca ccttggcgcg ggcatctctc 600

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tggccccctc tcgagagttc cgctccacct ccactggtgg cggtttccaa gtccgttccg 660

cctcctgctc ctcctcacac ggcacgaaac cgtcacggca ccggcagcac gggggattcc 720

tttcccaccg ctccttccct ttcccttcct cgcccgccgt tttaaatagc cagccccatc 780

cccagcttct ctccccaacc tcagcttctc tcgttgttcg gagcgcacac acaacccgat 840

ccccaatccc ctcgtctctc ctcgcgagcc tcgtcgatcc ccgcttcaag gtacggcgat 900

catcctccct ttctctacct tctcttctct agactaggtc ggcgatccat ggttagggcc 960

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ccctttttg tttggttttg tctgattggg ctgtagatca gagtatactg tttcaaacta 1440

cctactggat atatttatta aatttgaatc tgtatgtgtg tcacatatat cttcataatt 1500

aaaatggatg gaaagatata tggataggta catgtgttgc tgtgggtttt actggtactt 1560

tgttagatat acatgcttag atacatgaag caacatgatg ttacagttca ataattcttg 1620

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atatctaata gacaagcctg ctttttaatt attttgatat acttggatga tggcatacag 1800

cagctatgtg tggattttta aatacccagc atcatgagca tgcatgaccc tgccttagta 1860

tgctgtttat ttgcttgaga cttctttttt tgttggtact caccttttgt agtttggtga 1920

ctcttctgca ggtg 1934

<210> SEQ ID NO 30
<211> LENGTH: 796
<212> TYPE: DNA
<213> ORGANISM: Saccharum ravennae

<400> SEQUENCE: 30

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aaaagtagag aaattagaaa aaaatcacgt ttttgtggtc ttgatttcta gcctccacaa 120

aatctttggt tttacatttt ttgtttgatt ttggtttcag aagtccttat ttatatgtgc 180

tagtttggca gcacttaaaa tcgttagaga gagcctaaac aaaagccttt tcaaaacgac 240

cttgagccag attggttgat ggccaaaatt tgattgtcaa aacttaggca agccaagatt 300

ttagcagcta tttggtttgg taccaaaatt tgccaatgat ctgttctttt gccttttcaa 360

ccggtttatc agccgtactt cagcttattc tctctcacag aacactattg aatcagccga 420

aaagccaccg cagaacagga ccagtatctc acaaatggca tgccaaatat actcaccgtc 480

agtgagcccg tttaacggcg tcgacaagtc taacggccac caaccagcga accaccagcg 540

tcaagctagc caagcgaagc agacggccga gacgttgaca ccttggcgcg ggcatctctc 600

tggccccctc tcgagagttc cgctccacct ccactggtgg cggtttccaa gtccgttccg 660

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cctcctgctc ctcctcacac ggcacgaaac cgtcacggca ccggcagcac gggggattcc 720

tttcccaccg ctccttccct ttcccttcct cgcccgccgt tttaaatagc cagccccatc 780

cccagcttct ctcccc 796

<210> SEQ ID NO 31
<211> LENGTH: 1649
<212> TYPE: DNA
<213> ORGANISM: Saccharum ravennae

<400> SEQUENCE: 31

aggcaagcca agattttagc agctatttgg tttggtacca aaatttgcca atgatctgtt 60

cttttgcctt ttcaaccggt ttatcagccg tacttcagct tattctctct cacagaacac 120

tattgaatca gccgaaaagc caccgcagaa caggaccagt atctcacaaa tggcatgcca 180

aatatactca ccgtcagtga gcccgtttaa cggcgtcgac aagtctaacg gccaccaacc 240

agcgaaccac cagcgtcaag ctagccaagc gaagcagacg gccgagacgt tgacaccttg 300

gcgcgggcat ctctctggcc ccctctcgag agttccgctc cacctccact ggtggcggtt 360

tccaagtccg ttccgcctcc tgctcctcct cacacggcac gaaaccgtca cggcaccggc 420

agcacggggg attcctttcc caccgctcct tcccttccc ttcctcgccc gccgttttaa 480

atagccagcc ccatccccag cttctctccc caacctcagc ttctctcgtt gttcggagcg 540

cacacacaac ccgatcccca atcccctcgt ctctcctcgc gagcctcgtc gatccccgct 600

tcaaggtacg gcgatcatcc tccctttctc taccttctct tctctagact aggtcggcga 660

tccatggtta gggcctgcta gttctgttcc tgtttttccg tggctgcgag gtacaataga 720

tctgatggcg ttatgatggt taacttgtca tactcctgcg gtgtgcggtc tatagtgctt 780

ttaggacatc aatttgacct ggctcgttcg agatcggcga tccatggtta ggaccctagg 840

cggtggagtc gggttagatc cgcgctgttt gtgttagtag atggatgcga cctttacttc 900

agacacgttc tgattgttaa cttgtcagca cctgggagtc ctgggatggt tctagctggt 960

tcgcagatga gatcgatttc atgatctgct gtatcttgtt tcgttaggtt ccttttaatc 1020

tatccgtggt attatgctaa cctatgatat ggttcgatcg tgctagctac gtcctgtgtc 1080

ataatttttа gcatgccctt ttttgtttgg ttttgtctga ttgggctgta gatcagagta 1140

tactgtttca aactacctac tggatatatt tattaaattt gaatctgtat gtgtgtcaca 1200

tatatcttca taattaaaat ggatggaaag atatatggat aggtacatgt gttgctgtgg 1260

gttttactgg tactttgtta gatatacatg cttagataca tgaagcaaca tgatgttaca 1320

gttcaataat tcttgtttac ctaataaaca aataaggata ggtgtatgtt gctgtgggtt 1380

ttgctggtac tttgttagat atatatgctt agatatatga agcaacatcc tgctacggtt 1440

taataattat tgtttatatc taatagacaa gcctgctttt taattatttt gatatacttg 1500

gatgatggca tacagcagct atgtgtggat ttttaaatac ccagcatcat gagcatgcat 1560

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tttgtagttt ggtgactctt ctgcaggtg 1649

<210> SEQ ID NO 32
<211> LENGTH: 511
<212> TYPE: DNA
<213> ORGANISM: Saccharum ravennae

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<400> SEQUENCE: 32

aggcaagcca agattttagc agctatttgg tttggtacca aaatttgcca atgatctgtt 60

cttttgcctt ttcaaccggt ttatcagccg tacttcagct tattctctct cacagaacac 120

tattgaatca gccgaaaagc caccgcagaa caggaccagt atctcacaaa tggcatgcca 180

aatatactca ccgtcagtga gcccgtttaa cggcgtcgac aagtctaacg gccaccaacc 240

agcgaaccac cagcgtcaag ctagccaagc gaagcagacg gccgagacgt tgacaccttg 300

gcgcgggcat ctctctggcc ccctctcgag agttccgctc cacctccact ggtggcggtt 360

tccaagtccg ttccgcctcc tgctcctcct cacacggcac gaaaccgtca cggcaccggc 420

agcacggggg attcctttcc caccgctcct tccctttccc ttcctcgccc gccgttttaa 480

atagccagcc ccatccccag cttctctccc c 511

<210> SEQ ID NO 33
<211> LENGTH: 2631
<212> TYPE: DNA
<213> ORGANISM: Setaria viridis

<400> SEQUENCE: 33

actgccgcga cacgcctcac tggcgggagg gctccgagcg ctctctcccc ggcggccggc 60

ggagcagcga tctggattgg agagaataga ggaaagagag ggaaaaggag agagatagcg 120

caaagagctg aaaagataag gttgtgcggg ctgtggtgat tagaggacca ctaatccctc 180

catctcctaa tgacgcggtg cccaagacca gtgccgcggc acaccagcgt ctaagtgaac 240

ttccgctaac cttccggtca ttgcgcctga aagatgtcat gtggcgaggc ccccctctca 300

gtagattgcc aactgcctac cgtgccactc ttccatgcat gattgctccc gtctatcccg 360

tttctcacaa cagatagaca acagtaagca tcactaaagc aagcatgtgt agaaccttaa 420

aaaaaggctt atactaccag tatactatca accagcatgc cgtttttgaa gtatccagga 480

ttagaagctt ctactgcgct tttatattat agctgtggac ctgtggtaac ctttctcttt 540

tggcgcttgc ttaatctcgg ccgtgctggt ccatgcttag gcactaggca gagatagagc 600

cgggggtgaa tggggctaaa gctcagctgc tcgaggggcc gtgggctggt ttccactagc 660

ctacagctgt gccacgtgcg gccgcgcaag ccgaagcaag cacgctgagc cgttggacag 720

cttgtcataa tgccattacg tggattacag gtaactggcc ctgtaactac tcgttcggcc 780

atcatcaaac gacgacgtcc gctaggcgac gacacgggta atgcacgcag ccacccaggc 840

gcgcgcgcta gcggagcacg gtcaggtgac acgggcgtcg tgacgcttcc gagttgaagg 900

ggttaacgcc agaaacagtg tttggccagg gtatgaacat aacaaaaaat attcacacga 960

aagaatggaa gtatggagct gctactgtgt aaatgccaag caggaaactc acgcccgcta 1020

acatccaacg gccaacagct cgacgtgccg gtcagcagag acatcggaac actggtgatt 1080

ggtggagccg gcagtatgcg ccccagcacg gccgaggtgg tggtggcccg tggccctgct 1140

gtctgcgcgg ctcgggacaa cttgaaactg ggccaccgcc tcgtcgcaac tcgcaacccg 1200

ttggcggaag aaaggaatgg ctcgtagggg cccgggtaga atccaagaat gttgcgctgg 1260

gcttcgattc acataacatg ggcctgaagc tctaaaacga cggcccggtc accgggcgat 1320

ggaaagagac cggatcctcc tcgtgaattc tggaaggcca cacgagagcg acccaccacc 1380

gacgcggagg agtcgtgcgt ggtccaacac ggccggcggg ctgggctgcg accttaacca 1440

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gcaagactca gatcagattc cgatccccag ttcttcccca atcaccttgt ggtctctcgt 1560

gtcgcggttc ccagggacgc ctccggctcg tcgctcgaca gcgatctccg ccccagcaag 1620

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cagtcgttct tgctgtcgac tagtttgttt tgatatccat gtagtacaag ttacttaaaa 1980

tttaggtcca atatattttg catgcttttg gcctgttatt cttgccaaca agttgtcctg 2040

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tatagttctg tgatacatct atctgatttt ttttggtcta ttggtgccta acttatctga 2160

aaatcatgga acatgaggct agtttgatca tggtttagtt cattgtgatt aataatgtat 2220

gatttagtag ctattttggt gatcgtgtca ttttatttgt gaatggaatc attgtatgta 2280

aatgaagcta gttcaggggt tatgatgtag ctggctttgt attctaaagg ctgctattat 2340

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ttcactagga aggacagaac attgttaata ttttggcaca tctgtcttat tctcatcctt 2460

tgtttgaaca tgttagcctg ttcaaacaga tactgttgta atgtcctagt tatataggta 2520

catatgtgtt ctctattgag tttatggact tttgtgtgtg aagttatatt tcattttgct 2580

caaaactcat gtttgcaagc tttctgacat tattctattg ttctgaaaca g 2631

<210> SEQ ID NO 34
<211> LENGTH: 1493
<212> TYPE: DNA
<213> ORGANISM: Setaria viridis

<400> SEQUENCE: 34

actgccgcga cacgcctcac tggcgggagg gctccgagcg ctctctcccc ggcggccggc 60

ggagcagcga tctggattgg agagaataga ggaaagagag ggaaaaggag agagatagcg 120

caaagagctg aaaagataag gttgtgcggg ctgtggtgat tagaggacca ctaatccctc 180

catctcctaa tgacgcggtg cccaagacca gtgccgcggc acaccagcgt ctaagtgaac 240

ttccgctaac cttccggtca ttgcgcctga aagatgtcat gtggcgaggc ccccctctca 300

gtagattgcc aactgcctac cgtgccactc ttccatgcat gattgctccc gtctatcccg 360

tttctcacaa cagatagaca acagtaagca tcactaaagc aagcatgtgt agaaccttaa 420

aaaaaggctt atactaccag tatactatca accagcatgc cgtttttgaa gtatccagga 480

ttagaagctt ctactgcgct tttatattat agctgtggac ctgtggtaac ctttctcttt 540

tggcgcttgc ttaatctcgg ccgtgctggt ccatgcttag gcactaggca gagatagagc 600

cgggggtgaa tggggctaaa gctcagctgc tcgaggggcc gtgggctggt ttccactagc 660

ctacagctgt gccacgtgcg gccgcgcaag ccgaagcaag cacgctgagc cgttggacag 720

cttgtcataa tgccattacg tggattacag gtaactggcc ctgtaactac tcgttcggcc 780

atcatcaaac gacgacgtcc gctaggcgac gacacgggta atgcacgcag ccacccaggc 840

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gcgcgcgcta gcggagcacg gtcaggtgac acgggcgtcg tgacgcttcc gagttgaagg 900

ggttaacgcc agaaacagtg tttggccagg gtatgaacat aacaaaaaat attcacacga 960

aagaatggaa gtatggagct gctactgtgt aaatgccaag caggaaactc acgcccgcta 1020

acatccaacg gccaacagct cgacgtgccg gtcagcagag acatcggaac actggtgatt 1080

ggtggagccg gcagtatgcg ccccagcacg gccgaggtgg tggtggcccg tggccctgct 1140

gtctgcgcgg ctcgggacaa cttgaaactg ggccaccgcc tcgtcgcaac tcgcaacccg 1200

ttggcggaag aaaggaatgg ctcgtagggg cccgggtaga atccaagaat gttgcgctgg 1260

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gacgcggagg agtcgtgcgt ggtccaacac ggccggcggg ctgggctgcg accttaacca 1440

gcaaggcacg ccacgacccg cctcgccctc gaggcataaa taccctccca tcc 1493

<210> SEQ ID NO 35
<211> LENGTH: 127
<212> TYPE: DNA
<213> ORGANISM: Setaria viridis

<400> SEQUENCE: 35

cgttgccgca agactcagat cagattccga tccccagttc ttccccaatc accttgtggt 60

ctctcgtgtc gcggttccca gggacgcctc cggctcgtcg ctcgacagcg atctccgccc 120

cagcaag 127

<210> SEQ ID NO 36
<211> LENGTH: 1011
<212> TYPE: DNA
<213> ORGANISM: Setaria viridis

<400> SEQUENCE: 36

gtatagattc agttccttgc tccgatccca atctggttga gatgttgctc cgatgcgact 60

tgattatgtc atatatctgc ggtttgcacc gatctgaagc ctagggtttc tcgagcgacc 120

cagttgtttg caatttgcga tttgctcgtt tgttgcgcat cgtagtttat gtttggagta 180

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gtaaaaagta gatgtgaaag tcacgtattg ggacaaattg atggttaagt gctatagttc 480

tatagttctg tgatacatct atctgatttt ttttggtcta ttggtgccta acttatctga 540

aaatcatgga acatgaggct agtttgatca tggtttagtt cattgtgatt aataatgtat 600

gatttagtag ctattttggt gatcgtgtca ttttatttgt gaatggaatc attgtatgta 660

aatgaagcta gttcaggggt tatgatgtag ctggctttgt attctaaagg ctgctattat 720

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tgtttgaaca tgttagcctg ttcaaacaga tactgttgta atgtcctagt tatataggta 900

catatgtgtt ctctattgag tttatggact tttgtgtgtg aagttatatt tcattttgct 960

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caaaactcat gtttgcaagc tttctgacat tattctattg ttctgaaaca g 1011

<210> SEQ ID NO 37
<211> LENGTH: 2173
<212> TYPE: DNA
<213> ORGANISM: Setaria viridis

<400> SEQUENCE: 37

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acctgtggta acctttctct tttggcgctt gcttaatctc ggccgtgctg gtccatgctt 120

aggcactagg cagagataga gccgggggtg aatggggcta aagctcagct gctcgagggg 180

ccgtgggctg gtttccacta gcctacagct gtgccacgtg cggccgcgca agccgaagca 240

agcacgctga gccgttggac agcttgtcat aatgccatta cgtggattac aggtaactgg 300

ccctgtaact actcgttcgg ccatcatcaa acgacgacgt ccgctaggcg acgacacggg 360

taatgcacgc agccacccag gcgcgcgcgc tagcggagca cggtcaggtg acacgggcgt 420

cgtgacgctt ccgagttgaa ggggttaacg ccagaaacag tgtttggcca gggtatgaac 480

ataacaaaaa atattcacac gaaagaatgg aagtatggag ctgctactgt gtaaatgcca 540

agcaggaaac tcacgcccgc taacatccaa cggccaacag ctcgacgtgc cggtcagcag 600

agacatcgga acactggtga ttggtggagc cggcagtatg cgccccagca cggccgaggt 660

ggtggtggcc cgtggccctg ctgtctgcgc ggctcgggac aacttgaaac tgggccaccg 720

cctcgtcgca actcgcaacc cgttggcgga agaaaggaat ggctcgtagg ggcccgggta 780

gaatccaaga atgttgcgct gggcttcgat tcacataaca tgggcctgaa gctctaaaac 840

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atctaagaat ctagattagg ctcagtcgtt cttgctgtcg actagtttgt tttgatatcc 1500

atgtagtaca agttacttaa aatttaggtc caatatattt tgcatgcttt tggcctgtta 1560

ttcttgccaa caagttgtcc tggtaaaaag tagatgtgaa agtcacgtat tgggacaaat 1620

tgatggttaa gtgctatagt tctatagttc tgtgatacat ctatctgatt ttttttggtc 1680

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gtgaatggaa tcattgtatg taaatgaagc tagttcaggg gttatgatgt agctggcttt 1860

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catctgtctt attctcatcc tttgtttgaa catgttagcc tgttcaaaca gatactgttg 2040

taatgtccta gttatatagg tacatatgtg ttctctattg agtttatgga cttttgtgtg 2100

tgaagttata tttcattttg ctcaaaactc atgtttgcaa gctttctgac attattctat 2160

tgttctgaaa cag 2173

<210> SEQ ID NO 38
<211> LENGTH: 1035
<212> TYPE: DNA
<213> ORGANISM: Setaria viridis

<400> SEQUENCE: 38

gccgtttttg aagtatccag gattagaagc ttctactgcg cttttatatt atagctgtgg 60

acctgtggta acctttctct tttggcgctt gcttaatctc ggccgtgctg gtccatgctt 120

aggcactagg cagagataga gccgggggtg aatggggcta aagctcagct gctcgagggg 180

ccgtgggctg gtttccacta gcctacagct gtgccacgtg cggccgcgca agccgaagca 240

agcacgctga gccgttggac agcttgtcat aatgccatta cgtggattac aggtaactgg 300

ccctgtaact actcgttcgg ccatcatcaa acgacgacgt ccgctaggcg acgacacggg 360

taatgcacgc agccacccag gcgcgcgcgc tagcggagca cggtcaggtg acacgggcgt 420

cgtgacgctt ccgagttgaa ggggttaacg ccagaaacag tgtttggcca gggtatgaac 480

ataacaaaaa atattcacac gaaagaatgg aagtatggag ctgctactgt gtaaatgcca 540

agcaggaaac tcacgcccgc taacatccaa cggccaacag ctcgacgtgc cggtcagcag 600

agacatcgga acactggtga ttggtggagc cggcagtatg cgccccagca cggccgaggt 660

ggtggtggcc cgtggccctg ctgtctgcgc ggctcgggac aacttgaaac tgggccaccg 720

cctcgtcgca actcgcaacc cgttggcgga agaaaggaat ggctcgtagg ggcccgggta 780

gaatccaaga atgttgcgct gggcttcgat tcacataaca tgggcctgaa gctctaaaac 840

gacggcccgg tcaccgggcg atggaaagag accggatcct cctcgtgaat tctggaaggc 900

cacacgagag cgacccacca ccgacgcgga ggagtcgtgc gtggtccaac acggccggcg 960

ggctgggctg cgaccttaac cagcaaggca cgccacgacc cgcctcgccc tcgaggcata 1020

aataccctcc catcc 1035

<210> SEQ ID NO 39
<211> LENGTH: 1819
<212> TYPE: DNA
<213> ORGANISM: Setaria viridis

<400> SEQUENCE: 39

cacgggtaat gcacgcagcc acccaggcgc gcgcgctagc ggagcacggt caggtgacac 60

gggcgtcgtg acgcttccga gttgaagggg ttaacgccag aaacagtgtt tggccagggt 120

atgaacataa caaaaaatat tcacacgaaa gaatggaagt atggagctgc tactgtgtaa 180

atgccaagca ggaaactcac gcccgctaac atccaacggc caacagctcg acgtgccggt 240

cagcagagac atcggaacac tggtgattgg tggagccggc agtatgcgcc ccagcacggc 300

cgaggtggtg gtggcccgtg gccctgctgt ctgcgcggct cgggacaact tgaaactggg 360

ccaccgcctc gtcgcaactc gcaacccgtt ggcggaagaa aggaatggct cgtaggggcc 420

cgggtagaat ccaagaatgt tgcgctgggc ttcgattcac ataacatggg cctgaagctc 480

-continued

taaaacgacg gcccggtcac cgggcgatgg aaagagaccg gatcctcctt gtgaattctg 540

gaaggccaca cgagagcgac ccaccaccga cgcggaggag tcgtgcgtgg tccaacacgg 600

ccggcgggct gggctgcgac cttaaccagc aaggcacgcc acgacccgcc tcgccctcga 660

ggcataaata ccctcccatc ccgttgccgc aagactcaga tcagattccg atccccagtt 720

cttccccaat caccttgtgg tctctcgtgt cgcggttccc agggacgcct ccggctcgtc 780

gctcgacagc gatctccgcc ccagcaaggt atagattcag ttccttgctc cgatcccaat 840

ctggttgaga tgttgctccg atgcgacttg attatgtcat atatctgcgg tttgcaccga 900

tctgaagcct agggtttctc gagcgaccca gttgtttgca atttgcgatt tgctcgtttg 960

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tgcttaatca cgccatgtga cgcggttact tgcagaggct gggttagtgg gttctgttat 1080

gtcgtgatct aagaatctag attaggctca gtcgttcttg ctgtcgacta gtttgttttg 1140

atatccatgt agtacaagtt acttaaaatt taggtccaat atattttgca tgcttttggc 1200

ctgttattct tgccaacaag ttgtcctggt aaaaagtaga tgtgaaagtc acgtattggg 1260

acaaattgat ggttaagtgc tatagttcta tagttctgtg atacatctat ctgatttttt 1320

ttggtctatt ggtgcctaac ttatctgaaa atcatggaac atgaggctag tttgatcatg 1380

gtttagttca ttgtgattaa taatgtatga tttagtagct attttggtga tcgtgtcatt 1440

ttatttgtga atggaatcat tgtatgtaaa tgaagctagt tcaggggtta tgatgtagct 1500

ggctttgtat tctaaaggct gctattattc atccatcgat ttcacctata tgtaatccag 1560

agctttcgat gtgaaatttg tctgatcctt cactaggaag gacagaacat tgttaatatt 1620

ttggcacatc tgtcttattc tcatcctttg tttgaacatg ttagcctgtt caaacagata 1680

ctgttgtaat gtcctagtta tataggtaca tatgtgttct ctattgagtt tatggacttt 1740

tgtgtgtgaa gttatatttc attttgctca aaactcatgt ttgcaagctt tctgacatta 1800

ttctattgtt ctgaaacag 1819

<210> SEQ ID NO 40
<211> LENGTH: 681
<212> TYPE: DNA
<213> ORGANISM: Setaria viridis

<400> SEQUENCE: 40

cacgggtaat gcacgcagcc acccaggcgc gcgcgctagc ggagcacggt caggtgacac 60

gggcgtcgtg acgcttccga gttgaagggg ttaacgccag aaacagtgtt tggccagggt 120

atgaacataa caaaaaatat tcacacgaaa gaatggaagt atggagctgc tactgtgtaa 180

atgccaagca ggaaactcac gcccgctaac atccaacggc caacagctcg acgtgccggt 240

cagcagagac atcggaacac tggtgattgg tggagccggc agtatgcgcc ccagcacggc 300

cgaggtggtg gtggcccgtg gccctgctgt ctgcgcggct cgggacaact tgaaactggg 360

ccaccgcctc gtcgcaactc gcaacccgtt ggcggaagaa aggaatggct cgtaggggcc 420

cgggtagaat ccaagaatgt tgcgctgggc ttcgattcac ataacatggg cctgaagctc 480

taaaacgacg gcccggtcac cgggcgatgg aaagagaccg gatcctcctt gtgaattctg 540

gaaggccaca cgagagcgac ccaccaccga cgcggaggag tcgtgcgtgg tccaacacgg 600

ccggcgggct gggctgcgac cttaaccagc aaggcacgcc acgacccgcc tcgccctcga 660

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ggcataaata ccctcccatc c 681

<210> SEQ ID NO 41
<211> LENGTH: 1922
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 41

gtcgtgcccc tctctagaga taatgagcat tgcatgtcta agttataaaa aattaccaca 60

tatttttttt tgtcacactt gtgtttgaag tgcagtttat ctatctctat acatatattt 120

aaacttcact atatgaataa tatagtctat agtattaaaa taatatcaat gttttagatg 180

attatataac tgaactgcta gacatggtct aaaggacaac cgagtatttt gacaacatga 240

ctctacagtt ttatcttttt agtgtgcatg tgttcttttt acttttgcaa atagcttcac 300

ctatataata cttcatccat tttattagta catccattta ctaaattttt agtacatcta 360

ttttattcta ttttagcctc taaattaaga aaacttaaac tctattttag ttttttattt 420

aataatttag atataaaata gaataaaata aagtgactaa aaaataacta aatacctttt 480

aagaaataaa aaaactaagg aaccattttt cttgttccga gtagataatg acagcctgtt 540

caacgccgtc gacgagtcta acggacacca accagcgaac cagcagcgtc gcgtcgggcc 600

aagcgaagca gacggcacgg catctctgta gctgcctctg gacccctctc gagagttccg 660

ctccaccgtt ggacttgctc cgctgtcggc atccagaaat tgcgtggcgg agcggcagac 720

gtgagccggc acggcaggcg gcctcctctc acggcaccgg cagctacggg ggattccttt 780

cccaccgctc cttcgctttc ccttcctcgc ccgccgtaat aaatagaccc cctccacacc 840

ctctttcccc aacctcgtgt tcgttcggag cgcgcacaca cacaaccaga tctcccccaa 900

atccacccgt cggcacctcc gcttcaaggt acgccgctca tcctcctccc ccccctctct 960

ctaccttctc tagatcggcg tttcggtcca tggttagggc ccggtagttc tacttctgtt 1020

catgtttgtg ttagatccgt gtttgtgtta gatccgtgct gctagatttc gtacacggat 1080

gcgacctgta catcagacat gttctgattg ctaacttgcc agtgtttctc tttggggaat 1140

cctgggatgg ctctagccgt tccgcagacg ggatcgattt catgaatttt ttttgtttcg 1200

ttgcataggg tttggtttgc ccttttcctt tatttcaata tatgccgtgc acttgtttgt 1260

cgggtcatct tttcatgttt tttttggctt ggttgtgatg atgtggtctg gttgggcggt 1320

cgttctagat cggagtagaa tactgtttca aactacctgg tggatttatt aaaggatctg 1380

tatgtatgtg ccatacatct tcatagttac gagtttaaga tgatggatgg aaatatcgat 1440

ctaggatagg tatacatgtt gatgcgggtt ttactgatgc atatacagag atgctttttt 1500

ttcgcttggt tgtgatgatg tggtctggtc gggcggtcgt tctagatcgg agtagaatac 1560

tgtttcaaac tacctggtgg atttattaat tttggatctg tatgtgtgtc atacatcttc 1620

atagttacga gtttaagatc gatggaaata tcgatctagg ataggtatac atgttgatgt 1680

gggttttact gatgcatata catggcatat gcagcatcta ttcatatgct ctaaccttga 1740

gtacctatct attataataa acaagtatgt tttataatta ttttgatctt gatatacttg 1800

gatgatggca tatgcagcag ctatatgtgg attttttttag ccctgccttc atacgctatt 1860

tatttgcttg gtactgtttc ttttgtcgat gctcaccctg ttgtttggtg atacttctgc 1920

ag 1922

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<210> SEQ ID NO 42
<211> LENGTH: 850
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 42

gtcgtgcccc tctctagaga taatgagcat tgcatgtcta agttataaaa aattaccaca 60

tatttttttt tgtcacactt gtgtttgaag tgcagtttat ctatctctat acatatattt 120

aaacttcact atatgaataa tatagtctat agtattaaaa taatatcaat gttttagatg 180

attatataac tgaactgcta gacatggtct aaaggacaac cgagtatttt gacaacatga 240

ctctacagtt ttatcttttt agtgtgcatg tgttcttttt acttttgcaa atagcttcac 300

ctatataata cttcatccat tttattagta catccattta ctaaattttt agtacatcta 360

ttttattcta ttttagcctc taaattaaga aaacttaaac tctattttag ttttttattt 420

aataatttag atataaaata gaataaaata aagtgactaa aaaataacta aatacctttt 480

aagaaataaa aaaactaagg aaccattttt cttgttccga gtagataatg acagcctgtt 540

caacgccgtc gacgagtcta acggacacca accagcgaac cagcagcgtc gcgtcgggcc 600

aagcgaagca gacggcacgg catctctgta gctgcctctg gacccctctc gagagttccg 660

ctccaccgtt ggacttgctc cgctgtcggc atccagaaat tgcgtggcgg agcggcagac 720

gtgagccggc acggcaggcg gcctcctctc acggcaccgg cagctacggg ggattccttt 780

cccaccgctc cttcgctttc ccttcctcgc ccgccgtaat aaatagaccc cctccacacc 840

ctctttcccc 850

<210> SEQ ID NO 43
<211> LENGTH: 78
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 43

aacctcgtgt tcgttcggag cgcgcacaca cacaaccaga tctcccccaa atccacccgt 60

cggcacctcc gcttcaag 78

<210> SEQ ID NO 44
<211> LENGTH: 994
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 44

gtacgccgct catcctcctc ccccccctct ctctaccttc tctagatcgg cgtttcggtc 60

catggttagg gcccggtagt tctacttctg ttcatgtttg tgttagatcc gtgtttgtgt 120

tagatccgtg ctgctagatt tcgtacacgg atgcgacctg tacatcagac atgttctgat 180

tgctaacttg ccagtgtttc tctttgggga atcctgggat ggctctagcc gttccgcaga 240

cgggatcgat ttcatgaatt ttttttgttt cgttgcatag ggtttggttt gccctttcc 300

tttatttcaa tatatgccgt gcacttgttt gtcgggtcat cttttcatgt tttttttggc 360

ttggttgtga tgatgtggtc tggttgggcg gtcgttctag atcggagtag aatactgttt 420

caaactacct ggtggattta ttaaaggatc tgtatgtatg tgccatacat cttcatagtt 480

acgagtttaa gatgatggat ggaaatatcg atctaggata ggtatacatg ttgatgcggg 540

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ttttactgat gcatatacag agatgctttt ttttcgcttg gttgtgatga tgtggtctgg 600

tcgggcggtc gttctagatc ggagtagaat actgtttcaa actacctggt ggatttatta 660

attttggatc tgtatgtgtg tcatacatct tcatagttac gagtttaaga tcgatggaaa 720

tatcgatcta ggataggtat acatgttgat gtgggtttta ctgatgcata tacatggcat 780

atgcagcatc tattcatatg ctctaacctt gagtacctat ctattataat aaacaagtat 840

gttttataat tattttgatc ttgatatact tggatgatgg catatgcagc agctatatgt 900

ggatttttt agccctgcct tcatacgcta tttatttgct tggtactgtt tcttttgtcg 960

atgctcaccc tgttgtttgg tgatacttct gcag 994

<210> SEQ ID NO 45
<211> LENGTH: 1971
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 45

gtcgtgcccc tctctagaga taaagagcat tgcatgtcta agttataaaa aattaccaca 60

tatttttttt gtcacacttg tttgaagtgc agtttatcta tctttataca tatatttaaa 120

ctttactcta cgaataatat aatctatagt actacaataa tatcagtgtt ttagagaatc 180

atataaatga acagttagac atggtctaaa ggacaattga gtattttgac aacaggactc 240

tacagtttta tctttttagt gtgcatgtgt tctccttttt tttttgcaaa tagcttcacc 300

tatataatac ttcatccatt ttattagtac atccatttag ggtttagggt taatggtttt 360

tatagactaa tttttttagt acatctattt tattctattt tagcctctaa attaagaaaa 420

ctaaaactct attttagttt ttttatttaa taatttagat ataaaataga ataaaataaa 480

gtgactaaaa attaaacaaa tacccttttaa gaaattaaaa aaactaagga aacatttttc 540

ttgtttcgag tagataatgc cagcctgtta aacgccgtcg acgagtctaa cggacaccaa 600

ccagcgaacc agcagcgtcg cgtcgggcca agcgaagcag acggcacggc atctctgtcg 660

ctgcctctgg acccctctcg agagttccgc tccaccgttg gacttgctcc gctgtcggca 720

tccagaaatt gcgtggcgga gcggcagacg tgagccggca cggcaggcgg cctcctcctc 780

ctctcacggc accggcagct acgggggatt cctttcccac cgctccttcg ctttcccttc 840

ctcgcccgcc gtaataaata gacacccccc ccacaccttc tttccccaac ctcgtgttgt 900

tcggagcgca cacacacaca accagatctc ccccaaatcc acccgtcggc acctccgctt 960

caaggtacgc cgctcatcct ccccccccc tctctacctt ctctagatcg gcgttccggt 1020

ccatggttag ggcccggtag ttctacttct gttcatgttt gtgttagatc cgtgtttgtg 1080

ttagatccgt gctgctagcg ttcgtacacg gatgcgacct gtacgtcaga cacgttctga 1140

ttgctaactt gccagtgttt ctctttgggg aatcctggga tggctctagc cgttccgcag 1200

acgggatcga tttcatgatt ttttttgttt cgttgcatag ggtttggttt gccctttcc 1260

tttatttcaa tatatgccgt gcacttgttt gtcgggtcat cttttcatgc tttttttgt 1320

cttggttgtg atgatgtggt ctggttgggc ggtcgttcta gatcggagaa gaattctgtt 1380

tcaaactacc tggtggattt attaattttg gatctgtatg tgtgtgccat acatattcat 1440

agttacgaat tgaagatgat ggatggaaat atcgatctag gataggtata catgttgatg 1500

cgggttttac tgatgcatat acagagatgc tttttgttcg cttggttgtg atgatgtggt 1560

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ctggttgggc ggtcgttcat tcgttctaga tcggagtaga atactgtttc aaactacctg 1620

gtgtatttat taattttgga actgtatgtg tgtgtcatac atcttcatag ttacgagttt 1680

aagatggatg gaaatatcga tctaggatag gtatacatgt tgatgtgggt tttactgatg 1740

catatacatg atggcatatg cagcatctat tcatatgctc taaccttgag tacctatcta 1800

ttataataaa caagtatgtt ttataattat tttgatcttg atatacttgg atgatggcat 1860

atgcagcagc tatatgtgga ttttttttagc cctgccttca tacgctattt atttgcttgg 1920

tactgtttct tttgtcgatg ctcaccctgt tgtttggtga tacttctgca g 1971

<210> SEQ ID NO 46
<211> LENGTH: 887
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 46

gtcgtgcccc tctctagaga taaagagcat tgcatgtcta agttataaaa aattaccaca 60

tatttttttt gtcacacttg tttgaagtgc agtttatcta tctttataca tatatttaaa 120

ctttactcta cgaataatat aatctatagt actacaataa tatcagtgtt ttagagaatc 180

atataaatga acagttagac atggtctaaa ggacaattga gtattttgac aacaggactc 240

tacagtttta tctttttagt gtgcatgtgt tctccttttt tttttgcaaa tagcttcacc 300

tatataatac ttcatccatt ttattagtac atccatttag ggtttagggt taatggtttt 360

tatagactaa tttttttagt acatctattt tattctattt tagcctctaa attaagaaaa 420

ctaaaactct attttagttt ttttatttaa taatttagat ataaaataga ataaaataaa 480

gtgactaaaa attaaacaaa tacccttaa gaaattaaaa aaactaagga aacatttttc 540

ttgtttcgag tagataatgc cagcctgtta aacgccgtcg acgagtctaa cggacaccaa 600

ccagcgaacc agcagcgtcg cgtcgggcca agcgaagcag acggcacggc atctctgtcg 660

ctgcctctgg acccctctcg agagttccgc tccaccgttg gacttgctcc gctgtcggca 720

tccagaaatt gcgtggcgga gcggcagacg tgagccggca cggcaggcgg cctcctcctc 780

ctctcacggc accggcagct acgggggatt cctttcccac cgctccttcg ctttcccttc 840

ctcgcccgcc gtaataaata gacacccccc ccacaccttc tttcccc 887

<210> SEQ ID NO 47
<211> LENGTH: 77
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 47

aacctcgtgt tgttcggagc gcacacacac acaaccagat ctcccccaaa tccacccgtc 60

ggcacctccg cttcaag 77

<210> SEQ ID NO 48
<211> LENGTH: 1007
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 48

gtacgccgct catcctcccc ccccctctc taccttctct agatcggcgt tccggtccat 60

ggttagggcc cggtagttct acttctgttc atgtttgtgt tagatccgtg tttgtgttag 120

-continued

atccgtgctg ctagcgttcg tacacggatg cgacctgtac gtcagacacg ttctgattgc 180

taacttgcca gtgtttctct ttggggaatc ctgggatggc tctagccgtt ccgcagacgg 240

gatcgatttc atgatttttt ttgtttcgtt gcatagggtt tggtttgccc ttttccttta 300

tttcaatata tgccgtgcac ttgtttgtcg ggtcatcttt tcatgctttt ttttgtcttg 360

gttgtgatga tgtggtctgg ttgggcggtc gttctagatc ggagaagaat tctgtttcaa 420

actacctggt ggatttatta attttggatc tgtatgtgtg tgccatacat attcatagtt 480

acgaattgaa gatgatggat ggaaatatcg atctaggata ggtatacatg ttgatgcggg 540

ttttactgat gcatatacag agatgctttt tgttcgcttg gttgtgatga tgtggtctgg 600

ttgggcggtc gttcattcgt tctagatcgg agtagaatac tgtttcaaac tacctggtgt 660

atttattaat tttggaactg tatgtgtgtg tcatacatct tcatagttac gagtttaaga 720

tggatggaaa tatcgatcta ggataggtat acatgttgat gtgggtttta ctgatgcata 780

tacatgatgg catatgcagc atctattcat atgctctaac cttgagtacc tatctattat 840

aataaacaag tatgttttat aattattttg atcttgatat acttggatga tggcatatgc 900

agcagctata tgtggatttt tttagccctg ccttcatacg ctatttattt gcttggtact 960

gtttcttttg tcgatgctca ccctgttgtt tggtgatact tctgcag 1007

<210> SEQ ID NO 49
<211> LENGTH: 2005
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 49

gtcgtgcccc tctctagaga taaagagcat tgcatgtcta aagtataaaa aattaccaca 60

tatttttttg tcacacttat ttgaagtgta gtttatctat ctctatacat atatttaaac 120

ttcactctac aaataatata gtctataata ctaaaataat attagtgttt tagaggatca 180

tataaataaa ctgctagaca tggtctaaag gataattgaa tattttgaca atctacagtt 240

ttatcttttt agtgtgcatg tgatctctct gtttttttttg caaatagctt gacctatata 300

atacttcatc cattttatta gtacatccat ttaggattta gggttgatgg tttctataga 360

ctaatttttа gtacatccat tttattcttt ttagtctcta aatttttttaa aactaaaact 420

ctattttagt tttttattta ataatttaga tataaaatga aataaaataa attgactaca 480

aataaaacaa atacccttta agaaataaaa aaactaagca aacatttttc ttgtttcgag 540

tagataatga caggctgttc aacgccgtcg acgagtctaa cggacaccaa ccagcgaacc 600

agcagcgtcg cgtcgggcca agcgaagcag acggcacggc atctctgtag ctgcctctgg 660

acccctctcg agagttccgc tccaccgttg gacttgctcc gctgtcggca tccagaaatt 720

gcgtggcgga gcggcagacg tgaggcggca cggcaggcgg cctcttcctc ctctcacggc 780

accggcagct acgggggatt cctttcccac cgctccttcg ctttcccttc ctcgcccgcc 840

gtaataaata gacacccccт ccacaccctc tttccccaac ctcgtgttcg ttcggagcgc 900

acacacacgc aaccagatct cccccaaatc cagccgtcgg cacctccgct tcaaggtacg 960

ccgctcatcc tccccccccc cctctctcta ccttctctag atcggcgatc cggtccatgg 1020

ttagggcccg gtagttctac ttctgttcat gtttgtgtta gagcaaacat gttcatgttc 1080

atgtttgtga tgatgtggtc tggttgggcg gtcgttctag atcggagtag gatactgttt 1140

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gttacgagtt taagatgatg gatggaaata tcgatctagg ataggtatac atgttgatgc 1260

gggttttact gatgcatata cagagatgct ttttttctcg cttggttgtg atgatatggt 1320

ctggttgggc ggtcgttcta gatcggagta gaatactgtt tcaaactacc tggtggattt 1380

attaaaggat aaagggtcgt tctagatcgg agtagaatac tgtttcaaac tacctggtgg 1440

atttattaaa ggatctgtat gtatgtgcct acatcttcat agttacgagt ttaagatgat 1500

ggatggaaat atcgatctag gataggtata catgttgatg cgggttttac tgatgcatat 1560

acagagatgc tttttttcgc ttggttgtga tgatgtggtc tggttgggcg gtcgttctag 1620

atcggagtag aatactgttt caaactacct ggtggattta ttaattttgt atctttatgt 1680

gtgtgccata catcttcata gttacgagtt taagatgatg gatggaaata ttgatctagg 1740

ataggtatac atgttgatgt gggttttact gatgcatata catgatggca tatgcggcat 1800

ctattcatat gctctaacct tgagtaccta tctattataa taaacaagta tgttttataa 1860

ttattttgat cttgatatac ttggatgatg gcatatgcag cagctatatg tggatttttt 1920

agccctgcct tcatacgcta tttatttgct tggtactgtt tcttttgtcc gatgctcacc 1980

ctgttgttgg gtgatacttc tgcag 2005

<210> SEQ ID NO 50
<211> LENGTH: 877
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 50

gtcgtgcccc tctctagaga taaagagcat tgcatgtcta aagtataaaa aattaccaca 60

tatttttttg tcacacttat ttgaagtgta gtttatctat ctctatacat atatttaaac 120

ttcactctac aaataatata gtctataata ctaaaataat attagtgttt tagaggatca 180

tataaataaa ctgctagaca tggtctaaag gataattgaa tattttgaca atctacagtt 240

ttatcttttt agtgtgcatg tgatctctct gttttttttg caaatagctt gacctatata 300

atacttcatc cattttatta gtacatccat ttaggattta gggttgatgg tttctataga 360

ctaattttta gtacatccat tttattcttt ttagtctcta aatttttaa aactaaaact 420

ctattttagt tttttattta ataatttaga tataaaatga aataaaataa attgactaca 480

aataaaacaa atacccttta agaaataaaa aaactaagca aacatttttc ttgtttcgag 540

tagataatga caggctgttc aacgccgtcg acgagtctaa cggacaccaa ccagcgaacc 600

agcagcgtcg cgtcgggcca agcgaagcag acggcacggc atctctgtag ctgcctctgg 660

acccctctcg agagttccgc tccaccgttg gacttgctcc gctgtcggca tccagaaatt 720

gcgtggcgga gcggcagacg tgaggcggca cggcaggcgg cctcttcctc ctctcacggc 780

accggcagct acgggggatt cctttcccac cgctccttcg ctttcccttc ctcgcccgcc 840

gtaataaata gacacccccc ccacaccctc tttcccc 877

<210> SEQ ID NO 51
<211> LENGTH: 78
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 51

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aacctcgtgt tcgttcggag cgcacacaca cgcaaccaga tctcccccaa atccagccgt 60

cggcacctcc gcttcaag 78

<210> SEQ ID NO 52
<211> LENGTH: 1050
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 52

gtacgccgct catcctcccc ccccccctct ctctaccttc tctagatcgg cgatccggtc 60

catggttagg gcccggtagt tctacttctg ttcatgtttg tgttagagca aacatgttca 120

tgttcatgtt tgtgatgatg tggtctggtt gggcggtcgt tctagatcgg agtaggatac 180

tgtttcaagc tacctggtgg atttattaat tttgtatctg tatgtgtgtg ccatacatct 240

tcatagttac gagtttaaga tgatggatgg aaatatcgat ctaggatagg tatacatgtt 300

gatgcgggtt ttactgatgc atatacagag atgctttttt tctcgcttgg ttgtgatgat 360

atggtctggt tgggcggtcg ttctagatcg gagtagaata ctgtttcaaa ctacctggtg 420

gatttattaa aggataaagg gtcgttctag atcggagtag aatactgttt caaactacct 480

ggtggattta ttaaaggatc tgtatgtatg tgcctacatc ttcatagtta cgagtttaag 540

atgatggatg gaaatatcga tctaggatag gtatacatgt tgatgcgggt tttactgatg 600

catatacaga gatgcttttt ttcgcttggt tgtgatgatg tggtctggtt gggcggtcgt 660

tctagatcgg agtagaatac tgtttcaaac tacctggtgg atttattaat tttgtatctt 720

tatgtgtgtg ccatacatct tcatagttac gagtttaaga tgatggatgg aaatattgat 780

ctaggatagg tatacatgtt gatgtgggtt ttactgatgc atatacatga tggcatatgc 840

ggcatctatt catatgctct aaccttgagt acctatctat tataataaac aagtatgttt 900

tataattatt ttgatcttga tatacttgga tgatggcata tgcagcagct atatgtggat 960

tttttagccc tgccttcata cgctatttat ttgcttggta ctgtttcttt tgtccgatgc 1020

tcaccctgtt gttgggtgat acttctgcag 1050

<210> SEQ ID NO 53
<211> LENGTH: 2005
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 53

gtcgtgcccc tctctagaga taaagagcat tgcatgtcta aagtataaaa aattaccaca 60

tatttttttg tcacacttat ttgaagtgta gtttatctat ctctatacat atatttaaac 120

ttcactctac aaataatata gtctataata ctaaaataat attagtgttt tagaggatca 180

tataaataaa ctgctagaca tggtctaaag gataattgaa tattttgaca atctacagtt 240

ttatcttttt agtgtgcatg tgatctctct gttttttttg caaatagctt gacctatata 300

atacttcatc cattttatta gtacatccat ttaggattta gggttgatgg tttctataga 360

ctaattttta gtacatccat tttattcttt ttagtctcta aatttttaa aactaaaact 420

ctattttagt tttttattta ataatttaga tataaaatga aataaaataa attgactaca 480

aataaaacaa atacccttta agaaataaaa aaactaagca aacatttttc ttgtttcgag 540

tagataatga caggctgttc aacgccgtcg acgagtctaa cggacaccaa ccagcgaacc 600

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agcagcgtcg cgtcgggcca agcgaagcag acggcacggc atctctgtag ctgcctctgg 660

acccctctcg agagttccgc tccaccgttg gacttgctcc gctgtcggca tccagaaatt 720

gcgtggcgga gcggcagacg tgaggcggca cggcaggcgg cctcttcctc ctctcacggc 780

accggcagct acgggggatt cctttcccac cgctccttcg ctttcccttc ctcgcccgcc 840

gtaataaata gacacccccc ccacaccctc tttccccaac ctcgtgttcg ttcggagcgc 900

acacacacgc aaccagatct cccccaaatc cagccgtcgg cacctccgct tcaaggtacg 960

ccgctcatcc tccccccccc cctctctcta ccttctctag atcggcgatc cggtccatgg 1020

ttagggcccg gtagttctac ttctgttcat gtttgtgtta gagcaaacat gttcatgttc 1080

atgtttgtga tgatgtggtc tggttgggcg gtcgttctag atcggagtag gatactgttt 1140

caagctacct ggtggattta ttaattttgt atctgtatgt gtgtgccata catcttcata 1200

gttacgagtt taagatgatg gatggaaata tcgatctagg ataggtatac atgttgatgc 1260

gggttttact gatgcatata cagagatgct ttttttctcg cttggttgtg atgatatggt 1320

ctggttgggc ggtcgttcta gatcggagta gaatactgtt tcaaactacc tggtggattt 1380

attaaaggat aaagggtcgt tctagatcgg agtagaatac tgtttcaaac tacctggtgg 1440

atttattaaa ggatctgtat gtatgtgcct acatcttcat agttacgagt ttaagatgat 1500

ggatggaaat atcgatctag gataggtata catgttgatg cgggttttac tgatgcatat 1560

acagagatgc ttttttcgc ttggttgtga tgatgtggtc tggttgggcg gtcgttctag 1620

atcggagtag aatactgttt caaactacct ggtggattta ttaattttgt atctttatgt 1680

gtgtgccata catcttcata gttacgagtt taagatgatg gatggaaata ttgatctagg 1740

ataggtatac atgttgatgt gggttttact gatgcatata catgatggca tatgcggcat 1800

ctattcatat gctctaacct tgagtaccta tctattataa taaacaagta tgttttataa 1860

ttattttgat cttgatatac ttggatgatg gcatatgcag cagctatatg tggatttttt 1920

agccctgcct tcatacgcta tttatttgct tggtactgtt tcttttgtcc gatgctcacc 1980

ctgttgtttg gtgatacttc tgcag 2005

<210> SEQ ID NO 54
<211> LENGTH: 1050
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 54

gtacgccgct catcctcccc ccccccctct ctctaccttc tctagatcgg cgatccggtc 60

catggttagg gcccggtagt tctacttctg ttcatgtttg tgttagagca aacatgttca 120

tgttcatgtt tgtgatgatg tggtctggtt gggcggtcgt tctagatcgg agtaggatac 180

tgtttcaagc tacctggtgg atttattaat tttgtatctg tatgtgtgtg ccatacatct 240

tcatagttac gagtttaaga tgatggatgg aaatatcgat ctaggatagg tatacatgtt 300

gatgcgggtt ttactgatgc atatacagag atgctttttt tctcgcttgg ttgtgatgat 360

atggtctggt tgggcggtcg ttctagatcg gagtagaata ctgtttcaaa ctacctggtg 420

gatttattaa aggataaagg gtcgttctag atcggagtag aatactgttt caaactacct 480

ggtggattta ttaaaggatc tgtatgtatg tgcctacatc ttcatagtta cgagtttaag 540

atgatggatg gaaatatcga tctaggatag gtatacatgt tgatgcgggt tttactgatg 600

-continued

catatacaga gatgcttttt ttcgcttggt tgtgatgatg tggtctggtt gggcggtcgt 660

tctagatcgg agtagaatac tgtttcaaac tacctggtgg atttattaat tttgtatctt 720

tatgtgtgtg ccatacatct tcatagttac gagtttaaga tgatggatgg aaatattgat 780

ctaggatagg tatacatgtt gatgtgggtt ttactgatgc atatacatga tggcatatgc 840

ggcatctatt catatgctct aaccttgagt acctatctat tataataaac aagtatgttt 900

tataattatt ttgatcttga tatacttgga tgatggcata tgcagcagct atatgtggat 960

tttttagccc tgccttcata cgctatttat ttgcttggta ctgtttcttt tgtccgatgc 1020

tcaccctgtt gtttggtgat acttctgcag 1050

<210> SEQ ID NO 55
<211> LENGTH: 1632
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 55

ccaagtccaa atgtcaattc ccttgaagat gatctatttt tatcttttgc attttgttat 60

ggaagtttgc aaatagcaac aaatgctaag tcaatttgcc aaagtctttg gagatgctct 120

tagtctataa ttgaacaata tttgtaaaat acaaaaaaaa atagtactat ttttatttta 180

aaaaattttt ggaagtaaac aaggccgagg atggggaaac ggaagtccaa cacgtcgttt 240

tctaagttgg gctcaaaagc ccatcacgga actgacctgc tatgggtcgg aggagagcgc 300

gtccagatgg ttccagaggc tggtggtggt gggccaaacg cggaactccg ccaccgccac 360

ggcctcgtgc gcaagcgcag cgcgttgccg tgagccgtga cgtaaccctc cgttgcccac 420

gataaaagct ccacccccga ccccggcccc ccgatttccc ctacggacca gtctcccccc 480

gatcgcaatc gcgaattcgt cgcaccatcg gcacgcagac gaacgaagca aggctctccc 540

catcggctcg tcaaggtatg cgttccctag atttgttccc ttcctctctc ggtttgtcta 600

tatatatgca tgtatggtcg attcccgatc tcgtcgattc tcggtttcgc cttccgtacg 660

aagattcgtt tagattgttc atatgttctg ttgtgttacc agattgatcg gatcaacttg 720

atccagttat cttcgctcct ccgattagat ccgtttctat ttcagtatat atatactagt 780

atagtatcta gggttcacac tgttgaccga ctggttactt ggaattgatc cgtgctgagt 840

tcagttgttg ccgtccataa aggcccgtgc tattgtctgt tctgaaacga aatcctgtag 900

atttcttagg gttagtgttc aattcatcaa aaggttgatt agtgaattat caaatttgag 960

agggttaaat cattctcatc atgttgtctc gaatgtaatc ccaaagatat tatagactgt 1020

gtttcgattt gatggattga tttgtgtatc atctaaatca acaaggctaa gtcatcagtt 1080

catagaatca tgtttaggtt tccgttcaat agactagttt tatcaatata taaaattata 1140

agaagggtag ggtaaatcac gttgcctcaa atgccatcct gtatggtttg gtttcaattc 1200

aattagtttg gttgattagg gtatgctctg gattaagatg gttaaatctt ccctagcatc 1260

ttccctgcct atccttactt gatccgtttc ggatatgttg gaagtacagc gagcttattt 1320

catgttgata gtgacccctt tcagattata ctattgaata ttgtatgttt gccacttctg 1380

tatgttgaat tatcctgcta aattagcaat ggaattagca tattggcaat tggtatgcat 1440

ggacctaatc aggacggatg tggttatgtt agtttcaatt cattgtcaat tcattgttca 1500

cctgcgttag atatatatga tgatttttac gtgtagttca tagttcttga gttttggatc 1560

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tttcttatct gatatatgct ttcctgtgcc tgtgctttat tgtgtcttac catgcgattt 1620

ttgtctatgc ag 1632

<210> SEQ ID NO 56
<211> LENGTH: 401
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 56

ccaagtccaa atgtcaattc ccttgaagat gatctatttt tatcttttgc attttgttat 60

ggaagtttgc aaatagcaac aaatgctaag tcaatttgcc aaagtctttg gagatgctct 120

tagtctataa ttgaacaata tttgtaaaat acaaaaaaaa atagtactat ttttatttta 180

aaaaattttt ggaagtaaac aaggccgagg atggggaaac ggaagtccaa cacgtcgttt 240

tctaagttgg gctcaaaagc ccatcacgga actgacctgc tatgggtcgg aggagagcgc 300

gtccagatgg ttccagaggc tggtggtggt gggccaaacg cggaactccg ccaccgccac 360

ggcctcgtgc gcaagcgcag cgcgttgccg tgagccgtga c 401

<210> SEQ ID NO 57
<211> LENGTH: 154
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 57

gtaaccctcc gttgcccacg ataaaagctc cacccccgac cccggccccc cgatttcccc 60

tacggaccag tctccccccg atcgcaatcg cgaattcgtc gcaccatcgg cacgcagacg 120

aacgaagcaa ggctctcccc atcggctcgt caag 154

<210> SEQ ID NO 58
<211> LENGTH: 1077
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 58

gtatgcgttc cctagatttg ttcccttcct ctctcggttt gtctatatat atgcatgtat 60

ggtcgattcc cgatctcgtc gattctcggt ttcgccttcc gtacgaagat tcgtttagat 120

tgttcatatg ttctgttgtg ttaccagatt gatcggatca acttgatcca gttatcttcg 180

ctcctccgat tagatccgtt tctatttcag tatatatata ctagtatagt atctagggtt 240

cacactgttg accgactggt tacttggaat tgatccgtgc tgagttcagt tgttgccgtc 300

cataaaggcc cgtgctattg tctgttctga aacgaaatcc tgtagatttc ttagggttag 360

tgttcaattc atcaaaaggt tgattagtga attatcaaat ttgagagggt taaatcattc 420

tcatcatgtt gtctcgaatg taatcccaaa gatattatag actgtgtttc gatttgatgg 480

attgatttgt gtatcatcta aatcaacaag gctaagtcat cagttcatag aatcatgttt 540

aggtttccgt tcaatagact agttttatca atatataaaa ttataagaag ggtagggtaa 600

atcacgttgc ctcaaatgcc atcctgtatg gtttggtttc aattcaatta gtttggttga 660

ttagggtatg ctctggatta agatggttaa atcttcccta gcatcttccc tgcctatcct 720

tacttgatcc gtttcggata tgttggaagt acagcgagct tatttcatgt tgatagtgac 780

ccctttcaga ttatactatt gaatattgta tgtttgccac ttctgtatgt tgaattatcc 840

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tgctaaatta gcaatggaat tagcatattg gcaattggta tgcatggacc taatcaggac 900

ggatgtggtt atgttagttt caattcattg tcaattcatt gttcacctgc gttagatata 960

tatgatgatt tttacgtgta gttcatagtt cttgagtttt ggatctttct tatctgatat 1020

atgctttcct gtgcctgtgc tttattgtgt cttaccatgc gatttttgtc tatgcag 1077

<210> SEQ ID NO 59
<211> LENGTH: 2000
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 59

cactagctgc gcatgataaa gccacaagcc aaaattaatt attatgggtg agaataaata 60

cgtaccagca ccggccatag aaaaagtaca ttattaaagg tctaatttgg aaacagtctg 120

aaaacgacgt gcgctgcaga ggtaaatgta attttcggca ctaaaaccat tatcaactaa 180

ttcattcaat aacagttatt tagaaaatgt atagctcgct ctaaaaaaac agtttagaaa 240

aacagtcaaa ataattcgac caacaaacag ttaataaggt tcattaaata tataatgcac 300

ggtgctattt gatcttttaa aggaaaaaga ggaatagtcg tgggcgccag gcgggaattg 360

gggcgcggga gtctgccgga cgacgcgttc cgtccgaacg gccggacccg acgaggcccc 420

cccgccgccc cacgtcgcag aaccgtccgt gggtggtaat ctggccgggt acaccagccg 480

tcccccttggg cggcctcaca gcactgggct cacacgtgag ttttgttctg ggcttcggat 540

cgcaccatat gggcctcggc atcagaaaga cggggcccgt ctgggataga agagacagga 600

acctcctcgt ggattccaga agccagccac gagcgaccac cgacgcggag gatactcgtc 660

gtccaagtcc aacacggcgg gcgggcgggc ggacgcgtgg gctgggctaa ctgcctaacc 720

ttaacctcca aggcacgcca aggcccgctt ctcccacccg acataaatat ccccccatcc 780

aggcaaggcg cagagcctca gaccagattc cgatcaatca cccataagct ccccccaaat 840

ctgttcctcg tctcccgtct cgcggtttcc tacttccctc ggacgcctcc ggcaagtcgc 900

tcgaccgcgc gattccgccc gctcaaggta tcaactcggt tcaccactcc aatctacgtc 960

tgatttagat gttacttcca tctatgtcta atttagatgt tactccgatg cgattggatt 1020

atgtttatgc ggtttgcact gctctggaaa ctggaatcta gggtttcgag tgatttgatc 1080

gatcgcgatc tgtgatttcg ttgcgccttg tgtatgcttg gagtgatcta ggcttgtata 1140

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aatgcgagac tggtctatgg gtgctttgac cagtaatgcg agactagtta tttgatcatg 1500

gtgcagttcc tagtgattac gaacaacaat ttggtagctc agttcattca gcattggttt 1560

ctacgatcct tatcatttta cttctgaatg aatttattta tttaagatat tacagtgcaa 1620

taaactgctg tataatatca gtaacaaact gctattacta gtaaatgcct agattcataa 1680

taattcatta ttctacttga aaatgatctt aggccttttt atgcggtcct acgcatcctt 1740

ccacaggact tgctgtttgt ttgtttttg taatccctcg ctgggacgca gaatggttca 1800

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tctgtgctaa taatttttt gcatatataa gtttatagtt ctcattattc atgtggctat 1860

ggtagcctgt aaaatctatt gtaataacat attagtcagc catacatctg ttccaacttg 1920

ctcaattgca aatcatatct ccacttaaag cacatgtttg caagctttct gacaagtttc 1980

tttgtgtttg attgaaacag 2000

<210> SEQ ID NO 60
<211> LENGTH: 791
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 60

cactagctgc gcatgataaa gccacaagcc aaaattaatt attatgggtg agaataaata 60

cgtaccagca ccggccatag aaaaagtaca ttattaaagg tctaatttgg aaacagtctg 120

aaaacgacgt gcgctgcaga ggtaaatgta attttcggca ctaaaaccat tatcaactaa 180

ttcattcaat aacagttatt tagaaaatgt atagctcgct ctaaaaaaac agtttagaaa 240

aacagtcaaa ataattcgac caacaaacag ttaataaggt tcattaaata tataatgcac 300

ggtgctattt gatcttttaa aggaaaaaga ggaatagtcg tgggcgccag gcgggaattg 360

gggcgcggga gtctgccgga cgacgcgttc cgtccgaacg gccggacccg acgaggcccc 420

cccgccgccc cacgtcgcag aaccgtccgt gggtggtaat ctggccgggt acaccagccg 480

tcccccttggg cggcctcaca gcactgggct cacacgtgag ttttgttctg ggcttcggat 540

cgcaccatat gggcctcggc atcagaaaga cggggcccgt ctgggataga agagacagga 600

acctcctcgt ggattccaga agccagccac gagcgaccac cgacgcggag gatactcgtc 660

gtccaagtcc aacacggcgg gcgggcgggc ggacgcgtgg gctgggctaa ctgcctaacc 720

ttaacctcca aggcacgcca aggcccgctt ctcccacccg acataaatat ccccccatcc 780

aggcaaggcg c 791

<210> SEQ ID NO 61
<211> LENGTH: 136
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 61

agagcctcag accagattcc gatcaatcac ccataagctc cccccaaatc tgttcctcgt 60

ctcccgtctc gcggtttcct acttccctcg gacgcctccg gcaagtcgct cgaccgcgcg 120

attccgcccg ctcaag 136

<210> SEQ ID NO 62
<211> LENGTH: 1073
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 62

gtatcaactc ggttcaccac tccaatctac gtctgattta gatgttactt ccatctatgt 60

ctaatttaga tgttactccg atgcgattgg attatgttta tgcggtttgc actgctctgg 120

aaactggaat ctagggtttc gagtgatttg atcgatcgcg atctgtgatt tcgttgcgcc 180

ttgtgtatgc ttggagtgat ctaggcttgt atatgcggca tcgcgatctg acgcggttgc 240

tttgtagagg ctgggggtct aggctgtgat tttagaatca aataaagctg ttccttaccg 300

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tagatgtttc ctacatgttc tgtccagtac tccagtgcta tattcacatt gtttgaggct 360

tgagttttgt cgatcagtgg tcatgagaaa aatatatctc atgattttag aggcacctat 420

tgggaaaggt agatggttcc gttttacatg ttttatagac cttgtggcat ggctcctttg 480

ttctatgggt gctttatttt cctgaataac agtaatgcga gactggtcta tgggtgcttt 540

gaccagtaat gcgagactag ttatttgatc atggtgcagt tcctagtgat tacgaacaac 600

aatttggtag ctcagttcat tcagcattgg tttctacgat ccttatcatt ttacttctga 660

atgaatttat ttatttaaga tattacagtg caataaactg ctgtataata tcagtaacaa 720

actgctatta ctagtaaatg cctagattca taataattca ttattctact tgaaaatgat 780

cttaggcctt tttatgcggt cctacgcatc cttccacagg acttgctgtt tgtttgtttt 840

ttgtaatccc tcgctgggac gcagaatggt tcatctgtgc taataatttt tttgcatata 900

taagtttata gttctcatta ttcatgtggc tatggtagcc tgtaaaatct attgtaataa 960

catattagtc agccatacat ctgttccaac ttgctcaatt gcaaatcata tctccactta 1020

aagcacatgt ttgcaagctt tctgacaagt ttctttgtgt ttgattgaaa cag 1073

<210> SEQ ID NO 63
<211> LENGTH: 2064
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 63

cattaaaagt cattatgtgc atgcgtcgta actaacatgg atatgttgct gcactatctc 60

ctcgcactag ctgcgcatga taaagccaca agccaaaatt aattattatg ggtgagaata 120

aatacgtacc agcaccggcc atagaaaaag tacattatta aaggtctaat ttggaaacag 180

tctgaaaacg acgtgcgctg cagaggtaaa tgtaattttc ggcactaaaa ccattatcaa 240

ctaattcatt caataacagt tatttagaaa atgtatagct cgctctaaaa aaacagttta 300

gaaaaacagt caaaataatt cgaccaacaa acagttaata aggttcatta aatatataat 360

gcacggtgct atttgatctt ttaaaggaaa aagaggaata gtcgtgggcg ccaggcggga 420

attggggcgc gggagtctgc cggacgacgc gttccgtccg aacggccgga cccgacgagg 480

ccccccgccc gccccacgtc gcagaaccgt ccgtgggtgg taatctggcc gggtacacca 540

gccgtcccct tgggcggcct cacagcactg ggctcacacg tgagttttgt tctgggcttc 600

ggatcgcacc atatgggcct cggcatcaga aagacggggc ccgtctggga tagaagagac 660

aggaacctcc tcgtggattc cagaagccag ccacgagcga ccaccgacgc ggaggatact 720

cgtcgtccaa gtccaacacg gcgggcgggc gggcggacgc gtgggctggg ctaactgcct 780

aaccttaacc tccaaggcac gccaaggccc gcttctccca cccgacataa atatcccccc 840

atccaggcaa ggcgcagagc ctcagaccag attccgatca atcacccata agctcccccc 900

aaatctgttc ctcgtctccc gtctcgcggt ttcctacttc cctcggacgc ctccggcaag 960

tcgctcgacc gcgcgattcc gcccgctcaa ggtatcaact cggttcacca ctccaatcta 1020

cgtctgattt agatgttact tccatctatg tctaatttag atgttactcc gatgcgattg 1080

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catggtgcag ttcctagtga ttacgaacaa caatttggta gctcagttca ttcagcattg 1620

gtttctacga tccttatcat tttacttctg aatgaattta tttatttaag atattacagt 1680

gcaataaact gctgtataat atcagtaaca aactgctatt actagtaaat gcctagattc 1740

ataataattc attattctac ttgaaaatga tcttaggcct ttttatgcgg tcctacgcat 1800

ccttccacag gacttgctgt ttgtttgttt tttgtaatcc ctcgctggga cgcagaatgg 1860

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ctatggtagc ctgtaaaatc tattgtaata acatattagt cagccataca tctgttccaa 1980

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tttctttgtg tttgattgaa acag 2064

<210> SEQ ID NO 64
<211> LENGTH: 855
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 64

cattaaaagt cattatgtgc atgcgtcgta actaacatgg atatgttgct gcactatctc 60

ctcgcactag ctgcgcatga taaagccaca agccaaaatt aattattatg ggtgagaata 120

aatacgtacc agcaccggcc atagaaaaag tacattatta aaggtctaat ttggaaacag 180

tctgaaaacg acgtgcgctg cagaggtaaa tgtaattttc ggcactaaaa ccattatcaa 240

ctaattcatt caataacagt tatttagaaa atgtatagct cgctctaaaa aaacagttta 300

gaaaaacagt caaaataatt cgaccaacaa acagttaata aggttcatta aatatataat 360

gcacggtgct atttgatctt ttaaaggaaa aagaggaata gtcgtgggcg ccaggcggga 420

attggggcgc gggagtctgc cggacgacgc gttccgtccg aacggccgga cccgacgagg 480

ccccccgcc gccccacgtc gcagaaccgt ccgtgggtgg taatctggcc gggtacacca 540

gccgtcccct tgggcggcct cacagcactg ggctcacacg tgagttttgt tctgggcttc 600

ggatcgcacc atatgggcct cggcatcaga aagacggggc ccgtctggga tagaagagac 660

aggaacctcc tcgtggattc cagaagccag ccacgagcga ccaccgacgc ggaggatact 720

cgtcgtccaa gtccaacacg gcgggcgggc gggcggacgc gtgggctggg ctaactgcct 780

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atccaggcaa ggcgc 855

<210> SEQ ID NO 65
<211> LENGTH: 2000
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 65

agaagtaaaa aaaaagttcg tttcagaatc ataaaggtaa gttaaaaaaa gaccatacaa 60

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aaaagaggta tttaatgata aactataatc cagaatttgt taggatagta tataagaata 120

agaccttgtt tagtttcaaa aaaatttgca aaattttcca gattcctcgt cacatcaaat 180

ctttagaggt atgcatggag tattaaatat agacaagacc taaataagaa aacatgaaat 240

gttcacgaaa aaaatcaagc caatgcatga tcgaagcaaa cggtatagta acggtgttaa 300

cctgatccat tgatctttgt aatctttaac ggccacctac cgcgggcagc aaacggcgtc 360

cccctcctcg atatctccgc ggcggcctct ggctttttcc gcggaattgc gcggtgggga 420

cggattccac gagaccgcaa cgcaaccgcc tctcgccgct gggccccaca ccgctcggtg 480

ccgtagcccg tagcctcacg ggattctttc tccctcctcc cccgtgtata aattggcttc 540

atcccctccc tgcctcatcc atccaaatcc cactccccaa tcccatcccg tcggagaaat 600

tcatcgaagc gaagcgaagc gaatcctccc gatcctctca aggtacgcga gttttcgaat 660

cccctccaga cccctcgtat gctttccctg ttcgttttcg tcgtagcgtt tgattaggta 720

tgctttccct gttcgtgttc gtcgtagggt tcgattaggt cgtgtgaggc catggcctgc 780

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aggctgtaaa agggacacta cttattagct tgttgtttaa tctttttatt agtagattat 1320

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taatcataga tcactgtagt tgattgttga atcatgtgtc aaatacccgt atacataaca 1440

ctacacattt gcttagttgt ttccttaact catgcaaatt gaacaccatg tatgatttgc 1500

atggtgctgt aatgttaaat actacagtcc tgttggtact tgtttagtaa gaatctgctt 1560

catacaacta tatgctatgc ctgatgataa tcatatatct ttgtgtaatt aataattagt 1620

tgactgttga ataatgtatc gagtacatac catggcacaa ttgcttagtc acttccttaa 1680

ccatgcatat tgaactgacc ccttcatgtt ctgctgaatt gttctattct gattagacca 1740

tacatcatgt attgcaatct ttatttgcaa ttgtaatgta atggttcggt tctcaaatgt 1800

taaatgctat agttgtgcta ctttctaatg ttaaatgcta tagctgtgct acttgtaaga 1860

tctgcttcat agtttagtta aattaggatg atgagctttg atgctgtaac tttgtttgat 1920

tatgttcata gttgatcagt ttttgttaga ctcacagtaa cttatggtct cactcttctt 1980

ctggtctttg atgtttgcag 2000

<210> SEQ ID NO 66
<211> LENGTH: 565
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 66

agaagtaaaa aaaaagttcg tttcagaatc ataaaggtaa gttaaaaaaa gaccatacaa 60

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aaaagaggta tttaatgata aactataatc cagaatttgt taggatagta tataagaata 120

agaccttgtt tagtttcaaa aaaatttgca aaattttcca gattcctcgt cacatcaaat 180

ctttagaggt atgcatggag tattaaatat agacaagacc taaataagaa aacatgaaat 240

gttcacgaaa aaaatcaagc caatgcatga tcgaagcaaa cggtatagta acggtgttaa 300

cctgatccat tgatctttgt aatctttaac ggccacctac cgcgggcagc aaacggcgtc 360

cccctcctcg atatctccgc ggcggcctct ggctttttcc gcggaattgc gcggtgggga 420

cggattccac gagaccgcaa cgcaaccgcc tctcgccgct gggccccaca ccgctcggtg 480

ccgtagcccg tagcctcacg ggattctttc tccctcctcc cccgtgtata aattggcttc 540

atcccctccc tgcctcatcc atcca 565

<210> SEQ ID NO 67
<211> LENGTH: 77
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 67

aatcccactc cccaatccca tcccgtcgga gaaattcatc gaagcgaagc gaagcgaatc 60

ctcccgatcc tctcaag 77

<210> SEQ ID NO 68
<211> LENGTH: 1358
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 68

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gtagcgtttg attaggtatg ctttccctgt tcgtgttcgt cgtagggttc gattaggtcg 120

tgtgaggcca tggcctgctg tgataaattt atttgttgtt atatcggatc tgtagtcgat 180

ttgggggtcg tggtgtagat ccgcgggctg tgatgaagtt atttggtgtg attgtgctcg 240

cgtgattctg cgcgttgagc tcgagtagat ctgatggttg gacgaccgat tggttcgttg 300

gctggctgcg ctaaggttgg gctgggctca tgttgcgttc gctgttgcgc gtgattccgc 360

ggatggactt gcgcttgatt gccgccagat cacgttacga ttatgtgatt tcgtttggaa 420

ctttttagat ttgtagcttc tgcttattat atgacagatg cgcctactgc tcatatgcct 480

gtggtaaata atggatggct gtgggtcaaa ctagttgatt gtcgagtcat gtatcatata 540

caggtgtata gacttgcgtc taattgtttg catgttgcag ttatatgatt tgttttagat 600

tgtttgttcc actcatctag gctgtaaaag ggacactact tattagcttg ttgtttaatc 660

tttttattag tagattatat tggtaatgtt ttactaatta ttattatgtt atatgtgact 720

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atacccgtat acataacact acacatttgc ttagttgttt ccttaactca tgcaaattga 840

acaccatgta tgatttgcat ggtgctgtaa tgttaaatac tacagtcctg ttggtacttg 900

tttagtaaga atctgcttca tacaactata tgctatgcct gatgataatc atatatcttt 960

gtgtaattaa taattagttg actgttgaat aatgtatcga gtacatacca tggcacaatt 1020

gcttagtcac ttccttaacc atgcatattg aactgacccc ttcatgttct gctgaattgt 1080

tctattctga ttagaccata catcatgtat tgcaatcttt atttgcaatt gtaatgtaat 1140

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ggttcggttc tcaaatgtta aatgctatag ttgtgctact ttctaatgtt aaatgctata 1200

gctgtgctac ttgtaagatc tgcttcatag tttagttaaa ttaggatgat gagctttgat 1260

gctgtaactt tgtttgatta tgttcatagt tgatcagttt ttgttagact cacagtaact 1320

tatggtctca ctcttcttct ggtctttgat gtttgcag 1358

<210> SEQ ID NO 69
<211> LENGTH: 2622
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 69

actgccgcga cacgcctcac tggcgggagg gctccgagcg ctctctcccc ggcggccggc 60

ggagcagcga tctggattgg agagaataga ggaaagagag ggaaaaggag agagatagcg 120

caaagagctg aaaagataag gttgtgcggg ctgtggtgat tagaggacca ctaatccctc 180

catctcctaa tgacgcggtg cccaagacca gtgccgcggc acaccagcgt ctaagtgaac 240

ttccgctaac cttccggtca ttgcgcctga aagatgtcat gtggcgaggc ccccctctca 300

gtagattgcc aactgcctac cgtgccactc ttccatgcat gattgctccc gtctatcccg 360

tttctcacaa cagatagaca acagtaagca tcactaaagc aagcatgtgt agaaccttaa 420

aaaaaggctt atactaccag tatactatca accagcatgc cgtttttgaa gtatccagga 480

ttagaagctt ctactgcgct tttatattat agctgtggac ctgtggtaac ctttctcttt 540

tggcgcttgc ttaatctcgg ccgtgctggt ccatgcttag gcactaggca gagatagagc 600

cgggggtgaa tggggctaaa gctcagctgc tcgaggggcc gtgggctggt ttccactagc 660

ctacagctgt gccacgtgcg gccgcgcaag ccgaagcaag cacgctgagc cgttggacag 720

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gcgcgcgcta gcggagcacg gtcaggtgac acgggcgtcg tgacgcttcc gagttgaagg 900

ggttaacgcc agaaacagtg tttggccagg gtatgaacat aacaaaaaat attcacacga 960

aagaatggaa gtatggagct gctactgtgt aaatgccaag caggaaactc acgcccgcta 1020

acatccaacg gccaacagct cgacgtgccg gtcagcagag catcggaaca ctggtgattg 1080

gtggagccgg cagtatgcgc cccagcacgg ccgaggtggt ggtggcccgt ggccctgctg 1140

tctgcgcggc tcgggacaac ttgaaactgg gccaccgcct cgtcgcaact cgcaacccgt 1200

tggcggaaga aaggaatggc tcgtaggggc ccgggtagaa tcgaagaatg ttgcgctggg 1260

cttcgattca cataacatgg gcctgaagct ctaaaacgac ggcccggtcg ccgcgcgatg 1320

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gattatgtca tatatctgcg gtttgcaccg atctgaagcc tagggtttct cgagcgaccc 1740

agttatttgc aatttgcgat ttgctcgttt gttgcgcagc gtagtttatg tttggagtaa 1800

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tcgaggattt gtatgcggcg tcggcgctac ctgcttaatc acgccatgtg acgcggttac 1860

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ttgctgtcga ctagtttgtt ttgatatcca tgtagtacaa gttacttaaa atttaggtcc 1980

aatatatttt gcatgctttt ggcctgttat tcttgccaac aagttgtcct ggtaaaaagt 2040

agatgtgaaa gtcacgtatt gggacaaatt gatggtttag tgctatagtt ctatagttct 2100

gtgatacatc tatctgattt tttttggtct attggtgcct aacttatctg aaaatcatgg 2160

aacatgaggc tagtttgatc atggtttagt tcattgtgat taataatgta tgatttagta 2220

gctattttgg tgatcgtgtc attttatttg tgaatggaat cattgtatgt aaatgaagct 2280

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aaggacagaa cattgttaat attttggcac atctgtctta ttctcatcct ttgtttgaac 2460

atgttagcct gttcaaacag atactgttgt aatgtcctag ttatataggt acatatgtgt 2520

tctctattga gtttatggac ttttgtgtgt gaagttatat ttcattttgc tcaaaactca 2580

tgtttgcaag ctttctgaca ttattctatt gttctgaaac ag 2622

<210> SEQ ID NO 70
<211> LENGTH: 1492
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 70

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ggagcagcga tctggattgg agagaataga ggaaagagag ggaaaaggag agagatagcg 120

caaagagctg aaaagataag gttgtgcggg ctgtggtgat tagaggacca ctaatccctc 180

catctcctaa tgacgcggtg cccaagacca gtgccgcggc acaccagcgt ctaagtgaac 240

ttccgctaac cttccggtca ttgcgcctga aagatgtcat gtggcgaggc ccccctctca 300

gtagattgcc aactgcctac cgtgccactc ttccatgcat gattgctccc gtctatcccg 360

tttctcacaa cagatagaca acagtaagca tcactaaagc aagcatgtgt agaaccttaa 420

aaaaaggctt atactaccag tatactatca accagcatgc cgtttttgaa gtatccagga 480

ttagaagctt ctactgcgct tttatattat agctgtggac ctgtggtaac ctttctcttt 540

tggcgcttgc ttaatctcgg ccgtgctggt ccatgcttag gcactaggca gagatagagc 600

cgggggtgaa tggggctaaa gctcagctgc tcgaggggcc gtgggctggt ttccactagc 660

ctacagctgt gccacgtgcg gccgcgcaag ccgaagcaag cacgctgagc cgttggacag 720

cttgtcataa tgccattacg tggattacac gtaactggcc ctgtaactac tcgttcggcc 780

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gcgcgcgcta gcggagcacg gtcaggtgac acgggcgtcg tgacgcttcc gagttgaagg 900

ggttaacgcc agaaacagtg tttggccagg gtatgaacat aacaaaaaat attcacacga 960

aagaatggaa gtatggagct gctactgtgt aaatgccaag caggaaactc acgcccgcta 1020

acatccaacg gccaacagct cgacgtgccg gtcagcagag catcggaaca ctggtgattg 1080

gtggagccgg cagtatgcgc cccagcacgg ccgaggtggt ggtggcccgt ggccctgctg 1140

tctgcgcggc tcgggacaac ttgaaactgg gccaccgcct cgtcgcaact cgcaacccgt 1200

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tggcggaaga aaggaatggc tcgtaggggc ccgggtagaa tcgaagaatg ttgcgctggg 1260

cttcgattca cataacatgg gcctgaagct ctaaaacgac ggcccggtcg ccgcgcgatg 1320

gaaagagacc ggatcctcct cgtgaattct ggaaggccac acgagagcga cccaccaccg 1380

acgcggagga gtcgtgcgtg gtccaacacg gccggcgggc tgggctgcga ccttaaccag 1440

caaggcacgc cacgacccgc cccgccctcg aggcataaat accctcccat cc 1492

<210> SEQ ID NO 71
<211> LENGTH: 127
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 71

cgttgccgca agactcagat cagattccga tccccagttc ttccccaatc accttgtggt 60

ctctcgtgtc gcggttccca gggacgcctc cggctcgtcg ctcgacagcg atctccgccc 120

cagcaag 127

<210> SEQ ID NO 72
<211> LENGTH: 1003
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 72

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cttgcagagg ctgggttctg ttatgtcgtg atctaagaat ctagattagg ctcagtcgtt 300

cttgctgtcg actagtttgt tttgatatcc atgtagtaca agttacttaa aatttaggtc 360

caatatattt tgcatgcttt tggcctgtta ttcttgccaa caagttgtcc tggtaaaaag 420

tagatgtgaa agtcacgtat tgggacaaat tgatggttta gtgctatagt tctatagttc 480

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atgtttgcaa gctttctgac attattctat tgttctgaaa cag 1003

<210> SEQ ID NO 73
<211> LENGTH: 2622
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 73

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caaagagctg aaaagataag gttgtgcggg ctgtggtgat tagaggacca ctaatccctc 180

catctcctaa tgacgcggtg cccaagacca gtgccgcggc acaccagcgt ctaagtgaac 240

ttccgctaac cttccggtca ttgcgcctga aagatgtcat gtggcgaggc ccccctctca 300

gtagattgcc aactgcctac cgtgccactc ttccatgcat gattgctccc gtctatcccg 360

tttctcacaa cagatagaca acagtaagca tcactaaagc aagcatgtgt agaaccttaa 420

aaaaaggctt atactaccag tatactatca accagcatgc cgtttttgaa gtatccagga 480

ttagaagctt ctactgcgct tttatattat agctgtggac ccgtggtaac ctttctcttt 540

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gcgcgcgcta gcggagcacg gtcaggtgac acgggcgtcg tgacgcttcc gagttgaagg 900

ggttaacgcc agaaacagtg tttggccagg gtatgaacat aacaaaaaat attcacacga 960

aagaatggaa gtatggagct gctactgtgt aaatgccaag caggaaactc acgcccgcta 1020

acatccaacg gccaacagct cgacgtgccg gtcagcagag catcggaaca ctggtgattg 1080

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tctgcgcggc tcgggacaac ttgaaactgg gccaccgcct cgtcgcaact cgcaacccgt 1200

tggcggaaga aaggaatggc tcgtaggggc ccgggtagaa tcgaagaatg ttgcgctggg 1260

cttcgattca cataacatgg gcctgaagct ctaaaacgac ggcccggtcg ccgcgcgatg 1320

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aacatgaggc tagtttgatc atggtttagt tcattgtgat taataatgta tgatttagta 2220

gctattttgg tgatcgtgtc attttatttg tgaatggaat cattgtatgt aaatgaagct 2280

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aaggacagaa cattgttaat attttggcac atctgtctta ttctcatcct ttgtttgaac 2460

atgttagcct gttcaaacag atactgttgt aatgtcctag ttatataggt acatatgtgt 2520

tctctattga gtttatggac ttttgtgtgt gaagttatat ttcattttgc tcaaaactca 2580

tgtttgcaag ctttctgaca ttattctatt gttctgaaac ag 2622

<210> SEQ ID NO 74
<211> LENGTH: 1492
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 74

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ggagcagcga tctggattgg agagaataga ggaaagagag ggaaaaggag agagatagcg 120

caaagagctg aaaagataag gttgtgcggg ctgtggtgat tagaggacca ctaatccctc 180

catctcctaa tgacgcggtg cccaagacca gtgccgcggc acaccagcgt ctaagtgaac 240

ttccgctaac cttccggtca ttgcgcctga aagatgtcat gtggcgaggc ccccctctca 300

gtagattgcc aactgcctac cgtgccactc ttccatgcat gattgctccc gtctatcccg 360

tttctcacaa cagatagaca acagtaagca tcactaaagc aagcatgtgt agaaccttaa 420

aaaaaggctt atactaccag tatactatca accagcatgc cgtttttgaa gtatccagga 480

ttagaagctt ctactgcgct tttatattat agctgtggac ccgtggtaac ctttctcttt 540

tggcgcttgc ttaatctcgg ccgtgctggt ccatgcttag gcactaggca gagatagagc 600

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gcgcgcgcta gcggagcacg gtcaggtgac acgggcgtcg tgacgcttcc gagttgaagg 900

ggttaacgcc agaaacagtg tttggccagg gtatgaacat aacaaaaaat attcacacga 960

aagaatggaa gtatggagct gctactgtgt aaatgccaag caggaaactc acgcccgcta 1020

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tggcggaaga aaggaatggc tcgtaggggc ccgggtagaa tcgaagaatg ttgcgctggg 1260

cttcgattca cataacatgg gcctgaagct ctaaaacgac ggcccggtcg ccgcgcgatg 1320

gaaagagacc ggatcctcct cgtgaattct ggaaggccac acgagagcga cccaccaccg 1380

acgcggagga gtcgtgcgtg gtccaacacg gccggcgggc tgggctgcga ccttaaccag 1440

caaggcacgc cacgacccgc cccgccctcg aggcataaat accctcccat cc 1492

<210> SEQ ID NO 75
<211> LENGTH: 2164
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 75

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aggcactagg cagagataga gccgggggtg aatggggcta aagctcagct gctcgagggg 180

ccgtgggctg gtttccacta gcctacagct gtgccacgtg cggccgcgca agccgaagca 240

agcacgctga gccgttggac agcttgtcat aatgccatta cgtggattac acgtaactgg 300

ccctgtaact actcgttcgg ccatcatcaa acgacgacgt ccgctaggcg acgacacggg 360

taatgcacgc agccacccag gcgcgcgcgc tagcggagca cggtcaggtg acacgggcgt 420

cgtgacgctt ccgagttgaa ggggttaacg ccagaaacag tgtttggcca gggtatgaac 480

ataacaaaaa atattcacac gaaagaatgg aagtatggag ctgctactgt gtaaatgcca 540

agcaggaaac tcacgcccgc taacatccaa cggccaacag ctcgacgtgc cggtcagcag 600

agcatcggaa cactggtgat tggtggagcc ggcagtatgc gccccagcac ggccgaggtg 660

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aatcgaagaa tgttgcgctg ggcttcgatt cacataacat gggcctgaag ctctaaaacg 840

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tctagattag gctcagtcgt tcttgctgtc gactagtttg ttttgatatc catgtagtac 1500

aagttactta aaatttaggt ccaatatatt ttgcatgctt ttggcctgtt attcttgcca 1560

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aggctgctat tattcatcca tcgatttcac ctatatgtaa tccagagctt ttgatgtgaa 1920

atttgtctga tccttcacta ggaaggacag aacattgtta atattttggc acatctgtct 1980

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agttatatag gtacatatgt gttctctatt gagtttatgg acttttgtgt gtgaagttat 2100

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acag 2164

<210> SEQ ID NO 76

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<211> LENGTH: 1034
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 76

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aggcactagg cagagataga gccgggggtg aatggggcta aagctcagct gctcgagggg 180

ccgtgggctg gtttccacta gcctacagct gtgccacgtg cggccgcgca agccgaagca 240

agcacgctga gccgttggac agcttgtcat aatgccatta cgtggattac acgtaactgg 300

ccctgtaact actcgttcgg ccatcatcaa acgacgacgt ccgctaggcg acgacacggg 360

taatgcacgc agccacccag gcgcgcgcgc tagcggagca cggtcaggtg acacgggcgt 420

cgtgacgctt ccgagttgaa ggggttaacg ccagaaacag tgtttggcca gggtatgaac 480

ataacaaaaa atattcacac gaaagaatgg aagtatggag ctgctactgt gtaaatgcca 540

agcaggaaac tcacgcccgc taacatccaa cggccaacag ctcgacgtgc cggtcagcag 600

agcatcggaa cactggtgat tggtggagcc ggcagtatgc gccccagcac ggccgaggtg 660

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acacgagagc gacccaccac cgacgcggag gagtcgtgcg tggtccaaca cggccggcgg 960

gctgggctgc gaccttaacc agcaaggcac gccacgaccc gccccgccct cgaggcataa 1020

ataccctccc atcc 1034

<210> SEQ ID NO 77
<211> LENGTH: 1810
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 77

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atgaacataa caaaaaatat tcacacgaaa gaatggaagt atggagctgc tactgtgtaa 180

atgccaagca ggaaactcac gcccgctaac atccaacggc caacagctcg acgtgccggt 240

cagcagagca tcggaacact ggtgattggt ggagccggca gtatgcgccc cagcacggcc 300

gaggtggtgg tggcccgtgg ccctgctgtc tgcgcggctc gggacaactt gaaactgggc 360

caccgcctcg tcgcaactcg caacccgttg gcggaagaaa ggaatggctc gtaggggccc 420

gggtagaatc gaagaatgtt gcgctgggct tcgattcaca taacatgggc ctgaagctct 480

aaaacgacgg cccggtcgcc gcgcgatgga aagagaccgg atcctcctcg tgaattctgg 540

aaggccacac gagagcgacc caccaccgac gcggaggagt cgtgcgtggt ccaacacggc 600

cggcgggctg ggctgcgacc ttaaccagca aggcacgcca cgacccgccc cgccctcgag 660

gcataaatac cctcccatcc cgttgccgca agactcagat cagattccga tccccagttc 720

ttccccaatc accttgtggt ctctcgtgtc gcggttccca gggacgcctc cggctcgtcg 780

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aatggaatca ttgtatgtaa atgaagctag ttcaggggtt acgatgtagc tggctttgta 1500

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tgtcctagtt atataggtac atatgtgttc tctattgagt ttatggactt ttgtgtgtga 1740

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tctgaaacag 1810

<210> SEQ ID NO 78
<211> LENGTH: 680
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 78

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gggcgtcgtg acgcttccga gttgaagggg ttaacgccag aaacagtgtt tggccagggt 120

atgaacataa caaaaaatat tcacacgaaa gaatggaagt atggagctgc tactgtgtaa 180

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cagcagagca tcggaacact ggtgattggt ggagccggca gtatgcgccc cagcacggcc 300

gaggtggtgg tggcccgtgg ccctgctgtc tgcgcggctc gggacaactt gaaactgggc 360

caccgcctcg tcgcaactcg caacccgttg gcggaagaaa ggaatggctc gtaggggccc 420

gggtagaatc gaagaatgtt gcgctgggct tcgattcaca taacatgggc ctgaagctct 480

aaaacgacgg cccggtcgcc gcgcgatgga aagagaccgg atcctcctcg tgaattctgg 540

aaggccacac gagagcgacc caccaccgac gcggaggagt cgtgcgtggt ccaacacggc 600

cggcgggctg ggctgcgacc ttaaccagca aggcacgcca cgacccgccc cgccctcgag 660

gcataaatac cctcccatcc 680

<210> SEQ ID NO 79
<211> LENGTH: 1940
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 79

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agagtgaagt catcatcata tttaccatgg cgcgcgtagg agcgcttcgt cgaagaccca 180

taggggggcg gtactcgcac cgtggttgtt tcctgttatg taatatcgga tgggggagca 240

gtcggctagg ttggtcccat cggtactggt cgtcccctag tgcgctagat gcgcgatgtt 300

tgtcctcaaa aactcttttc ttcttaataa caatcatacg caaatttttt gcgtattcga 360

gaaaaaaaga agattctatc tgtttttttt ttgaaatggc tccaatttat aggaggagcc 420

cgtttaacgg cgtcgacaaa tctaacggac accaaccagc gaatgagcga acccaccagc 480

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atgtactttt ttagacggaa tattgatatg tatacatgtg tagatacatg aagcaacatg 1620

ctgctgtagt ctaataattc ctgttcatct aataatcaag tatgtatatg ttctgtgtgt 1680

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tacagtttaa tcattattgt ttatccaata aacaaacatg ctttttaatt tatcttgata 1800

tgcttggatg acggaatatg cagagatttt aagtacccag catcatgagc atgcatgacc 1860

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ttctggtgat cctactgcag 1940

<210> SEQ ID NO 80
<211> LENGTH: 837
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 80

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gtcggctagg ttggtcccat cggtactggt cgtcccctag tgcgctagat gcgcgatgtt 300

tgtcctcaaa aactcttttc ttcttaataa caatcatacg caaatttttt gcgtattcga 360

gaaaaaaaga agattctatc tgtttttttt ttgaaatggc tccaatttat aggaggagcc 420

cgtttaacgg cgtcgacaaa tctaacggac accaaccagc gaatgagcga acccaccagc 480

gccaagctag ccaagcgaag cagacggccg agacgctgac acccttgcct tggcgcggca 540

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ttcccttcct cgcccgccat cataaatagc caccctccc agcttccttc gccacat 837

<210> SEQ ID NO 81
<211> LENGTH: 86
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 81

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gagcctcgtc gatccctcgc ttcaag 86

<210> SEQ ID NO 82
<211> LENGTH: 1017
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 82

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gcgttatgat ggttagcctg tcatgctctt gcgatctgtg gttcctttag gaaaggcatt 180

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agactgttcc aaaccatctg ctggatttat taaatttgga tctggatgtg tcacatacac 540

cttcataatt aaaatggatg gaaatatctc ttatctttta gatatggata ggcatttata 600

tgatgctgtg agttttacta gtactttctt agaatatatg tacttttttа gacggaatat 660

tgatatgtat acatgtgtag atacatgaag caacatgctg ctgtagtcta ataattcctg 720

ttcatctaat aatcaagtat gtatatgttc tgtgtgtttt attggtattt gattagatat 780

atacatgctt agatacatac atgaagcagc atgctgctac agtttaatca ttattgttta 840

tccaataaac aaacatgctt tttaatttat cttgatatgc ttggatgacg gaatatgcag 900

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agattttaag tacccagcat catgagcatg catgaccctg cgttagtatg ctgtttattt 960

gcttgagact ctttcttttg tagatactca ccctgttttc tggtgatcct actgcag 1017

<210> SEQ ID NO 83
<211> LENGTH: 1845
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 83

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cctagtgcgc tagatgcgcg atgtttgtcc tcaaaaactc ttttcttctt aataacaatc 240

atacgcaaat tttttgcgta ttcgagaaaa aaagaagatt ctatctgttt tttttttgaa 300

atggctccaa tttataggag gagcccgttt aacggcgtcg acaaatctaa cggacaccaa 360

ccagcgaatg agcgaaccca ccagcgccaa gctagccaag cgaagcagac ggccgagacg 420

ctgacaccct tgccttggcg cggcatctcc gtcgctggct cgctggctct ggcccccttcg 480

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<210> SEQ ID NO 84

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<211> LENGTH: 742
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 84

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cctagtgcgc tagatgcgcg atgtttgtcc tcaaaaactc ttttcttctt aataacaatc 240

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atggctccaa tttataggag gagcccgttt aacggcgtcg acaaatctaa cggacaccaa 360

ccagcgaatg agcgaaccca ccagcgccaa gctagccaag cgaagcagac ggccgagacg 420

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<210> SEQ ID NO 85
<211> LENGTH: 1504
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 85

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ccgttccgcc ttcgcgtggg acttgttccg ttcatccgtt ggcggcatcc ggaaattgcg 240

tggcgtagag cacggggccc tcctctcaca cggcacggaa ccgtcacgag ctcacggcac 300

cggcagcacg gcggggattc cttccccacc accgctcctt ccctttccct tcctcgcccg 360

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tccgtcggcg ttatgatggt tagcctgtca tgctcttgcg atctgtggtt cctttaggaa 660

aggcattaat ttaatccctg atggttcgag atcggtgatc catggttagt accctaagct 720

gtggagtcgg gtttagatcc gcgctgttcg taggcgatct gttctgattg ttaacttgtc 780

agtacctgcg aatcctcggt ggttctagct ggttcggaga tcagatcgat tccattatct 840

gctatacatc ttgtttcgtt gcctaggctc cgtttaatct atccatcgta tgatgttagc 900

ctttgatatg attcgatcgt gctagctatg tcctgtggac ttaattgtca ggtcctaatt 960

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tatgcagaga ttttaagtac ccagcatcat gagcatgcat gaccctgcgt tagtatgctg 1440

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gcag 1504

<210> SEQ ID NO 86
<211> LENGTH: 401
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 86

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gctggctctg gccccttcgc gagagttccg gtccacctcc acctgtgtcg gtttccaact 180

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tggcgtagag cacggggccc tcctctcaca cggcacggaa ccgtcacgag ctcacggcac 300

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ccatcataaa tagccacccc tcccagcttc cttcgccaca t 401

<210> SEQ ID NO 87
<211> LENGTH: 1157
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 87

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cgtcgatccc tcgcttcaag gtatggctat cgtccttcct ctctctctct ttaccttatc 180

tagatcggcg atccatggtt agggcctgct agttctccgt tcgtgtttgt cgatggctgt 240

gaggcacaat agatccgtcg gcgttatgat ggttagcctg tcatgctctt gcgatctgtg 300

gttcctttag gaaaggcatt aatttaatcc ctgatggttc gagatcggtg atccatggtt 360

agtaccctaa gctgtggagt cgggtttaga tccgcgctgt tcgtaggcga tctgttctga 420

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tcaggtccta atttttagga agactgttcc aaaccatctg ctggatttat taaatttgga 660

tctggatgtg tcacatacac cttcataatt aaaatggatg gaaatatctc ttatctttta 720

gatatggata ggcatttata tgatgctgtg agttttacta gtactttctt agaatatatg 780

tacttttta gacggaatat tgatatgtat acatgtgtag atacatgaag caacatgctg 840

ctgtagtcta ataattcctg ttcatctaat aatcaagtat gtatatgttc tgtgtgtttt 900

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attggtattt gattagatat atacatgctt agatacatac atgaagcagc atgctgctac 960

agtttaatca ttattgttta tccaataaac aaacatgctt tttaatttat cttgatatgc 1020

ttggatgacg gaatatgcag agattttaag tacccagcat catgagcatg catgaccctg 1080

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tggtgatcct actgcag 1157

<210> SEQ ID NO 88
<211> LENGTH: 54
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 88

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<210> SEQ ID NO 89
<211> LENGTH: 798
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 89

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agagtgaagt catcatcata tttaccatgg cgcgcgtagg agcgcttcgt cgaagaccca 180

taggggggcg gtactcgcac cgtggttgtt tcctgttatg taatatcgga tgggggagca 240

gtcggctagg ttggtcccat cggtactggt cgtcccctag tgcgctagat gcgcgatgtt 300

tgtcctcaaa aactcttttc ttcttaataa caatcatacg caaatttttt gcgtattcga 360

gaaaaaaaga agattctatc tgttttttttt ttgaaatggc tccaatttat aggaggagcc 420

cgtttaacgg cgtcgacaaa tctaacggac accaaccagc gaatgagcga acccaccagc 480

gccaagctag ccaagcgaag cagacggccg agacgctgac acccttgcct tggcgcggca 540

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gcatccggaa attgcgtggc gtagagcacg gggccctcct ctcacacggc acggaaccgt 720

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ttcccttcct cgcccgcc 798

<210> SEQ ID NO 90
<211> LENGTH: 3393
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 90

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aaaagaaatg catttgcagt tgtctgtcct aatcaatcta ctagcagact cacattattg 180

atgtaggaaa taaaattcag cctgtgacgt ggatgcaaca actgcactgc acaggatacc 240

atcttagccg ttgtgtcaca atttgctttg ctaatgtttt gagaaaccca gctttgacaa 300

acgtaagatc gatgagggcc ttacgtttgg cacaatatgt attgtaatcc ggcacggcaa 360

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gttagactcg gtagtgttta gccggcatct ttatgtttgg cacaatttaa tttaattcgg 420

catggtaggt tagactgcag cgtgagccgg tcattgcaag ttattatgac atgttagagc 480

atctccaaca agttggaaaa aatgacttgg tatatcatgg tatatcatga gttttagcaa 540

cttattaatt catttgacaa gtaaaaaaaa gatccctctt caacaatttg ctattccaac 600

tcgctaaaat aaaaaaaaat taggctcacc taggccgatc tgcgttgccg cgggagagga 660

gggtaaaaga ttttgcgcta ggagaggtgg aggaacaggg cgcgggagcc ggccacggtg 720

aaatcacggg atagcaacct cacccgcgcg cgcaaattta cgcgtgtggc atggaggaat 780

agaaagttgg aaaagatagc aagttcattt agggagttgt tggagaagaa tatttgtgct 840

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tacaataagg tgaactgtta tatcgatcga ttttttttttg agcacatatc gatcgaattt 1020

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gattattttt aaactatgaa aacaataacc gaactactcg ctctcttcta attagtaaag 1140

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cttgcgatct gtggttcctt taggaaaggc attaatttaa tccctgatgg ttcgagatcg 2580

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aagcaacatg ctgctgtagt ctaataattc ctgttcatct aataatcaag tatgtatatg 3120

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tatcttgata tgcttggatg acggaatatg cagagatttt aagtacccag catcatgagc 3300

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tcaccctgtt ttctggtgat cctactgcag gtg 3393

<210> SEQ ID NO 91
<211> LENGTH: 2287
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 91

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aaaagaaatg catttgcagt tgtctgtcct aatcaatcta ctagcagact cacattattg 180

atgtaggaaa taaaattcag cctgtgacgt ggatgcaaca actgcactgc acaggatacc 240

atcttagccg ttgtgtcaca atttgctttg ctaatgtttt gagaaaccca gctttgacaa 300

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cttattaatt catttgacaa gtaaaaaaaa gatccctctt caacaatttg ctattccaac 600

tcgctaaaat aaaaaaaaat taggctcacc taggccgatc tgcgttgccg cgggagagga 660

gggtaaaaga ttttgcgcta ggagaggtgg aggaacaggg cgcgggagcc ggccacggtg 720

aaatcacggg atagcaacct cacccgcgcg cgcaaattta cgcgtgtggc atggaggaat 780

agaaagttgg aaaagatagc aagttcattt agggagttgt tggagaagaa tatttgtgct 840

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tatacacaat aaagtggtat aataagcggc aagttattat gacatatata agagcaagta 960

tacaataagg tgaactgtta tatcgatcga ttttttttttg agcacatatc gatcgaattt 1020

attgtaagat agaaaagaga agatataaaa acttatagtg atgaacaata ataatataaa 1080

gattattttt aaactatgaa aacaataacc gaactactcg ctctcttcta attagtaaag 1140

taaaggcttc tcattgtata tatataaaaa aattcgttct gatttcttat attcaagacg 1200

gggagagtgc tgagtgctaa cttactagtc tacgagagaa gcttcaaatc aaacagtgta 1260

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acctaccatg gatcacatcg taaaaaaaaa accctaccat ggatcctatc tgttttcttt 1560

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gccacat 2287

<210> SEQ ID NO 92
<211> LENGTH: 1020
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 92

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gcgttatgat ggttagcctg tcatgctctt gcgatctgtg gttcctttag gaaaggcatt 180

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cttcataatt aaaatggatg gaaatatctc ttatctttta gatatggata ggcatttata 600

tgatgctgtg agttttacta gtactttctt agaatatatg tacttttttа gacggaatat 660

tgatatgtat acatgtgtag atacatgaag caacatgctg ctgtagtcta ataattcctg 720

ttcatctaat aatcaagtat gtatatgttc tgtgtgtttt attggtattt gattagatat 780

atacatgctt agatacatac atgaagcagc atgctgctac agtttaatca ttattgttta 840

tccaataaac aaacatgctt tttaatttat cttgatatgc ttggatgacg gaatatgcag 900

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<210> SEQ ID NO 93
<211> LENGTH: 3393
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 93

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aaaagaaatg catttgcagt tgtctgtcct aatcaatcta ctagcagact cacattattg 180

atgtaggaaa taaaattcag cctgtgacgt ggatgcaaca actgcactgc acaggatacc 240

atcttagccg ttgtgtcaca atttgctttg ctaatgtttt gagaaaccca gctttgacaa 300

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gttagactcg gtagtgttta gccggcatct ttatgtttgg cacaatttaa tttaattcgg 420

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atctccaaca agttggaaaa aatgacttgg tatatcatgg tatatcatga gttttagcaa 540

cttattaatt catttgacaa gtaaaaaaaa gatccctctt caacaatttg ctattccaac 600

tcgctaaaat aaaaaaaaat taggctcacc taggccgatc tgcgttgccg cgggagagga 660

gggtaaaaga ttttgcgcta ggagaggtgg aggaacaggg cgcgggagcc ggccacggtg 720

aaatcacggg atagcaacct cacccgcgcg cgcaaattta cgcgtgtggc atggaggaat 780

agaaagttgg aaaagatagc aagttcattt agggagttgt tggagaagaa tatttgtgct 840

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tacaataagg tgaactgtta tatcgatcga ttttttttttg agcacatatc gatcgaattt 1020

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gattattttt aaactatgaa aacaataacc gaactactcg ctctcttcta attagtaaag 1140

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aggaggagcc cgtttaacgg cgtcgacaaa tctaacggac accaaccagc gaatgagcga 1920

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tctttacctt atctagatcg gcgatccatg gttagggcct gctagttctc cgttcgtgtt 2460

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aagcaacatg ctgctgtagt ctaataattc ctgttcatct aataatcaag tatgtatatg 3120

ttctgtgtgt tttattggta tttgattaga tatatacatg cttagataca tacatgaagc 3180

agcatgctgc tacagtttaa tcattattgt ttatccaata aacaaacatg ctttttaatt 3240

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tcaccctgtt ttctggtgat cctactgcag gtc 3393

<210> SEQ ID NO 94
<211> LENGTH: 1020
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 94

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gcgttatgat ggttagcctg tcatgctctt gcgatctgtg gttcctttag gaaaggcatt 180

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agactgttcc aaaccatctg ctggatttat taaatttgga tctggatgtg tcacatacac 540

cttcataatt aaaatggatg gaaatatctc ttatctttta gatatggata ggcatttata 600

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tgatgctgtg agttttacta gtactttctt agaatatatg tacttttttа gacggaatat 660

tgatatgtat acatgtgtag atacatgaag caacatgctg ctgtagtcta ataattcctg 720

ttcatctaat aatcaagtat gtatatgttc tgtgtgtttt attggtattt gattagatat 780

atacatgctt agatacatac atgaagcagc atgctgctac agtttaatca ttattgttta 840

tccaataaac aaacatgctt tttaatttat cttgatatgc ttggatgacg gaatatgcag 900

agattttaag tacccagcat catgagcatg catgaccctg cgttagtatg ctgtttattt 960

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<210> SEQ ID NO 95
<211> LENGTH: 2166
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 95

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ttctgtgaag tgattctcca tgctgatttt aaaagtttat gataaaaaat caaagagaat 180

aactttcagc cacagaatca cttctctcag agaatcaact tatatggaga atcagaatca 240

gatggagctc taccaaactg gccctaggca ttaacctacc atggatcaca tcgtaaaaaa 300

aaaaccctac catggatcct atctgttttc tttttgccct gaaagagtga agtcatcatc 360

atatttacca tggcgcgcgt aggagcgctt cgtcgaagac ccataggggg gcggtactcg 420

caccgtggtt gtttcctgtt atgtaatatc ggatgggggа gcagtcggct aggttggtcc 480

catcggtact ggtcgtcccc tagtgcgcta gatgcgcgat gtttgtcctc aaaaactctt 540

ttcttcttaa taacaatcat acgcaaattt tttgcgtatt cgagaaaaaa agaagattct 600

atctgttttt tttttgaaat ggctccaatt tataggagga gcccgtttaa cggcgtcgac 660

aaatctaacg gacaccaacc agcgaatgag cgaacccacc agcgccaagc tagccaagcg 720

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agatatatac atgcttagat acatacatga agcagcatgc tgctacagtt taatcattat 1980

tgtttatcca ataaacaaac atgcttttta atttatcttg atatgcttgg atgacggaat 2040

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ttatttgctt gagactcttt cttttgtaga tactcaccct gttttctggt gatcctactg 2160

caggtg 2166

<210> SEQ ID NO 96
<211> LENGTH: 1060
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 96

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ttctgtgaag tgattctcca tgctgatttt aaaagtttat gataaaaaat caaagagaat 180

aactttcagc cacagaatca cttctctcag agaatcaact tatatggaga atcagaatca 240

gatggagctc taccaaactg gccctaggca ttaacctacc atggatcaca tcgtaaaaaa 300

aaaaccctac catggatcct atctgttttc tttttgccct gaaagagtga agtcatcatc 360

atatttacca tggcgcgcgt aggagcgctt cgtcgaagac ccataggggg gcggtactcg 420

caccgtggtt gtttcctgtt atgtaatatc ggatggggga gcagtcggct aggttggtcc 480

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ttcttcttaa taacaatcat acgcaaattt tttgcgtatt cgagaaaaaa agaagattct 600

atctgttttt tttttgaaat ggctccaatt tataggagga gcccgtttaa cggcgtcgac 660

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<210> SEQ ID NO 97
<211> LENGTH: 2166
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 97

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ggaagcgatt gtctgaaatg aactaaaagg ctgagagctg gaaaaagtag cttattctga 120

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ttctgtgaag tgattctcca tgctgatttt aaaagtttat gataaaaaat caaagagaat 180

aactttcagc cacagaatca cttctctcag agaatcaact tatatggaga atcagaatca 240

gatggagctc taccaaactg gccctaggca ttaacctacc atggatcaca tcgtaaaaaa 300

aaaaccctac catggatcct atctgttttc tttttgccct gaaagagtga agtcatcatc 360

atatttacca tggcgcgcgt aggagcgctt cgtcgaagac ccataggggg gcggtactcg 420

caccgtggtt gtttcctgtt atgtaatatc ggatgggga gcagtcggct aggttggtcc 480

catcggtact ggtcgtcccc tagtgcgcta gatgcgcgat gtttgtcctc aaaaactctt 540

ttcttcttaa taacaatcat acgcaaattt tttgcgtatt cgagaaaaaa agaagattct 600

atctgttttt tttttgaaat ggctccaatt tataggagga gcccgtttaa cggcgtcgac 660

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tgtttatcca ataaacaaac atgcttttta atttatcttg atatgcttgg atgacggaat 2040

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caggtc 2166

<210> SEQ ID NO 98
<211> LENGTH: 1943
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

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<400> SEQUENCE: 98

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agagtgaagt catcatcata tttaccatgg cgcgcgtagg agcgcttcgt cgaagaccca 180

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gtcggctagg ttggtcccat cggtactggt cgtcccctag tgcgctagat gcgcgatgtt 300

tgtcctcaaa aactcttttc ttcttaataa caatcatacg caaatttttt gcgtattcga 360

gaaaaaaaga agattctatc tgtttttttt ttgaaatggc tccaatttat aggaggagcc 420

cgtttaacgg cgtcgacaaa tctaacggac accaaccagc gaatgagcga acccaccagc 480

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tttattggta tttgattaga tatatacatg cttagataca tacatgaagc agcatgctgc 1740

tacagtttaa tcattattgt ttatccaata aacaaacatg ctttttaatt tatcttgata 1800

tgcttggatg acggaatatg cagagatttt aagtacccag catcatgagc atgcatgacc 1860

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<210> SEQ ID NO 99
<211> LENGTH: 1943
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 99

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gtcggctagg ttggtcccat cggtactggt cgtcccctag tgcgctagat gcgcgatgtt 300

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gaaaaaaaga agattctatc tgtttttttt ttgaaatggc tccaatttat aggaggagcc 420

cgtttaacgg cgtcgacaaa tctaacggac accaaccagc gaatgagcga acccaccagc 480

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<210> SEQ ID NO 100
<211> LENGTH: 1943
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 100

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<210> SEQ ID NO 101
<211> LENGTH: 1020
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 101

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<210> SEQ ID NO 102
<211> LENGTH: 1943
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 102

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tgtcctcaaa aactcttttc ttcttaataa caatcatacg caaatttttt gcgtattcga 360

gaaaaaaaga agattctatc tgtttttttt ttgaaatggc tccaatttat aggaggagcc 420

cgtttaacgg cgtcgacaaa tctaacggac accaaccagc gaatgagcga acccaccagc 480

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<210> SEQ ID NO 103
<211> LENGTH: 1020
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 103

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<210> SEQ ID NO 104
<211> LENGTH: 1943
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

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<400> SEQUENCE: 104

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<210> SEQ ID NO 105
<211> LENGTH: 1020
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 105

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<210> SEQ ID NO 106
<211> LENGTH: 1943
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 106

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<210> SEQ ID NO 107
<211> LENGTH: 1020
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 107

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tgatgctgtg agttttacta gtactttctt agaatatatg tacttttttа gacggaatat 660

tgatatgtat acatgtgtag atacatgaag caacatgctg ctgtagtcta ataattcctg 720

ttcatctaat aatcaagtat gtatatgttc tgtgtgtttt attggtattt gattagatat 780

atacatgctt agatacatac atgaagcagc atgctgctac agtttaatca ttattgttta 840

tccaataaac aaacatgctt tttaatttat cttgatatgc ttggatgacg gaatatgcag 900

agattttaag tacccagcat catgagcatg catgaccctg cgttagtatg ctgtttattt 960

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<210> SEQ ID NO 108

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<211> LENGTH: 1943
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 108

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agagtgaagt catcatcata tttaccatgg cgcgcgtagg agcgcttcgt cgaagaccca 180

taggggggcg gtactcgcac cgtggttgtt tcctgttatg taatatcgga tgggggagca 240

gtcggctagg ttggtcccat cggtactggt cgtcccctag tgcgctagat gcgcgatgtt 300

tgtcctcaaa aactcttttc ttcttaataa caatcatacg caaatttttt gcgtattcga 360

gaaaaaaaga agattctatc tgtttttttt ttgaaatggc tccaatttat aggaggagcc 420

cgtttaacgg cgtcgacaaa tctaacggac accaaccagc gaatgagcga acccaccagc 480

gccaagctag ccaagcgaag cagacggccg agacgctgac acccttgcct tggcgcggca 540

tctccgtcgc tggctcgctg gctctggccc cttcgcgaga gttccggtcc acctccacct 600

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cctcgtcgat ccctcgcttc aaggtatggc tatcgtcctt cctctctctc tctttacctt 960

atctagatcg gcgatccatg gttagggcct gctagttctc cgttcgtgtt tgtcgatggc 1020

tgtgaggcac aatagatccg tcggcgttat gatggttagc ctgtcatgct cttgcgatct 1080

gtggttcctt taggaaaggc attaatttaa tccctgatgg ttcgagatcg gtgatccatg 1140

gttagtaccc taagctgtgg agtcgggttt agatccgcgc tgttcgtagg cgatctgttc 1200

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atgtactttt ttagacggaa tattgatatg tatacatgtg tagatacatg aagcaacatg 1620

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tttattggta tttgattaga tatatacatg cttagataca tacatgaagc agcatgctgc 1740

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tgcttggatg acggaatatg cagagatttt aagtacccag catcatgagc atgcatgacc 1860

ctgcgttagt atgctgttta tttgcttgag actctttctt ttgtagatac tcaccctgtt 1920

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<210> SEQ ID NO 109
<211> LENGTH: 1020
<212> TYPE: DNA

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<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 109

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cgggtttaga tccgcgctgt tcgtaggcga tctgttctga ttgttaactt gtcagtacct 300

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agactgttcc aaaccatctg ctggatttat taaatttgga tctggatgtg tcacatacac 540

cttcataatt aaaatggatg gaaatatctc ttatctttta gatatggata ggcatttata 600

tgatgctgtg agttttacta gtactttctt agaatatatg tacttttta gacggaatat 660

tgatatgtat acatgtgtag atacatgaag caacatgctg ctgtagtcta ataattcctg 720

ttcatctaat aatcaagtat gtatatgttc tgtgtgtttt attggtattt gattagatat 780

atacatgctt agatacatac atgaagcagc atgctgctac agtttaatca ttattgttta 840

tccaataaac aaacatgctt tttaatttat cttgatatgc ttggatgacg gaatatgcag 900

agattttaag tacccagcat catgagcatg catgaccctg cgttagtatg ctgtttattt 960

gcttgagact ctttcttttg tagatactca ccctgttttc tggtgatcct actgcagggt 1020

<210> SEQ ID NO 110
<211> LENGTH: 1943
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 110

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taggggggcg gtactcgcac cgtggttgtt tcctgttatg taatatcgga tgggggagca 240

gtcggctagg ttggtcccat cggtactggt cgtcccctag tgcgctagat gcgcgatgtt 300

tgtcctcaaa aactcttttc ttcttaataa caatcatacg caaatttttt gcgtattcga 360

gaaaaaaaga agattctatc tgttttttttt ttgaaatggc tccaatttat aggaggagcc 420

cgtttaacgg cgtcgacaaa tctaacggac accaaccagc gaatgagcga acccaccagc 480

gccaagctag ccaagcgaag cagacggccg agacgctgac acccttgcct tggcgcggca 540

tctccgtcgc tggctcgctg gctctggccc cttcgcgaga gttccggtcc acctccacct 600

gtgtcggttt ccaactccgt tccgccttcg cgtgggactt gttccgttca tccgttggcg 660

gcatccggaa attgcgtggc gtagagcacg gggccctcct ctcacacggc acggaaccgt 720

cacgagctca cggcaccggc agcacggcgg ggattccttc cccaccaccg ctccttccct 780

ttcccttcct cgcccgccat cataaatagc cacccctccc agcttccttc gccacatcct 840

ctcatcatct tctctcgtgt agcacgcgca gcccgatccc caatcccctc tcctcgcgag 900

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cctcgtcgat ccctcgcttc aaggtatggc tatcgtcctt cctctctctc tctttacctt 960

atctagatcg gcgatccatg gttagggcct gctagttctc cgttcgtgtt tgtcgatggc 1020

tgtgaggcac aatagatccg tcggcgttat gatggttagc ctgtcatgct cttgcgatct 1080

gtggttcctt taggaaaggc attaatttaa tccctgatgg ttcgagatcg gtgatccatg 1140

gttagtaccc taagctgtgg agtcgggttt agatccgcgc tgttcgtagg cgatctgttc 1200

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atgtactttt ttagacggaa tattgatatg tatacatgtg tagatacatg aagcaacatg 1620

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tacagtttaa tcattattgt ttatccaata aacaaacatg ctttttaatt tatcttgata 1800

tgcttggatg acggaatatg cagagatttt aagtacccag catcatgagc atgcatgacc 1860

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<210> SEQ ID NO 111
<211> LENGTH: 1020
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 111

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gcgttatgat ggttagcctg tcatgctctt gcgatctgtg gttcctttag gaaaggcatt 180

aatttaatcc ctgatggttc gagatcggtg atccatggtt agtaccctaa gctgtggagt 240

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atgattcgat cgtgctagct atgtcctgtg gacttaattg tcaggtccta atttttagga 480

agactgttcc aaaccatctg ctggatttat taaatttgga tctggatgtg tcacatacac 540

cttcataatt aaaatggatg gaaatatctc ttatctttta gatatggata ggcatttata 600

tgatgctgtg agttttacta gtactttctt agaatatatg tacttttttа gacggaatat 660

tgatatgtat acatgtgtag atacatgaag caacatgctg ctgtagtcta ataattcctg 720

ttcatctaat aatcaagtat gtatatgttc tgtgtgtttt attggtattt gattagatat 780

atacatgctt agatacatac atgaagcagc atgctgctac agtttaatca ttattgttta 840

tccaataaac aaacatgctt tttaatttat cttgatatgc ttggatgacg gaatatgcag 900

agattttaag tacccagcat catgagcatg catgaccctg cgttagtatg ctgtttattt 960

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gcttgagact ctttcttttg tagatactca ccctgttttc tggtgatcct actgcagcgt 1020

<210> SEQ ID NO 112
<211> LENGTH: 1943
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 112

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agagtgaagt catcatcata tttaccatgg cgcgcgtagg agcgcttcgt cgaagaccca 180

taggggggcg gtactcgcac cgtggttgtt tcctgttatg taatatcgga tgggggagca 240

gtcggctagg ttggtcccat cggtactggt cgtcccctag tgcgctagat gcgcgatgtt 300

tgtcctcaaa aactcttttc ttcttaataa caatcatacg caaatttttt gcgtattcga 360

gaaaaaaaga agattctatc tgttttttt ttgaaatggc tccaatttat aggaggagcc 420

cgtttaacgg cgtcgacaaa tctaacggac accaaccagc gaatgagcga acccaccagc 480

gccaagctag ccaagcgaag cagacggccg agacgctgac acccttgcct tggcgcggca 540

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cctcgtcgat ccctcgcttc aaggtatggc tatcgtcctt cctctctctc tctttacctt 960

atctagatcg gcgatccatg gttagggcct gctagttctc cgttcgtgtt tgtcgatggc 1020

tgtgaggcac aatagatccg tcggcgttat gatggttagc ctgtcatgct cttgcgatct 1080

gtggttcctt taggaaaggc attaatttaa tccctgatgg ttcgagatcg gtgatccatg 1140

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atgtactttt ttagacggaa tattgatatg tatacatgtg tagatacatg aagcaacatg 1620

ctgctgtagt ctaataattc ctgttcatct aataatcaag tatgtatatg ttctgtgtgt 1680

tttattggta tttgattaga tatatacatg cttagataca tacatgaagc agcatgctgc 1740

tacagtttaa tcattattgt ttatccaata aacaaacatg ctttttaatt tatcttgata 1800

tgcttggatg acggaatatg cagagatttt aagtacccag catcatgagc atgcatgacc 1860

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<210> SEQ ID NO 113
<211> LENGTH: 1020
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 113

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gcgttatgat ggttagcctg tcatgctctt gcgatctgtg gttcctttag gaaaggcatt 180

aatttaatcc ctgatggttc gagatcggtg atccatggtt agtaccctaa gctgtggagt 240

cgggtttaga tccgcgctgt tcgtaggcga tctgttctga ttgttaactt gtcagtacct 300

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agactgttcc aaaccatctg ctggatttat taaatttgga tctggatgtg tcacatacac 540

cttcataatt aaaatggatg gaaatatctc ttatctttta gatatggata ggcatttata 600

tgatgctgtg agttttacta gtactttctt agaatatatg tacttttta gacggaatat 660

tgatatgtat acatgtgtag atacatgaag caacatgctg ctgtagtcta ataattcctg 720

ttcatctaat aatcaagtat gtatatgttc tgtgtgtttt attggtattt gattagatat 780

atacatgctt agatacatac atgaagcagc atgctgctac agtttaatca ttattgttta 840

tccaataaac aaacatgctt tttaatttat cttgatatgc ttggatgacg gaatatgcag 900

agattttaag tacccagcat catgagcatg catgaccctg cgttagtatg ctgtttattt 960

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<210> SEQ ID NO 114
<211> LENGTH: 1848
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 114

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cctagtgcgc tagatgcgcg atgtttgtcc tcaaaaactc ttttcttctt aataacaatc 240

atacgcaaat tttttgcgta ttcgagaaaa aaagaagatt ctatctgttt tttttttgaa 300

atggctccaa tttataggag gagcccgttt aacggcgtcg acaaatctaa cggacaccaa 360

ccagcgaatg agcgaaccca ccagcgccaa gctagccaag cgaagcagac ggccgagacg 420

ctgacaccct tgccttggcg cggcatctcc gtcgctggct cgctggctct ggcccccttcg 480

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gatggttcga gatcggtgat ccatggttag taccctaagc tgtggagtcg ggtttagatc 1080

cgcgctgttc gtaggcgatc tgttctgatt gttaacttgt cagtacctgc gaatcctcgg 1140

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accatctgct ggatttatta aatttggatc tggatgtgtc acatacacct tcataattaa 1380

aatggatgga aatatctctt atcttttaga tatggatagg catttatatg atgctgtgag 1440

ttttactagt actttcttag aatatatgta ctttttttaga cggaatattg atatgtatac 1500

atgtgtagat acatgaagca acatgctgct gtagtctaat aattcctgtt catctaataa 1560

tcaagtatgt atatgttctg tgtgttttat tggtatttga ttagatatat acatgcttag 1620

atacatacat gaagcagcat gctgctacag tttaatcatt attgtttatc caataaacaa 1680

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ttcttttgta gatactcacc ctgttttctg gtgatcctac tgcaggtc 1848

<210> SEQ ID NO 115
<211> LENGTH: 1507
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 115

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gctggctctg gccccttcgc gagagttccg gtccacctcc acctgtgtcg gtttccaact 180

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tggcgtagag cacggggccc tcctctcaca cggcacggaa ccgtcacgag ctcacggcac 300

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gtggagtcgg gtttagatcc gcgctgttcg taggcgatct gttctgattg ttaacttgtc 780

agtacctgcg aatcctcggt ggttctagct ggttcggaga tcagatcgat tccattatct 840

gctatacatc ttgtttcgtt gcctaggctc cgtttaatct atccatcgta tgatgttagc 900

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tagatatata catgcttaga tacatacatg aagcagcatg ctgctacagt ttaatcatta 1320

ttgtttatcc aataaacaaa catgcttttt aatttatctt gatatgcttg gatgacggaa 1380

tatgcagaga ttttaagtac ccagcatcat gagcatgcat gaccctgcgt tagtatgctg 1440

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gcaggtc 1507

<210> SEQ ID NO 116
<211> LENGTH: 1160
<212> TYPE: DNA
<213> ORGANISM: Coix lacryma-jobi

<400> SEQUENCE: 116

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gaggcacaat agatccgtcg gcgttatgat ggttagcctg tcatgctctt gcgatctgtg 300

gttcctttag gaaaggcatt aatttaatcc ctgatggttc gagatcggtg atccatggtt 360

agtaccctaa gctgtggagt cgggtttaga tccgcgctgt tcgtaggcga tctgttctga 420

ttgttaactt gtcagtacct gcgaatcctc ggtggttcta gctggttcgg agatcagatc 480

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tcaggtccta atttttagga agactgttcc aaaccatctg ctggatttat taaatttgga 660

tctggatgtg tcacatacac cttcataatt aaaatggatg gaaatatctc ttatctttta 720

gatatggata ggcatttata tgatgctgtg agttttacta gtactttctt agaatatatg 780

tacttttttа gacggaatat tgatatgtat acatgtgtag atacatgaag caacatgctg 840

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agtttaatca ttattgttta tccaataaac aaacatgctt tttaatttat cttgatatgc 1020

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<210> SEQ ID NO 117
<211> LENGTH: 2625
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 117

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caaagagctg aaaagataag gttgtgcggg ctgtggtgat tagaggacca ctaatccctc 180

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gtgatacatc tatctgattt tttttggtct attggtgcct aacttatctg aaaatcatgg 2160

aacatgaggc tagtttgatc atggtttagt tcattgtgat taataatgta tgatttagta 2220

gctattttgg tgatcgtgtc attttatttg tgaatggaat cattgtatgt aaatgaagct 2280

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gatttcacct atatgtaatc cagagctttt gatgtgaaat ttgtctgatc cttcactagg 2400

aaggacagaa cattgttaat attttggcac atctgtctta ttctcatcct ttgtttgaac 2460

atgttagcct gttcaaacag atactgttgt aatgtcctag ttatataggt acatatgtgt 2520

tctctattga gtttatggac ttttgtgtgt gaagttatat ttcattttgc tcaaaactca 2580

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<210> SEQ ID NO 118
<211> LENGTH: 1006
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 118

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cttgctgtcg actagtttgt tttgatatcc atgtagtaca agttacttaa aatttaggtc 360

caatatattt tgcatgcttt tggcctgtta ttcttgccaa caagttgtcc tggtaaaaag 420

tagatgtgaa agtcacgtat tgggacaaat tgatggttta gtgctatagt tctatagttc 480

tgtgatacat ctatctgatt ttttttggtc tattggtgcc taacttatct gaaaatcatg 540

gaacatgagg ctagtttgat catggtttag ttcattgtga ttaataatgt atgatttagt 600

agctattttg gtgatcgtgt cattttattt gtgaatggaa tcattgtatg taaatgaagc 660

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cgatttcacc tatatgtaat ccagagcttt tgatgtgaaa tttgtctgat ccttcactag 780

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catgttagcc tgttcaaaca gatactgttg taatgtccta gttatatagg tacatatgtg 900

ttctctattg agtttatgga cttttgtgtg tgaagttata tttcattttg ctcaaaactc 960

atgtttgcaa gctttctgac attattctat tgttctgaaa caggtg 1006

<210> SEQ ID NO 119
<211> LENGTH: 2625
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 119

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caaagagctg aaaagataag gttgtgcggg ctgtggtgat tagaggacca ctaatccctc 180

catctcctaa tgacgcggtg cccaagacca gtgccgcggc acaccagcgt ctaagtgaac 240

ttccgctaac cttccggtca ttgcgcctga aagatgtcat gtggcgaggc ccccctctca 300

gtagattgcc aactgcctac cgtgccactc ttccatgcat gattgctccc gtctatcccg 360

tttctcacaa cagatagaca acagtaagca tcactaaagc aagcatgtgt agaaccttaa 420

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aaaaaggctt atactaccag tatactatca accagcatgc cgtttttgaa gtatccagga 480

ttagaagctt ctactgcgct tttatattat agctgtggac ccgtggtaac ctttctcttt 540

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cgggggtgaa tggggctaaa gctcagctgc tcgaggggcc gtgggctggt ttccactagc 660

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gcgcgcgcta gcggagcacg gtcaggtgac acgggcgtcg tgacgcttcc gagttgaagg 900

ggttaacgcc agaaacagtg tttggccagg gtatgaacat aacaaaaaat attcacacga 960

aagaatggaa gtatggagct gctactgtgt aaatgccaag caggaaactc acgcccgcta 1020

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tctgcgcggc tcgggacaac ttgaaactgg gccaccgcct cgtcgcaact cgcaacccgt 1200

tggcggaaga aaggaatggc tcgtaggggc ccgggtagaa tcgaagaatg ttgcgctggg 1260

cttcgattca cataacatgg gcctgaagct ctaaaacgac ggcccggtcg ccgcgcgatg 1320

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ttgctgtcga ctagtttgtt ttgatatcca tgtagtacaa gttacttaaa atttaggtcc 1980

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gtgatacatc tatctgattt tttttggtct attggtgcct aacttatctg aaaatcatgg 2160

aacatgaggc tagtttgatc atggtttagt tcattgtgat taataatgta tgatttagta 2220

gctattttgg tgatcgtgtc attttatttg tgaatggaat cattgtatgt aaatgaagct 2280

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gatttcacct atatgtaatc cagagctttt gatgtgaaat ttgtctgatc cttcactagg 2400

aaggacagaa cattgttaat attttggcac atctgtctta ttctcatcct ttgtttgaac 2460

atgttagcct gttcaaacag atactgttgt aatgtcctag ttatataggt acatatgtgt 2520

tctctattga gtttatggac ttttgtgtgt gaagttatat ttcattttgc tcaaaactca 2580

tgtttgcaag ctttctgaca ttattctatt gttctgaaac agggt 2625

<210> SEQ ID NO 120

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<211> LENGTH: 1006
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 120

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cttgcagagg ctgggttctg ttatgtcgtg atctaagaat ctagattagg ctcagtcgtt 300

cttgctgtcg actagtttgt tttgatatcc atgtagtaca agttacttaa aatttaggtc 360

caatatattt tgcatgcttt tggcctgtta ttcttgccaa caagttgtcc tggtaaaaag 420

tagatgtgaa agtcacgtat tgggacaaat tgatggttta gtgctatagt tctatagttc 480

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<210> SEQ ID NO 121
<211> LENGTH: 2625
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 121

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caaagagctg aaaagataag gttgtgcggg ctgtggtgat tagaggacca ctaatccctc 180

catctcctaa tgacgcggtg cccaagacca gtgccgcggc acaccagcgt ctaagtgaac 240

ttccgctaac cttccggtca ttgcgcctga aagatgtcat gtggcgaggc ccccctctca 300

gtagattgcc aactgcctac cgtgccactc ttccatgcat gattgctccc gtctatcccg 360

tttctcacaa cagatagaca acagtaagca tcactaaagc aagcatgtgt agaaccttaa 420

aaaaaggctt atactaccag tatactatca accagcatgc cgtttttgaa gtatccagga 480

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aaggacagaa cattgttaat attttggcac atctgtctta ttctcatcct ttgtttgaac 2460

atgttagcct gttcaaacag atactgttgt aatgtcctag ttatataggt acatatgtgt 2520

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<210> SEQ ID NO 122
<211> LENGTH: 1006
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 122

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cagttatttg caatttgcga tttgctcgtt tgttgcgcag cgtagtttat gtttggagta 180

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cttgctgtcg actagtttgt tttgatatcc atgtagtaca agttacttaa aatttaggtc 360

caatatattt tgcatgcttt tggcctgtta ttcttgccaa caagttgtcc tggtaaaaag 420

tagatgtgaa agtcacgtat tgggacaaat tgatggttta gtgctatagt tctatagttc 480

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<210> SEQ ID NO 123
<211> LENGTH: 2167
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 123

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aggcactagg cagagataga gccgggggtg aatggggcta aagctcagct gctcgagggg 180

ccgtgggctg gtttccacta gcctacagct gtgccacgtg cggccgcgca agccgaagca 240

agcacgctga gccgttggac agcttgtcat aatgccatta cgtggattac acgtaactgg 300

ccctgtaact actcgttcgg ccatcatcaa acgacgacgt ccgctaggcg acgacacggg 360

taatgcacgc agccacccag gcgcgcgcgc tagcggagca cggtcaggtg acacgggcgt 420

cgtgacgctt ccgagttgaa ggggttaacg ccagaaacag tgtttggcca gggtatgaac 480

ataacaaaaa atattcacac gaaagaatgg aagtatggag ctgctactgt gtaaatgcca 540

agcaggaaac tcacgcccgc taacatccaa cggccaacag ctcgacgtgc cggtcagcag 600

agcatcggaa cactggtgat tggtggagcc ggcagtatgc gccccagcac ggccgaggtg 660

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gctgggctgc gaccttaacc agcaaggcac gccacgaccc gccccgccct cgaggcataa 1020

ataccctccc atcccgttgc cgcaagactc agatcagatt ccgatcccca gttcttcccc 1080

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agcgatctcc gccccagcaa ggtatagatt cagttccttg ctccgatccc aatctggttg 1200

agatgttgct ccgatgcgac ttgattatgt catatatctg cggtttgcac cgatctgaag 1260

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aagttactta aaatttaggt ccaatatatt ttgcatgctt ttggcctgtt attcttgcca 1560

acaagttgtc ctggtaaaaa gtagatgtga aagtcacgta ttgggacaaa ttgatggttt 1620

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aggctgctat tattcatcca tcgatttcac ctatatgtaa tccagagctt ttgatgtgaa 1920

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agttatatag gtacatatgt gttctctatt gagtttatgg acttttgtgt gtgaagttat 2100

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acaggtg 2167

<210> SEQ ID NO 124
<211> LENGTH: 1813
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 124

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aaaacgacgg cccggtcgcc gcgcgatgga aagagaccgg atcctcctcg tgaattctgg 540

aaggccacac gagagcgacc caccaccgac gcggaggagt cgtgcgtggt ccaacacggc 600

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tgtcctagtt atataggtac atatgtgttc tctattgagt ttatggactt ttgtgtgtga 1740

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<210> SEQ ID NO 125
<211> LENGTH: 1813
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 125

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aaggccacac gagagcgacc caccaccgac gcggaggagt cgtgcgtggt ccaacacggc 600

cggcgggctg ggctgcgacc ttaaccagca aggcacgcca cgacccgccc cgccctcgag 660

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tctgaaacag ggt 1813

<210> SEQ ID NO 126
<211> LENGTH: 1813
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 126

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aaaacgacgg cccggtcgcc gcgcgatgga aagagaccgg atcctcctcg tgaattctgg 540

aaggccacac gagagcgacc caccaccgac gcggaggagt cgtgcgtggt ccaacacggc 600

cggcgggctg ggctgcgacc ttaaccagca aggcacgcca cgacccgccc cgccctcgag 660

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tggtgcctaa cttatctgaa aatcatggaa catgaggcta gtttgatcat ggtttagttc 1380

attgtgatta ataatgtatg atttagtagc tattttggtg atcgtgtcat tttatttgtg 1440

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aatggaatca ttgtatgtaa atgaagctag ttcaggggtt acgatgtagc tggctttgta 1500

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tctgaaacag ggc 1813

<210> SEQ ID NO 127
<211> LENGTH: 1006
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 127

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cagttatttg caatttgcga tttgctcgtt tgttgcgcag cgtagtttat gtttggagta 180

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cttgctgtcg actagtttgt tttgatatcc atgtagtaca agttacttaa aatttaggtc 360

caatatattt tgcatgcttt tggcctgtta ttcttgccaa caagttgtcc tggtaaaaag 420

tagatgtgaa agtcacgtat tgggacaaat tgatggttta gtgctatagt tctatagttc 480

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<210> SEQ ID NO 128
<211> LENGTH: 2634
<212> TYPE: DNA
<213> ORGANISM: Setaria viridis

<400> SEQUENCE: 128

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ggagcagcga tctggattgg agagaataga ggaaagagag ggaaaaggag agagatagcg 120

caaagagctg aaaagataag gttgtgcggg ctgtggtgat tagaggacca ctaatccctc 180

catctcctaa tgacgcggtg cccaagacca gtgccgcggc acaccagcgt ctaagtgaac 240

ttccgctaac cttccggtca ttgcgcctga aagatgtcat gtggcgaggc ccccctctca 300

gtagattgcc aactgcctac cgtgccactc ttccatgcat gattgctccc gtctatcccg 360

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tttctcacaa cagatagaca acagtaagca tcactaaagc aagcatgtgt agaaccttaa 420

aaaaaggctt atactaccag tatactatca accagcatgc cgtttttgaa gtatccagga 480

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catatgtgtt ctctattgag tttatggact tttgtgtgtg aagttatatt tcattttgct 2580

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<210> SEQ ID NO 129
<211> LENGTH: 1014
<212> TYPE: DNA
<213> ORGANISM: Setaria viridis

<400> SEQUENCE: 129

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aaatcatgga acatgaggct agtttgatca tggtttagtt cattgtgatt aataatgtat 600

gatttagtag ctattttggt gatcgtgtca ttttatttgt gaatggaatc attgtatgta 660

aatgaagcta gttcaggggt tatgatgtag ctggctttgt attctaaagg ctgctattat 720

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tgtttgaaca tgttagcctg ttcaaacaga tactgttgta atgtcctagt tatataggta 900

catatgtgtt ctctattgag tttatggact tttgtgtgtg aagttatatt tcattttgct 960

caaaactcat gtttgcaagc tttctgacat tattctattg ttctgaaaca ggtg 1014

<210> SEQ ID NO 130
<211> LENGTH: 2634
<212> TYPE: DNA
<213> ORGANISM: Setaria viridis

<400> SEQUENCE: 130

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caaagagctg aaaagataag gttgtgcggg ctgtggtgat tagaggacca ctaatccctc 180

catctcctaa tgacgcggtg cccaagacca gtgccgcggc acaccagcgt ctaagtgaac 240

ttccgctaac cttccggtca ttgcgcctga aagatgtcat gtggcgaggc ccccctctca 300

gtagattgcc aactgcctac cgtgccactc ttccatgcat gattgctccc gtctatcccg 360

tttctcacaa cagatagaca acagtaagca tcactaaagc aagcatgtgt agaaccttaa 420

aaaaaggctt atactaccag tatactatca accagcatgc cgtttttgaa gtatccagga 480

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acatccaacg gccaacagct cgacgtgccg gtcagcagag acatcggaac actggtgatt 1080

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gcaagactca gatcagattc cgatccccag ttcttcccca atcaccttgt ggtctctcgt 1560

gtcgcggttc ccagggacgc ctccggctcg tcgctcgaca gcgatctccg ccccagcaag 1620

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cagtcgttct tgctgtcgac tagtttgttt tgatatccat gtagtacaag ttacttaaaa 1980

tttaggtcca atatattttg catgcttttg gcctgttatt cttgccaaca agttgtcctg 2040

gtaaaaagta gatgtgaaag tcacgtattg ggacaaattg atggttaagt gctatagttc 2100

tatagttctg tgatacatct atctgatttt ttttggtcta ttggtgccta acttatctga 2160

aaatcatgga acatgaggct agtttgatca tggtttagtt cattgtgatt aataatgtat 2220

gatttagtag ctattttggt gatcgtgtca ttttatttgt gaatggaatc attgtatgta 2280

aatgaagcta gttcaggggt tatgatgtag ctggctttgt attctaaagg ctgctattat 2340

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tgtttgaaca tgttagcctg ttcaaacaga tactgttgta atgtcctagt tatataggta 2520

catatgtgtt ctctattgag tttatggact tttgtgtgtg aagttatatt tcattttgct 2580

caaaactcat gtttgcaagc tttctgacat tattctattg ttctgaaaca gggt 2634

<210> SEQ ID NO 131
<211> LENGTH: 1014
<212> TYPE: DNA
<213> ORGANISM: Setaria viridis

<400> SEQUENCE: 131

gtatagattc agttccttgc tccgatccca atctggttga gatgttgctc cgatgcgact 60

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cagttgtttg caatttgcga tttgctcgtt tgttgcgcat cgtagtttat gtttggagta 180

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cagtcgttct tgctgtcgac tagtttgttt tgatatccat gtagtacaag ttacttaaaa 360

tttaggtcca atatattttg catgcttttg gcctgttatt cttgccaaca agttgtcctg 420

gtaaaaagta gatgtgaaag tcacgtattg ggacaaattg atggttaagt gctatagttc 480

tatagttctg tgatacatct atctgatttt ttttggtcta ttggtgccta acttatctga 540

aaatcatgga acatgaggct agtttgatca tggtttagtt cattgtgatt aataatgtat 600

gatttagtag ctattttggt gatcgtgtca ttttatttgt gaatggaatc attgtatgta 660

aatgaagcta gttcaggggt tatgatgtag ctggctttgt attctaaagg ctgctattat 720

tcatccatcg atttcaccta tatgtaatcc agagctttcg atgtgaaatt tgtctgatcc 780

ttcactagga aggacagaac attgttaata ttttggcaca tctgtcttat tctcatcctt 840

tgtttgaaca tgttagcctg ttcaaacaga tactgttgta atgtcctagt tatataggta 900

catatgtgtt ctctattgag tttatggact tttgtgtgtg aagttatatt tcattttgct 960

caaaactcat gtttgcaagc tttctgacat tattctattg ttctgaaaca gggt 1014

<210> SEQ ID NO 132
<211> LENGTH: 2176
<212> TYPE: DNA
<213> ORGANISM: Setaria viridis

<400> SEQUENCE: 132

gccgtttttg aagtatccag gattagaagc ttctactgcg cttttatatt atagctgtgg 60

acctgtggta acctttctct tttggcgctt gcttaatctc ggccgtgctg gtccatgctt 120

aggcactagg cagagataga gccgggggtg aatggggcta aagctcagct gctcgagggg 180

ccgtgggctg gtttccacta gcctacagct gtgccacgtg cggccgcgca agccgaagca 240

agcacgctga gccgttggac agcttgtcat aatgccatta cgtggattac aggtaactgg 300

ccctgtaact actcgttcgg ccatcatcaa acgacgacgt ccgctaggcg acgacacggg 360

taatgcacgc agccacccag gcgcgcgcgc tagcggagca cggtcaggtg acacgggcgt 420

cgtgacgctt ccgagttgaa ggggttaacg ccagaaacag tgtttggcca gggtatgaac 480

ataacaaaaa atattcacac gaaagaatgg aagtatggag ctgctactgt gtaaatgcca 540

agcaggaaac tcacgcccgc taacatccaa cggccaacag ctcgacgtgc cggtcagcag 600

agacatcgga acactggtga ttggtggagc cggcagtatg cgccccagca cggccgaggt 660

ggtggtggcc cgtggccctg ctgtctgcgc ggctcgggac aacttgaaac tgggccaccg 720

cctcgtcgca actcgcaacc cgttggcgga agaaaggaat ggctcgtagg ggcccgggta 780

gaatccaaga atgttgcgct gggcttcgat tcacataaca tgggcctgaa gctctaaaac 840

gacggcccgg tcaccgggcg atggaaagag accggatcct cctcgtgaat tctggaaggc 900

cacacgagag cgacccacca ccgacgcgga ggagtcgtgc gtggtccaac acggccggcg 960

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atctaagaat ctagattagg ctcagtcgtt cttgctgtcg actagtttgt tttgatatcc 1500

atgtagtaca agttacttaa aatttaggtc caatatattt tgcatgcttt tggcctgtta 1560

ttcttgccaa caagttgtcc tggtaaaaag tagatgtgaa agtcacgtat tgggacaaat 1620

tgatggttaa gtgctatagt tctatagttc tgtgatacat ctatctgatt ttttttggtc 1680

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gtgaatggaa tcattgtatg taaatgaagc tagttcaggg gttatgatgt agctggcttt 1860

gtattctaaa ggctgctatt attcatccat cgatttcacc tatatgtaat ccagagcttt 1920

cgatgtgaaa tttgtctgat ccttcactag gaaggacaga acattgttaa tattttggca 1980

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taatgtccta gttatatagg tacatatgtg ttctctattg agtttatgga cttttgtgtg 2100

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tgttctgaaa caggtg 2176

<210> SEQ ID NO 133
<211> LENGTH: 1822
<212> TYPE: DNA
<213> ORGANISM: Setaria viridis

<400> SEQUENCE: 133

cacgggtaat gcacgcagcc acccaggcgc gcgcgctagc ggagcacggt caggtgacac 60

gggcgtcgtg acgcttccga gttgaagggg ttaacgccag aaacagtgtt tggccagggt 120

atgaacataa caaaaaatat tcacacgaaa gaatggaagt atggagctgc tactgtgtaa 180

atgccaagca ggaaactcac gcccgctaac atccaacggc caacagctcg acgtgccggt 240

cagcagagac atcggaacac tggtgattgg tggagccggc agtatgcgcc ccagcacggc 300

cgaggtggtg gtggcccgtg gccctgctgt ctgcgcggct cgggacaact tgaaactggg 360

ccaccgcctc gtcgcaactc gcaacccgtt ggcggaagaa aggaatggct cgtaggggcc 420

cgggtagaat ccaagaatgt tgcgctgggc ttcgattcac ataacatggg cctgaagctc 480

taaaacgacg gcccggtcac cgggcgatgg aaagagaccg gatcctcctt gtgaattctg 540

gaaggccaca cgagagcgac ccaccaccga cgcggaggag tcgtgcgtgg tccaacacgg 600

ccggcgggct gggctgcgac cttaaccagc aaggcacgcc acgacccgcc tcgccctcga 660

ggcataaata ccctcccatc ccgttgccgc aagactcaga tcagattccg atccccagtt 720

cttccccaat caccttgtgg tctctcgtgt cgcggttccc agggacgcct ccggctcgtc 780

gctcgacagc gatctccgcc ccagcaaggt atagattcag ttccttgctc cgatcccaat 840

ctggttgaga tgttgctccg atgcgacttg attatgtcat atatctgcgg tttgcaccga 900

tctgaagcct agggtttctc gagcgaccca gttgtttgca atttgcgatt tgctcgtttg 960

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tgcttaatca cgccatgtga cgcggttact tgcagaggct gggttagtgg gttctgttat 1080

gtcgtgatct aagaatctag attaggctca gtcgttcttg ctgtcgacta gtttgttttg 1140

atatccatgt agtacaagtt acttaaaatt taggtccaat atattttgca tgcttttggc 1200

ctgttattct tgccaacaag ttgtcctggt aaaaagtaga tgtgaaagtc acgtattggg 1260

acaaattgat ggttaagtgc tatagttcta tagttctgtg atacatctat ctgatttttt 1320

ttggtctatt ggtgcctaac ttatctgaaa atcatggaac atgaggctag tttgatcatg 1380

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ggctttgtat tctaaaggct gctattattc atccatcgat ttcacctata tgtaatccag 1560

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tgtgtgtgaa gttatatttc attttgctca aaactcatgt ttgcaagctt tctgacatta 1800

ttctattgtt ctgaaacagg tg 1822

<210> SEQ ID NO 134
<211> LENGTH: 1822
<212> TYPE: DNA
<213> ORGANISM: Setaria viridis

<400> SEQUENCE: 134

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gggcgtcgtg acgcttccga gttgaagggg ttaacgccag aaacagtgtt tggccagggt 120

atgaacataa caaaaaatat tcacacgaaa gaatggaagt atggagctgc tactgtgtaa 180

atgccaagca ggaaactcac gcccgctaac atccaacggc caacagctcg acgtgccggt 240

cagcagagac atcggaacac tggtgattgg tggagccggc agtatgcgcc ccagcacggc 300

cgaggtggtg gtggcccgtg gccctgctgt ctgcgcggct cgggacaact tgaaactggg 360

ccaccgcctc gtcgcaactc gcaacccgtt ggcggaagaa aggaatggct cgtaggggcc 420

cgggtagaat ccaagaatgt tgcgctgggc ttcgattcac ataacatggg cctgaagctc 480

taaaacgacg gcccggtcac cgggcgatgg aaagagaccg gatcctcctc gtgaattctg 540

gaaggccaca cgagagcgac ccaccaccga cgcggaggag tcgtgcgtgg tccaacacgg 600

ccggcgggct gggctgcgac cttaaccagc aaggcacgcc acgacccgcc tcgccctcga 660

ggcataaata ccctcccatc ccgttgccgc aagactcaga tcagattccg atccccagtt 720

cttccccaat caccttgtgg tctctcgtgt cgcggttccc agggacgcct ccggctcgtc 780

gctcgacagc gatctccgcc ccagcaaggt atagattcag ttccttgctc cgatcccaat 840

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tgcttaatca cgccatgtga cgcggttact tgcagaggct gggttagtgg gttctgttat 1080

gtcgtgatct aagaatctag attaggctca gtcgttcttg ctgtcgacta gtttgttttg 1140

atatccatgt agtacaagtt acttaaaatt taggtccaat atattttgca tgcttttggc 1200

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ctgttattct tgccaacaag ttgtcctggt aaaaagtaga tgtgaaagtc acgtattggg 1260

acaaattgat ggttaagtgc tatagttcta tagttctgtg atacatctat ctgatttttt 1320

ttggtctatt ggtgcctaac ttatctgaaa atcatggaac atgaggctag tttgatcatg 1380

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tgtgtgtgaa gttatatttc attttgctca aaactcatgt ttgcaagctt tctgacatta 1800

ttctattgtt ctgaaacagg tg 1822

<210> SEQ ID NO 135
<211> LENGTH: 681
<212> TYPE: DNA
<213> ORGANISM: Setaria viridis

<400> SEQUENCE: 135

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gggcgtcgtg acgcttccga gttgaagggg ttaacgccag aaacagtgtt tggccagggt 120

atgaacataa caaaaaatat tcacacgaaa gaatggaagt atggagctgc tactgtgtaa 180

atgccaagca ggaaactcac gcccgctaac atccaacggc caacagctcg acgtgccggt 240

cagcagagac atcggaacac tggtgattgg tggagccggc agtatgcgcc ccagcacggc 300

cgaggtggtg gtggcccgtg gccctgctgt ctgcgcggct cgggacaact tgaaactggg 360

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cgggtagaat ccaagaatgt tgcgctgggc ttcgattcac ataacatggg cctgaagctc 480

taaaacgacg gcccggtcac cgggcgatgg aaagagaccg gatcctcctc gtgaattctg 540

gaaggccaca cgagagcgac ccaccaccga cgcggaggag tcgtgcgtgg tccaacacgg 600

ccggcgggct gggctgcgac cttaaccagc aaggcacgcc acgacccgcc tcgccctcga 660

ggcataaata ccctcccatc c 681

<210> SEQ ID NO 136
<211> LENGTH: 1822
<212> TYPE: DNA
<213> ORGANISM: Setaria viridis

<400> SEQUENCE: 136

cacgggtaat gcacgcagcc acccaggcgc gcgcgctagc ggagcacggt caggtgacac 60

gggcgtcgtg acgcttccga gttgaagggg ttaacgccag aaacagtgtt tggccagggt 120

atgaacataa caaaaaatat tcacacgaaa gaatggaagt atggagctgc tactgtgtaa 180

atgccaagca ggaaactcac gcccgctaac atccaacggc caacagctcg acgtgccggt 240

cagcagagac atcggaacac tggtgattgg tggagccggc agtatgcgcc ccagcacggc 300

cgaggtggtg gtggcccgtg gccctgctgt ctgcgcggct cgggacaact tgaaactggg 360

ccaccgcctc gtcgcaactc gcaacccgtt ggcggaagaa aggaatggct cgtaggggcc 420

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taaaacgacg gcccggtcac cgggcgatgg aaagagaccg gatcctcctt gtgaattctg 540

gaaggccaca cgagagcgac ccaccaccga cgcggaggag tcgtgcgtgg tccaacacgg 600

ccggcgggct gggctgcgac cttaaccagc aaggcacgcc acgacccgcc tcgccctcga 660

ggcataaata ccctcccatc ccgttgccgc aagactcaga tcagattccg atccccagtt 720

cttccccaat caccttgtgg tctctcgtgt cgcggttccc agggacgcct ccggctcgtc 780

gctcgacagc gatctccgcc ccagcaaggt atagattcag ttccttgctc cgatcccaat 840

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tgcttaatca cgccatgtga cgcggttact tgcagaggct gggttagtgg gttctgttat 1080

gtcgtgatct aagaatctag attaggctca gtcgttcttg ctgtcgacta gtttgttttg 1140

atatccatgt agtacaagtt acttaaaatt taggtccaat atattttgca tgcttttggc 1200

ctgttattct tgccaacaag ttgtcctggt aaaaagtaga tgtgaaagtc acgtattggg 1260

acaaattgat ggttaagtgc tatagttcta tagttctgtg atacatctat ctgatttttt 1320

ttggtctatt ggtgcctaac ttatctgaaa atcatggaac atgaggctag tttgatcatg 1380

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ttctattgtt ctgaaacagg gt 1822

<210> SEQ ID NO 137
<211> LENGTH: 1925
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 137

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tatttttttt tgtcacactt gtgtttgaag tgcagtttat ctatctctat acatatattt 120

aaacttcact atatgaataa tatagtctat agtattaaaa taatatcaat gttttagatg 180

attatataac tgaactgcta gacatggtct aaaggacaac cgagtatttt gacaacatga 240

ctctacagtt ttatcttttt agtgtgcatg tgttcttttt acttttgcaa atagcttcac 300

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ttttattcta ttttagcctc taaattaaga aaacttaaac tctattttag ttttttattt 420

aataatttag atataaaata gaataaaata aagtgactaa aaaataacta aatacctttt 480

aagaaataaa aaaactaagg aaccattttt cttgttccga gtagataatg acagcctgtt 540

caacgccgtc gacgagtcta acggacacca accagcgaac cagcagcgtc gcgtcgggcc 600

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ctccaccgtt ggacttgctc cgctgtcggc atccagaaat tgcgtggcgg agcggcagac 720

gtgagccggc acggcaggcg gcctcctctc acggcaccgg cagctacggg ggattccttt 780

cccaccgctc cttcgctttc ccttcctcgc ccgccgtaat aaatagaccc cctccacacc 840

ctctttcccc aacctcgtgt tcgttcggag cgcgcacaca cacaaccaga tctcccccaa 900

atccacccgt cggcacctcc gcttcaaggt acgccgctca tcctcctccc ccccctctct 960

ctaccttctc tagatcggcg tttcggtcca tggttagggc ccggtagttc tacttctgtt 1020

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cgggtcatct tttcatgttt tttttggctt ggttgtgatg atgtggtctg gttgggcggt 1320

cgttctagat cggagtagaa tactgtttca aactacctgg tggatttatt aaaggatctg 1380

tatgtatgtg ccatacatct tcatagttac gagtttaaga tgatggatgg aaatatcgat 1440

ctaggatagg tatacatgtt gatgcgggtt ttactgatgc atatacagag atgctttttt 1500

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gatgatggca tatgcagcag ctatatgtgg attttttttag ccctgccttc atacgctatt 1860

tatttgcttg gtactgtttc ttttgtcgat gctcaccctg ttgtttggtg atacttctgc 1920

aggtc 1925

<210> SEQ ID NO 138
<211> LENGTH: 997
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 138

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cgggatcgat ttcatgaatt ttttttgttt cgttgcatag ggtttggttt gccctttcc 300

tttatttcaa tatatgccgt gcacttgttt gtcgggtcat cttttcatgt tttttttggc 360

ttggttgtga tgatgtggtc tggttgggcg gtcgttctag atcggagtag aatactgttt 420

caaactacct ggtggattta ttaaaggatc tgtatgtatg tgccatacat cttcatagtt 480

acgagtttaa gatgatggat ggaaatatcg atctaggata ggtatacatg ttgatgcggg 540

ttttactgat gcatatacag agatgctttt ttttcgcttg gttgtgatga tgtggtctgg 600

tcgggcggtc gttctagatc ggagtagaat actgtttcaa actacctggt ggatttatta 660

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tatcgatcta ggataggtat acatgttgat gtgggtttta ctgatgcata tacatggcat 780

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gttttataat tattttgatc ttgatatact tggatgatgg catatgcagc agctatatgt 900

ggatttttt agccctgcct tcatacgcta tttatttgct tggtactgtt tcttttgtcg 960

atgctcaccc tgttgtttgg tgatacttct gcaggtc 997

<210> SEQ ID NO 139
<211> LENGTH: 1925
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 139

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aaacttcact atatgaataa tatagtctat agtattaaaa taatatcaat gttttagatg 180

attatataac tgaactgcta gacatggtct aaaggacaac cgagtatttt gacaacatga 240

ctctacagtt ttatcttttt agtgtgcatg tgttcttttt acttttgcaa atagcttcac 300

ctatataata cttcatccat tttattagta catccattta ctaaattttt agtacatcta 360

ttttattcta ttttagcctc taaattaaga aaacttaaac tctattttag ttttttattt 420

aataatttag atataaaata gaataaaata aagtgactaa aaaataacta aataccttt 480

aagaaataaa aaaactaagg aaccattttt cttgttccga gtagataatg acagcctgtt 540

caacgccgtc gacgagtcta acggacacca accagcgaac cagcagcgtc gcgtcgggcc 600

aagcgaagca gacggcacgg catctctgta gctgcctctg gacccctctc gagagttccg 660

ctccaccgtt ggacttgctc cgctgtcggc atccagaaat tgcgtggcgg agcggcagac 720

gtgagccggc acggcaggcg gcctcctctc acggcaccgg cagctacggg ggattccttt 780

cccaccgctc cttcgctttc ccttcctcgc ccgccgtaat aaatagaccc cctccacacc 840

ctctttcccc aacctcgtgt tcgttcggag cgcgcacaca cacaaccaga tctcccccaa 900

atccacccgt cggcacctcc gcttcaaggt acgccgctca tcctcctccc ccccctctct 960

ctaccttctc tagatcggcg tttcggtcca tggttagggc ccggtagttc tacttctgtt 1020

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gcgacctgta catcagacat gttctgattg ctaacttgcc agtgtttctc tttggggaat 1140

cctgggatgg ctctagccgt tccgcagacg ggatcgattt catgaatttt ttttgtttcg 1200

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cgggtcatct tttcatgttt tttttggctt ggttgtgatg atgtggtctg gttgggcggt 1320

cgttctagat cggagtagaa tactgtttca aactacctgg tggatttatt aaaggatctg 1380

tatgtatgtg ccatacatct tcatagttac gagtttaaga tgatggatgg aaatatcgat 1440

ctaggatagg tatacatgtt gatgcgggtt ttactgatgc atatacagag atgctttttt 1500

ttcgcttggt tgtgatgatg tggtctggtc gggcggtcgt tctagatcgg agtagaatac 1560

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gatgatggca tatgcagcag ctatatgtgg attttttttag ccctgccttc atacgctatt 1860

tatttgcttg gtactgtttc ttttgtcgat gctcaccctg ttgtttggtg atacttctgc 1920

agggt 1925

<210> SEQ ID NO 140
<211> LENGTH: 997
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 140

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tagatccgtg ctgctagatt tcgtacacgg atgcgacctg tacatcagac atgttctgat 180

tgctaacttg ccagtgtttc tctttgggga atcctgggat ggctctagcc gttccgcaga 240

cgggatcgat ttcatgaatt ttttttgttt cgttgcatag ggtttggttt gccctttcc 300

tttatttcaa tatatgccgt gcacttgttt gtcgggtcat cttttcatgt tttttttggc 360

ttggttgtga tgatgtggtc tggttgggcg gtcgttctag atcggagtag aatactgttt 420

caaactacct ggtggattta ttaaaggatc tgtatgtatg tgccatacat cttcatagtt 480

acgagtttaa gatgatggat ggaaatatcg atctaggata ggtatacatg ttgatgcggg 540

ttttactgat gcatatacag agatgctttt ttttcgcttg gttgtgatga tgtggtctgg 600

tcgggcggtc gttctagatc ggagtagaat actgtttcaa actacctggt ggatttatta 660

attttggatc tgtatgtgtg tcatacatct tcatagttac gagtttaaga tcgatggaaa 720

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ggatttttt agccctgcct tcatacgcta tttatttgct tggtactgtt tcttttgtcg 960

atgctcaccc tgttgtttgg tgatacttct gcagggt 997

<210> SEQ ID NO 141
<211> LENGTH: 1974
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 141

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tatttttttt gtcacacttg tttgaagtgc agtttatcta tctttataca tatatttaaa 120

ctttactcta cgaataatat aatctatagt actacaataa tatcagtgtt ttagagaatc 180

atataaatga acagttagac atggtctaaa ggacaattga gtattttgac aacaggactc 240

tacagtttta tctttttagt gtgcatgtgt tctccttttt tttttgcaaa tagcttcacc 300

tatataatac ttcatccatt ttattagtac atccatttag ggtttagggt taatggtttt 360

tatagactaa tttttttagt acatctattt tattctattt tagcctctaa attaagaaaa 420

ctaaaactct attttagttt ttttatttaa taatttagat ataaaataga ataaaataaa 480

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gtgactaaaa attaaacaaa tacccttaa gaaattaaaa aaactaagga aacatttttc 540

ttgtttcgag tagataatgc cagcctgtta aacgccgtcg acgagtctaa cggacaccaa 600

ccagcgaacc agcagcgtcg cgtcgggcca agcgaagcag acggcacggc atctctgtcg 660

ctgcctctgg acccctctcg agagttccgc tccaccgttg gacttgctcc gctgtcggca 720

tccagaaatt gcgtggcgga gcggcagacg tgagccggca cggcaggcgg cctcctcctc 780

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tcggagcgca cacacacaca accagatctc ccccaaatcc acccgtcggc acctccgctt 960

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ccatggttag ggcccggtag ttctacttct gttcatgttt gtgttagatc cgtgtttgtg 1080

ttagatccgt gctgctagcg ttcgtacacg gatgcgacct gtacgtcaga cacgttctga 1140

ttgctaactt gccagtgttt ctctttgggg aatcctggga tggctctagc cgttccgcag 1200

acgggatcga tttcatgatt ttttttgttt cgttgcatag ggtttggttt gccctttcc 1260

tttatttcaa tatatgccgt gcacttgttt gtcgggtcat cttttcatgc tttttttgt 1320

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agttacgaat tgaagatgat ggatggaaat atcgatctag gataggtata catgttgatg 1500

cgggttttac tgatgcatat acagagatgc tttttgttcg cttggttgtg atgatgtggt 1560

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atgcagcagc tatatgtgga ttttttttagc cctgccttca tacgctattt atttgcttgg 1920

tactgtttct tttgtcgatg ctcaccctgt tgtttggtga tacttctgca ggtc 1974

<210> SEQ ID NO 142
<211> LENGTH: 1010
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 142

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ggttagggcc cggtagttct acttctgttc atgtttgtgt tagatccgtg tttgtgttag 120

atccgtgctg ctagcgttcg tacacggatg cgacctgtac gtcagacacg ttctgattgc 180

taacttgcca gtgtttctct ttggggaatc ctgggatggc tctagccgtt ccgcagacgg 240

gatcgatttc atgatttttt ttgtttcgtt gcatagggtt tggtttgccc ttttccttta 300

tttcaatata tgccgtgcac ttgtttgtcg ggtcatcttt tcatgctttt ttttgtcttg 360

gttgtgatga tgtggtctgg ttgggcggtc gttctagatc ggagaagaat tctgtttcaa 420

actacctggt ggatttatta attttggatc tgtatgtgtg tgccatacat attcatagtt 480

acgaattgaa gatgatggat ggaaatatcg atctaggata ggtatacatg ttgatgcggg 540

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ttgggcggtc gttcattcgt tctagatcgg agtagaatac tgtttcaaac tacctggtgt 660

atttattaat tttggaactg tatgtgtgtg tcatacatct tcatagttac gagtttaaga 720

tggatggaaa tatcgatcta ggataggtat acatgttgat gtgggtttta ctgatgcata 780

tacatgatgg catatgcagc atctattcat atgctctaac cttgagtacc tatctattat 840

aataaacaag tatgttttat aattattttg atcttgatat acttggatga tggcatatgc 900

agcagctata tgtggatttt tttagccctg ccttcatacg ctatttattt gcttggtact 960

gtttcttttg tcgatgctca ccctgttgtt tggtgatact tctgcaggtc 1010

<210> SEQ ID NO 143
<211> LENGTH: 1974
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 143

gtcgtgcccc tctctagaga taaagagcat tgcatgtcta agttataaaa aattaccaca 60

tatttttttt gtcacacttg tttgaagtgc agtttatcta tctttataca tatatttaaa 120

ctttactcta cgaataatat aatctatagt actacaataa tatcagtgtt ttagagaatc 180

atataaatga acagttagac atggtctaaa ggacaattga gtattttgac aacaggactc 240

tacagtttta tctttttagt gtgcatgtgt tctccttttt tttttgcaaa tagcttcacc 300

tatataatac ttcatccatt ttattagtac atccatttag ggtttagggt taatggtttt 360

tatagactaa tttttttagt acatctattt tattctattt tagcctctaa attaagaaaa 420

ctaaaactct attttagttt ttttatttaa taatttagat ataaaataga ataaaataaa 480

gtgactaaaa attaaacaaa tacccttttaa gaaattaaaa aaactaagga aacatttttc 540

ttgtttcgag tagataatgc cagcctgtta aacgccgtcg acgagtctaa cggacaccaa 600

ccagcgaacc agcagcgtcg cgtcgggcca agcgaagcag acggcacggc atctctgtcg 660

ctgcctctgg acccctctcg agagttccgc tccaccgttg gacttgctcc gctgtcggca 720

tccagaaatt gcgtggcgga gcggcagacg tgagccggca cggcaggcgg cctcctcctc 780

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ttagatccgt gctgctagcg ttcgtacacg gatgcgacct gtacgtcaga cacgttctga 1140

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acgggatcga tttcatgatt ttttttgttt cgttgcatag ggtttggttt gccctttcc 1260

tttatttcaa tatatgccgt gcacttgttt gtcgggtcat cttttcatgc tttttttgt 1320

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ctggttgggc ggtcgttcat tcgttctaga tcggagtaga atactgtttc aaactacctg 1620

gtgtatttat taattttgga actgtatgtg tgtgtcatac atcttcatag ttacgagttt 1680

aagatggatg gaaatatcga tctaggatag gtatacatgt tgatgtgggt tttactgatg 1740

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atgcagcagc tatatgtgga ttttttttagc cctgccttca tacgctattt atttgcttgg 1920

tactgtttct tttgtcgatg ctcaccctgt tgtttggtga tacttctgca gggt 1974

<210> SEQ ID NO 144
<211> LENGTH: 1010
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 144

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ggttagggcc cggtagttct acttctgttc atgtttgtgt tagatccgtg tttgtgttag 120

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tggatggaaa tatcgatcta ggataggtat acatgttgat gtgggtttta ctgatgcata 780

tacatgatgg catatgcagc atctattcat atgctctaac cttgagtacc tatctattat 840

aataaacaag tatgttttat aattattttg atcttgatat acttggatga tggcatatgc 900

agcagctata tgtggatttt tttagccctg ccttcatacg ctatttattt gcttggtact 960

gtttcttttg tcgatgctca ccctgttgtt tggtgatact tctgcagggt 1010

<210> SEQ ID NO 145
<211> LENGTH: 2008
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 145

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tatttttttg tcacacttat ttgaagtgta gtttatctat ctctatacat atatttaaac 120

ttcactctac aaataatata gtctataata ctaaaataat attagtgttt tagaggatca 180

tataaataaa ctgctagaca tggtctaaag gataattgaa tattttgaca atctacagtt 240

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atacttcatc cattttatta gtacatccat ttaggattta gggttgatgg tttctataga 360

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ctaattttta gtacatccat tttattcttt ttagtctcta aatttttaa aactaaaact 420

ctattttagt tttttattta ataatttaga tataaaatga aataaaataa attgactaca 480

aataaaacaa atacccttta agaaataaaa aaactaagca aacatttttc ttgtttcgag 540

tagataatga caggctgttc aacgccgtcg acgagtctaa cggacaccaa ccagcgaacc 600

agcagcgtcg cgtcgggcca agcgaagcag acggcacggc atctctgtag ctgcctctgg 660

acccctctcg agagttccgc tccaccgttg gacttgctcc gctgtcggca tccagaaatt 720

gcgtggcgga gcggcagacg tgaggcggca cggcaggcgg cctcttcctc ctctcacggc 780

accggcagct acgggggatt cctttcccac cgctccttcg ctttcccttc ctcgcccgcc 840

gtaataaata gacacccccc ccacaccctc tttccccaac ctcgtgttcg ttcggagcgc 900

acacacacgc aaccagatct cccccaaatc cagccgtcgg cacctccgct tcaaggtacg 960

ccgctcatcc tccccccccc cctctctcta ccttctctag atcggcgatc cggtccatgg 1020

ttagggcccg gtagttctac ttctgttcat gtttgtgtta gagcaaacat gttcatgttc 1080

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ggatggaaat atcgatctag gataggtata catgttgatg cgggttttac tgatgcatat 1560

acagagatgc tttttttcgc ttggttgtga tgatgtggtc tggttgggcg gtcgttctag 1620

atcggagtag aatactgttt caaactacct ggtggattta ttaattttgt atctttatgt 1680

gtgtgccata catcttcata gttacgagtt taagatgatg gatggaaata ttgatctagg 1740

ataggtatac atgttgatgt gggttttact gatgcatata catgatggca tatgcggcat 1800

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ctgttgttgg gtgatacttc tgcaggtc 2008

<210> SEQ ID NO 146
<211> LENGTH: 1053
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 146

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tgttcatgtt tgtgatgatg tggtctggtt gggcggtcgt tctagatcgg agtaggatac 180

tgtttcaagc tacctggtgg atttattaat tttgtatctg tatgtgtgtg ccatacatct 240

tcatagttac gagtttaaga tgatggatgg aaatatcgat ctaggatagg tatacatgtt 300

gatgcgggtt ttactgatgc atatacagag atgctttttt tctcgcttgg ttgtgatgat 360

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atggtctggt tgggcggtcg ttctagatcg gagtagaata ctgtttcaaa ctacctggtg 420

gatttattaa aggataaagg gtcgttctag atcggagtag aatactgttt caaactacct 480

ggtggattta ttaaaggatc tgtatgtatg tgcctacatc ttcatagtta cgagtttaag 540

atgatggatg gaaatatcga tctaggatag gtatacatgt tgatgcgggt tttactgatg 600

catatacaga gatgcttttt ttcgcttggt tgtgatgatg tggtctggtt gggcggtcgt 660

tctagatcgg agtagaatac tgtttcaaac tacctggtgg atttattaat tttgtatctt 720

tatgtgtgtg ccatacatct tcatagttac gagtttaaga tgatggatgg aaatattgat 780

ctaggatagg tatacatgtt gatgtgggtt ttactgatgc atatacatga tggcatatgc 840

ggcatctatt catatgctct aaccttgagt acctatctat tataataaac aagtatgttt 900

tataattatt ttgatcttga tatacttgga tgatggcata tgcagcagct atatgtggat 960

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tcaccctgtt gttgggtgat acttctgcag gtc 1053

<210> SEQ ID NO 147
<211> LENGTH: 2008
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 147

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ttcactctac aaataatata gtctataata ctaaaataat attagtgttt tagaggatca 180

tataaataaa ctgctagaca tggtctaaag gataattgaa tattttgaca atctacagtt 240

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atacttcatc cattttatta gtacatccat ttaggattta gggttgatgg tttctataga 360

ctaatttttа gtacatccat tttattcttt ttagtctcta aatttttttaa aactaaaact 420

ctattttagt tttttattta ataatttaga tataaaatga aataaaataa attgactaca 480

aataaaacaa ataccctttа agaaataaaa aaactaagca aacatttttc ttgtttcgag 540

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ccgctcatcc tccccccccc cctctctcta ccttctctag atcggcgatc cggtccatgg 1020

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ataggtatac atgttgatgt gggttttact gatgcatata catgatggca tatgcggcat 1800

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ctgttgtttg gtgatacttc tgcaggtc 2008

<210> SEQ ID NO 148
<211> LENGTH: 1053
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 148

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tgttcatgtt tgtgatgatg tggtctggtt gggcggtcgt tctagatcgg agtaggatac 180

tgtttcaagc tacctggtgg atttattaat tttgtatctg tatgtgtgtg ccatacatct 240

tcatagttac gagtttaaga tgatggatgg aaatatcgat ctaggatagg tatacatgtt 300

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ggtggattta ttaaaggatc tgtatgtatg tgcctacatc ttcatagtta cgagtttaag 540

atgatggatg gaaatatcga tctaggatag gtatacatgt tgatgcgggt tttactgatg 600

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tatgtgtgtg ccatacatct tcatagttac gagtttaaga tgatggatgg aaatattgat 780

ctaggatagg tatacatgtt gatgtgggtt ttactgatgc atatacatga tggcatatgc 840

ggcatctatt catatgctct aaccttgagt acctatctat tataataaac aagtatgttt 900

tataattatt ttgatcttga tatacttgga tgatggcata tgcagcagct atatgtggat 960

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tcaccctgtt gtttggtgat acttctgcag gtc 1053

<210> SEQ ID NO 149
<211> LENGTH: 2008
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 149

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ttcactctac aaataatata gtctataata ctaaaataat attagtgttt tagaggatca 180

tataaataaa ctgctagaca tggtctaaag gataattgaa tattttgaca atctacagtt 240

ttatcttttt agtgtgcatg tgatctctct gttttttttg caaatagctt gacctatata 300

atacttcatc cattttatta gtacatccat ttaggattta gggttgatgg tttctataga 360

ctaattttta gtacatccat tttattcttt ttagtctcta aatttttttaa aactaaaact 420

ctattttagt tttttattta ataatttaga tataaaatga aataaaataa attgactaca 480

aataaaacaa atacccttta agaaataaaa aaactaagca aacatttttc ttgtttcgag 540

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agcagcgtcg cgtcgggcca agcgaagcag acggcacggc atctctgtag ctgcctctgg 660

acccctctcg agagttccgc tccaccgttg gacttgctcc gctgtcggca tccagaaatt 720

gcgtggcgga gcggcagacg tgaggcggca cggcaggcgg cctcttcctc ctctcacggc 780

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gtaataaata gacacccccc ccacaccctc tttccccaac ctcgtgttcg ttcggagcgc 900

acacacacgc aaccagatct cccccaaatc cagccgtcgg cacctccgct tcaaggtacg 960

ccgctcatcc tccccccccc cctctctcta ccttctctag atcggcgatc cggtccatgg 1020

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ataggtatac atgttgatgt gggttttact gatgcatata catgatggca tatgcggcat 1800

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<210> SEQ ID NO 150
<211> LENGTH: 1053
<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 150

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tgttcatgtt tgtgatgatg tggtctggtt gggcggtcgt tctagatcgg agtaggatac 180

tgtttcaagc tacctggtgg atttattaat tttgtatctg tatgtgtgtg ccatacatct 240

tcatagttac gagtttaaga tgatggatgg aaatatcgat ctaggatagg tatacatgtt 300

gatgcgggtt ttactgatgc atatacagag atgctttttt tctcgcttgg ttgtgatgat 360

atggtctggt tgggcggtcg ttctagatcg gagtagaata ctgtttcaaa ctacctggtg 420

gatttattaa aggataaagg gtcgttctag atcggagtag aatactgttt caaactacct 480

ggtggattta ttaaaggatc tgtatgtatg tgcctacatc ttcatagtta cgagtttaag 540

atgatggatg gaaatatcga tctaggatag gtatacatgt tgatgcgggt tttactgatg 600

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tataattatt ttgatcttga tatacttgga tgatggcata tgcagcagct atatgtggat 960

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tcaccctgtt gttgggtgat acttctgcag ggt 1053

<210> SEQ ID NO 151
<211> LENGTH: 1635
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 151

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tagtctataa ttgaacaata tttgtaaaat acaaaaaaaa atagtactat ttttatttta 180

aaaaattttt ggaagtaaac aaggccgagg atggggaaac ggaagtccaa cacgtcgttt 240

tctaagttgg gctcaaaagc ccatcacgga actgacctgc tatgggtcgg aggagagcgc 300

gtccagatgg ttccagaggc tggtggtggt gggccaaacg cggaactccg ccaccgccac 360

ggcctcgtgc gcaagcgcag cgcgttgccg tgagccgtga cgtaaccctc cgttgcccac 420

gataaaagct ccacccccga ccccggcccc ccgatttccc ctacggacca gtctcccccc 480

gatcgcaatc gcgaattcgt cgcaccatcg gcacgcagac gaacgaagca aggctctccc 540

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tatatatgca tgtatggtcg attcccgatc tcgtcgattc tcggtttcgc cttccgtacg 660

aagattcgtt tagattgttc atatgttctg ttgtgttacc agattgatcg gatcaacttg 720

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tcagttgttg ccgtccataa aggcccgtgc tattgtctgt tctgaaacga aatcctgtag 900

atttcttagg gttagtgttc aattcatcaa aaggttgatt agtgaattat caaatttgag 960

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agggttaaat cattctcatc atgttgtctc gaatgtaatc ccaaagatat tatagactgt 1020

gtttcgattt gatggattga tttgtgtatc atctaaatca acaaggctaa gtcatcagtt 1080

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catgttgata gtgacccctt tcagattata ctattgaata ttgtatgttt gccacttctg 1380

tatgttgaat tatcctgcta aattagcaat ggaattagca tattggcaat tggtatgcat 1440

ggacctaatc aggacggatg tggttatgtt agtttcaatt cattgtcaat tcattgttca 1500

cctgcgttag atatatatga tgatttttac gtgtagttca tagttcttga gttttggatc 1560

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<210> SEQ ID NO 152
<211> LENGTH: 1080
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 152

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tgttcatatg ttctgttgtg ttaccagatt gatcggatca acttgatcca gttatcttcg 180

ctcctccgat tagatccgtt tctatttcag tatatatata ctagtatagt atctagggtt 240

cacactgttg accgactggt tacttggaat tgatccgtgc tgagttcagt tgttgccgtc 300

cataaaggcc cgtgctattg tctgttctga aacgaaatcc tgtagatttc ttagggttag 360

tgttcaattc atcaaaaggt tgattagtga attatcaaat ttgagagggt taaatcattc 420

tcatcatgtt gtctcgaatg taatcccaaa gatattatag actgtgtttc gatttgatgg 480

attgatttgt gtatcatcta aatcaacaag gctaagtcat cagttcatag aatcatgttt 540

aggtttccgt tcaatagact agttttatca atatataaaa ttataagaag ggtagggtaa 600

atcacgttgc ctcaaatgcc atcctgtatg gtttggtttc aattcaatta gtttggttga 660

ttagggtatg ctctggatta agatggttaa atcttcccta gcatcttccc tgcctatcct 720

tacttgatcc gtttcggata tgttggaagt acagcgagct tatttcatgt tgatagtgac 780

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<210> SEQ ID NO 153
<211> LENGTH: 2067
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 153

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aatacgtacc agcaccggcc atagaaaaag tacattatta aaggtctaat ttggaaacag 180

tctgaaaacg acgtgcgctg cagaggtaaa tgtaatttttc ggcactaaaa ccattatcaa 240

ctaattcatt caataacagt tatttagaaa atgtatagct cgctctaaaa aaacagttta 300

gaaaaacagt caaaataatt cgaccaacaa acagttaata aggttcatta aatatataat 360

gcacggtgct atttgatctt ttaaaggaaa aagaggaata gtcgtgggcg ccaggcggga 420

attggggcgc gggagtctgc cggacgacgc gttccgtccg aacggccgga cccgacgagg 480

ccccccgcc gccccacgtc gcagaaccgt ccgtgggtgg taatctggcc gggtacacca 540

gccgtcccct tgggcggcct cacagcactg ggctcacacg tgagttttgt tctgggcttc 600

ggatcgcacc atatgggcct cggcatcaga aagacggggc ccgtctggga tagaagagac 660

aggaacctcc tcgtggattc cagaagccag ccacgagcga ccaccgacgc ggaggatact 720

cgtcgtccaa gtccaacacg gcgggcgggc gggcggacgc gtgggctggg ctaactgcct 780

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tttctttgtg tttgattgaa acaggtg 2067

<210> SEQ ID NO 154
<211> LENGTH: 1076
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

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<400> SEQUENCE: 154

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aaactggaat ctagggtttc gagtgatttg atcgatcgcg atctgtgatt tcgttgcgcc 180

ttgtgtatgc ttggagtgat ctaggcttgt atatgcggca tcgcgatctg acgcggttgc 240

tttgtagagg ctgggggtct aggctgtgat tttagaatca aataaagctg ttccttaccg 300

tagatgtttc ctacatgttc tgtccagtac tccagtgcta tattcacatt gtttgaggct 360

tgagttttgt cgatcagtgg tcatgagaaa aatatatctc atgattttag aggcacctat 420

tgggaaaggt agatggttcc gttttacatg ttttatagac cttgtggcat ggctcctttg 480

ttctatgggt gctttatttt cctgaataac agtaatgcga gactggtcta tgggtgcttt 540

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aagcacatgt ttgcaagctt tctgacaagt ttctttgtgt ttgattgaaa caggtg 1076

<210> SEQ ID NO 155
<211> LENGTH: 2067
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 155

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aatacgtacc agcaccggcc atagaaaaag tacattatta aaggtctaat ttggaaacag 180

tctgaaaacg acgtgcgctg cagaggtaaa tgtaattttc ggcactaaaa ccattatcaa 240

ctaattcatt caataacagt tatttagaaa atgtatagct cgctctaaaa aaacagttta 300

gaaaaacagt caaaataatt cgaccaacaa acagttaata aggttcatta aatatataat 360

gcacggtgct atttgatctt ttaaaggaaa aagaggaata gtcgtgggcg ccaggcggga 420

attggggcgc gggagtctgc cggacgacgc gttccgtccg aacggccgga cccgacgagg 480

ccccccgccc gccccacgtc gcagaaccgt ccgtgggtgg taatctggcc gggtacacca 540

gccgtcccct tgggcggcct cacagcactg ggctcacacg tgagttttgt tctgggcttc 600

ggatcgcacc atatgggcct cggcatcaga aagacggggc ccgtctggga tagaagagac 660

aggaacctcc tcgtggattc cagaagccag ccacgagcga ccaccgacgc ggaggatact 720

cgtcgtccaa gtccaacacg gcgggcgggc gggcggacgc gtgggctggg ctaactgcct 780

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tatatgcggc atcgcgatct gacgcggttg ctttgtagag gctgggggtc taggctgtga 1260

ttttagaatc aaataaagct gttccttacc gtagatgttt cctacatgtt ctgtccagta 1320

ctccagtgct atattcacat tgtttgaggc ttgagttttg tcgatcagtg gtcatgagaa 1380

aaatatatct catgatttta gaggcaccta ttgggaaagg tagatggttc cgttttacat 1440

gttttataga ccttgtggca tggctccttt gttctatggg tgctttattt tcctgaataa 1500

cagtaatgcg agactggtct atgggtgctt tgaccagtaa tgcgagacta gttatttgat 1560

catggtgcag ttcctagtga ttacgaacaa caatttggta gctcagttca ttcagcattg 1620

gtttctacga tccttatcat tttacttctg aatgaattta tttatttaag atattacagt 1680

gcaataaact gctgtataat atcagtaaca aactgctatt actagtaaat gcctagattc 1740

ataataattc attattctac ttgaaaatga tcttaggcct ttttatgcgg tcctacgcat 1800

ccttccacag gacttgctgt ttgtttgttt tttgtaatcc ctcgctggga cgcagaatgg 1860

ttcatctgtg ctaataattt ttttgcatat ataagtttat agttctcatt attcatgtgg 1920

ctatggtagc ctgtaaaatc tattgtaata acatattagt cagccataca tctgttccaa 1980

cttgctcaat tgcaaatcat atctccactt aaagcacatg tttgcaagct ttctgacaag 2040

tttctttgtg tttgattgaa acagggt 2067

<210> SEQ ID NO 156
<211> LENGTH: 1076
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 156

gtatcaactc ggttcaccac tccaatctac gtctgattta gatgttactt ccatctatgt 60

ctaatttaga tgttactccg atgcgattgg attatgttta tgcggtttgc actgctctgg 120

aaactggaat ctagggtttc gagtgatttg atcgatcgcg atctgtgatt tcgttgcgcc 180

ttgtgtatgc ttggagtgat ctaggcttgt atatgcggca tcgcgatctg acgcggttgc 240

tttgtagagg ctgggggtct aggctgtgat tttagaatca aataaagctg ttccttaccg 300

tagatgtttc ctacatgttc tgtccagtac tccagtgcta tattcacatt gtttgaggct 360

tgagttttgt cgatcagtgg tcatgagaaa aatatatctc atgattttag aggcacctat 420

tgggaaaggt agatggttcc gttttacatg ttttatagac cttgtggcat ggctcctttg 480

ttctatgggt gctttatttt cctgaataac agtaatgcga gactggtcta tgggtgcttt 540

gaccagtaat gcgagactag ttatttgatc atggtgcagt tcctagtgat tacgaacaac 600

aatttggtag ctcagttcat tcagcattgg tttctacgat ccttatcatt ttacttctga 660

atgaatttat ttatttaaga tattacagtg caataaactg ctgtataata tcagtaacaa 720

actgctatta ctagtaaatg cctagattca taataattca ttattctact tgaaaatgat 780

cttaggcctt tttatgcggt cctacgcatc cttccacagg acttgctgtt tgtttgtttt 840

-continued

ttgtaatccc tcgctgggac gcagaatggt tcatctgtgc taataatttt tttgcatata 900

taagtttata gttctcatta ttcatgtggc tatggtagcc tgtaaaatct attgtaataa 960

catattagtc agccatacat ctgttccaac ttgctcaatt gcaaatcata tctccactta 1020

aagcacatgt ttgcaagctt tctgacaagt ttctttgtgt ttgattgaaa cagggt 1076

<210> SEQ ID NO 157
<211> LENGTH: 2003
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 157

agaagtaaaa aaaaagttcg tttcagaatc ataaaggtaa gttaaaaaaa gaccatacaa 60

aaaagaggta tttaatgata aactataatc cagaatttgt taggatagta tataagaata 120

agaccttgtt tagtttcaaa aaaatttgca aaattttcca gattcctcgt cacatcaaat 180

ctttagaggt atgcatggag tattaaatat agacaagacc taaataagaa aacatgaaat 240

gttcacgaaa aaaatcaagc caatgcatga tcgaagcaaa cggtatagta acggtgttaa 300

cctgatccat tgatctttgt aatctttaac ggccacctac cgcgggcagc aaacggcgtc 360

cccctcctcg atatctccgc ggcggcctct ggctttttcc gcggaattgc gcggtgggga 420

cggattccac gagaccgcaa cgcaaccgcc tctcgccgct gggccccaca ccgctcggtg 480

ccgtagcccg tagcctcacg ggattctttc tccctcctcc cccgtgtata aattggcttc 540

atcccctccc tgcctcatcc atccaaatcc cactccccaa tcccatcccg tcggagaaat 600

tcatcgaagc gaagcgaagc gaatcctccc gatcctctca aggtacgcga gttttcgaat 660

cccctccaga cccctcgtat gctttccctg ttcgttttcg tcgtagcgtt tgattaggta 720

tgctttccct gttcgtgttc gtcgtagggt tcgattaggt cgtgtgaggc catggcctgc 780

tgtgataaat ttatttgttg ttatatcgga tctgtagtcg atttgggggt cgtggtgtag 840

atccgcgggc tgtgatgaag ttatttggtg tgattgtgct cgcgtgattc tgcgcgttga 900

gctcgagtag atctgatggt tggacgaccg attggttcgt tggctggctg cgctaaggtt 960

gggctgggct catgttgcgt tcgctgttgc gcgtgattcc gcggatggac ttgcgcttga 1020

ttgccgccag atcacgttac gattatgtga tttcgtttgg aacttttag atttgtagct 1080

tctgcttatt atatgacaga tgcgcctact gctcatatgc ctgtggtaaa taatggatgg 1140

ctgtgggtca aactagttga ttgtcgagtc atgtatcata tacaggtgta tagacttgcg 1200

tctaattgtt tgcatgttgc agttatatga tttgttttag attgtttgtt ccactcatct 1260

aggctgtaaa agggacacta cttattagct tgttgtttaa tctttttatt agtagattat 1320

attggtaatg ttttactaat tattattatg ttatatgtga cttctgctca tgcctgatta 1380

taatcataga tcactgtagt tgattgttga atcatgtgtc aaatacccgt atacataaca 1440

ctacacattt gcttagttgt ttccttaact catgcaaatt gaacaccatg tatgatttgc 1500

atggtgctgt aatgttaaat actacagtcc tgttggtact tgtttagtaa gaatctgctt 1560

catacaacta tatgctatgc ctgatgataa tcatatatct ttgtgtaatt aataattagt 1620

tgactgttga ataatgtatc gagtacatac catggcacaa ttgcttagtc acttccttaa 1680

ccatgcatat tgaactgacc ccttcatgtt ctgctgaatt gttctattct gattagacca 1740

tacatcatgt attgcaatct ttatttgcaa ttgtaatgta atggttcggt tctcaaatgt 1800

-continued

taaatgctat agttgtgcta ctttctaatg ttaaatgcta tagctgtgct acttgtaaga 1860

tctgcttcat agtttagtta aattaggatg atgagctttg atgctgtaac tttgtttgat 1920

tatgttcata gttgatcagt ttttgttaga ctcacagtaa cttatggtct cactcttctt 1980

ctggtctttg atgtttgcag cgg 2003

<210> SEQ ID NO 158
<211> LENGTH: 1361
<212> TYPE: DNA
<213> ORGANISM: Sorghum bicolor

<400> SEQUENCE: 158

gtacgcgagt tttcgaatcc cctccagacc cctcgtatgc tttccctgtt cgttttcgtc 60

gtagcgtttg attaggtatg ctttccctgt tcgtgttcgt cgtagggttc gattaggtcg 120

tgtgaggcca tggcctgctg tgataaattt atttgttgtt atatcggatc tgtagtcgat 180

ttgggggtcg tggtgtagat ccgcgggctg tgatgaagtt atttggtgtg attgtgctcg 240

cgtgattctg cgcgttgagc tcgagtagat ctgatggttg gacgaccgat tggttcgttg 300

gctggctgcg ctaaggttgg gctgggctca tgttgcgttc gctgttgcgc gtgattccgc 360

ggatggactt gcgcttgatt gccgccagat cacgttacga ttatgtgatt tcgtttggaa 420

ctttttagat ttgtagcttc tgcttattat atgacagatg cgcctactgc tcatatgcct 480

gtggtaaata atggatggct gtgggtcaaa ctagttgatt gtcgagtcat gtatcatata 540

caggtgtata gacttgcgtc taattgtttg catgttgcag ttatatgatt tgttttagat 600

tgtttgttcc actcatctag gctgtaaaag ggacactact tattagcttg ttgtttaatc 660

tttttattag tagattatat tggtaatgtt ttactaatta ttattatgtt atatgtgact 720

tctgctcatg cctgattata atcatagatc actgtagttg attgttgaat catgtgtcaa 780

atacccgtat acataacact acacatttgc ttagttgttt ccttaactca tgcaaattga 840

acaccatgta tgatttgcat ggtgctgtaa tgttaaatac tacagtcctg ttggtacttg 900

tttagtaaga atctgcttca tacaactata tgctatgcct gatgataatc atatatcttt 960

gtgtaattaa taattagttg actgttgaat aatgtatcga gtacatacca tggcacaatt 1020

gcttagtcac ttccttaacc atgcatattg aactgacccc ttcatgttct gctgaattgt 1080

tctattctga ttagaccata catcatgtat tgcaatcttt atttgcaatt gtaatgtaat 1140

ggttcggttc tcaaatgtta aatgctatag ttgtgctact ttctaatgtt aaatgctata 1200

gctgtgctac ttgtaagatc tgcttcatag tttagttaaa ttaggatgat gagctttgat 1260

gctgtaactt tgtttgatta tgttcatagt tgatcagttt ttgttagact cacagtaact 1320

tatggtctca ctcttcttct ggtctttgat gtttgcagcg g 1361

<210> SEQ ID NO 159
<211> LENGTH: 1812
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1812)
<223> OTHER INFORMATION: Codon redesigned coding sequence.

<400> SEQUENCE: 159

atggtccgtc ctgtagaaac cccaacccgt gaaatcaaaa aactcgacgg cctgtgggca 60

-continued

ttcagtctgg atcgcgaaaa ctgtggaatt gatcagcgtt ggtgggaaag cgcgttacaa 120

gaaagccggg caattgctgt gccaggcagt tttaacgatc agttcgccga tgcagatatt 180

cgtaattatg cgggcaacgt ctggtatcag cgcgaagtct ttataccgaa aggttgggca 240

ggccagcgta tcgtgctgcg tttcgatgcg gtcactcatt acggcaaagt gtgggtcaat 300

aatcaggaag tgatggagca tcagggcggc tatacgccat ttgaagccga tgtcacgccg 360

tatgttattg ccgggaaaag tgtacgtatc accgtttgtg tgaacaacga actgaactgg 420

cagactatcc cgccgggaat ggtgattacc gacgaaaacg gcaagaaaaa gcagtcttac 480

ttccatgatt tctttaacta tgccggaatc catcgcagcg taatgctcta caccacgccg 540

aacacctggg tggacgatat caccgtggtg acgcatgtcg cgcaagactg taaccacgcg 600

tctgttgact ggcaggtggt ggccaatggt gatgtcagcg ttgaactgcg tgatgcggat 660

caacaggtgg ttgcaactgg acaaggcact agcgggactt tgcaagtggt gaatccgcac 720

ctctggcaac cgggtgaagg ttatctctat gaactgtgcg tcacagccaa aagccagaca 780

gagtgtgata tctacccgct tcgcgtcggc atccggtcag tggcagtgaa gggcgaacag 840

ttcctgatta accacaaacc gttctacttt actggctttg gtcgtcatga agatgcggac 900

ttgcgtggca aaggattcga taacgtgctg atggtgcacg accacgcatt aatggactgg 960

attggggcca actcctaccg tacctcgcat tacccttacg ctgaagagat gctcgactgg 1020

gcagatgaac atggcatcgt ggtgattgat gaaactgctg ctgtcggctt taacctctct 1080

ttaggcattg gtttcgaagc gggcaacaag ccgaaagaac tgtacagcga agaggcagtc 1140

aacggggaaa ctcagcaagc gcacttacag gcgattaaag agctgatagc gcgtgacaaa 1200

aaccacccaa gcgtggtgat gtggagtatt gccaacgaac cggatacccg tccgcaaggt 1260

gcacgggaat atttcgcgcc actggcggaa gcaacgcgta aactcgaccc gacgcgtccg 1320

atcacctgcg tcaatgtaat gttctgcgac gctcacaccg ataccatcag cgatctcttt 1380

gatgtgctgt gcctgaaccg ttattacgga tggtatgtcc aaagcggcga tttggaaacg 1440

gcagagaagg tactggaaaa agaacttctg gcctggcagg agaaactgca tcagccgatt 1500

atcatcaccg aatacggcgt ggatacgtta gccgggctgc actcaatgta caccgacatg 1560

tggagtgaag agtatcagtg tgcatggctg gatatgtatc accgcgtctt tgatcgcgtc 1620

agcgccgtcg tcggtgaaca ggtatggaat ttcgccgatt ttgcgacctc gcaaggcata 1680

ttgcgcgttg gcggtaacaa gaaagggatc ttcactcgcg accgcaaacc gaagtcggcg 1740

gcttttctgc tgcaaaaacg ctggactggc atgaacttcg gtgaaaaacc gcagcaggga 1800

ggcaaacaat ga 1812

<210> SEQ ID NO 160
<211> LENGTH: 2001
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(2001)
<223> OTHER INFORMATION: Codon redesigned coding sequence.

<400> SEQUENCE: 160

atggtccgtc ctgtagaaac cccaacccgt gaaatcaaaa aactcgacgg cctgtgggca 60

ttcagtctgg atcgcgaaaa ctgtggaatt gatcagcgtt ggtgggaaag cgcgttacaa 120

-continued

gaaagccggg caattgctgt gccaggcagt tttaacgatc agttcgccga tgcagatatt 180

cgtaattatg cgggcaacgt ctggtatcag cgcgaagtct ttataccgaa aggttgggca 240

ggccagcgta tcgtgctgcg tttcgatgcg gtcactcatt acggcaaagt gtgggtcaat 300

aatcaggaag tgatggagca tcagggcggc tatacgccat ttgaagccga tgtcacgccg 360

tatgttattg ccgggaaaag tgtacgtaag tttctgcttc tacctttgat atatatataa 420

taattatcat taattagtag taatataata tttcaaatat ttttttcaaa ataaaagaat 480

gtagtatata gcaattgctt ttctgtagtt tataagtgtg tatattttaa tttataactt 540

ttctaatata tgaccaaaat ttgttgatgt gcaggtatca ccgtttgtgt gaacaacgaa 600

ctgaactggc agactatccc gccgggaatg gtgattaccg acgaaaacgg caagaaaaag 660

cagtcttact tccatgattt ctttaactat gccggaatcc atcgcagcgt aatgctctac 720

accacgccga acacctgggt ggacgatatc accgtggtga cgcatgtcgc gcaagactgt 780

aaccacgcgt ctgttgactg gcaggtggtg gccaatggtg atgtcagcgt tgaactgcgt 840

gatgcggatc aacaggtggt tgcaactgga caaggcacta gcgggacttt gcaagtggtg 900

aatccgcacc tctggcaacc gggtgaaggt tatctctatg aactgtgcgt cacagccaaa 960

agccagacag agtgtgatat ctacccgctt cgcgtcggca tccggtcagt ggcagtgaag 1020

ggcgaacagt tcctgattaa ccacaaaccg ttctacttta ctggctttgg tcgtcatgaa 1080

gatgcggact tgcgtggcaa aggattcgat aacgtgctga tggtgcacga ccacgcatta 1140

atggactgga ttggggccaa ctcctaccgt acctcgcatt acccttacgc tgaagagatg 1200

ctcgactggg cagatgaaca tggcatcgtg gtgattgatg aaactgctgc tgtcggcttt 1260

aacctctctt taggcattgg tttcgaagcg ggcaacaagc cgaaagaact gtacagcgaa 1320

gaggcagtca acggggaaac tcagcaagcg cacttacagg cgattaaaga gctgatagcg 1380

cgtgacaaaa accacccaag cgtggtgatg tggagtattg ccaacgaacc ggatacccgt 1440

ccgcaaggtg cacgggaata tttcgcgcca ctggcggaag caacgcgtaa actcgacccg 1500

acgcgtccga tcacctgcgt caatgtaatg ttctgcgacg ctcacaccga taccatcagc 1560

gatctctttg atgtgctgtg cctgaaccgt tattacggat ggtatgtcca aagcggcgat 1620

ttggaaacgg cagagaaggt actggaaaaa gaacttctgg cctggcagga gaaactgcat 1680

cagccgatta tcatcaccga atacggcgtg gatacgttag ccgggctgca ctcaatgtac 1740

accgacatgt ggagtgaaga gtatcagtgt gcatggctgg atatgtatca ccgcgtcttt 1800

gatcgcgtca gcgccgtcgt cggtgaacag gtatggaatt tcgccgattt tgcgacctcg 1860

caaggcatat tgcgcgttgg cggtaacaag aaagggatct tcactcgcga ccgcaaaccg 1920

aagtcggcgg cttttctgct gcaaaaacgc tggactggca tgaacttcgg tgaaaaaccg 1980

cagcagggag gcaaacaatg a 2001

<210> SEQ ID NO 161
<211> LENGTH: 253
<212> TYPE: DNA
<213> ORGANISM: Agrobacterium tumefaciens

<400> SEQUENCE: 161

gatcgttcaa acatttggca ataaagtttc ttaagattga atcctgttgc cggtcttgcg 60

atgattatca tataatttct gttgaattac gttaagcatg taataattaa catgtaatgc 120

-continued

atgacgttat ttatgagatg ggtttttatg attagagtcc cgcaattata catttaatac 180

gcgatagaaa acaaaatata gcgcgcaaac taggataaat tatcgcgcgc ggtgtcatct 240

atgttactag atc 253

<210> SEQ ID NO 162
<211> LENGTH: 210
<212> TYPE: DNA
<213> ORGANISM: Triticum aestivum

<400> SEQUENCE: 162

ctgcatgcgt ttggacgtat gctcattcag gttggagcca atttggttga tgtgtgtgcg 60

agttcttgcg agtctgatga gacatctctg tattgtgttt ctttccccag tgttttctgt 120

acttgtgtaa tcggctaatc gccaacagat tcggcgatga ataaatgaga aataaattgt 180

tctgattttg agtgcaaaaa aaaaggaatt 210

<210> SEQ ID NO 163
<211> LENGTH: 1204
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1204)
<223> OTHER INFORMATION: Chimeric transcriptional regulatory expression element group.

<400> SEQUENCE: 163

ggtccgattg agacttttca acaaagggta atatccggaa acctcctcgg attccattgc 60

ccagctatct gtcactttat tgtgaagata gtggaaaagg aaggtggctc ctacaaatgc 120

catcattgcg ataaaggaaa ggccatcgtt gaagatgcct ctgccgacag tggtcccaaa 180

gatggacccc cacccacgag gagcatcgtg gaaaaagaag acgttccaac cacgtcttca 240

aagcaagtgg attgatgtga tggtccgatt gagacttttc aacaaagggt aatatccgga 300

aacctcctcg gattccattg cccagctatc tgtcacttta ttgtgaagat agtggaaaag 360

gaaggtggct cctacaaatg ccatcattgc gataaaggaa aggccatcgt tgaagatgcc 420

tctgccgaca gtggtcccaa agatggaccc ccacccacga ggagcatcgt ggaaaaagaa 480

gacgttccaa ccacgtcttc aaagcaagtg gattgatgtg atatctccac tgacgtaagg 540

gatgacgcac aatcccacta tccttcgcaa gacccttcct ctatataagg aagttcattt 600

catttggaga ggacacgctg acaagctgac tctagcagat cctctagaac catcttccac 660

acactcaagc cacactattg gagaacacac agggacaaca caccataaga tccaagggag 720

gcctccgccg ccgccggtaa ccaccccgcc cctctcctct ttctttctcc gttttttttt 780

ccgtctcggt ctcgatcttt ggccttggta gtttgggtgg gcgagaggcg gcttcgtgcg 840

cgcccagatc ggtgcgcggg aggggcggga tctcgcggct ggggctctcg ccggcgtgga 900

tccggcccgg atctcgcggg gaatggggct ctcggatgta gatctgcgat ccgccgttgt 960

tgggggagat gatggggggt ttaaaatttc cgccgtgcta aacaagatca ggaagagggg 1020

aaaagggcac tatggtttat atttttatat atttctgctg cttcgtcagg cttagatgtg 1080

ctagatcttt ctttcttctt tttgtgggta gaatttgaat ccctcagcat tgttcatcgg 1140

tagtttttct tttcatgatt tgtgacaaat gcagcctcgt gcggagcttt tttgtaggta 1200

gaag 1204

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<210> SEQ ID NO 164
<211> LENGTH: 1399
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 164

tcgaggtcat tcatatgctt gagaagagag tcgggatagt ccaaaataaa acaaaggtaa 60

gattacctgg tcaaaagtga aaacatcagt taaaaggtgg tataaagtaa aatatcggta 120

ataaaaggtg gcccaaagtg aaatttactc ttttctacta ttataaaaat tgaggatgtt 180

tttgtcggta ctttgatacg tcatttttgt atgaattggt ttttaagttt attcgctttt 240

ggaaatgcat atctgtattt gagtcgggtt ttaagttcgt ttgcttttgt aaatacagag 300

ggatttgtat aagaaatatc tttagaaaaa cccatatgct aatttgacat aatttttgag 360

aaaaatatat attcaggcga attctcacaa tgaacaataa taagattaaa atagctttcc 420

cccgttgcag cgcatgggta ttttttctag taaaaataaa agataaactt agactcaaaa 480

catttacaaa aacaacccct aaagttccta aagcccaaag tgctatccac gatccatagc 540

aagcccagcc caacccaacc caacccaacc caccccagtc cagccaactg gacaatagtc 600

tccacacccc cccactatca ccgtgagttg tccgcacgca ccgcacgtct cgcagccaaa 660

aaaaaaaaga aagaaaaaaa agaaaaagaa aaaacagcag gtgggtccgg gtcgtggggg 720

ccggaaacgc gaggaggatc gcgagccagc gacgaggccg gccctccctc cgcttccaaa 780

gaaacgcccc ccatcgccac tatatacata ccccccccctc tcctcccatc cccccaaccc 840

taccaccacc accaccacca cctccacctc ctccccccctc gctgccggac gacgagctcc 900

tccccctcc ccctccgccg ccgccgcgcc ggtaaccacc ccgcccctct cctctttctt 960

tctccgtttt ttttccgtc tcggtctcga tctttggcct tggtagtttg ggtgggcgag 1020

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tctcgccggc gtggatccgg cccggatctc gcggggaatg gggctctcgg atgtagatct 1140

gcgatccgcc gttgttgggg gagatgatgg ggggtttaaa atttccgccg tgctaaacaa 1200

gatcaggaag aggggaaaag ggcactatgg tttatatttt tatatatttc tgctgcttcg 1260

tcaggcttag atgtgctaga tctttctttc ttctttttgt gggtagaatt tgaatccctc 1320

agcattgttc atcggtagtt tttcttttca tgatttgtga caaatgcagc ctcgtgcgga 1380

gctttttgt aggtagaag 1399

<210> SEQ ID NO 165
<211> LENGTH: 2181
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 165

gacaacaaca tgcttctcat caacatggag ggaagaggga gggagaaagt gtcgcctggt 60

cacctccatt gtcacactag ccactggcca gctctcccac accaccaatg ccaggggcga 120

gctttagcac agccaccgct tcacctccac caccgcacta ccctagcttc gcccaacagc 180

caccgtcaac gcctcctctc cgtcaacata agagagagag agaagaggag agtagccatg 240

tggggaggag gaatagtaca tggggcctac cgtttggcaa gttattttgg gttgccaagt 300

taggccaata aggggaggga tttggccatc cggttggaaa ggttattggg gtagtatctt 360

-continued

tttactagaa ttgtcaaaaa aaaatagttt gagagccatt tggagaggat gttgcctgtt 420

agaggtgctc ttaggacatc aaattccata aaaacatcag aaaaattctc tcgatgaaga 480

tttataacca ctaaaactgc cctcaattcg aagggagttc aaaacaatta aaatcatgtt 540

cgaattgagt ttcaatttca ctttaacccc tttgaaatct caatggtaaa acatcaaccc 600

gtcaggtagc atggttcttt ttattccttt caaaaagagt taattacaaa cagaatcaaa 660

actaacagtt aggcccaagg cccatccgag caaacaatag atcatgggcc aggcctgcca 720

ccaccctccc cctcctggct cccgctcttg aatttcaaaa tccaaaaata tcggcacgac 780

tggccgccga cggagcgggc ggaaaatgac ggaacaaccc ctcgaattct accccaacta 840

cgcccaccaa cccacacgcc actgacaatc cggtcccacc cttgtgggcc cacctacaag 900

cgagacgtca gtcgctcgca gcaaccagtg ggcccacctc ccagtgagcg gcgggtagat 960

ctggactctt acccacccac actaaacaaa acggcatgaa tattttgcac taaaaccctc 1020

agaaaaattc cgatattcca aaccagtaca gttcctgacc gttggaggag ccaaagtgga 1080

gcggagtgta aaattgggaa acttaatcga gggggttaaa cgcaaaaacg ccgaggcgcc 1140

tcccgctcta tagaaagggg aggagtggga ggtggaaacc ctaccacacc gcagagaaag 1200

gcgtcttcgt actcgcctct ctccgcgccc tcctccgccg ccgctcgccg ccgttcgtct 1260

ccgccgccac cggctagcca tccaggtaaa acaaacaaaa acggatctga tgcttccatt 1320

cctccgtttc tcgtagtagc gcgcttcgat ctgtgggtgg atctgggtga tcctggggtg 1380

tggttcgttc tgtttgatag atctgtcggt ggatctggcc ttctgtggtt gtcgatgtcc 1440

ggatctgcgt tttgatcagt ggtagttcgt ggatctggcg aaatgttttg gatctggcag 1500

tgagacgcta agaatcggga aatgatgcaa tattaggggg gtttcggatg gggatccact 1560

gaattagtct gtctccctgc tgataatctg ttccttttg gtagatctgg ttagtgtatg 1620

tttgtttcgg atagatctga tcaatgcttg tttgtttttt caaattttct acctaggttg 1680

tataggaatg gcatgcggat ctggttggat tgccatgatc cgtgctgaaa tgccccttg 1740

gttgatggat cttgatattt tactgctgtt cacctagatt tgtactcccg tttatactta 1800

atttgttgct tattatgaat agatctgtaa cttaggcaca tgtatggacg gagtatgtgg 1860

atctgtagta tgtacattgc tgcgagctaa gaactatttc agagcaagca cagaaaaaaa 1920

tatttagaca gattgggcaa ctatttgatg gtctttggta tcatgctttg tagtgctcgt 1980

ttctgcgtag taatcttttg atctgatctg aagataggtg ctattatatt cttaaaggtc 2040

attagaacgc tatctgaaag gctgtattat gtggattggt tcacctgtga ctccctgttc 2100

gtcttgtctt gataaatcct gtgataaaaa aaattcttaa ggcgtaattt gttgaaatct 2160

tgttttgtcc tatgcagcct g 2181

<210> SEQ ID NO 166
<211> LENGTH: 1653
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1653)
<223> OTHER INFORMATION: Codon redesigned coding sequence.

<400> SEQUENCE: 166

atggaagacg ccaaaaacat aaagaaaggc ccggcgccat tctatcctct agaggatgga 60

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accgctggag agcaactgca taaggctatg aagagatacg ccctggttcc tggaacaatt 120

gcttttacag atgcacatat cgaggtgaac atcacgtacg cggaatactt cgaaatgtcc 180

gttcggttgg cagaagctat gaaacgatat gggctgaata caaatcacag aatcgtcgta 240

tgcagtgaaa actctcttca attctttatg ccggtgttgg gcgcgttatt tatcggagtt 300

gcagttgcgc ccgcgaacga catttataat gaacgtgaat tgctcaacag tatgaacatt 360

tcgcagccta ccgtagtgtt tgtttccaaa aaggggttgc aaaaaatttt gaacgtgcaa 420

aaaaaattac caataatcca gaaaattatt atcatggatt ctaaaacgga ttaccaggga 480

tttcagtcga tgtacacgtt cgtcacatct catctacctc ccggttttaa tgaatacgat 540

tttgtaccag agtcctttga tcgtgacaaa acaattgcac tgataatgaa ttcctctgga 600

tctactgggt tacctaaggg tgtggccctt ccgcatagaa ctgcctgcgt cagattctcg 660

catgccagag atcctatttt tggcaatcaa atcattccgg atactgcgat tttaagtgtt 720

gttccattcc atcacggttt tggaatgttt actacactcg gatatttgat atgtggattt 780

cgagtcgtct taatgtatag atttgaagaa gagctgtttt tacgatccct tcaggattac 840

aaaattcaaa gtgcgttgct agtaccaacc ctattttcat tcttcgccaa aagcactctg 900

attgacaaat acgatttatc taatttacac gaaattgctt ctgggggcgc acctctttcg 960

aaagaagtcg gggaagcggt tgcaaaacgc ttccatcttc cagggatacg acaaggatat 1020

gggctcactg agactacatc agctattctg attacacccg agggggatga taaaccgggc 1080

gcggtcggta aagttgttcc atttttgaa gcgaaggttg tggatctgga taccgggaaa 1140

acgctgggcg ttaatcagag aggcgaatta tgtgtcagag gacctatgat tatgtccggt 1200

tatgtaaaca atccggaagc gaccaacgcc ttgattgaca aggatggatg gctacattct 1260

ggagacatag cttactggga cgaagacgaa cacttcttca tagttgaccg cttgaagtct 1320

ttaattaaat acaaaggata tcaggtggcc cccgctgaat tggaatcgat attgttacaa 1380

caccccaaca tcttcgacgc gggcgtggca ggtcttcccg acgatgacgc cggtgaactt 1440

cccgccgccg ttgttgtttt ggagcacgga aagacgatga cggaaaaaga gatcgtggat 1500

tacgtcgcca gtcaagtaac aaccgcgaaa aagttgcgcg gaggagttgt gtttgtggac 1560

gaagtaccga aaggtcttac cggaaaactc gacgcaagaa aaatcagaga gatcctcata 1620

aaggccaaga agggcggaaa gtccaaattg taa 1653

<210> SEQ ID NO 167
<211> LENGTH: 936
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(936)
<223> OTHER INFORMATION: Codon redesigned coding sequence.

<400> SEQUENCE: 167

atggcttcca aggtgtacga ccccgagcaa cgcaaacgca tgatcactgg gcctcagtgg 60

tgggctcgct gcaagcaaat gaacgtgctg gactccttca tcaactacta tgattccgag 120

aagcacgccg agaacgccgt gatttttctg catggtaacg ctgcctccag ctacctgtgg 180

aggcacgtcg tgcctcacat cgagcccgtg gctagatgca tcatccctga tctgatcgga 240

atgggtaagt ccggcaagag cgggaatggc tcatatcgcc tcctggatca ctacaagtac 300

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ctcaccgctt ggttcgagct gctgaacctt ccaaagaaaa tcatctttgt gggccacgac 360

tggggggctt gtctggcctt tcactactcc tacgagcacc aagacaagat caaggccatc 420

gtccatgctg agagtgtcgt ggacgtgatc gagtcctggg acgagtggcc tgacatcgag 480

gaggatatcg ccctgatcaa gagcgaagag ggcgagaaaa tggtgcttga gaataacttc 540

ttcgtcgaga ccatgctccc aagcaagatc atgcggaaac tggagcctga ggagttcgct 600

gcctacctgg agccattcaa ggagaagggc gaggttagac ggcctaccct ctcctggcct 660

cgcgagatcc ctctcgttaa gggaggcaag cccgacgtcg tccagattgt ccgcaactac 720

aacgcctacc ttcgggccag cgacgatctg cctaagatgt tcatcgagtc cgaccctggg 780

ttctttttcca acgctattgt cgagggagct aagaagttcc ctaacaccga gttcgtgaag 840

gtgaagggcc tccacttcag ccaggaggac gctccagatg aaatgggtaa gtacatcaag 900

agcttcgtgg agcgcgtgct gaagaacgag cagtaa 936

<210> SEQ ID NO 168
<211> LENGTH: 675
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(675)
<223> OTHER INFORMATION: Chimeric transcriptional regulatory expression element group.

<400> SEQUENCE: 168

ggtccgatgt gagacttttc aacaaagggt aatatccgga aacctcctcg gattccattg 60

cccagctatc tgtcacttta ttgtgaagat agtggaaaag gaaggtggct cctacaaatg 120

ccatcattgc gataaaggaa aggccatcgt tgaagatgcc tctgccgaca gtggtcccaa 180

agatggaccc ccacccacga ggagcatcgt ggaaaaagaa gacgttccaa ccacgtcttc 240

aaagcaagtg gattgatgtg atggtccgat gtgagacttt tcaacaaagg gtaatatccg 300

gaaacctcct cggattccat tgcccagcta tctgtcactt tattgtgaag atagtggaaa 360

aggaaggtgg ctcctacaaa tgccatcatt gcgataaagg aaaggccatc gttgaagatg 420

cctctgccga cagtggtccc aaagatggac ccccacccac gaggagcatc gtggaaaaag 480

aagacgttcc aaccacgtct tcaaagcaag tggattgatg tgatatctcc actgacgtaa 540

gggatgacgc acaatcccac tatccttcgc aagacccttc ctctatataa ggaagttcat 600

ttcatttgga gaggaaccat cttccacaca ctcaagccac actattggag aacacacagg 660

gacaacacac cataa 675

<210> SEQ ID NO 169
<211> LENGTH: 622
<212> TYPE: DNA
<213> ORGANISM: Cauliflower mosaic virus

<400> SEQUENCE: 169

ggtccgattg agacttttca acaaagggta atatccggaa acctcctcgg attccattgc 60

ccagctatct gtcactttat tgtgaagata gtggaaaagg aaggtggctc ctacaaatgc 120

catcattgcg ataaaggaaa ggccatcgtt gaagatgcct ctgccgacag tggtcccaaa 180

gatggacccc cacccacgag gagcatcgtg gaaaaagaag acgttccaac cacgtcttca 240

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aagcaagtgg attgatgtga tggtccgatt gagacttttc aacaaagggt aatatccgga 300

aacctcctcg gattccattg cccagctatc tgtcacttta ttgtgaagat agtggaaaag 360

gaaggtggct cctacaaatg ccatcattgc gataaaggaa aggccatcgt tgaagatgcc 420

tctgccgaca gtggtcccaa agatggaccc ccacccacga ggagcatcgt ggaaaaagaa 480

gacgttccaa ccacgtcttc aaagcaagtg gattgatgtg atatctccac tgacgtaagg 540

gatgacgcac aatcccacta tctagacgca agacccttcc tctatataag gaagttcatt 600

tcatttggag aggacacgct ga 622

<210> SEQ ID NO 170
<211> LENGTH: 1446
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1446)
<223> OTHER INFORMATION: Chimeric transcriptional regulatory expression element group.

<400> SEQUENCE: 170

ggtccgattg agacttttca acaaagggta atatccggaa acctcctcgg attccattgc 60

ccagctatct gtcactttat tgtgaagata gtggaaaagg aaggtggctc ctacaaatgc 120

catcattgcg ataaaggaaa ggccatcgtt gaagatgcct ctgccgacag tggtcccaaa 180

gatggacccc cacccacgag gagcatcgtg gaaaaagaag acgttccaac cacgtcttca 240

aagcaagtgg attgatgtga tggtccgatt gagacttttc aacaaagggt aatatccgga 300

aacctcctcg gattccattg cccagctatc tgtcacttta ttgtgaagat agtggaaaag 360

gaaggtggct cctacaaatg ccatcattgc gataaaggaa aggccatcgt tgaagatgcc 420

tctgccgaca gtggtcccaa agatggaccc ccacccacga ggagcatcgt ggaaaaagaa 480

gacgttccaa ccacgtcttc aaagcaagtg gattgatgtg atatctccac tgacgtaagg 540

gatgacgcac aatcccacta tccttcgcaa gacccttcct ctatataagg aagttcattt 600

catttggaga ggacacgctg acaagctgac tctagcagat ctaccgtctt cggtacgcgc 660

tcactccgcc ctctgccttt gttactgcca cgtttctctg aatgctctct tgtgtggtga 720

ttgctgagag tggtttagct ggatctagaa ttacactctg aaatcgtgtt ctgcctgtgc 780

tgattacttg ccgtcctttg tagcagcaaa atatagggac atggtagtac gaaacgaaga 840

tagaacctac acagcaatac gagaaatgtg taatttggtg cttagcggta tttatttaag 900

cacatgttgg tgttataggg cacttggatt cagaagtttg ctgttaattt aggcacaggc 960

ttcatactac atgggtcaat agtataggga ttcatattat aggcgatact ataataattt 1020

gttcgtctgc agagcttatt atttgccaaa attagatatt cctattctgt ttttgtttgt 1080

gtgctgttaa attgttaacg cctgaaggaa taaatataaa tgacgaaatt ttgatgttta 1140

tctctgctcc tttattgtga ccataagtca agatcagatg cacttgtttt aaatattgtt 1200

gtctgaagaa ataagtactg acagtatttt gatgcattga tctgcttgtt tgttgtaaca 1260

aaatttaaaa ataaagagtt tccttttttgt tgctctcctt acctcctgat ggtatctagt 1320

atctaccaac tgacactata ttgcttctct ttacatacgt atcttgctcg atgccttctc 1380

cctagtgttg accagtgtta ctcacatagt ctttgctcat ttcattgtaa tgcagatacc 1440

aagcgg 1446

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<210> SEQ ID NO 171
<211> LENGTH: 1165
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1165)
<223> OTHER INFORMATION: Chimeric transcriptional regulatory expression element group.

<400> SEQUENCE: 171

ggtccgatgt gagacttttc aacaaagggt aatatccgga aacctcctcg gattccattg 60

cccagctatc tgtcacttta ttgtgaagat agtggaaaag gaaggtggct cctacaaatg 120

ccatcattgc gataaaggaa aggccatcgt tgaagatgcc tctgccgaca gtggtcccaa 180

agatggaccc ccacccacga ggagcatcgt ggaaaaagaa gacgttccaa ccacgtcttc 240

aaagcaagtg gattgatgtg atggtccgat gtgagacttt tcaacaaagg gtaatatccg 300

gaaacctcct cggattccat tgcccagcta tctgtcactt tattgtgaag atagtggaaa 360

aggaaggtgg ctcctacaaa tgccatcatt gcgataaagg aaaggccatc gttgaagatg 420

cctctgccga cagtggtccc aaagatggac ccccacccac gaggagcatc gtggaaaaag 480

aagacgttcc aaccacgtct tcaaagcaag tggattgatg tgatatctcc actgacgtaa 540

gggatgacgc acaatcccac tatccttcgc aagacccttc ctctatataa ggaagttcat 600

ttcatttgga gaggacacgc tgacaagctg actctagcag atcctctaga accatcttcc 660

acacactcaa gccacactat tggagaacac acagggacaa cacaccataa gatccaaggg 720

aggcctccgc cgccgccggt aaccaccccg cccctctcct ctttctttct ccgttttttt 780

ttccgtctcg gtctcgatct ttggccttgg tagtttgggt gggcgagagg cggcttcgtg 840

cgcgcccaga tcggtgcgcg ggaggggcgg gatctcgcgg ggaatggggc tctcggatgt 900

agatctgcga tccgccgttg ttgggggaga tgatgggggg tttaaaattt gcgccgtgct 960

aaacaagatc aggaagaggg gaaaagggca ctatggttta tatttttata tatttctgct 1020

gcttcgtcag gcttagatgt gctagatctt tctttcttct ttttgtgggt agaatttgaa 1080

tccctcagca ttgttcatcg gtagtttttc ttttcatgat ttgtgacaaa tgcagcctcg 1140

tgcggagctt ttttgtaggt agaag 1165

<210> SEQ ID NO 172
<211> LENGTH: 1751
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1751)
<223> OTHER INFORMATION: Chimeric transcriptional regulatory expression element group.

<400> SEQUENCE: 172

tcgaggtcat tcatatgctt gagaagagag tcgggatagt ccaaaataaa acaaaggtaa 60

gattacctgg tcaaaagtga aaacatcagt taaaaggtgg tataaagtaa aatatcggta 120

ataaaaggtg gcccaaagtg aaatttactc ttttctacta ttataaaaat tgaggatgtt 180

tttgtcggta ctttgatacg tcatttttgt atgaattggt ttttaagttt attcgctttt 240

ggaaatgcat atctgtattt gagtcgggtt ttaagttcgt ttgcttttgt aaatacagag 300

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ggatttgtat aagaaatatc tttagaaaaa cccatatgct aatttgacat aatttttgag 360

aaaaatatat attcaggcga attagcttag gcctcatcgt tgaagatgcc tctgccgaca 420

gtggtcccaa agatggaccc ccacccacga ggagcatcgt ggaaaaagaa gacgttccaa 480

ccacgtcttc aaagcaagtg gattgatgtg atatctccac tgacgtaagg gatgacgcac 540

aatcccacta tccttcgagg cctcatcgtt gaagatgcct ctgccgacag tggtcccaaa 600

gatggacccc cacccacgag gagcatcgtg gaaaaagaag acgttccaac cacgtcttca 660

aagcaagtgg attgatgtga tatctccact gacgtaaggg atgacgcaca atcccactat 720

ccttcgaagc taattctcac aatgaacaat aataagatta aaatagcttt cccccgttgc 780

agcgcatggg tatttttttct agtaaaaata aaagataaac ttagactcaa aacatttaca 840

aaaacaaccc ctaaagttcc taaagcccaa agtgctatcc acgatccata gcaagcccag 900

cccaacccaa cccaacccaa cccaccccag tccagccaac tggacaatag tctccacacc 960

cccccactat caccgtgagt tgtccgcacg caccgcacgt ctcgcagcca aaaaaaaaaa 1020

gaaagaaaaa aaagaaaaag aaaaaacagc aggtgggtcc gggtcgtggg ggccggaaac 1080

gcgaggagga tcgcgagcca gcgacgaggc cggccctccc tccgcttcca aagaaacgcc 1140

ccccatcgcc actatataca tacccccccc tctcctccca tccccccaac cctaccacca 1200

ccaccaccac cacctccacc tcctcccccc tcgctgccgg acgacgagct cctccccct 1260

ccccctccgc cgccgccgcg ccggtaacca ccccgccccc ctcctctttc tttctccgtt 1320

ttttttccg tctcggtctc gatctttggc cttggtagtt tgggtgggcg agaggcggct 1380

tcgtgcgcgc ccagatcggt gcgcgggagg ggcgggatct cgcggctggg gctctcgccg 1440

gcgtggatcc ggcccggatc tcgcggggaa tggggctctc ggatgtagat ctgcgatccg 1500

ccgttgttgg gggagatgat gggggggttta aaatttccgc cgtgctaaac aagatcagga 1560

agaggggaaa agggcactat ggtttatatt tttatatatt tctgctgctt cgtcaggctt 1620

agatgtgcta gatctttctt tcttcttttt gtgggtagaa tttgaatccc tcagcattgt 1680

tcatcggtag tttttctttt catgatttgt gacaaatgca gcctcgtgcg gagctttttt 1740

gtaggtagaa g 1751

<210> SEQ ID NO 173
<211> LENGTH: 1101
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1101)
<223> OTHER INFORMATION: Chimeric transcriptional regulatory expression element group.

<400> SEQUENCE: 173

ggtccgattg agacttttca acaaagggta atatccggaa acctcctcgg attccattgc 60

ccagctatct gtcactttat tgtgaagata gtggaaaagg aaggtggctc ctacaaatgc 120

catcattgcg ataaaggaaa ggccatcgtt gaagatgcct ctgccgacag tggtcccaaa 180

gatggacccc cacccacgag gagcatcgtg gaaaaagaag acgttccaac cacgtcttca 240

aagcaagtgg attgatgtga tggtccgatt gagacttttc aacaaagggt aatatccgga 300

aacctcctcg gattccattg cccagctatc tgtcacttta ttgtgaagat agtggaaaag 360

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gaaggtggct cctacaaatg ccatcattgc gataaaggaa aggccatcgt tgaagatgcc 420

tctgccgaca gtggtcccaa agatggaccc ccacccacga ggagcatcgt ggaaaaagaa 480

gacgttccaa ccacgtcttc aaagcaagtg gattgatgtg atatctccac tgacgtaagg 540

gatgacgcac aatcccacta tccttcgcaa gacccttcct ctatataagg aagttcattt 600

catttggaga ggacacgctg accgccgccg ccggtaacca ccccgccccc ctcctctttc 660

tttctccgtt ttttttccg tctcggtctc gatctttggc cttggtagtt tgggtgggcg 720

agaggcggct tcgtgcgcgc ccagatcggt gcgcgggagg ggcgggatct cgcggctggg 780

gctctcgccg gcgtggatcc ggcccggatc tcgcggggaa tggggctctc ggatgtagat 840

ctgcgatccg ccgttgttgg gggagatgat gggggggttta aaatttccgc cgtgctaaac 900

aagatcagga agaggggaaa agggcactat ggtttatatt tttatatatt tctgctgctt 960

cgtcaggctt agatgtgcta gatctttctt tcttcttttt gtgggtagaa tttgaatccc 1020

tcagcattgt tcatcggtag ttttttctttt catgatttgt gacaaatgca gcctcgtgcg 1080

gagctttttt gtaggtagaa g 1101

<210> SEQ ID NO 174
<211> LENGTH: 200
<212> TYPE: DNA
<213> ORGANISM: Cauliflower mosaic virus

<400> SEQUENCE: 174

aaatcaccag tctctctcta caaatctatc tctctctatt tttctccaga ataatgtgtg 60

agtagttccc agataaggga attagggttc ttatagggtt tcgctcatgt gttgagcata 120

taagaaaccc ttagtatgta tttgtatttg taaaatactt ctatcaataa aatttctaat 180

tcctaaaacc aaaatccagt 200

<210> SEQ ID NO 175
<211> LENGTH: 300
<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 175

attaatcgat cctccgatcc cttaattacc ataccattac accatgcatc aatatccata 60

tatatataaa ccctttcgca cgtacttata ctatgttttg tcatacatat atatgtgtcg 120

aacgatcgat ctatcactga tatgatatga ttgatccatc agcctgatct ctgtatcttg 180

ttatttgtat accgtcaaat aaaagtttct tccacttgtg ttaataatta gctactctca 240

tctcatgaac cctatatata actagtttaa tttgctgtca attgaacatg atgatcgatg 300

<210> SEQ ID NO 176
<211> LENGTH: 623
<212> TYPE: DNA
<213> ORGANISM: Cauliflower mosaic virus

<400> SEQUENCE: 176

ggtccgatgt gagacttttc aacaaagggt aatatccgga aacctcctcg gattccattg 60

cccagctatc tgtcacttta ttgtgaagat agtggaaaag gaaggtggct cctacaaatg 120

ccatcattgc gataaaggaa aggccatcgt tgaagatgcc tctgccgaca gtggtcccaa 180

agatggaccc ccacccacga ggagcatcgt ggaaaaagaa gacgttccaa ccacgtcttc 240

-continued

aaagcaagtg gattgatgtg atggtccgat gtgagacttt tcaacaaagg gtaatatccg 300

gaaacctcct cggattccat tgcccagcta tctgtcactt tattgtgaag atagtggaaa 360

aggaaggtgg ctcctacaaa tgccatcatt gcgataaagg aaaggccatc gttgaagatg 420

cctctgccga cagtggtccc aaagatggac ccccacccac gaggagcatc gtggaaaaag 480

aagacgttcc aaccacgtct tcaaagcaag tggattgatg tgatatctcc actgacgtaa 540

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<212> TYPE: DNA
<213> ORGANISM: Cauliflower mosaic virus

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<210> SEQ ID NO 178
<211> LENGTH: 804
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atcgtgttct gcctgtgctg attacttgcc gtcctttgta gcagcaaaat atagggacat 180

ggtagtacga aacgaagata gaacctacac agcaatacga gaaatgtgta atttggtgct 240

tagcggtatt tatttaagca catgttggtg ttatagggca cttggattca gaagtttgct 300

gttaatttag gcacaggctt catactacat gggtcaatag tatagggatt catattatag 360

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<212> TYPE: DNA
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 179

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ataaaaggtg gcccaaagtg aaatttactc ttttctacta ttataaaaat tgaggatgtt 180

tttgtcggta ctttgatacg tcatttttgt atgaattggt ttttaagttt attcgctttt 240

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ggaaatgcat atctgtattt gagtcgggtt ttaagttcgt ttgcttttgt aaatacagag 300

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cccgttgcag cgcatgggta ttttttctag taaaaataaa agataaactt agactcaaaa 480

catttacaaa aacaacccct aaagttccta aagcccaaag tgctatccac gatccatagc 540

aagcccagcc caacccaacc caacccagcc caccccagtc cagccaactg gacaatagtc 600

tccacacccc cccactatca ccgtgagttg tccgcacgca ccgcacgtct cgcagccaaa 660

aaaaaaaaga aagaaaaaaa agaaaaagaa aaaacagcag gtgggtccgg gtcgtggggg 720

ccggaaacgc gaggaggatc gcgagccagc gacgaggccg gccctccctc cgcttccaaa 780

gaaacgcccc ccatcgccac tatatacata ccccccccctc tcctcccatc cccccaaccc 840

taccaccacc accaccacca cctccacctc ctcccccctc gctgccggac gacgagctcc 900

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tctccgtttt tttttccgtc tcggtctcga tctttggcct tggtagtttg ggtgggcgag 1020

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cgcccccgtg gatccggccc ggatctcgcg gggaatgggg ctctcggatg tagatctgcg 1140

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caggaagagg ggaaaagggc actatggttt atatttttat atatttctgc tgcttcgtca 1260

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tttttgtagg tagaag 1396

<210> SEQ ID NO 180
<211> LENGTH: 2625
<212> TYPE: DNA
<213> ORGANISM: Setaria italica

<400> SEQUENCE: 180

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caaagagctg aaaagataag gttgtgcggg ctgtggtgat tagaggacca ctaatccctc 180

catctcctaa tgacgcggtg cccaagacca gtgccgcggc acaccagcgt ctaagtgaac 240

ttccgctaac cttccggtca ttgcgcctga aagatgtcat gtggcgaggc ccccctctca 300

gtagattgcc aactgcctac cgtgccactc ttccatgcat gattgctccc gtctatcccg 360

tttctcacaa cagatagaca acagtaagca tcactaaagc aagcatgtgt agaaccttaa 420

aaaaaggctt atactaccag tatactatca accagcatgc cgtttttgaa gtatccagga 480

ttagaagctt ctactgcgct tttatattat agctgtggac ccgtggtaac ctttctcttt 540

tggcgcttgc ttaatctcgg ccgtgctggt ccatgcttag gcactaggca gagatagagc 600

cgggggtgaa tggggctaaa gctcagctgc tcgaggggcc gtgggctggt ttccactagc 660

ctacagctgt gccacgtgcg gccgcgcaag ccgaagcaag cacgctgagc cgttggacag 720

cttgtcataa tgccattacg tggattacac gtaactggcc ctgtaactac tcgttcggcc 780

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aagaatggaa gtatggagct gctactgtgt aaatgccaag caggaaactc acgcccgcta 1020

acatccaacg gccaacagct cgacgtgccg gtcagcagag catcggaaca ctggtgattg 1080

gtggagccgg cagtatgcgc cccagcacgg ccgaggtggt ggtggcccgt ggccctgctg 1140

tctgcgcggc tcgggacaac ttgaaactgg gccaccgcct cgtcgcaact cgcaacccgt 1200

tggcggaaga aaggaatggc tcgtaggggc ccgggtagaa tcgaagaatg ttgcgctggg 1260

cttcgattca cataacatgg gcctgaagct ctaaaacgac ggcccggtcg ccgcgcgatg 1320

gaaagagacc ggatcctcct cgtgaattct ggaaggccac acgagagcga cccaccaccg 1380

acgcggagga gtcgtgcgtg gtccaacacg gccggcgggc tgggctgcga ccttaaccag 1440

caaggcacgc cacgacccgc cccgccctcg aggcataaat accctcccat cccgttgccg 1500

caagactcag atcagattcc gatccccagt tcttccccaa tcaccttgtg gtctctcgtg 1560

tcgcggttcc cagggacgcc tccggctcgt cgctcgacag cgatctccgc cccagcaagg 1620

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gattatgtca tatatctgcg gtttgcaccg atctgaagcc tagggtttct cgagcgaccc 1740

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tcgaggattt gtatgcggcg tcggcgctac ctgcttaatc acgccatgtg acgcggttac 1860

ttgcagaggc tgggttctgt tatgtcgtga tctaagaatc tagattaggc tcagtcgttc 1920

ttgctgtcga ctagtttgtt ttgatatcca tgtagtacaa gttacttaaa atttaggtcc 1980

aatatatttt gcatgctttt ggcctgttat tcttgccaac aagttgtcct ggtaaaaagt 2040

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gctattttgg tgatcgtgtc attttatttg tgaatggaat cattgtatgt aaatgaagct 2280

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aaggacagaa cattgttaat attttggcac atctgtctta ttctcatcct ttgtttgaac 2460

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<210> SEQ ID NO 181
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<212> TYPE: DNA
<213> ORGANISM: Zea mays subsp. Mexicana

<400> SEQUENCE: 181

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ttcactctac aaataatata gtctataata ctaaaataat attagtgttt tagaggatca 180

tataaataaa ctgctagaca tggtctaaag gataattgaa tattttgaca atctacagtt 240

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atacttcatc cattttatta gtacatccat ttaggattta gggttgatgg tttctataga 360

ctaatttttа gtacatccat tttattcttt ttagtctcta aatttttttaa aactaaaact 420

ctattttagt tttttattta ataatttaga tataaaatga aataaaataa attgactaca 480

aataaaacaa ataccctttа agaaatаaaa aaactaagca aacatttttc ttgtttcgag 540

tagataatga caggctgttc aacgccgtcg acgagtctaa cggacaccaa ccagcgaacc 600

agcagcgtcg cgtcgggcca agcgaagcag acggcacggc atctctgtag ctgcctctgg 660

acccctctcg agagttccgc tccaccgttg gacttgctcc gctgtcggca tccagaaatt 720

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accggcagct acgggggatt cctttcccac cgctccttcg ctttcccttc ctcgcccgcc 840

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acacacacgc aaccagatct cccccaaatc cagccgtcgg cacctccgct tcaaggtacg 960

ccgctcatcc tccccccccc cctctctcta ccttctctag atcggcgatc cggtccatgg 1020

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atcggagtag aatactgttt caaactacct ggtggattta ttaattttgt atctttatgt 1680

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<400> SEQUENCE: 182

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tgttcatgtt tgtgatgatg tggtctggtt gggcggtcgt tctagatcgg agtaggatac 180

tgtttcaagc tacctggtgg atttattaat tttgtatctg tatgtgtgtg ccatacatct 240

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gatgcgggtt ttactgatgc atatacagag atgctttttt tctcgcttgg ttgtgatgat 360

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gatttattaa aggataaagg gtcgttctag atcggagtag aatactgttt caaactacct 480

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<400> SEQUENCE: 183

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caaagagctg aaaagataag gttgtgcggg ctgtggtgat tagaggacca ctaatccctc 180

catctcctaa tgacgcggtg cccaagacca gtgccgcggc acaccagcgt ctaagtgaac 240

ttccgctaac cttccggtca ttgcgcctga aagatgtcat gtggcgaggc ccccctctca 300

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tctctattga gtttatggac ttttgtgtgt gaagttatat ttcattttgc tcaaaactca   2580

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What is claimed is:

1. A DNA molecule comprising a DNA sequence selected from the group consisting of:

a) a sequence with at least 85 percent sequence identity to any of SEQ ID NOs: 1-158 and 180-183;

b) a sequence comprising any of SEQ ID NOs: 1-158 and 180-183; and

c) a fragment of any of SEQ ID NOs: 1-158 and 180-183, wherein the fragment has gene-regulatory activity;

wherein said sequence is operably linked to a heterologous transcribable polynucleotide molecule.

2. The DNA molecule of claim **1**, wherein said sequence has at least 90 percent sequence identity to the DNA sequence of any of SEQ ID NOs: 1-158 and 180-183.

3. The DNA molecule of claim **1**, wherein said sequence has at least 95 percent sequence identity to the DNA sequence of any of SEQ ID NOs: 1-158 and 180-183.

4. The DNA molecule of claim **1**, wherein the DNA sequence comprises gene regulatory activity.

5. The DNA molecule of claim **1**, wherein the heterologous transcribable polynucleotide molecule comprises a gene of agronomic interest.

6. The DNA molecule of claim **5**, wherein the gene of agronomic interest confers herbicide tolerance in plants.

7. The DNA molecule of claim **5**, wherein the gene of agronomic interest confers pest resistance in plants.

8. A transgenic plant cell comprising a heterologous DNA molecule comprising a sequence selected from the group consisting of:

a) a sequence with at least 85 percent sequence identity to any of SEQ ID NOs: 1-158 and 180-183;

b) a sequence comprising any of SEQ ID NOs: 1-158 and 180-183; and

c) a fragment of any of SEQ ID NOs: 1-158 and 180-183, wherein the fragment has gene-regulatory activity;

wherein said sequence is operably linked to a heterologous transcribable polynucleotide molecule.

9. The transgenic plant cell of claim **8**, wherein said transgenic plant cell is a monocotyledonous plant cell.

10. The transgenic plant cell of claim **8**, wherein said transgenic plant cell is a dicotyledonous plant cell.

11. A transgenic plant, or part thereof, comprising the DNA molecule of claim **1**.

12. A progeny plant of the transgenic plant of claim **11**, or a part thereof, wherein the progeny plant or part thereof comprises said DNA molecule.

13. A transgenic seed, wherein the seed comprises the DNA molecule of claim **1**.

14. A method of producing a commodity product comprising obtaining a transgenic plant or part thereof according to claim **11** and producing the commodity product therefrom.

15. The method of claim **14**, wherein the commodity product is protein concentrate, protein isolate, grain, starch, seeds, meal, flour, biomass, or seed oil.

16. A commodity product comprising the DNA molecule of claim **1**.

17. The commodity product of claim **16**, wherein the commodity product is protein concentrate, protein isolate, grain, starch, seeds, meal, flour, biomass, or seed oil.

18. A method of expressing a transcribable polynucleotide molecule comprising obtaining a transgenic plant according to claim **11** and cultivating plant, wherein the transcribable polynucleotide is expressed.

* * * * *