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(54) Title: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER			
(57) Abstract			
Compositions and methods for the detection and therapy of breast cancer are disclosed. The compounds provided include nucleotide sequences that are preferentially expressed in breast tumor tissue, as well as polypeptides encoded by such nucleotide sequences. Vaccines and pharmaceutical compositions comprising such compounds are also provided and may be used, for example, for the prevention and treatment of breast cancer. The polypeptides may also be used for the production of antibodies, which are useful for diagnosing and monitoring the progression of breast cancer patient.			

COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER

TECHNICAL FIELD

The present invention relates generally to the detection and therapy of breast cancer. The invention is more specifically related to nucleotide sequences that are preferentially expressed in breast tumor tissue and to polypeptides encoded by such nucleotide sequences. The nucleotide sequences and polypeptides may be used in vaccines and pharmaceutical compositions for the prevention and treatment of breast cancer. The polypeptides may also be used for the production of compounds, such as antibodies, useful for diagnosing and monitoring the progression of breast cancer in a patient.

BACKGROUND OF THE INVENTION

Breast cancer is a significant health problem for women in the United States and throughout the world. Although advances have been made in detection and treatment of the disease, breast cancer remains the second leading cause of cancer-related deaths in women, affecting more than 180,000 women in the United States each year. For women in North America, the life-time odds of getting breast cancer are now one in eight

No vaccine or other universally successful method for the prevention or treatment of breast cancer is currently available. Management of the disease currently relies on a combination of early diagnosis (through routine breast screening procedures) and aggressive treatment, which may include one or more of a variety of treatments such as surgery, radiotherapy, chemotherapy and hormone therapy. The course of treatment for a particular breast cancer is often selected based on a variety of prognostic parameters, including an analysis of specific tumor markers. See, e.g., Porter-Jordan and Lippman, *Breast Cancer* 8:73-100 (1994). However, the use of established markers often leads to a result that is difficult to interpret, and the high mortality observed in

breast cancer patients indicates that improvements are needed in the treatment, diagnosis and prevention of the disease.

Accordingly, there is a need in the art for improved methods for therapy and diagnosis of breast cancer. The present invention fulfills these needs and further
5 provides other related advantages.

SUMMARY OF THE INVENTION

Briefly stated, the subject invention provides compositions and methods for the diagnosis and therapy of breast cancer. In one aspect, isolated DNA molecules are provided, comprising (a) a nucleotide sequence preferentially expressed in breast
10 cancer tissue, relative to normal tissue; (b) a variant of such a sequence that contains one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% (preferably no more than 5%) of the nucleotide positions, such that the antigenic and/or immunogenic properties of the polypeptide encoded by the nucleotide sequence are retained; or (c) a nucleotide sequence encoding an epitope of a polypeptide
15 encoded by at least one of the above sequences. In one embodiment, the isolated DNA molecule comprises a human endogenous retroviral sequence recited in SEQ ID NO:1. In other embodiments, the isolated DNA molecule comprises a nucleotide sequence recited in any one of SEQ ID NO: 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247,
20 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297.

In related embodiments, the isolated DNA molecule encodes an epitope of a polypeptide, wherein the polypeptide is encoded by a nucleotide sequence that: (a) hybridizes to a sequence recited in any one of SEQ ID NO: 1, 3-26, 28-77, 142, 143,
25 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297 under stringent conditions; and (b) is at least 80% identical to a sequence recited in any one of SEQ ID NO: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219,

221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297; and wherein RNA corresponding to said nucleotide sequence is expressed at a greater level in human breast tumor tissue than in normal breast tissue.

5 In another embodiment, the present invention provides an isolated DNA molecule encoding an epitope of a polypeptide, the polypeptide being encoded by: (a) a nucleotide sequence transcribed from the sequence of SEQ ID NO: 141; or (b) a variant of said nucleotide sequence that contains one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide
10 positions, such that the antigenic and/or immunogenic properties of the polypeptide encoded by the nucleotide sequence are retained. Isolated DNA and RNA molecules comprising a nucleotide sequence complementary to a DNA molecule as described above are also provided.

In related aspects, the present invention provides recombinant expression
15 vectors comprising a DNA molecule as described above and host cells transformed or transfected with such expression vectors.

In further aspects, polypeptides, comprising an amino acid sequence encoded by a DNA molecule as described above, and monoclonal antibodies that bind to such polypeptides are provided.

20 In yet another aspect, methods are provided for determining the presence of breast cancer in a patient. In one embodiment, the method comprises detecting, within a biological sample, a polypeptide as described above. In another embodiment, the method comprises detecting, within a biological sample, an RNA molecule encoding a polypeptide as described above. In yet another embodiment, the method
25 comprises (a) intradermally injecting a patient with a polypeptide as described above; and (b) detecting an immune response on the patient's skin and therefrom detecting the presence of breast cancer in the patient. In further embodiments, the present invention provides methods for determining the presence of breast cancer in a patient as described
above wherein the polypeptide is encoded by a nucleotide sequence selected from the
30 group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208,

215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

In a related aspect, diagnostic kits useful in the determination of breast cancer are provided. The diagnostic kits generally comprise either one or more monoclonal antibodies as described above, or one or more monoclonal antibodies that bind to a polypeptide encoded by a nucleotide sequence selected from the group consisting of sequences provided in SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 and 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and a detection reagent.

Within a related aspect, the diagnostic kit comprises a first polymerase chain reaction primer and a second polymerase chain reaction primer, at least one of the primers being specific for an RNA molecule described herein. In one embodiment, at least one of the primers comprises at least about 10 contiguous nucleotides of an RNA molecule as described above, or an RNA molecule encoding a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

Within another related aspect, the diagnostic kit comprises at least one oligonucleotide probe, the probe being specific for a DNA molecule described herein. In one embodiment, the probe comprises at least about 15 contiguous nucleotides of a DNA molecule as described above, or a DNA molecule selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

In another related aspect, the present invention provides methods for monitoring the progression of breast cancer in a patient. In one embodiment, the method comprises: (a) detecting an amount, in a biological sample, of a polypeptide as described above at a first point in time; (b) repeating step (a) at a subsequent point in time; and (c) comparing the amounts of polypeptide detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient. In another

embodiment, the method comprises (a) detecting an amount, within a biological sample, of an RNA molecule encoding a polypeptide as described above at a first point in time; (b) repeating step (a) at a subsequent point in time; and (c) comparing the amounts of RNA molecules detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient. In yet other embodiments, the present invention provides methods for monitoring the progression of breast cancer in a patient as described above wherein the polypeptide is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

In still other aspects, pharmaceutical compositions, which comprise a polypeptide as described above in combination with a physiologically acceptable carrier, and vaccines, which comprise a polypeptide as described above in combination with an immune response enhancer or adjuvant, are provided. In yet other aspects, the present invention provides pharmaceutical compositions and vaccines comprising a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 and 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

In related aspects, the present invention provides methods for inhibiting the development of breast cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as described above.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the differential display PCR products, separated by gel electrophoresis, obtained from cDNA prepared from normal breast tissue (lanes 1 and 2)

and from cDNA prepared from breast tumor tissue from the same patient (lanes 3 and 4). The arrow indicates the band corresponding to B18Ag1.

Figure 2 is a northern blot comparing the level of B18Ag1 mRNA in breast tumor tissue (lane 1) with the level in normal breast tissue.

5 Figure 3 shows the level of B18Ag1 mRNA in breast tumor tissue compared to that in various normal and non-breast tumor tissues as determined by RNase protection assays.

Figure 4 is a genomic clone map showing the location of additional retroviral sequences obtained from ends of XbaI restriction digests (provided in SEQ ID
10 NO:3 - SEQ ID NO:10) relative to B18Ag1.

Figures 5A and 5B show the sequencing strategy, genomic organization and predicted open reading frame for the retroviral element containing B18Ag1.

Figure 6 shows the nucleotide sequence of the representative breast tumor-specific cDNA B18Ag1.

15 Figure 7 shows the nucleotide sequence of the representative breast tumor-specific cDNA B17Ag1.

Figure 8 shows the nucleotide sequence of the representative breast tumor-specific cDNA B17Ag2.

Figure 9 shows the nucleotide sequence of the representative breast
20 tumor-specific cDNA B13Ag2a.

Figure 10 shows the nucleotide sequence of the representative breast tumor-specific cDNA B13Ag1b.

Figure 11 shows the nucleotide sequence of the representative breast tumor-specific cDNA B13Ag1a.

25 Figure 12 shows the nucleotide sequence of the representative breast tumor-specific cDNA B11Ag1.

Figure 13 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA3c.

Figure 14 shows the nucleotide sequence of the representative breast
30 tumor-specific cDNA B9CG1.

Figure 15 shows the nucleotide sequence of the representative breast tumor-specific cDNA B9CG3.

Figure 16 shows the nucleotide sequence of the representative breast tumor-specific cDNA B2CA2.

5 Figure 17 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA1.

Figure 18 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA2.

10 Figure 19 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA3.

Figure 20 shows the nucleotide sequence of the representative breast tumor-specific cDNA B4CA1.

Figure 21A depicts RT-PCR analysis of breast tumor genes in breast tumor tissues (lanes 1-8) and normal breast tissues (lanes 9-13) and H₂O (lane 14).

15 Figure 21B depicts RT-PCR analysis of breast tumor genes in prostate tumors (lane 1, 2), colon tumors (lane 3), lung tumor (lane 4), normal prostate (lane 5), normal colon (lane 6), normal kidney (lane 7), normal liver (lane 8), normal lung (lane 9), normal ovary (lanes 10, 18), normal pancreases (lanes 11, 12), normal skeletal muscle (lane 13), normal skin (lane 14), normal stomach (lane 15), normal testes (lane 20 16), normal small intestine (lane 17), HBL-100 (lane 19), MCF-12A (lane 20), breast tumors (lanes 21-23), H₂O (lane 24), and colon tumor (lane 25).

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the diagnosis, monitoring and therapy of breast cancer.

25 The compositions described herein include polypeptides, nucleic acid sequences and antibodies. Polypeptides of the present invention generally comprise at least a portion of a protein that is expressed at a greater level in human breast tumor tissue than in normal breast tissue (*i.e.*, the level of RNA encoding the polypeptide is at least 2-fold higher in tumor tissue). Such polypeptides are referred to herein as breast tumor-

specific polypeptides, and cDNA molecules encoding such polypeptides are referred to as breast tumor-specific cDNAs. Nucleic acid sequences of the subject invention generally comprise a DNA or RNA sequence that encodes all or a portion of a polypeptide as described above, or that is complementary to such a sequence.

5 Antibodies are generally immune system proteins, or fragments thereof, that are capable of binding to a portion of a polypeptide as described above. Antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies.

10 Polypeptides within the scope of this invention include, but are not limited to, polypeptides (and epitopes thereof) encoded by a human endogenous retroviral sequence, such as the sequence designated B18Ag1 (Figure 5 and SEQ ID NO:1). Also within the scope of the present invention are polypeptides encoded by other sequences within the retroviral genome containing B18Ag1 (SEQ ID NO: 141).

15 Such sequences include, but are not limited to, the sequences recited in SEQ ID NO:3 - SEQ ID NO:10. B18Ag1 has homology to the *gag* p30 gene of the endogenous human retroviral element S71, as described in Werner et al., *Virology* 174:225-238 (1990) and also shows homology to about thirty other retroviral *gag* genes. As discussed in more detail below, the present invention also includes a number of additional breast tumor-specific polypeptides, such as those encoded by the nucleotide sequences recited in
20 SEQ ID NO: 11-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including
25 full length proteins containing the sequences recited herein. A polypeptide comprising an epitope of a protein containing a sequence as described herein may consist entirely of the epitope, or may contain additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may (but, need not) possess immunogenic or antigenic properties.

An "epitope," as used herein is a portion of a polypeptide that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Epitopes may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides derived from the native polypeptide for the ability to react with antigen-specific antisera and/or T-cell lines or clones. An epitope of a polypeptide is a portion that reacts with such antisera and/or T-cells at a level that is similar to the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. B-cell and T-cell epitopes may also be predicted via computer analysis. Polypeptides comprising an epitope of a polypeptide that is preferentially expressed in a tumor tissue (with or without additional amino acid sequence) are within the scope of the present invention.

The compositions and methods of the present invention also encompass variants of the above polypeptides and nucleic acid sequences encoding such polypeptides. A polypeptide "variant," as used herein, is a polypeptide that differs from the native polypeptide in substitutions and/or modifications, such that the antigenic and/or immunogenic properties of the polypeptide are retained. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antisera and/or T-cells as described above. Nucleic acid variants may contain one or more substitutions, deletions, insertions and/or modifications such that the antigenic and/or immunogenic properties of the encoded polypeptide are retained. One preferred variant of the polypeptides described herein is a variant that contains nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide positions.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another

amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr;
5 (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenic or antigenic properties, secondary structure and hydrophobic nature of the polypeptide. For
10 example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a
15 polypeptide may be conjugated to an immunoglobulin Fc region.

In general, nucleotide sequences encoding all or a portion of the polypeptides described herein may be prepared using any of several techniques. For example, cDNA molecules encoding such polypeptides may be cloned on the basis of the breast tumor-specific expression of the corresponding mRNAs, using differential
20 display PCR. This technique compares the amplified products from RNA template prepared from normal and breast tumor tissue. cDNA may be prepared by reverse transcription of RNA using a (dT)₁₂AG primer. Following amplification of the cDNA using a random primer, a band corresponding to an amplified product specific to the tumor RNA may be cut out from a silver stained gel and subcloned into a suitable
25 vector (*e.g.*, the T-vector, Novagen, Madison, WI). Nucleotide sequences encoding all or a portion of the breast tumor-specific polypeptides disclosed herein may be amplified from cDNA prepared as described above using the random primers shown in SEQ ID NO.:87-125.

Alternatively, a gene encoding a polypeptide as described herein (or a
30 portion thereof) may be amplified from human genomic DNA, or from breast tumor

cDNA, via polymerase chain reaction. For this approach, B18Ag1 sequence-specific primers may be designed based on the sequence provided in SEQ ID NO:1, and may be purchased or synthesized. One suitable primer pair for amplification from breast tumor cDNA is (5'ATG GCT ATT TTC GGG GGC TGA CA) (SEQ ID NO.:126) and
5 (5'CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO.:127). An amplified portion of B18Ag1 may then be used to isolate the full length gene from a human genomic DNA library or from a breast tumor cDNA library, using well known techniques, such as those described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY (1989). Other sequences within
10 the retroviral genome of which B18Ag1 is a part may be similarly prepared by screening human genomic libraries using B18Ag1-specific sequences as probes. Nucleotides translated into protein from the retroviral genome shown in SEQ ID NO: 141 may then be determined by cloning the corresponding cDNAs, predicting the open reading frames and cloning the appropriate cDNAs into a vector containing a viral
15 promoter, such as T7. The resulting constructs can be employed in a translation reaction, using techniques known to those of skill in the art, to identify nucleotide sequences which result in expressed protein. Similarly, primers specific for the remaining breast tumor-specific polypeptides described herein may be designed based on the nucleotide sequences provided in SEQ ID NO:11 - SEQ ID NO:86 and SEQ ID
20 NO:142 - SEQ ID NO:297.

Recombinant polypeptides encoded by the DNA sequences described above may be readily prepared from the DNA sequences. For example, supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter.
25 Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

In general, any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this
30 invention. Expression may be achieved in any appropriate host cell that has been

transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO.

5 Such techniques may also be used to prepare polypeptides comprising epitopes or variants of the native polypeptides. For example, variants of a native polypeptide may generally be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis, and sections of the DNA sequence may be removed to permit preparation of truncated polypeptides. Portions and other
10 variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing
15 amino acid chain. *See* Merrifield, *J. Am. Chem. Soc.* 85:2149-2146 (1963). Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division, Foster City, CA, and may be operated according to the manufacturer's instructions.

 In specific embodiments, polypeptides of the present invention
20 encompass amino acid sequences encoded by a DNA molecule having a sequence recited in any one of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297, variants of such polypeptides that are encoded by DNA molecules containing
25 one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide positions, and epitopes of the above polypeptides. Polypeptides within the scope of the present invention also include polypeptides (and epitopes thereof) encoded by DNA sequences that hybridize to a DNA molecule having a sequence recited in any one of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-
30 166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240,

243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297 under stringent conditions, wherein the DNA sequences are at least 80% identical in overall sequence to a recited sequence and wherein RNA corresponding to the nucleotide sequence is expressed at a greater level in human breast
5 tumor tissue than in normal breast tissue. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65°C and two washes of 30 minutes each in 0.2 X SSC, 0.1% SDS at 65°C. DNA molecules according to the present invention include molecules that encode any of the
10 above polypeptides.

In another aspect of the present invention, antibodies are provided. Such antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen
15 comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole
20 limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

25 Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519 (1976), and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may
30 be produced, for example, from spleen cells obtained from an animal immunized as

described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and
5 then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having
10 high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from
15 the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Antibodies may be used, for example, in methods for detecting breast
20 cancer in a patient. Such methods involve using an antibody to detect the presence or absence of a breast tumor-specific polypeptide as described herein in a suitable biological sample. As used herein, suitable biological samples include tumor or normal tissue biopsy, mastectomy, blood, lymph node, serum or urine samples, or other tissue, homogenate, or extract thereof obtained from a patient.

25 There are a variety of assay formats known to those of ordinary skill in the art for using an antibody to detect polypeptide markers in a sample. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, the assay may be performed in a Western blot format, wherein a protein preparation from the biological sample is submitted to gel electrophoresis,
30 transferred to a suitable membrane and allowed to react with the antibody. The

presence of the antibody on the membrane may then be detected using a suitable detection reagent, as described below.

In another embodiment, the assay involves the use of antibody immobilized on a solid support to bind to the polypeptide and remove it from the remainder of the sample. The bound polypeptide may then be detected using a second antibody or reagent that contains a reporter group. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized antibody after incubation of the antibody with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the antibody is indicative of the reactivity of the sample with the immobilized antibody, and as a result, indicative of the concentration of polypeptide in the sample.

The solid support may be any material known to those of ordinary skill in the art to which the antibody may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose filter or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681.

The antibody may be immobilized on the solid support using a variety of techniques known to those in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the antibody, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of

antibody ranging from about 10 ng to about 1 μ g, and preferably about 100-200 ng, is sufficient to immobilize an adequate amount of polypeptide.

Covalent attachment of antibody to a solid support may also generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the antibody. For example, the antibody may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook (1991) at A12-A13).

In certain embodiments, the assay for detection of polypeptide in a sample is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the biological sample, such that the polypeptide within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20TM (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with breast cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least, 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium

may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support
5 with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard
10 methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed
15 and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different
20 reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of breast cancer, the signal
25 detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value established from non-tumor tissue. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients, without breast cancer. In general, a sample generating a signal that is three standard
30 deviations above the predetermined cut-off value may be considered positive for breast

cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, p. 106-7 (Little Brown and Co., 1985). Briefly, in this embodiment, the cut-off value may be determined from a plot of
5 pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered
10 positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for breast cancer.

In a related embodiment, the assay is performed in a flow-through or
15 strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, the polypeptide within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody
20 may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of breast cancer. Typically, the
25 concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that, would be sufficient to generate a positive signal in the two-antibody sandwich assay, in
30 the format discussed above. Preferably, the amount of antibody immobilized on the

membrane ranges from about 25 ng to about 1 µg, and more preferably from about 50 ng to about 1 µg. Such tests can typically be performed with a very small amount of biological sample.

The presence or absence of breast cancer in a patient may also be
5 determined by evaluating the level of mRNA encoding a breast tumor-specific polypeptide as described herein within the biological sample (*e.g.*, a biopsy, mastectomy and/or blood sample from a patient) relative to a predetermined cut-off value. Such an evaluation may be achieved using any of a variety of methods known to those of ordinary skill in the art such as, for example, *in situ* hybridization and
10 amplification by polymerase chain reaction.

For example, polymerase chain reaction may be used to amplify sequences from cDNA prepared from RNA that is isolated from one of the above biological samples. Sequence-specific primers for use in such amplification may be designed based on the sequences provided in any one of SEQ ID NO: 1, 11-86 and 142-
15 297, and may be purchased or synthesized. In the case of B18Ag1, as noted herein, one suitable primer pair is B18Ag1-2 (5'ATG GCT ATT TTC GGG GGC TGA CA) (SEQ ID NO.:126) and B18Ag1-3 (5'CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO.:127). The PCR reaction products may then be separated by gel electrophoresis and visualized according to methods well known to those of ordinary skill in the art.
20 Amplification is typically performed on samples obtained from matched pairs of tissue (tumor and non-tumor tissue from the same individual) or from unmatched pairs of tissue (tumor and non-tumor tissue from different individuals). The amplification reaction is preferably performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the
25 tumor sample as compared to the same dilution of the non-tumor sample is considered positive.

As used herein, the term "primer/probe specific for a DNA/RNA molecule" means an oligonucleotide sequence that has at least about 80% identity preferably at least about 90% and more preferably at least about 95%, identity to the
30 DNA/RNA molecule in question. Primers and/or probes which may be usefully

employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the polymerase chain reaction primers comprise at least about 10 contiguous nucleotides of a DNA/RNA molecule encoding one of the polypeptides disclosed herein. Preferably, oligonucleotide probes for use in
5 the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA/RNA molecule encoding one of the polypeptides disclosed herein. Techniques for both PCR based assays and *in situ* hybridization assays are well known in the art.

Conventional RT-PCR protocols using agarose and ethidium bromide
10 staining while important in defining gene specificity do not lend themselves to diagnostic kit development because of the time and effort required in making them quantitative (i.e., construction of saturation and/or titration curves), and their sample throughput. This problem is overcome by the development of procedures such as real time RT-PCR which allows for assays to be performed in single tubes, and in turn can
15 be modified for use in 96 well plate formats. Instrumentation to perform such methodologies are available from Perkin Elmer/Applied Biosystems Division. Alternatively, other high throughput assays using labeled probes (e.g., digoxigenin) in combination with labeled (e.g., enzyme fluorescent, radioactive) antibodies to such probes can also be used in the development of 96 well plate assays.

20 In yet another method for determining the presence or absence of breast cancer in a patient, one or more of the breast tumor-specific polypeptides described may be used in a skin test. As used herein, a "skin test" is any assay performed directly on a patient in which a delayed-type hypersensitivity (DTH) reaction (such as swelling, reddening or dermatitis) is measured following intradermal injection of one or more
25 polypeptides as described above. Such injection may be achieved using any suitable device sufficient to contact the polypeptide or polypeptides with dermal cells of the patient, such as a tuberculin syringe or 1 mL syringe. Preferably, the reaction is measured at least 48 hours after injection, more preferably 48-72 hours.

The DTH reaction is a cell-mediated immune response, which is greater
30 in patients that have been exposed previously to a test antigen (*i.e.*, an immunogenic

portion of a polypeptide employed, or a variant thereof). The response may be measured visually, using a ruler. In general, a response that is greater than about 0.5 cm in diameter, preferably greater than about 5.0 cm in diameter, is a positive response, indicative of breast cancer.

5 The breast tumor-specific polypeptides described herein are preferably formulated, for use in a skin test, as pharmaceutical compositions containing at least one polypeptide and a physiologically acceptable carrier, such as water, saline, alcohol, or a buffer. Such compositions typically contain one or more of the above polypeptides in an amount ranging from about 1 μ g to 100 μ g, preferably from about 10 μ g to 50 μ g
10 in a volume of 0.1 mL. Preferably, the carrier employed in such pharmaceutical compositions is a saline solution with appropriate preservatives, such as phenol and/or Tween 80TM.

 In other aspects of the present invention, the progression and/or response to treatment of a breast cancer may be monitored by performing any of the above assays
15 over a period of time, and evaluating the change in the level of the response (*i.e.*, the amount of polypeptide or mRNA detected or, in the case of a skin test, the extent of the immune response detected). For example, the assays may be performed every month to every other month for a period of 1 to 2 years. In general, breast cancer is progressing in those patients in whom the level of the response increases over time. In contrast,
20 breast cancer is not progressing when the signal detected either remains constant or decreases with time.

 In further aspects of the present invention, the compounds described herein may be used for the immunotherapy of breast cancer. In these aspects, the compounds (which may be polypeptides, antibodies or nucleic acid molecules) are
25 preferably incorporated into pharmaceutical compositions or vaccines. Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more polypeptides and an immune response enhancer, such as an adjuvant or a liposome (into which the compound is incorporated). Pharmaceutical compositions and vaccines may additionally contain a delivery system,
30 such as biodegradable microspheres which are disclosed, for example, in U.S. Patent

Nos. 4,897,268 and 5,075,109. Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, including one or more separate polypeptides.

Alternatively, a vaccine may contain DNA encoding one or more of the
5 polypeptides as described above, such that the polypeptide is generated *in situ*. In such vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and
10 terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication
15 competent virus. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749 (1993), and reviewed by Cohen, *Science* 259:1691-1692 (1993). The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the
20 cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a
25 wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention.

Any of a variety of adjuvants may be employed in the vaccines of this invention to nonspecifically enhance the immune response. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI), Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ), alum, biodegradable microspheres, monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

The above pharmaceutical compositions and vaccines may be used, for example, for the therapy of breast cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with breast cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of breast cancer or to treat a patient afflicted with breast cancer. To prevent the development of breast cancer, a pharmaceutical composition or vaccine comprising one or more polypeptides as described herein may be administered to a patient. Alternatively, naked DNA or plasmid or viral vector encoding the polypeptide may be administered. For treating a patient with breast cancer, the pharmaceutical composition or vaccine may comprise one or more polypeptides, antibodies or nucleotide sequences complementary to DNA encoding a polypeptide as described herein (e.g., antisense RNA or antisense deoxyribonucleotide oligonucleotides).

Routes and frequency of administration, as well as dosage, will vary from individual to individual. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered for a 52-week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients.

- A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*.
- 5 Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about
- 10 100 μ g to 5 mg. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

PREPARATION OF BREAST TUMOR-SPECIFIC CDNAS USING DIFFERENTIAL DISPLAY RT-PCR

This Example illustrates the preparation of cDNA molecules encoding breast tumor-specific polypeptides using a differential display screen.

A. Preparation of B18Ag1 cDNA and Characterization of mRNA Expression

Tissue samples were prepared from breast tumor and normal tissue of a patient with breast cancer that was confirmed by pathology after removal from the patient. Normal RNA and tumor RNA was extracted from the samples and mRNA was isolated and converted into cDNA using a (dT)₁₂AG (SEQ ID NO.:130) anchored 3' primer. Differential display PCR was then executed using a randomly chosen primer (CTTCAACCTC) (SEQ ID NO.:103). Amplification conditions were standard buffer containing 1.5 mM MgCl₂, 20 pmol of primer, 500 pmol dNTP, and 1 unit of *Taq* DNA polymerase (Perkin-Elmer, Branchburg, NJ). Forty cycles of amplification were performed using 94°C denaturation for 30 seconds, 42°C annealing for 1 minute, and 72°C extension for 30 seconds. An RNA fingerprint containing 76 amplified products was obtained. Although the RNA fingerprint of breast tumor tissue was over 98% identical to that of the normal breast tissue, a band was repeatedly observed to be specific to the RNA fingerprint pattern of the tumor. This band was cut out of a silver stained gel, subcloned into the T-vector (Novagen, Madison, WI) and sequenced.

The sequence of the cDNA, referred to as B18Ag1, is provided in SEQ ID NO:1. A database search of GENBANK and EMBL revealed that the B18Ag1 fragment initially cloned is 77% identical to the endogenous human retroviral element S71, which is a truncated retroviral element homologous to the Simian Sarcoma Virus (SSV). S71 contains an incomplete *gag* gene, a portion of the *pol* gene and an LTR-like structure at the 3' terminus (*see* Werner et al., *Virology* 174:225-238 (1990)). B18Ag1

is also 64% identical to SSV in the region corresponding to the P30 (*gag*) locus. B18Ag1 contains three separate and incomplete reading frames covering a region which shares considerable homology to a wide variety of *gag* proteins of retroviruses which infect mammals. In addition, the homology to S71 is not just within the *gag* gene, but
5 spans several kb of sequence including an LTR.

B18Ag1-specific PCR primers were synthesized using computer analysis guidelines. RT-PCR amplification (94°C, 30 seconds; 60°C → 42°C, 30 seconds; 72°C, 30 seconds for 40 cycles) confirmed that B18Ag1 represents an actual mRNA sequence present at relatively high levels in the patient's breast tumor tissue. The primers used
10 in amplification were B18Ag1-1 (CTG CCT GAG CCA CAA ATG) (SEQ ID NO.:128) and B18Ag1-4 (CCG GAG GAG GAA GCT AGA GGA ATA) (SEQ ID NO.:129) at a 3.5 mM magnesium concentration and a pH of 8.5, and B18Ag1-2 (ATG GCT ATT TTC GGG GCC TGA CA) (SEQ ID NO.:126) and B18Ag1-3 (CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO.:127) at 2 mM magnesium at pH 9.5. The same
15 experiments showed exceedingly low to nonexistent levels of expression in this patient's normal breast tissue (*see* Figure 1). RT-PCR experiments were then used to show that B18Ag1 mRNA is present in nine other breast tumor samples (from Brazilian and American patients) but absent in, or at exceedingly low levels in, the normal breast tissue corresponding to each cancer patient. RT-PCR analysis has also shown that the
20 B18Ag1 transcript is not present in various normal tissues (including lymph node, myocardium and liver) and present at relatively low levels in PBMC and lung tissue. The presence of B18Ag1 mRNA in breast tumor samples, and its absence from normal breast tissue, has been confirmed by Northern blot analysis, as shown in Figure 2.

The differential expression of B18Ag1 in breast tumor tissue was also
25 confirmed by RNase protection assays. Figure 3 shows the level of B18Ag1 mRNA in various tissue types as determined in four different RNase protection assays. Lanes 1-12 represent various normal breast tissue samples, lanes 13-25 represent various breast tumor samples; lanes 26-27 represent normal prostate samples; lanes 28-29 represent prostate tumor samples; lanes 30-32 represent colon tumor samples; lane 33 represents
30 normal aorta; lane 34 represents normal small intestine; lane 35 represents normal skin,

lane 36 represents normal lymph node; lane 37 represents normal ovary; lane 38 represents normal liver; lane 39 represents normal skeletal muscle; lane 40 represents a first normal stomach sample, lane 41 represents a second normal stomach sample; lane 42 represents a normal lung; lane 43 represents normal kidney; and lane 44 represents normal pancreas. Interexperimental comparison was facilitated by including a positive control RNA of known β -actin message abundance in each assay and normalizing the results of the different assays with respect to this positive control.

RT-PCR and Southern Blot analysis has shown the B18Ag1 locus to be present in human genomic DNA as a single copy endogenous retroviral element. A genomic clone of approximately 12-18 kb was isolated using the initial B18Ag1 sequence as a probe. Four additional subclones were also isolated by XbaI digestion. Additional retroviral sequences obtained from the ends of the XbaI digests of these clones (located as shown in Figure 4) are shown as SEQ ID NO:3 - SEQ ID NO:10, where SEQ ID NO:3 shows the location of the sequence labeled 10 in Figure 4, SEQ ID NO:4 shows the location of the sequence labeled 11-29, SEQ ID NO:5 shows the location of the sequence labeled 3, SEQ ID NO:6 shows the location of the sequence labeled 6, SEQ ID NO:7 shows the location of the sequence labeled 12, SEQ ID NO:8 shows the location of the sequence labeled 13, SEQ ID NO:9 shows the location of the sequence labeled 14 and SEQ ID NO:10 shows the location of the sequence labeled 11-22.

Subsequent studies demonstrated that the 12-18 kb genomic clone contains a retroviral element of about 7.75 kb, as shown in Figures 5A and 5B. The sequence of this retroviral element is shown in SEQ ID NO: 141. The numbered line at the top of Figure 5A represents the sense strand sequence of the retroviral genomic clone. The box below this line shows the position of selected restriction sites. The arrows depict the different overlapping clones used to sequence the retroviral element. The direction of the arrow shows whether the single-pass subclone sequence corresponded to the sense or anti-sense strand. Figure 5B is a schematic diagram of the retroviral element containing B18Ag1 depicting the organization of viral genes within the element. The open boxes correspond to predicted reading frames, starting with a

methionine, found throughout the element. Each of the six likely reading frames is shown, as indicated to the left of the boxes, with frames 1-3 corresponding to those found on the sense strand.

Using the cDNA of SEQ ID NO:1 as a probe, a longer cDNA was
5 obtained (SEQ ID NO:227) which contains minor nucleotide differences (less than 1%) compared to the genomic sequence shown in SEQ ID NO:141.

B. Preparation of cDNA Molecules Encoding Other Breast Tumor-Specific Polypeptides

Normal RNA and tumor RNA was prepared and mRNA was isolated and
10 converted into cDNA using a (dT)₁₂AG anchored 3' primer, as described above. Differential display PCR was then executed using the randomly chosen primers SEQ ID NO.: 87-125. Amplification conditions were as noted above, and bands observed to be specific to the RNA fingerprint pattern of the tumor were cut out of a silver stained gel, subcloned into either the T-vector (Novagen, Madison, WI) or the pCRII vector
15 (Invitrogen, San Diego, CA) and sequenced. The sequences are provided in SEQ ID NO:11 - SEQ ID NO:86. Of the 79 sequences isolated, 67 were found to be novel (SEQ ID NO.:11-26 and 28-77) (*see also* Figures 6-20).

An extended DNA sequence (SEQ ID NO: 290) for the antigen B15Ag1 (originally identified partial sequence provided in SEQ ID NO: 27) was obtained in
20 further studies. Comparison of the sequence of SEQ ID NO: 290 with those in the gene bank as described above, revealed homology to the known human β -A activin gene.

Subsequent studies identified an additional 146 sequences (SEQ ID NOS:142-289), of which 115 appeared to be novel (SEQ ID NOS:142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-
25 240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291). To the best of the inventors' knowledge none of the previously identified sequences have heretofore been shown to be expressed at a greater level in human breast tumor tissue than in normal breast tissue.

In further studies, six different splice forms of the antigen B11Ag1 were
30 isolated, with each of the various splice forms containing slightly different versions of

the B11Ag1 coding frame. Splice junction sequences define individual exons which, in various patterns and arrangements, make up the various splice forms. Primers were designed to examine the expression pattern of each of the exons using RT-PCR as described below. Each exon was found to show the same expression pattern as the original B11Ag1 clone, with expression being breast tumor, prostate and testis-specific. The determined cDNA sequences for the isolated protein coding exons are provided in SEQ ID NO: 292-297, respectively.

EXAMPLE 2

10 PREPARATION OF B18Ag1 DNA FROM HUMAN GENOMIC DNA

This Example illustrates the preparation of B18Ag1 DNA by amplification from human genomic DNA.

B18Ag1 DNA may be prepared from 250 ng human genomic DNA using 20 pmol of B18Ag1 specific primers, 500 pmol dNTPS and 1 unit of *Taq* DNA polymerase (Perkin Elmer, Branchburg, NJ) using the following amplification parameters: 94°C for 30 seconds denaturing, 30 seconds 60°C to 42°C touchdown annealing in 2°C increments every two cycles and 72°C extension for 30 seconds. The last increment (a 42°C annealing temperature) should cycle 25 times. Primers were selected using computer analysis. Primers synthesized were B18Ag1-1, B18Ag1-2, B18Ag1-3, and B18Ag1-4. Primer pairs that may be used are 1+3, 1+4, 2+3, and 2+4.

Following gel electrophoresis, the band corresponding to B18Ag1 DNA may be excised and cloned into a suitable vector.

EXAMPLE 3

25 PREPARATION OF B18Ag1 DNA FROM BREAST TUMOR CDNA

This Example illustrates the preparation of B18Ag1 DNA by amplification from human breast tumor cDNA.

First strand cDNA is synthesized from RNA prepared from human breast tumor tissue in a reaction mixture containing 500 ng poly A+ RNA, 200 pmol of the primer (T)₁₂AG (*i.e.*, TTT TTT TTT TTT AG) (SEQ ID NO: 130), 1X first strand reverse transcriptase buffer, 6.7 mM DTT, 500 mmol dNTPs, and 1 unit AMV or
5 MMLV reverse transcriptase (from any supplier, such as Gibco-BRL (Grand Island, NY)) in a final volume of 30 μ l. After first strand synthesis, the cDNA is diluted approximately 25 fold and 1 μ l is used for amplification as described in Example 2. While some primer pairs can result in a heterogeneous population of transcripts, the primers B18Ag1-2 (5'ATG GCT ATT TTC GGG GGC TGA CA) (SEQ ID NO: 126)
10 and B18Ag1-3 (5'CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO: 127) yield a single 151 bp amplification product.

EXAMPLE 4

IDENTIFICATION OF B-CELL AND T-CELL EPITOPES OF B18Ag1

15

This Example illustrates the identification of B18Ag1 epitopes.

The B18Ag1 sequence can be screened using a variety of computer algorithms. To determine B-cell epitopes, the sequence can be screened for hydrophobicity and hydrophilicity values using the method of Hopp, *Prog. Clin. Biol.*
20 *Res. 172B:367-77* (1985) or, alternatively, Cease et al., *J. Exp. Med. 164:1779-84* (1986) or Spouge et al., *J. Immunol. 138:204-12* (1987). Additional Class II MHC (antibody or B-cell) epitopes can be predicted using programs such as AMPHI (*e.g.*, Margalit et al., *J. Immunol. 138:2213* (1987)) or the methods of Rothbard and Taylor (*e.g.*, *EMBO J. 7:93* (1988)).

25

Once peptides (15-20 amino acids long) are identified using these techniques, individual peptides can be synthesized using automated peptide synthesis equipment (available from manufacturers such as Perkin Elmer/Applied Biosystems Division, Foster City, CA) and techniques such as Merrifield synthesis. Following synthesis, the peptides can be used to screen sera harvested from either normal or breast
30 cancer patients to determine whether patients with breast cancer possess antibodies

reactive with the peptides. Presence of such antibodies in breast cancer patient would confirm the immunogenicity of the specific B-cell epitope in question. The peptides can also be tested for their ability to generate a serologic or humoral immune in animals (mice, rats, rabbits, chimps etc.) following immunization *in vivo*. Generation of a
5 peptide-specific antiserum following such immunization further confirms the immunogenicity of the specific B-cell epitope in question.

To identify T-cell epitopes, the B18Ag1 sequence can be screened using different computer algorithms which are useful in identifying 8-10 amino acid motifs within the B18Ag1 sequence which are capable of binding to HLA Class I MHC
10 molecules. (*see, e.g., Rammensee et al., Immunogenetics 41:178-228 (1995)*). Following synthesis such peptides can be tested for their ability to bind to class I MHC using standard binding assays (*e.g., Sette et al., J. Immunol. 153:5586-92 (1994)*) and more importantly can be tested for their ability to generate antigen reactive cytotoxic T-cells following *in vitro* stimulation of patient or normal peripheral mononuclear cells
15 using, for example, the methods of Bakker et al., *Cancer Res. 55:5330-34 (1995)*; Visseren et al., *J. Immunol. 154:3991-98 (1995)*; Kawakami et al., *J. Immunol. 154:3961-68 (1995)*; and Kast et al., *J. Immunol. 152:3904-12 (1994)*. Successful *in vitro* generation of T-cells capable of killing autologous (bearing the same Class I MHC molecules) tumor cells following *in vitro* peptide stimulation further confirms the
20 immunogenicity of the B18Ag1 antigen. Furthermore, such peptides may be used to generate murine peptide and B18Ag1 reactive cytotoxic T-cells following *in vivo* immunization in mice rendered transgenic for expression of a particular human MHC Class I haplotype (Vitiello et al., *J. Exp. Med. 173:1007-15 (1991)*).

A representative list of predicted B18Ag1 B-cell and T-cell epitopes,
25 broken down according to predicted HLA Class I MHC binding antigen, is shown below:

Predicted Th Motifs (B-cell epitopes) (SEQ ID NOS.: 131-133)

SSGGRTFDDFHRYLLVGI

30

QGAAQKPINLSKXIEVVQGHDE

SPGVFLEHLQEAYRIYTPFDLSA

Predicted HLA A2.1 Motifs (T-cell epitopes) (SEQ ID NOS.: 134-140)

YLLVGIQGA
5 GAAQKPINL
NLSKXIEVV
EVVQGHDES
HLQEAYRIY
NLAQVAQAA
10 FVAQAAPDS

EXAMPLE 5

CHARACTERIZATION OF BREAST TUMOR GENES DISCOVERED BY
DIFFERENTIAL DISPLAY PCR

15

The specificity and sensitivity of the breast tumor genes discovered by differential display PCR were determined using RT-PCR. This procedure enabled the rapid evaluation of breast tumor gene mRNA expression semiquantitatively without using large amounts of RNA. Using gene specific primers, mRNA expression levels in
20 a variety of tissues were examined, including 8 breast tumors, 5 normal breasts, 2 prostate tumors, 2 colon tumors, 1 lung tumor, and 14 other normal adult human tissues, including normal prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach and testes.

To ensure the semiquantitative nature of the RT-PCR, β -actin was used
25 as internal control for each of the tissues examined. Serial dilutions of the first strand cDNAs were prepared and RT-PCR assays performed using β -actin specific primers. A dilution was then selected that enabled the linear range amplification of β -actin template, and which was sensitive enough to reflect the difference in the initial copy number. Using this condition, the β -actin levels were determined for each reverse
30 transcription reaction from each tissue. DNA contamination was minimized by DNase

treatment and by assuring a negative result when using first strand cDNA that was prepared without adding reverse transcriptase.

Using gene specific primers, the mRNA expression levels were determined in a variety of tissues. To date, 38 genes have been successfully examined by RT-PCR, five of which exhibit good specificity and sensitivity for breast tumors (B15AG-1, B31GA1b, B38GA2a, B11A1a and B18AG1a). Figures 21A and 21B depict the results for three of these genes: B15AG-1 (SEQ ID NO:27), B31GA1b (SEQ ID NO:148) and B38GA2a (SEQ ID NO. 157). Table I summarizes the expression level of all the genes tested in normal breast tissue and breast tumors, and also in other tissues.

TABLE I

Percentage of Breast Cancer Antigens that are Expressed in Various Tissues

15	Breast Tissues	Over-expressed in Breast Tumors	84%
		Equally Expressed in Normals and Tumor	16%
20	Other Tissues	Over-expressed in Breast Tumors but not in any Normal Tissues	9%
		Over-expressed in Breast Tumors but Expressed in Some Normal Tissues	30%
		Over-expressed in Breast Tumors but Equally Expressed in All Other Tissues	61%

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purpose of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Frudakis, Tony N.
Smith, John M.
Reed, Steven G.
 - (ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
 - (iii) NUMBER OF SEQUENCES: 297
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SEED and BERRY LLP
 - (B) STREET: 6300 Columbia Center, 701 Fifth Avenue
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: USA
 - (F) ZIP: 98104-7092
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 04-APR-1997
 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Maki, David J.
 - (B) REGISTRATION NUMBER: 31,392
 - (C) REFERENCE/DOCKET NUMBER: 210121.419C2
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 622-4900
 - (B) TELEFAX: (206) 682-6031
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTA GAG ACC CAA TTG GGA CCT AAT TGG GAC CCA AAT TTC TCA AGT GGA	48
Leu Glu Thr Gln Leu Gly Pro Asn Trp Asp Pro Asn Phe Ser Ser Gly	
1 5 10 15	
GGG AGA ACT TTT GAC GAT TTC CAC CGG TAT CTC CTC GTG GGT ATT CAG	96
Gly Arg Thr Phe Asp Asp Phe His Arg Tyr Leu Leu Val Gly Ile Gln	
20 25 30	
GGA GCT GCC CAG AAA CCT ATA AAC TTG TCT AAG GCG ATT GAA GTC GTC	144
Gly Ala Ala Gln Lys Pro Ile Asn Leu Ser Lys Ala Ile Glu Val Val	
35 40 45	
CAG GGG CAT GAT GAG TCA CCA GGA GTG TTT TTA GAG CAC CTC CAG GAG	192
Gln Gly His Asp Glu Ser Pro Gly Val Phe Leu Glu His Leu Gln Glu	
50 55 60	
GCT TAT CGG ATT TAC ACC CCT TTT GAC CTG GCA GCC CCC GAA AAT AGC	240
Ala Tyr Arg Ile Tyr Thr Pro Phe Asp Leu Ala Ala Pro Glu Asn Ser	
65 70 75 80	
CAT GCT CTT AAT TTG GCA TTT GTG GCT CAG GCA GCC CCA GAT AGT AAA	288
His Ala Leu Asn Leu Ala Phe Val Ala Gln Ala Ala Pro Asp Ser Lys	
85 90 95	
AGG AAA CTC CAA AAA CTA GAG GGA TTT TGC TGG AAT GAA TAC CAG TCA	336
Arg Lys Leu Gln Lys Leu Glu Gly Phe Cys Trp Asn Glu Tyr Gln Ser	
100 105 110	
GCT TTT AGA GAT AGC CTA AAA GGT TTT	363
Ala Phe Arg Asp Ser Leu Lys Gly Phe	
115 120	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu Glu Thr Gln Leu Gly Pro Asn Trp Asp Pro Asn Phe Ser Ser Gly	
1 5 10 15	
Gly Arg Thr Phe Asp Asp Phe His Arg Tyr Leu Leu Val Gly Ile Gln	
20 25 30	
Gly Ala Ala Gln Lys Pro Ile Asn Leu Ser Lys Ala Ile Glu Val Val	
35 40 45	
Gln Gly His Asp Glu Ser Pro Gly Val Phe Leu Glu His Leu Gln Glu	
50 55 60	
Ala Tyr Arg Ile Tyr Thr Pro Phe Asp Leu Ala Ala Pro Glu Asn Ser	

65	70	75	80
His Ala Leu Asn Leu Ala Phe Val Ala Gln Ala Ala Pro Asp Ser Lys			
	85	90	95
Arg Lys Leu Gln Lys Leu Glu Gly Phe Cys Trp Asn Glu Tyr Gln Ser			
	100	105	110
Ala Phe Arg Asp Ser Leu Lys Gly Phe			
	115	120	

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCTTAGAATC	TTCATACCCC	GAAGTCTTGG	GAAAACTTTA	ATCAGTCACC	TACAGTCTAC	60
CACCCATTTA	GGAGGAGCAA	AGCTACCTCA	GCTCCTCCGG	AGCCGTTTTA	AGATCCCCCA	120
TCTTCAAAGC	CTAACAGATC	AAGCAGCTCT	CCGGTGCACA	ACCTGCGCCC	AGGTAAATGC	180
CAAAAAAGGT	CCTAAACCCA	GCCCAGGCCA	CCGTCTCCAA	GAAAACTCAC	CAGGAGAAAA	240
GTGGGAAATT	GACTTTACAG	AAGTAAAACC	ACACCGGGCT	GGGTACAAAT	ACCTTCTAGT	300
ACTGGTAGAC	ACCTTCTCTG	GATGGACTGA	AGCATTTGCT	ACCAAAAACG	AAACTGTCAA	360
TATGGTAGTT	AAGTTTTTAC	TCAATGAAAT	CATCCCTCGA	CGTGGGCTGC	CTGTTGCCAT	420
AGGGTCTGAT	AATGGAACGG	CCTTCGCCTT	GTCTATAGTT	TAATCAGTCA	GTAAGGCGTT	480
AAACATTCAA	TGGAAGCTCC	ATTGTGCCTA	TCGACCCAGA	GCTCTGGGCA	AGTAGAACGC	540
ATGAACTGCA	CCCTAAAAAA	ACACTCTTAC	AAAATTAATC	TTAAAAACCG	GTGTTAATTG	600
TGTTAGTCTC	CTTCCCCTAG	CCCTACTTAG	AGTTAAGGTG	CACCCCTTAC	TGGGCTGGGT	660
TCTTTACCTT	TTGAAATCAT	NTTNGGAAG	GGGCTGCCTA	TCTTTNCTTA	ACTAAAAAAN	720
GCCCATTGTT	CAAAAAATTC	NCAACTAATT	TNTACGTNCC	TACGTCTCCC	CAACAGGTAN	780
AAAAATCTNC	TGCCCTTTTC	AAGGAACCAT	CCCATCCATT	CCTNAACAAA	AGGCCTGCCN	840
TTCTTCCCCC	AGTTAACTNT	TTTTTNTTAA	AATTCCCAAA	AAANGAACCN	CCTGCTGGAA	900
AAACNCCCCC	CTCCAANCCC	CGGCCNAAGN	GGAAGGTTCC	CTTGAATCCC	NCCCCCNCNA	960
ANGGCCCCGA	ACCNTTAAAN	TNGTTCCNGG	GGGTNNGGCC	TAAAAGNCCN	ATTTGGTAAA	1020
CCTANAAATT	TTTTCTTTTN	TAAAAACCAC	NNTTTNNTTT	TTCTTAAACA	AAACCCNTNT	1080
TNTAGNANCN	TATTTCCNC	C				1101

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1087 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCTAGAGCTG	CGCCTGGATC	CCGCCACAGT	GAGGAGACCT	GAAGACCAGA	GAAAACACAG	60
CAAGTAGGCC	CTTTAAACTA	CTCACCTGTG	TTGTCTTCTA	ATTTATTCTG	TTTTATTTTG	120
TTTCCATCAT	TTTAAGGGGT	TAAAATCATC	TTGTTCAGAC	CTCAGCATAT	AAAATGACCC	180
ATCTGTAGAC	CTCAGGCTCC	AACCATACCC	CAAGAGTTGT	CTGGTTTTGT	TTAAATTACT	240
GCCAGGTTTC	AGCTGCAGAT	ATCCCTGGAA	GGAATATTCC	AGATTCCCTG	AGTAGTTTCC	300

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AGGTTAAAAT CCTATAGGCT TCTTCTGTTT TGAGGAAGAG TTCCTGTCAG AGAAAAACAT      360
GATTTTGGAT TTTTAACTTT AATGCTTGTG AAACGCTATA AAAAAAATTT TCTACCCCTA      420
GCTTTAAAGT ACTGTTAGTG AGAAATTAAA ATTCCCTCAG GAGGATTAAA CTGCCATTTC      480
AGTTACCCTA ATTCCAAATG TTTTGGTGGT TAGAATCTTC TTTAATGTC TTGAAGAAGT      540
GTTTTATATT TTCCCATCNA GATAAATTCT CTCNCNCCTT NNTTTTNTNT CTNNTTTTTT      600
AAAACGGANT CTTGCTCCGT TGTCCANGCT GGAATTTTN TTTTGGCCAA TCTCCGCTNC      660
CTTGCAANAA TNCTGCNTCC CAAAATTACC NCCTTTTTC CACCTCCACC CCNNGGAATT      720
ACCTGGAATT ANAGGCCCCC NCCCCCCCC CGGCTAATTT GTTTTTGTTT TTAGTAAAAA      780
ACGGGTTTCC TGTTTTAGTT AGGATGGCCC ANNTCTGACC CCNTNATCNT CCCCCTCNGC      840
CCTCNAATNT TNGGNNTANG GCTTACCCCC CCCNGNNGTT TTTCTCCCAT TNAAATTTTC      900
TNTGGANTCT TGAATNCCG GTTTTCCCTT TAAACCNAT TTTTTTTTN NNNCCCCCAN      960
TTTNCCTCC CCNTNTNTA ANGGGGGTTT CCCAANCCGG GTCCNCCCCC ANGTCCCCAA      1020
TTTTCTCCC CCCCCTCTT TTTCTTTNC CCCAAANTC CTATCTTTTC CTNNAATAT      1080
CNANTNT                                     1087

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

TCTAGACCAA GAAATGGGAG GATTTTAGAG TGA CTGATGA TTTCTCTATC ATCTGCAGTT      60
AGTAAACATT CTCCACAGTT TATGCAAAAA GTAACAAAAC CACTGCAGAT GACAAACACT      120
AGGTAACACA CATACTATCT CCCAAATACC TACCCACAAG CTCAACAATT TTAAACTGTT      180
AGGATCACTG GCTCTAATCA CCATGACATG AGGTCACCAC CAAACCATCA AGCGCTAAAC      240
AGACAGAATG TTTCCACTCC TGATCCACTG TGTGGGAAGA AGCACCGAAC TTACCCACTG      300
GGGGGCCTGC NTCANAANAA AAGCCCATGC CCCC GGNT NTNAAC CGGAACGAAT      360
NAACCCACCA TCCCACANNC TCCTCTGTT NTGGGCCCTG CATCTGTGG CCTCNTNTNC      420
TTTNGGGGAN ACNTGGGGAA GGTACCCCAT TTCNTTGACC CCNCNANAAA ACCCCNGTGG      480
CCCTTTGCCC TGATTCNCNT GGGCCTTTTC TCTTTTCCCT TTTGGGTTGT TTAAATTCCC      540
AATGTCCCN GAACCTCTC CNTNCTGCCC AAAACCTACC TAAATTNCTC NCTANGNNTT      600
TTCTTGGTGT TNCTTTTCAA AGGTNACCTT NCCTGTTCAN NCCCNACNAA AATTNTTCC      660
NTATNTTGGN CCCNAAAAA NNNATCNCC CNAATTGCC GAATGGTTN GGTTTTTCCT      720
NCTGGGGGAA ACCCTTTAAA TTTCCCTT GCGCGCCCC CCTTTTTC CCCC'TTNGA      780
AGGCAGNGG TTCTTCCCGA ACTTCCAATT NCAACAGCCN TGCCCATTN TGAAACCTT      840
TTCCTAAAAT TAAAAAATAN CCGGTTNNGG NNGGCCTCT TCCCCTCCNG GNGGGNNGNG      900
AAANTCCTTA CCCNAAAAA GGTTGCTTAG CCCCNGTCC CCACTCCCC NGGAAAAATN      960
AACCTTTTCN AAAAAAGGAA TATAANTTN CCACTCCTTN GTTCTCTTCC      1010

```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 950 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCTAGAGCTC	GCGGCCGCGA	GCTCTAATAC	GACTCACTAT	AGGGCGTCGA	CTCGATCTCA	60
GCTCACTGCA	ATCTCTGCCC	CCGGGGTCAT	GCGATTCTCC	TGCCCTCAGCC	TTCCAAGTAG	120
CTGGGATTAC	AGGCGTGCAA	CACCACACCC	GGCTAATTTT	GTATTTTTAA	TAGAGATGGG	180
GTTTTCCCTT	GTTGGCCANN	ATGGTCTCNA	ACCCCTGACC	TCNNGTGATC	CCCCCNCCCN	240
NGANCTCNNA	CTGCTGGGGA	TNNCCGNNNN	NNNCCTCCCN	NCNCNNNNNN	NCNCNNTCCN	300
TNNTCCTTNC	TCNNNNNNNN	CNNTCNNTCC	NNCTTCTCNC	CNNNTNTNT	CNNCNNCCNN	360
CNNNCCNCNT	NCCNCNNNT	TCNCNTNCNN	TNTCCNNCNC	NNTCNNCNCN	CNNNNCNTNN	420
CCNNTACNTC	NTNNNCNNNT	CCNTCTNTNN	CCTCNNCNCN	CNCTNCNCNT	TNTCTCCTCN	480
NTNNNNNNCT	CCNNNNNTCT	CNTCNCNNCN	TNCCTCNNTN	NCCNCNCCCC	NCCTCNCNNC	540
CTNNTTTNNN	CNNCWNNTCC	NTNCCNTTCN	NNTCCNNTNN	CNNCNTCNCN	NNCNTTNTTC	600
CCNCCNNTTC	CTTNCNCNTN	NNNTNTCNCN	CNCNTCNCNT	NTTNTCTCCT	NNNTCCCNNC	660
TCNNTTCNCC	CNNNTCCNCC	CCCCNCCNT	CTCTCNCNCN	NNTNNNTNTN	NNNCNTCCNC	720
TNTCNCNTTC	NTCNCNTCNC	TNCTNTCNCN	NNCNCNTCNC	TNCNTNTNT	CTNNNTCNCN	780
TCNCNTNTCN	CCNTCCNTTN	CTNTCTCCTN	TNTCCTTCCC	CTCNCCTNCT	CNTTCNCCNC	840
CCNNTNTNTN	TNNCNCNNT	NCTNNNCNNC	CNTCNTTTCN	TCTCTNCTNN	NNNTNNCCTC	900
MNCCNTNCC	CTNNTNCNCT	NCTNNTACCN	TNCTNCTCCN	TCTTCCTTCC		950

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1086 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCTAGAGCTC	GCGGCCGCGA	GCTCAATTAA	CCCTCACTAA	AGGGAGTCGA	CTCGATCAGA	60
CTGTTACTGT	GTCTATGTAG	AAAGAAGTAG	ACATAAGAGA	TTCCATTTTG	TTCTGTACTA	120
AGAAAAATTC	TTCTGCCTTG	AGATGCTGTT	AATCTGTAAC	CCTAGCCCCA	ACCCTGTGCT	180
CACAGAGACA	TGTGCTGTGT	TGACTCAAGG	TTCAATGGAT	TAGGGCTAT	GCTTTGTAA	240
AAAAGTGCTT	GAAGATAATA	TGCTTGTTAA	AAGTCATCAC	CATTCTCTAA	TCTCAAGTAC	300
CCAGGGACAC	AATACACTGC	GGAAGGCCGC	AGGGACCTCT	GTCTAGGAAA	GCCAGGTATT	360
GTCCAAGATT	TCTCCCCATG	TGATAGCCTG	AGATATGGCC	TCATGGGAAG	GGTAAGACCT	420
GACTGTCCCC	CAGCCCGACA	TCCCCCAGCC	CGACATCCCC	CAGCCCGACA	CCCGAAAAGG	480
GTCTGTGCTG	AGGAAGATTA	NTAAAAGAGG	AAGGCTCTTT	GCATTGAAGT	AAGAAGAAGG	540
CTCTGTCTCC	TGCTCGTCCC	TGGGCAATAA	AATGTCTTGG	TGTTAAACCC	GAATGTATGT	600
TCTACTTACT	GAGAATAGGA	GAAAACATCC	TTAGGGCTGG	AGGTGAGACA	CCCTGGCGGC	660
ATACTGCTCT	TTAATGCACG	AGATGTTTGT	NTAATTGCCA	TCCAGGGCCA	NCCCCTTTCC	720
TTAACTTTT	ATGANACAAA	AACTTTGTTC	NCTTTTCCTG	CGAACCTCTC	CCCCTATTAN	780
CCTATTGGCC	TGCCCATCCC	CTCCCCAAAN	GGTGAAAANA	TGTTCNTAAA	TNCGAGGGAA	840
TCCAAAACNT	TTTCCCGTTG	GTCCCTTTTC	CAACCCCGTC	CCTGGGCCNN	TTTCTCCCC	900
AACNTGTCCC	GGNTCCTTCN	TTCCCNCCCC	CTTCCCNGAN	AAAAAACCCC	GTNTGANGGN	960
GCCCCCTCAA	ATTATAACCT	TTCCNAAACA	AANNGGTTTCN	AAGGTGGTTT	GNTTCCGGTG	1020
CGGCTGGCCT	TGAGGTCCCC	CCTNCACCCC	AATTTGGAAN	CCNGTTTTTT	TTATTGCCCN	1080
NTCCCC						1086

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

NCCNTTTTAGA	TGTTGACAA	NTAAACAAGC	NGCTCAGGCA	GCTGAAAAAA	GCCACTGATA	60
AAGCATCCTG	GAGTATCAGA	GTTTACTGTT	AGATCAGCCT	CATTTGACTT	CCCCCTCCAC	120
ATGGTGTTTA	AATCCAGCTA	CACTACTTCC	TGACTCAAAC	TCCACTATTC	CTGTTCATGA	180
CTGTCAGGAA	CTGTTGGAAA	CTACTGAAAC	TGGCCGACCT	GATCTTCAA	ATGTGCCCCCT	240
AGGAAAGGTG	GATGCCACCG	TGTTACACAGA	CAGTACCNCC	TTCCTCGAGA	AGGGACTACG	300
AGGGGCCGGT	GCACTGTGA	CCAAGGAGAC	TNATGTGTG	TGGGCTCAGG	CTTACCANC	360
AAACACCTCA	NCNCNNAAGG	CTGAATTGAT	CGCCCTCACT	CAGGCTCTCG	GATGGGGTAA	420
GGGATATTAA	CGTTAACACT	GACAGCAGGT	ACGCCTTTGC	TACTGTGCAT	GTACGTGGAG	480
CCATCTACCA	GGAGCGTGGG	CTACTCACTC	GGCAGGTGGC	TGTNATCCAC	TGTAAANGGA	540
CATCAAAAGG	AAAACNNGGC	TGTTGCCCCG	GGTAACCANA	AANCTGATCN	NCAGCTCNAA	600
GATGCTGTGT	TGACTTTTAC	TCNCNCCTCT	TAAACTTGCT	GCCCACANTC	TCCTTTCCCA	660
ACCAGATCTG	CCTGACAATC	CCCATACTCA	AAAAAAAAAN	AANACTGGCC	CCGAACCCNA	720
ACCAATAAAA	ACGGGGANGG	TNGGTNGANC	NNCCTGACCC	AAAAATAATG	GATCCCCCGG	780
GCTGCAGGAA	TTCAATTCAN	CCTTATCNAT	ACCCCAACN	NGGNGGGGGG	GGCCNGTNCC	840
CATTNCCCCT	NTATTNATTC	TTTNCCCCC	CCCCCGGANT	CCTTTTNA	CTCGTGAAAG	900
GGAAAACCTG	NCTTACCAAN	TTATCNCCTG	GACCNTCCCC	TTCCNCGGTN	GNTTANAAAA	960
AAAAGCCNC	ANTCCCNTCC	NAAATTTGCA	CNGAAAGGNA	AGGAATTTAA	CCTTTATTTT	1020
TTNNTCCTTT	ANTTTGTNNN	CCCCCTTTTA	CCCAGGCGAA	CNGCCATCNT	TTAANAAAAA	1080
AAANAGAANG	TTTATTTTTT	CTTNGAACCA	TCCCAATANA	AANCACCCGC	NGGGGAACGG	1140
GGNGGNAGGC	CNCTACCCC	CTTTNTGTNG	GNGGGNC			1177

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

NCCNNTTNT	GATGTTGTCT	TTTTGGCCTC	TCTTTGGATA	CTTTCCTCT	CTTCAGAGGT	60
GAAAAGGGTC	AAAAGGAGCT	GTTGACAGTC	ATCCCAGGTG	GGCCAATGTG	TCCAGAGTAC	120
AGACTCCATC	AGTGAGGTCA	AAGCCTGGGG	CTTTTCAGAG	AAGGGAGGAT	TATGGGTTTT	180
CCAATTATAC	AAGTCAGAAG	TAGAAAGAAG	GGACATAAAC	CAGGAAGGGG	GTGGAGCACT	240
CATCACCCAG	AGGGACTTGT	GCCTCTCTCA	GTGGTAGTAG	AGGGGCTACT	TCCTCCCACC	300
ACGGTTGCAA	CCAAGAGGCA	ATGGGTGATG	AGCCTACAGG	GGACATANCC	GAGGAGACAT	360
GGGATGACCC	TAAGGGAGTA	GGCTGGTTTT	AAGGCGGTGG	GACTGGGTGA	GGGAACTCT	420
CCTCTTCTTC	AGAGAGAAGC	AGTACAGGGC	GAGCTGAACC	GGCTGAAGGT	CGAGGCGAAA	480
ACACGGTCTG	GCTCAGGAAG	ACCTTGGAAG	TAAAATTATG	AATGGTGCAT	GAATGGAGCC	540
ATGGAAGGGG	TGCTCCTGAC	CAAACTCAGC	CATTGATCAA	TGTTAGGGAA	ACTGATCAGG	600
GAAGCCGGGA	ATTTCATTA	CAACCCGCCA	CACAGCTTGA	ACATTGTGAG	GTTCAAGTGAC	660
CCTTCAAGGG	GCCACTCCAC	TCCAACTTTG	GCCATTCTAC	TTTGCNAAAT	TTCCAAAAC	720
TCCTTTTTTA	AGGCCGAATC	CNTANTCCCT	NAAAAACNAA	AAAAAATCTG	CNCCTATTCT	780
GGAAAAGGCC	CANCCCTTAC	CAGGCTGGAA	GAAATTTTNC	CTTTTTTTTT	TTTTTGAAGG	840
CNTTNTTAA	ATTGAACCTN	AATTCNCCCC	CCCCAAAAAA	AACCCNCCNG	GGGGGCGGAT	900
TTCCAAAAAC	NAATTCCTT	ACCAAAAAAC	AAAAACCCNC	CCTTNTTCCC	TTCCNCCCTN	960
TTCTTTTAAT	TAGGGAGAGA	TNAAGCCCCC	CAATTTCNG	GNCTNGATNN	GTTTCCCCCC	1020
CCCCCATTTT	CCNAACTTT	TTCCCANCA	GGAANCCNCC	CTTTTTTTNG	GTCNGATTNA	1080
NCAACCTTCC	AAACCATTTT	TCCNNAAAA	NTTGTNTNGG	NGGGAAAAAN	ACCTNNTTTT	1140

ATAGAN

1146

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTTCATTGGG TACGGGCCCC CTCGAGGTCTG ACGGTATCGA TAAGCTTGAT ATCGAATTCC	60
TGCAGCCCCG GGGATCCACT AGTTCTAGAG TCAGGAAGAA CCACCAACCT TCCTGATTTT	120
TATTGGCTCT GAGTTCTGAG GCCAGTTTTC TTCTTCTGTT GAGTATGCGG GATTGTCAGG	180
CAGATCTGGC TGTGGAAAGG AGACTGTGGG CAGCAAGTTT AGAGGCGTGA CTGAAAGTCA	240
CACTGCATCT TGAGCTGCTG AATCAGCTTT CTGGTTACCA CGGGCAACAG CCGTGTTTTC	300
CTTTTGATGT CCTTTACAGT GGATTACAGC CACCTGCTGA GGTGAGTAGC CCACGCTCCT	360
GGTAGATGGC TCCACGTACA TGCACAGTAG CAAAGGCGTA CCTGCTGTCA GTGTTAACGT	420
TAATATCCTT ACCCCATCGG AGAGCCTGAG TGAGGGCGAT CAATTCAGCC CTTTGTGCT	480
GAGGTGTTTG CTGGTTAAGC CCTGAACCCA CAACACATCT GTCTCCATGG TAACAGCTGC	540
ACCGG	545

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCTCCTAGGC TGGGCACAGT GGCTCATACC TGTAATCCTG ACCGTTTCAG AGGCTCAGGT	60
GGGGGGATCG CTTGAGCCCA AGATTTCAAG ACTAGTCTGG GTAACATAGT GAGACCCTAT	120
CTCTACGAAA AAATAAAAAA ATGAGCCTGG TGTAGTGGCA CACACCAGCT GAGGAGGGAG	180
AATCGAGCCT AGGAGA	196

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCTCCTAGGC TTGGGGGCTC TGA TAGAAA TTCAAGGAAC CTGGGATTCA AGTCCAAGT	60
TGACACCAAC TTACTGTG GNCTCCAATA AACTGCTTCT TTCCTATTCC CTCTCTATTA	120
AATAAAATAA GGAAAACGAT GTCTGTGTAT AGCCAAGTCA GNTATCCTAA AAGGAGATAC	180
TAAGTGACAT TAAATATCAG AATGTAAAAC CTGGGAACCA GGTTCACAGC CTGGGATTAA	240

ACTGACAGCA AGAAGACTGA ACAGTACTAC TGTGAAAAGC CCGAAGNGGC AATATGTTCA	300
CTCTACCGTT GAAGGATGGC TGGGAGAATG AATGCTCTGT CCCCAGTCC CAAGCTCACT	360
TACTATACCT CCTTTATAGC CTAGGAGA	388

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TAGTAGTTGC CTATAATCAT GTTTCCTCATT ATTTTCACAT TTTATTAACC AATTTCTGTT	60
TACCCTGAAA AATATGAGGG AAATATATGA AACAGGGAGG CAATGTTTCCG ATAATTGATC	120
ACAAGATATG ATTTCTACAT CAGATGCTCT TTCCTTTCCCT GTTTATTTCC TTTTATTTC	180
GGTTGTGGGG TCGAATGTAA TAGCTTTGTT TCAAGAGAGA GTTTTGGCAG TTTCTGTAGC	240
TTCTGACACT GTCATGTCT CCAGGCATCT ATTTGCACCT TAGGAGGTGT CGTGGGAGAC	300
TGAGAGGTCT ATTTTTCCTA TATTGGGCA ACTACTA	337

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TAGTAGTTGC CATACAGTGC CTTTCCATTT ATTTAACCCC CACCTGAACG GCATAAACTG	60
AGTGTTTCAGC TGGTGTTTTT TACTGTAAAC AATAAGGAGA CTTTGCTCTT CATTTAAACC	120
AAAATCATAT TTCATATTTT ACGCTCGAGG GTTTTTACCG GTTCCTTTTT AACTCCCTTA	180
AAACAGTTTT TAAGTCGTTT GGAACAAGAT ATTTTTTCTT TCCTGGCAGC TTTTAACATT	240
ATAGCAAATT TGTGTCTGGG GGAAGTCTGG TCACTGTTTC TCACAGTTGC AAATCAAGGC	300
ATTTGCAACC AAGAAAAAAA AATTTTTTTG TTTTATTTGA AACTGGACCG GATAAACGGT	360
GTTTGGAGCG GCTGCTGTAT ATAGTTTTAA ATGGTTTATT GCACCTCCTT AAGTTGCACT	420
TATGTGGGGG GGGGNTTTTG NATAGAAAGT NTTTANTCAC ANAGTCACAG GGAAGTTTNT	480
CTTTTGGNNA CTGAGCTAAA AAGGGCTGNT TTTCGGGTGG GGGCAGATGA AGGCTCACAG	540
GAGGCCTTTC TCTTAGAGGG GGGAAGTCT A	571

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TATATATTTA	ATAACTTAAA	TATATTTTGA	TCACCCACTG	GGGTGATAAG	ACAATAGATA	60
TAAAACTATT	TCCAAAAAGC	ATAAAACCAA	AGTTCATAC	CATACCAAAT	TCATACTGCT	120
TCCCCACCCC	GCACTGAAAC	TTCACCTTCT	AACTGTCTAC	CATACCAAAT	TCTACCCTTC	180
AAGTCTTTGG	TGCGTGCTCA	CTACTCTTTT	TTTTTTTTTT	TTTNTTTTGG	AGATGGAGTC	240
TGGCTGTGCA	GCCCAGGGGT	GGAGTACAAT	GGCACAACCT	CAGCTCACTG	NAACCTCCGC	300
CTCCCAGGTT	CATGAGATTC	TCCTGNNTCA	GCCTTCCCAG	TAGCTGGGAC	TACAGGTGTG	360
CATCACCATG	CCTGGNTAAT	CTTTTTTNGT	TTTNGGGTAG	AGATGGGGGT	TTTACATGTT	420
GGCCAGGNTG	GTNTCGAACT	CCTGACCTCA	AGTGATCCAC	CCACCTCAGG	CTCCCAAAGT	480
GCTAGGATTA	CAGACATGAG	CCACTGNGCC	CAGNCCTGGT	GCATGCTCAC	TTCTCTAGGC	540
AACTACTA						548

(2) INFORMATION FOR SEQ ID NO:16:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTCCGTTATG	CACATGCAGA	ATATTCTATC	GGTACTTCAG	CTATTACTCA	TTTTGATGGC	60
GCAATCCGAG	CCTATCCTCA	AGATGAGTAT	TTAGAAAGAA	TTGATTTAGC	GATAGACCAA	120
GCTGGTAAGC	ACTCTGACTA	CACGAAATTG	TTCAGATGTG	ATGGATTTAT	GACAGTTGAT	180
CTTTGGAAGA	GATTATTAAG	TGATTATTTT	AAAGGGAATC	CATTAATTCC	AGAATATCTT	240
GGTTTtagctc	AAGATGATAT	AGAAATAGAA	CAGAAAGAGA	CTACAAATGA	AGATGTATCA	300
CCAActgata	TTGAAGAGCC	TATAGTAGAA	AATGAATTAG	CTGCATTTAT	TAGCCTTACA	360
CATAGCGATT	TTCCTGATGA	ATCTTATATT	CAGCCATCGA	CATAGCATTa	CCTGATGGGC	420
AACCTTACGA	ATAATAGAAA	CTGGGTGCGG	GGCTATTGAT	GAATTCATCC	NCAGTAAATT	480
TGGATATNAC	AAAATATAAC	TCGATTGCAT	TTGGATGATG	GAATACTAAA	TCTGGCAAAA	540
GTAACTTTGG	AGCTACTAGT	AACCTCTCTT	TTTGAGATGC	AAAATTTTCT	TTTAGGGTTT	600
CTTATTCTCT	ACTTTACGGA	TATTGGAGCA	TAACGGGA			638

(2) INFORMATION FOR SEQ ID NO:17:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACTGATGGAT	GTCGCCGGAG	GCGAGGGGCC	TTATCTGATG	CTCGGCTGCC	TGTTCGTGAT	60
GTGCGCGGCG	ATTGGGCTGT	TTATCTCAAA	CACCGCCACG	GCGGTGCTGA	TGGCGCCTAT	120
TGCCTTAGCG	GCGGCGAAGT	CAATGGGCGT	CTCACCCTAT	CCTTTTGCCA	TGGTGGTGGC	180
GATGGCGGCT	TCGGCGGCGT	TTATGACCCC	GGTCTCCTCG	CCGGTTAACA	CCCTGGTGCT	240
TGGCCCTGSC	AAGTACTCAT	TTAGCGATTT	TGTCAAAATA	GGCGTG		286

(2) INFORMATION FOR SEQ ID NO:18:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TCGGTCATAG CAGCCCCTTC TTCTCAATTT CATCTGTCAC TACCCTGGTG TAGTATCTCA	60
TAGCCTTACA TTTTATAGC CTCCTCCCTG GTCTGTCTTT TGATTTTCCT GCCTGTAATC	120
CATATCACAC ATAACGCAA GTAAACATTT CTAAAGTGTG GTTATGCTCA TGTCACCTCT	180
GTGNCAAGAA ATAGTTTCCA TTACCGTCTT AATAAAATTC GGATTTGTTC TTTNCTATTN	240
TCACTCTTCA CCTATGACCG AA	262

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCGGTCATAG CAAAGCCAGT GGTTTGAGCT CTCTACTGTG TAAACTCCTA AACCAAGGCC	60
ATTTATGATA AATGGTGGCA GGATTTTAT TATAAACATG TACCCATGCA AATTCCTAT	120
AACTCTGAGA TATATTCTTC TACATTTAAA CAATAAAAT AATCTATTTT TAAAAGCCTA	180
ATTTGCGTAG TTAGGTAAGA GTGTTTAATG AGAGGGTATA AGGTATAAAT CACCAGTCAA	240
CGTTTCTCTG CCTATGACCG A	261

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TACAACGAGG CGACGTCGGT AAAATCGGAC ATGAAGCCAC CGCTGGTCTT TTCGTCCGAG	60
CGATAGGCGC CGGCCAGCCA GCGGAACGGT TGCCCGGATG GCGAAGCGAG CCGGAGTTCT	120
TCGGACTGAG TATGAATCTT GTTGTGAAAA TACTCGCCGC CTTCGTTCTGA CGACGTCGCG	180
TCGAAATCTT CGANCTCCTT ACGATCGAAG TCTTCGTGGG CGACGATCGC GGTCAGTTCC	240
GCCCCACCGA AATCATGGTT GAGCCGGATG CTGNCCCCGA AGNCCTCGTT TGTN	294

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTGGTAAAGG GCATGGACGC AGACGCCTGA CGTTTGGCTG AAAATCTTTC ATTGATTCGT	60
ATCAATGAAT AGGAAAATTC CCAAAGAGGG AATGTCCTGT TGCTCGCCAG TTTTNTGTT	120
GTTCTCATGG ANAAGGCAAN GAGCTCTTCA GACTATTGGN ATTNTCGTTC GGTCTTCTGC	180
CAACTAGTCG NCTTGCNANG ATCTTCAT	208

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

NCCNTTGAGC TGAGTGATTG AGATNTGTAA TGGTTGTAAG GGTGATTCAG GCGGATTAGG	60
GTGGCGGGTC ACCCGGCAGT GGTCTCCCG ACAGGCCAGC AGGATTGCG GCAGGTACGG	120
NC'TGCGCATC GCTCGACTAT ATGCTATGGC AGGCGAGCCG TGGAAGGNGG ATCAGGTCAC	180
GGCGCTGGAG CTTTCCACGG TCCATGNATT GNGATGGCTG TTCTAGGCGG CTGTTGCCAA	240
GCGTGATGGT ACGCTGGCTG GAGCATTGAT TTCTGGTGCC AAGGTGG	287

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTGGGTAAAG GGAGCAAGGA GAAGGCATGG AGAGGCTCAN GCTGGTCCTG GCCTACGACT	60
GGGCCAAGCT GTCGCCGGGG ATGGTGGAGA ACTGAAGCGG GACCTCCTCG AGGTCTCCG	120
NC'TTACTTC NCCGTCCAGG AGGAGGTCT TTCCGTGGTC TNGGAGGAGC GGGGGGAGAA	180
GATNCTCCTC ATGGTCNACA TCCC	204

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGGATTGGTC AGGAGCGGGT AGAGTGGCAC CATTGAGGGG ATATTCAAAA ATATTATTTT	60
GTCTAAATG ATAGTTGCTG AGTTTTTCTT TGACCCATGA GTTATATTGG AGTTTATTTT	120
TTAACTTTCC AATCGCATGG ACATGTTAGA CTTATTTTCT GTTAATGATT NCTATTTTTA	180

TTAAATTGGA TTTGAGAAAT TGGTTNTTAT TATATCAATT TTTGGTATTT GTTGAGTTTG 240
ACATTATAGC TTAGTATGTG ACCA 264

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 376 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTACAACGAG GGGAAACTCC GTCTCTACAA AAATTAAAAA ATTAGCCAGG TGTGGTGGTG 60
 TGCACCCGCA ATCCCAGCTA CTTGGGAGGT TGAGACACAA GANTCACCTA NATGTGGGAG 120
 GTCAAGGTTG CATGAGTCAT GATTGTGCCA CTGCACTCCA GCCTGGGTGA CAGACCGAGA 180
 CCCTGCCTCA AANAGANAANG AATAGGAAGT TCAGAAATCN TGGNTGTGGN GCCCAGCAAT 240
 CTGCATCTAT NCAACCCCTG CAGGCAANGC TGATGCAGCC TANGTTCAAG AGCTGCTGTT 300
 TCTGGAGGCA GCAGTTNGGG CTTCCATCCA GTATCACGGC CACACTCGCA CNAGCCATCT 360
 GTCCTCCGTN TGTNAC 376

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 372 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTACAACGAG GGGAAACTCC GTCTCTACAA AAATTAAAAA ATTAGCCAGG TGTGGTGGTG 60
 TGCACCTGTA ATCCCAGCTA CTTGGGCGGC TGAGACACAA GAACCACCTA AATGTGGGAG 120
 GGTCAAGGTT GCATGAGTCA TGATCGCGCC ACTGCACTCC AGCCTGGGTG ACAGACTGAG 180
 ACCCTGCCTC AAAAGAAAAA GAATAGGAAG TTCAGAAACC CTGGGTGTGG NGCCCAGCAA 240
 TCTGCATTTA AACAATCCCT GCAGGCAATG CTGATGCAGC CTAAGTTCAA GAGCTGCTGT 300
 TCTGGAGGCA GNAGTAAGGG CTTCCATCCA GCATCACGGN CAACACTGCA AAAGCACCTG 360
 TCCTCGTTGG TA 372

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTCTGTCCAC ATCTACAAGT TTTATTTATT TTGTGGGTTT TCAGGGTGAC TAAGTTTTTC 60
 CCTACATTGA AAAGAGAAGT TGCTAAAAGG TGCACAGGAA ATCATTTTTT TAAGTGAATA 120
 TGATAATATG GGTCCGTGCT TAATACAAC T GAGACATATT TGTTCTCTGT TTTTITAGAG 180

TCACCTCTTA	AAGTCCAATC	CCACAATGGT	GAAAAAAAAA	TAGAAAGTAT	TTGTTCTACC	240
TTTAAGGAGA	CTGCAGGGAT	TCTCCTTGAA	AACGGAGTAT	GGAATCAATC	TTAAATAAAT	300
ATGAAATTGG	TTGGTCTTCT	GGGATAAGAA	ATTCCCAACT	CAGTGTGCTG	AAATTACACT	360
GACTTTTTTT	GGGAAAAAAT	AGTCGAAAAT	GTCAATTGTT	TCCATAAAAT	ACATGTTACT	420
ATTAAAAGAT	ATTTAAAGAC	AAATTCTTTC	AGAGCTCTAA	GATTGGTGTG	GACAGAA	477

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TCTNCAACCT	CTTGANTGTC	AAAAACCTTN	TAGGCTATCT	CTAAAAGCTG	ACTGGTATTC	60
ATTCCAGCAA	AATCCCTCTA	GTTTTTGGAG	TTTCCTTTTA	CTATCTGGGG	CTGCCTGAGC	120
CACAAATGCC	AAATTAAGAG	CATGGCTATT	TTCGGGGGCT	GACAGGTCAA	AAGGGGTGTA	180
AATCCGATAA	GCCTCCTGGA	GGTGCTCTAA	AAACACTCCT	GGTGAATCAT	CATGCCCTCT	240
GACGACTTCA	ATCGNCTTAG	ACAAGTTTAT	AGGTTTCTGG	GCAGCTCCCT	GAATACCCAC	300
GAGGAGATAC	CGGTGGAAAT	CGTCAAAGT	TCTCCCTCCA	CTTGAGAAAT	TTGGGTCCCA	360
ATTAGGTCCC	AATTGGGTCT	CTAATCACTA	TTCTCTAGC	TTCTCTCTCC	GGNCTATTGG	420
TTGATGTGAG	GTTGAAGA					438

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAGAGGGTAC	CAGCCCCAAG	CCTTGACAAC	TTCCATAGGG	TGTCAAGCCT	GTGGGTGCAC	60
AGAAGTCAAA	AATTGAGTTT	TGGGATCCTC	AGCCTAGATT	TCAGAGGATA	TAAAGAAACA	120
CCTAACACCT	AGATATTTCAG	ACAAAAGTTT	ACTACAGGGA	TGAAGCTTTC	ACGGAAAACC	180
TCTACTAGGA	AAGTACAGAA	GAGAAATGTG	GGTTTGGAGC	CCCCAAACAG	AATCCCCCTCT	240
AGAACACTGC	CTAATGAAAC	TGTGAGAAGA	TGGCCACTGT	CATCCAGACA	CCAGAATGAT	300
AGACCCACCA	AAAACCTTATG	CCATATTGCC	TATAAAACCT	ACAGACACTC	AATGCCAGCC	360
CCATGAAAAA	AAAACCTGAGA	AGAAGACTGT	NCCCTACAAT	GCCACCGGAG	CAGAACTGCC	420
CCAGGCCATG	GAAGCACAGC	TCTTATATCA	ATGTGACCTG	GATGTTGAGA	CATGGAATCC	480
NANGAAATCN	TTTTAANACT	TCCACGGTTN	AATGACTGCC	CTATTANATT	CNGAACTTAN	540
ATCCNGGCCCT	GTGACCTCTT	TGCTTTGGCC	ATTCCCCCTT	TTTGAATG	CTNTTTTTTTT	600
CCCATGCCTG	TNCCCTCTTA					620

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTACAACGAG GGGGTCAATG TCATAAATGT CACAATAAAA CAATCTCTTC TTTTTTTTTT	60
TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT	100

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TAGTCTATGC GCCGGACAGA GCAGAATTAA ATTGGAAGTT GCCCTCCGGA CTTTCTACCC	60
ACACTCTTCC TGAAAAGAGA AAGAAAAGAG GCAGGAAAGA GGTTAGGATT TCATTTTCAA	120
GAGTCAGCTA ATTAGGAGAG CAGAGTTTAG ACAGCAGTAG GCACCCCATG ATACAAACCA	180
TGGACAAAGT CCCTGTTTAG TAACTGCCAG ACATGATCCT GCTCAGGTTT TGAAATCTCT	240
CTGCCCATAA AAGATGGAGA GCAGGAGTGC CATCCACATC AACACGTGTC CAAGAAAGAG	300
TCTCAGGGAG ACAAGGGTAT CAAAAACAA GATTCTTAAT GGGAAGGAAA TCAAACCAAA	360
AAATTAGATT TTTCTCTACA TATATATAAT ATACAGATAT TTAACACATT ATTCCAGAGG	420
TGGCTCCAGT CCTTGGGGCT TGAGAGATGG TGAAAACCTT TGTTCCACAT TAACTTCTGC	480
TCTCAAATTC TGAAGTATAT CAGAATGGGA CAGGCAATGT TTTGCTCCAC ACTGGGGCAC	540
AGACCCAAAT GGTTCGTGTC CCGAAGAAGA GAAGCCCGAA AGACATGAAG GATGCTTAAG	600
GGGGGTTGGG AAAGCCAAAT TGGTANTATC TTTTCTCCT GCCTGTGTTC CNGAAGTCTC	660
CNCTGAAGGA ATTCTTAAAA CCCTTTGTGA GGAAATGCCC CCTTACCATG ACAANTGGTC	720
CCATTGCTTT TAGGGNGATG GAAACACCAA GGGTTTGTAT CC	762

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TAGTCTATGC GTGTATTAACT CCCCCCTCCC TCAGTAACAA CCAAAGAGGC AGGAGCTGTT	60
ATTACCAACC CCATTTTACA GATGCATCAA TAATGACAGA GAAGTGAAGT GACTTGCGCA	120
CACAACCAGT AAATTGGCAG AGTCAGATTT GAATCCATGG AGTCTGGTCT GCACTTTCAA	180
TCACCGAATA CCCTTTCTAA GAAACGTGTG CTGAATGAGT GCATGGATAA ATCAGTGTCT	240
ACTCAACATC TTTGCCTAGA TATCCCGCAT AGACTA	276

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

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TAGTAGTTGC CAAATATTTG AAAATTTACC CAGAAGTGAT TGAAAAC TTTT 60
AAACAAATAA AGCCAAAAGG TAAAATAAAA ATATCTTTGC ACTCTCGTTA TTACCTATCC 120
ATAACTTTTT CACCGTAAGC TCTCCTGCTT GTTAGTGTAG TGTGGTTATA TTAAACTTTT 180
TAGTTATTAT TTTTATTCA CTTTCCACT AGAAAGTCAT TATTGATTTA GCACACATGT 240
TGATCTCATT TCATTTTTTC TTTTATAGG CAAAATTTGA TGCTATGCAA CAAAATACT 300
CAAGCCCATT ATCTTTTTTC CCCCCGAAAT CTGAAAATTG CAGGGGACAG AGGGAAGTTA 360
TCCCATTAAG AAATTGTAAA TATGTTGAGT TTATGTTTAA AAATGCACAA AACATAAGAA 420
AATTGTGTTT ACTTGAGCTG CTGATTGTAA GCAGTTTAT CTCAGGGGCA ACTACTA 477

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(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 631 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

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TAGTAGTTGC CAATTCAGAT GATCAGAAAT GCTGCTTTCC TCAGCATTGT CTTGTTAAAC 60
CGCATGCCAT TTGGAAC TTT GGCAGTGAGA AGCCAAAAGG AAGAGGTGAA TGACATATAT 120
ATATATATAT ATTCAATGAA AGTAAAATGT ATATGCTCAT ATACTTTCTA GTTATCAGAA 180
TGAGTTAAGC TTTATGCCAT TGGGCTGCTG CATATTTTAA TCAGAAGATA AAAGAAAATC 240
TGGGCATTTT TAGAATGTGA TACATGTTTT TTTAAACTG TTAAATATTA TTTCGATATT 300
TGTCTAAGAA CCGGAATGTT CTTAAAATTT ACTAAAACAG TATTGTTTGA GGAAGAGAAA 360
ACTGTACTGT TTGCCATTAT TACAGTCGTA CAAGTGCATG TCAAGTCACC CACTCTCTCA 420
GGCATCAGTA TCCACCTCAT AGCTTTACAC ATTTTGACGG GGAATATTGC AGCATCCTCA 480
GGCTGACAT CTGGGAAAGG CTCAGATCCA CCTACTGCTC CTTGCTCGTT GATTTGTTTT 540
AAAATATTGT GCCTGGTGTG ACTTTTAAGC CACAGCCCTG CCTAAAAGCC AGCAGAGAAC 600
AGAACCCGCA CCATTCTATA GGCAACTACT A 631

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(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 578 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

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TAGTAGTTGC CATCCCATAT TACAGAAGGC TCTGTATACA TGACTTATTT GGAAGTGATC 60
TGTTTTCTCT CCAAACCCAT TTATCGTAAT TTCACCAGTC TTGGATCAAT CTTGGTTTTCC 120
ACTGATACCA TGAAACCTAC TTGGAGCAGA CATTGCACAG TTTTCTGTGG TAAAACTAA 180
AGGTTTATTT GCTAAGCTGT CATCTTATGC TTAGTATTTT TTTTCTACAG TGGGGAATTG 240
CTGAGATTAC ATTTTGTTAT TCATTAGATA CTTTGGGATA ACTTGACACT GTCTTCTTTT 300
TTTCGCTTTT AATTGCTATC ATCATGCTTT TGAACAAGA ACACATTAGT CCTCAAGTAT 360

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TACATAAGCT	TGCTTGTTAC	GCCTGGTGGT	TTAAAGGACT	ATCTTTGGCC	TCAGGTTTAC	420
AAGAATGGGC	AAAGTGTTC	CTTATGTTCT	GTAGTTCTCA	ATAAAAGATT	GCCAGGGGCC	480
GGGTACTGTG	GCTCGCACTG	TAATCCCAGC	ACTTTGGGAA	GCTGAGGCTG	GCGGATCATG	540
TTAGGGCAGG	TGTTCGAAAC	CAGCCTGGGC	AACTACTA			578

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TAGTAGTTGC	CTGTAATCCC	AGCAACTCAG	GAGGCTGGGG	CAGGAGAATC	AGTTGAACCT	60
GGGAGGCAGA	AGTTGTAATT	AGCAAAGATC	GCACCATTGC	ACTTCAGCCT	GGGCAACAAG	120
AGTGAGATTC	CATCTCAAAA	ACAAAAA	GAAAAAGAAA	AGAAAAGGAA	AAAACGTATA	180
AACCCAGCCA	AAACAAAATG	ATCATTCTTT	TAATAAGCAA	GACTAATTTA	ATGTGTTTAT	240
TTAATCAAAG	CAGTTGAATC	TTCTGAGTTA	TTGGTGAAAA	TACCCATGTA	GTTAATTTAG	300
GGTTCCTACT	TGGGTGAACG	TTTGATGTTT	ACAGGTTATA	AAATGGTTAA	CAAGGAAAAAT	360
GATGCATAAA	GAATCTTATA	AACTACTAAA	AATAAATAAA	ATATAAATGG	ATAGGTGCTA	420
TGGATGGAGT	TTTTGTGTAA	TTTAAAATCT	TGAAGTCATT	TTGGATGCTC	ATTGGTTGTC	480
TGGTAATTTT	CATTAGGAAA	AGGTTATGAT	ATGGGGAAAC	TGTTTCTGGA	AATTGCGGAA	540
TGTTTCTCAT	CTGTAAAATG	CTAGTATCTC	AGGGCAACTA	CTA		583

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GATCTACTAG	TCATNTGGAT	TCTATCCATG	GCAGCTAAGC	CTTTCTGAAT	GGATTCTACT	60
GCTTTCTTGT	TCTTTAATCC	AGACCCTTAT	ATATGTTTAT	GTTACAGGC	AGGGCAATGT	120
TTAGTGAAAA	CAATTCTAAA	TTTTTTATTT	TGCATTTTCA	TGCTAATTTT	CGTCACACTC	180
CAGCAGGCTT	CCTGGGAGAA	TAAGGAGAAA	TACAGCTAAA	GACATTGTCC	CTGCTTACTT	240
ACAGCCTAAT	GGTATGCAA	ACCATTCAA	TAAAGTAACA	GGAAGTAC	TAACCAGGTA	300
GAATGGACCA	AAACTGATAT	AGAAAAATCA	GAGGAAGAGA	GGAACAAATA	TTTACTGAGT	360
CCTAGAATGT	ACAAGGCTTT	TTAATTACAT	ATTTTATGTA	AGGCCTGCAA	AAAACAGGTG	420
AGTAATCAAC	ATTTGTCCCA	TTTACATAT	AAGGAACTG	AAGCTTAAAT	TGAATAATTT	480
AATGCATAGA	TTTTATAGTT	AGACCATGTT	CAGGTCCCTA	TGTTATACTT	ACTAGCTGTA	540
TGAATATGAG	AAAATAATTT	TGTTATTTTC	TTGGCATCAG	TATTTTTCATC	TGCAAAATAA	600
AGCTAAAGTT	ATTTAGCAA	CAGTCAGCAT	AGTGCTGAT	ACATAGTAGG	TGCTCCAAAC	660
ATGATTACNC	TANTATTNGG	TATTANAAAA	ATCCAATATA	GGCNTGGATA	AAACCG	716

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTCTGTCCAC	ATATCATCCC	ACTTTAATTG	TTAATCAGCA	AAACTTTCAA	TGAAAAATCA	60
TCCATTTTAA	CCAGGATCAC	ACCAGGAAAC	TGAAGGTGTA	TTTTTTTTTA	CCTTAAAAAA	120
AAAAAAAAAA	ACCAAACAAA	CCAAAACAGA	TTAACAGCAA	AGAGTTCTAA	AAAATTTACA	180
TTTCTCTTAC	AAGTGTCTAT	CAGAGAACAA	TAGTTCTTAA	GTCTGTTAAA	TCTTGGCATT	240
AACAGAGAAA	CTTGATGAAN	AGTTGTACTT	GGAATATTGT	GGATTTTTTT	TTTTGTCTAA	300
TCTCCCCCTA	TTGTTTTGCC	AACAGTAATT	TAAATTTGTG	TGGAACATCC	CCGTAGTTGA	360
AGTGTAACA	ATGTATAGGA	AGGAATATAT	GATAAGATGA	TGCATCACAT	ATGCATTACA	420
TGTAGGGACC	TTCACAACTT	CATGCACTCA	GAAAACATGC	TTGAAGAGGA	GGAGAGGACG	480
GCCCAGGGTC	ACCATCCAGG	TGCCTTGAGG	ACAGAGAATG	CAGAAGTGGC	ACTGTTGAAA	540
TTTAGAAGAC	CATGTGTGAA	TGGTTTCAGG	CCTGGGATGT	TTGCCACCAA	GAAGTGCCTC	600
CGAGAAATTT	CTTTCCCAT	TGGAATACAG	GGTGGCTTGA	TGGGTACGGT	GGGTGACCCA	660
ACGAAGAAAA	TGAAATTCTG	CCCTTTCC				688

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 585 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TAGTAGTTGC	CGCNNACCTA	AAANTTGGAA	AGCATGATGT	CTAGGAAACA	TANTAAAATA	60
GGGTATGCCT	ATGTGCTACA	GAGAGATGTT	AGCATTTAAA	GTGCATANTT	TTATGTATTT	120
TGACAAATGC	ATATNCCTCT	ATAATCCACA	ACTGATTACG	AAGCTATTAC	AATTAAAAAG	180
TTTGGCCGGG	CGTGGTGGGC	GGTGGCTGAC	GCCTGTAATC	CCAGCACTTT	GGGAGGCCGA	240
GGCACGCGGA	TCACGAGGTC	GGGAGTTCAA	GACCATCCTG	GCTAACACGG	TGAAAGTCCA	300
TCTCTACTAA	AAATACGAAA	AAATTACCCC	GGCGTGGTGG	CGGGCGCCTG	TAGTCCCAGC	360
TACTCCGGAG	GCTGAGGCAG	GAGAATGGCG	TGAACCCAGG	ACACGGAGCT	TGCAGTGTGC	420
CAACATCACG	TCACTGCCCT	CCAGCCTGGG	GGACAGGAAC	AAGANTCCCG	TCCTCANAAA	480
AGAAAAATAC	TACTNATANT	TTCNACTTTA	TTTTAANTTA	CACAGAACTN	CCTCTTGGTA	540
CCCCCTTACC	ATTATCTCA	CCCACCTCCT	ATAGGGCACN	NCTAA		585

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 475 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TCTGTCCACA	CCAATCTTAG	AAGCTCTGAA	AAGAATTTGT	CTTTAAATAT	CTTTTAATAG	60
TAACATGTAT	TTTATGGACC	AAATTGACAT	TTTCGACTGT	TTTTTCCAAA	AAAGTCAGGT	120

GAATTCAGC	ACACTGAGTT	GGGAATTCT	TATCCCAGAA	GACCAACCAA	TTTCATATTT	180
ATTTAAGATT	GATTCCATAC	TCCGTTTCA	AGGAGAATCC	CTGCAGTCTC	CTTAAAGGTA	240
GAACAAATAC	TTCCTATTTT	TTTTTCACCA	TTGTGGGATT	GGACTTTAAG	AGGTGACTCT	300
AAAAAACAG	AGAACAAATA	TGTCTCAGTT	GTATTAAGCA	CGGACCCATA	TTATCATATT	360
CACTTAAAA	AATGATTTC	TGTGCACCTT	TTGGCAACTT	CTCTTTTCAA	TGTAGGGAAA	420
AACTTAGTCA	CCCTGAAAAC	CCACAAAATA	AATAAACTT	GTAGATGTGG	ACAGA	475

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TAAGAGGGTA	CATCGGGTAA	GAACGTAGGC	ACATCTAGAG	CTTAGAGAAG	TCTGGGGTAG	60
GAAAAAATC	TAAGTATTTA	TAAGGGTATA	GGTAACATTT	AAAAGTAGGG	CTAGCTGACA	120
TTATTTAGAA	AGAACACATA	CGGAGAGATA	AGGGCAAAGG	ACTAAGACCA	GAGGAACACT	180
AATATTTAGT	GATCACTTCC	ATTCTTGGTA	AAAATAGTAA	CTTTTAAGTT	AGCTTCAAGG	240
AAGATTTTGT	GCCATGATTA	GTTGTCAAAA	GTTAGTTCTC	TTGGGTTTAT	ATTACTAATT	300
TTGTTTAAAG	ATCCTTGTTA	GTGCTTTAAT	AAAGTCATGT	TATATCAAAC	GCTCTAAAAC	360
ATTGTAGCAT	GTAAATGTC	ACAATATACT	TACCATTGTG	TGTATATGGC	TGTACCTCT	420
CTA						423

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCTCCTAGGC	TAATGTGTGT	GTTTCTGTAA	AAGTAAAAAG	TTAAAAATTT	TAAAAATAGA	60
AAAAAGCTTA	TAGAATAAGA	ATATGAAGAA	AGAAAAATATT	TTTGTACATT	TGCACAATGA	120
GTTTATGTTT	TAAGCTAAGT	GTTATTACAA	AAGAGCCAAA	AAGGTTTTAA	AAATTA AAC	180
GTTTGTAAAG	TTACAGTACC	CTTATGTTAA	TTTATAATTG	AAGAAAGAAA	AACTTTTTTT	240
TATAAATGTA	GTGTAGCCTA	AGCATACAGT	ATTATAAAG	TCTGGCAGTG	TTCAATAATG	300
TCCTAGGCCT	TCACATTCAC	TCACTGACTC	ACCCAGAGCA	ACTTCCAGTC	CTGTAAGCTC	360
CATTGCGTGGT	AAGTGCCCTA	TACAGGTGCA	CCATTTATTT	TACAGTATTT	TTACTGTACC	420
TTCTCTATGT	TTCCATATGT	TTGATATAC	AAATACCACT	GGTTACTATN	GCCCNACAGG	480
TAATTCCAGT	AACACGGCCT	GTATACGTCT	GGTANCCCTA	GNGAAGA		527

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TCTTCAACCT	CGTAGGACAA	CTCTCATATG	CCTGGGCACT	ATTTTATAGGT	TACTACCTTG	60
GCTGCCCTTC	TTTAAGAAAA	AAAAAAGAAG	AAAAAAGAAC	TTTTCCACAA	GTTTCTCTTC	120
CTCTAGTTGG	AAAAATTAGAG	AAATCATGTT	TTTAATTTTG	TGTTATTTC	GATCACAAT	180
TCAAACACTT	GTAAACATTA	AGCTTCTGTT	CAATCCCCTG	GGAAAGAGGAT	TCATTCTGAT	240
ATTTACGGTT	CAAAAGAAAGT	TGTAATATTG	TGCTTGGAAC	ACAGAGAACC	AGTTATTAAC	300
TTCTACTAC	TATTATATAA	TAAATAATAA	C			331

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGCTTAGTAG	TTGCCAGGCA	AAATARCGTT	GATTCTCCTC	AGGAGCCACC	CCCAACACCC	60
CTGTTTGCTT	CTAGACCTAT	ACCTAGACTA	AAGTCCCAGC	AGACCCCTAG	AGGTGAGGTT	120
CAGAGTGACC	CTTGAGGAGA	TGTGCTACAC	TAGAAAAGAA	CTGCTTGACT	TTTCTAATTT	180
ATATAAGCAG	AAATCTGGAG	AAGAGTCATA	GGAATGGATA	TTAAGGGTGT	GAGATAATGG	240
CGGAAGGAAT	ATAGAGTTGG	ATCAGGCTGG	ACTTATTGAT	TTGAACCCAC	TAAGTAGAGA	300
TTCTGCTTTT	GATGTTGCAG	CTCAGGGAGT	TAAAAAAGGT	TTTAATGGTT	CTAATAGTTT	360
ATTTGCTTGG	TTAGCTGAAA	TATGGATAAA	AGATGGCCCA	CTGTGAGCAA	GCTGGAAATG	420
CCTGATCTCT	CTCAGTTTAA	TGTAGAGGAA	GGGATCCAAA	AGTTTAGGGA	GANTTGGATG	480
CTGGRAKTGG	ATTGGTCACT	TTGRGACCTA	CCCWTCCAG	CTGGGAGGGT	CCAGAAGATA	540
CACCCTTGAC	CAACGCTTTG	CGAAATGGAT	TTGTGATGGC	GGCAACTACT	AA	592

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGCTTAGTAG	TTGCCATTGC	GAGTGCTTGC	TCAACGAGCG	TTGAACATGG	CGGATTGTCT	60	
AGATTCAACG	GATTTGAGTT	TTACCAGCAA	AGCGAACC	AA	GCGCGGCCCA	GAGAATTATG	120
GGTTGGTTGG	CTTTGAAAAG	ATGGAAATCC	TGTAGGCCTA	GTCAGAAAAG	CCTTCTTGCA	180	
GAACAGTTGG	TTCTCGGGCG	AACGCTCATC	AAGATGCCCA	TTGGAAAGGC	TAGCGTGTAT	240	
TTGGGAGAGC	CTGATAGCGT	GTCTTCTGAT	GATGTTTGTG	CTTGGACAGT	GACAAAAGAT	300	
ATGCAAAGCA	AGTCCGAAGT	AGACGTCAAG	CTTCGTGAGC	AAATTATTGT	AGACTCCTAC	360	
TTATACTGTG	AGGAATGATA	GCCAAGGGTG	GGGACTTTAA	GACTAAGGTG	GTTTGTACTT	420	
GCGCCGATGA	TCCCAGGCAG	AAAGAMCTGA	TCGCTAGTTT	TATACGGGCA	ACTACTAAGC	480	
CGAATTCCAG	CACACTGGCG	GCCGTTACTA	ATTGGATCCG	ANCTCGGTAC	CAGCTTGATG	540	
CATASCTTGA	GTTWTCTATA	NTGTCNC				567	

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 908 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GAGCGAAAGA	CCGAGGGCAG	NGNNTANGNG	CGANGAAGCG	GAGAGGGCCA	AAAAGCAACC	60
GCTTTCCCCG	GGGGGTGCCG	ATTCATTAAAG	GCAGGTGGAG	GACAGGTTTC	CCGATGGAAG	120
GCGGCAGGGG	CGCAAGCAAT	TAATGTGAGT	AGGCCATTCA	TTAGCACCCG	GGCTTAACAT	180
TTAACTTCG	GGTTGGTATG	TGGTGGGAAT	TGTGAGCGGA	TAACAATTTT	ACACAGGAAA	240
CAGCTATGAC	CATGATTACG	CCAAGCTATT	TAGCTGACAT	TATAGAATAA	CTCAAGTTAT	300
GCATCAAGCT	TGGTACCGAG	TTCGGATCCA	CTAGTAACGG	CCGCCAGTGT	GTGGAATTCG	360
GCTTAGTAGT	TGCCGACCAT	GGAGTGCTAC	CTAGGCTAGA	ATACCTGAGY	TCCTCCCTAG	420
CCTCACTCAC	ATTAAATTGT	ATCTTTTCTA	CATTAGATGT	CCTCAGCGCC	TTATTTCTGC	480
TGGACWATCG	ATAAATTAAT	CCTGATAGGA	TGATAGCAGC	AGATTAATTA	CTGAGAGTAT	540
GTTAATGTGT	CATCCCTCCT	ATATAACGTA	TTTGCATTTT	AATGGAGCAA	TTCTGGAGAT	600
AATCCCTGAA	GGCAAAGGAA	TGAATCTTGA	GGGTGAGAAA	GCCAGAATCA	GTGTCCAGCT	660
GCAGTTGTGG	GAGAAGGTGA	TATTATGTAT	GTCTCAGAAG	TGACACCATA	TGGGCAACTA	720
CTAAGCCCGA	ATTCCAGCAC	ACTGGCGGGC	GTTACTAATG	GATCCGAGCT	CGGTACCAAG	780
CTTGATGCAT	AGCTTGAGTA	TCTATAGTGT	CACTAAATAG	CCTGGCGTTA	TCATGGTCAT	840
AGCTGTTTCC	TGTTGAAAT	TGTTATCCGC	TCCCAATTCC	CCCCACCATA	CGAGCCGGAA	900
CATAAAGT						908

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TGCCAACAAG	GAAAGTTTTA	AATTTCCCCT	TGAGGATTCT	TGGTGATCAT	CAAATTCAGT	60
GGTTTTTAAG	GTTGTTTTCT	GTCAAATAAC	TCTAACTTTA	AGCCAAACAG	TATATGGAAG	120
CACAGATAKA	ATATTACACA	GATAAAAGAG	GAGTTGATCT	AAAGTARAGA	TAGTTGGGGG	180
CTTTAATTTT	TGGAACCTAG	GTCTCCCCAT	CTTCTTCTGT	GCTGAGGAAC	TTCTTGGAAG	240
CGGGGATTCT	AAAGTTCTTT	GGAAGACAGT	TTGAAAACCA	CCATGTTGTT	CTCAGTACCT	300
TTATTTTTTAA	AAAGTAGGTG	AACATTTTGA	GAGAGAAAAG	GGCTTG GTTG	AGATGAAGTC	360
CCCCCCCCC	CTTTTTTTTT	TTTGTAGCTGA	AATAGATACC	CTATGTTNAA	RGAARGGATT	420
ATTATTTACC	ATGCCAYTAR	SCACATGCTC	TTTGATGGGC	NYCTCCSTAC	CCTCCTTAAG	480

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAGAGGGTAC	CGAGTGGAAT	TTCCGCTTCA	CTAGTCTGGT	GTGGCTAGTC	GGTTTCGTGG	60
TGGCCAACAT	TACGAAC TTC	CAACTCAACC	GTTCTTGAC	GTTCAAGCGG	GAGTACCGGC	120
GAGGATGGTG	GCGTGAATTC	TGGCCTTTCT	TTGCCGTGGG	ATCGGTAGCC	GCCATCATCG	180
GTATGTTTAT	CAAGATCTTC	TTTACTAACC	CGACCTCTCC	GATTTACCTG	CCCGAGCCGT	240
GGTTTAACGA	GGGGAGGGGG	ATCCAGTCAC	GCGAGTACTG	GTCCCAGATC	TCGCCATCG	300
TCGTGACAAT	GCCTATCAAC	TTCGTCTGTC	ATAAGTTGTG	GACCTTCCGA	ACGGTGAAGC	360
ACTCCGAAAA	CGTCCGGTGG	CTGCTGTGCG	GTGACTCCCA	AAATCTTGAT	AACAACAAGG	420
TAACCGAATC	GCGCTAAGGA	ACCCCGGCAT	CTCGGGTACT	CTGCATATGC	GTACCCCTTA	480
AGCCGAATTC	CAGCACACTG	GCGGCCGTTA	CTAATTGGAT	CCGAAC TCCG	TAACCAAGCC	540
TGATGCGTAA	CTTGAGTTAT	TCTATAGTGT	CCCTAAAATA	ACCTGGCGTT	A	591

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AAGAGGGTAC	CTGCCTTGAA	ATTTAAATGT	CTAAGGAAAR	TGGGAGATGA	TTAAGAGTTG	60
GTGTGGCYTA	GTCACACCAA	AATGTATTTA	TTACATCCTG	CTCCTTTCTA	GTTGACAGGA	120
AAGAAAGCTG	CTGTGGGGAA	AGGAGGGATA	AATACTGAAG	GGATT TACTA	AACAAATGTC	180
CATCACAGAG	TTTTCTTTT	TTTTTTTTTG	AGACAGAGTC	TTGCTCTGTC	ACCCAGGCTG	240
GAATGAAGWG	GTATGATCTC	AGTTGAATGC	AACCTCTACC	TCCTAGGTTT	AAGCGATTCT	300
CATGCCTCAG	CCTCCTGAGC	AGCTGGGACT	ATAGGCGCAT	GCTACCATGC	CAGGCTAATT	360
TTTATATTTT	TATTAGAGAC	GGGGTGTTGC	CATGTTGGCC	AGGCAGGTCT	CGAACTCCTG	420
GGCCTCAGAT	GATCTGCCCC	ACCGTACCCT	CTTA			454

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AAGAGGGTAC	CAAAAAAAG	AAAAAGGAAA	AAAAGAAAA	CAACTTGAT	AAGGCTTTCT	60
GCTGCATACA	GCTTTTTTTT	TTTAAATAAA	TGGTGCCAAC	AAATGTTTTT	GCATTCACAC	120
CAATTGCTGG	TTTGAAATC	GTACTCTTCA	AAGGTATTTG	TGCAGATCAA	TCCAATAGTG	180
ATGCCCCGTA	GGTTTTGTGG	ACTGCCACG	TTGTCTACCT	TCTCATGTAG	GAGCCATTGA	240
GAGACTGTTT	GGACATGCCT	GTGTTCATGT	AGCCGTGATG	TCCGGGGGCC	GTGTACATCA	300
TGTTACCGTG	GGGTGGGGTC	TGCATTGGCT	GCTGGGCATA	TGGCTGGGTG	CCCATCATGC	360
CCATCTGCAT	CTGCATAGGG	TATTGGGGCG	TTTGATCCAT	ATAGCCATGA	TTGCTGTGGT	420
AGCCACTGTT	CATCATTGGC	TGGGACATGC	TGTTACCCTC	TTA		463

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTTCAACCTC CCAAAGTGCT GGGATTACAG GACTGAGCCA CCACGCTCAG CCTAAGCCTC	60
TTTTTCACTA CCCTCTAAGC GATCTACCAC AGTGATGAGG GGCTAAAGAG CAGTGCAATT	120
TGATTACAAT AATGGAACCT AGATTTATTA ATTAACAATT TTCCTTAGC ATGTTGGTTC	180
CATAATTATT AAGAGTATGG ACTTACTTAG AAATGAGCTT TCATTTTAAG AATTCATCT	240
TTGACCTTCT CTATTAGTCT GAGCAGTATG AACTATACG TATTTTATT AACTAACCTA	300
CCTTGAGCTA TTACTTTTAA AAAGGCTATA TACATGAATG TGTATTGTCA ACTGTAAAGC	360
CCCACAGTAT TTAATTATAT CATGATGTCT TTGAGGTTG	399

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTTCAACCTC AATCAACCTT GGTAATTGAT AAAATCATCA CTTAACTTTC TGATATAATG	60
GCAATAATTA TCTGAGAAAA AAAAGTGGTG AAAGATTAAA CTTGCATTTT TCTCAGAATC	120
TTGAAGGATA TTTGAATAAT TCAAAAGCGG AATCAGTAGT ATCAGCCGAA GAAACTCACT	180
TAGCTAGAAC GTTGGACCCA TGGATCTAAG TCCCTGCCCT TCCACTAACC AGCTGATTGG	240
TTTTGTGTAA ACCTCCTACA CGCTTGGGCT TGCTCGCCTC ATTTGTCAAA GTAAAGGCTG	300
AAATAGGAAG ATAATGAACC GTGTCTTTT GGTCTCTTTT CCATCCATTA CTCTGATTTT	360
ACAAAGAGGC CTGTATTCCC CTGGTGAGGT TG	392

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TTCGGGTGAT GCCTCCTCAG GCTACAGTGA AGACTGGATT ACAGAAAGGT GCCAGCGAGA	60
TTTCAGATTC CTGTAAACCT CTAAAGAAAA GGAGTCGCGC CTCAACTGAT GTAGAAATGA	120
CTAGTTCAGC ATACNGAGAC ACNTCTGACT CCGATTCTAG AGGACTGAGT GACCTGCAN	179

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TTCGGGTGAT GCCTCCTCAG GCTACATCAT NATAGAAGCA AAGTAGAANA ATCNGGTTTG	60
TGCATTTTCC CACANACAAA ATTCAAATGA NTGGAAGAAA TTGGGANAGT AT	112

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TGAGCTTCCG CTTCTGACAA CTCAATAGAT AATCAAAGGA CAACTTTAAC AGGGATTCAC	60
AAAGGAGTAT ATCCAAATGC CAATAAACAT ATAAAAAGGA ATTCAGCTTC ATCATCATCA	120
GAAGWATGCA AATTAAACC ATAATGAGAA ACCACTATGT CCCACTAGAA TAGATAAAAT	180
CTTAAAAGAC TGGTAAACC AAGTGTGGT AAGGCAAGAG GAGCA	225

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GCTCCTCTTG CCTTACCAAC ACATTCTCAA AAACCTGTTA GAGTCCTAAG CATTCTCCTG	60
TTAGTATTGG GATTTTACCC CTGTCCTATA AAGATGTTAT GTACCAAAAA TGAAGTGGAG	120
GGCCATACCC TGAGGGAGGG GAGGGATCTC TAGTGTGTC AGAAGCGGAA GCTCA	175

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

AGCCATTTAC CACCCATGGA TGAATGGATT TTGTAATTCT AGCTGTTGTA TTTTGTGAAT	60
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TTGTTAATTT TGTGTTTTT CTGTGAAACA CATAATTGG ATATGGGAGG TAAAGGAGTG      120
TCCCAGTTGC TCCTGGTCAC TCCCTTTATA GCCATTACTG TCTGTTTCT TGTAACTCAG      180
GTTAGGTTTT GGTCTCTCTT GCTCCACTGC AAAAAAAAAA AAA                      223

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(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```

GTTCTGAAGGT GAACGTGTAG GTAGCGGATC TCACAACTGG GGAAGTGTCA AAGACGAATT      60
AACTGACTTG GATCAATCAA ATGTGACTGA GGAAACACCT GAAGGTGAAG AACATCATCC      120
AGTGGCAGAC ACTGAAAATA AGGAGAATGA AGTTGAAGAG GTAAAAGAGG AGGGTCCAAA      180
AGAGATGACT TTGGATGGGT GGTAAATGGC T                                211

```

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```

GCTCCTCTTG CCTTACCAAC TTTGCACCCA TCATCAACCA TG1GGCCAGG TTTGCAGCCC      60
AGGCTGCACA TCAGGGGACT GCCTCGCAAT ACTTCATGCT GTTGCTGCTG ACTGATGGTG      120
CTGTGACGGA TGTGGAAGCC ACACGTGAGG CTGTGGTGCG TGCCTCGAAC CTGCCCATGT      180
CAGTGATCAT TATGGGTGGT AAATGGCT                                208

```

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```

AGCCATTTAC CACCCATACT AAATTCTAGT TCAAACCTCCA ACTTCTTCCA TAAAACATCT      60
AACCACTGAC ACCAGTTGGC AATAGCTTCT TCCTTCTTFA ACCTCTTAGA GTATTTATGG      120
TCAATGCCAC ACATTTCTGC AACTGAATAA AGTTGGTAAG GCAAGAGGAG C              171

```

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs

58

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```

CCGGTGATGC CTCCTCAGGC TTGGGTGTGT CCACTCNACCT CACTGGCCTC TTCTCCAGCA      60
ACTGGTGAAN ATGTCCTCAN GAAAANCNCC ACACGCNGCT CAGGGTGGGG TGGAANCAT      120
CANAATCATC NGGC                                          134

```

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```

AGAGGGTACA TATGCAACAG TATATAAAGG AAGAAGTGCA CTGAGAGGAA CTTCATCAAG      60
GCCATTTAAT CAATAAGTGA TAGAGTCAAG GCTCAACCCA GGTGTGACGG ATTCACAGGTC      120
CCAAGCTCCT TACTGGTACC CTCTT                                          145

```

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```

TGCACTGAGA GGAATTCAAA GGGTTTATGC CAAAGAACAA ACCAGTCCTC TGCAGCCTAA      60
CTCATTTGTT TTTGGGCTGC GAAGCCATGT AGAGGGCGAT CAGGCAGTAG ATGGTCCCTC      120
CCACAGTCAG CGCCATGGTG GTCCGGTAAA GCATTTGGTC AGGCAGGCCT CGTTTCAGGT      180
AGACGGGCAC ACATCAGCTT TCTGGAAAAA CTTTGTAGC TCTGGAGCTT TGTTTTTCCC      240
AGCATAATCA TACTGTGG AATCGGAGGT CAGTTTAGTT GGTAAGGCAA GAGGAGC          297

```

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```

GCACTGAGAG GAACTTCCAA TACTATGTTG AATAGGAGTG GTGAGAGAGG GCATCCTTGT      60

```

CTTGTGCCCG	TTTTCAAAGG	GAATGCTTCC	AGCTTTTGCC	CATTTCAGTAT	AATATTAAAG	120
AATGTTTTAC	CATTTTCTGT	CTTGCTGT	TTTCTGTGTT	TTTGTGGTC	TCTTCATTCT	180
CCATTTTATAG	GCCTTTACAT	GTTAGGAATA	TATTTCTTTT	AATGATACTT	CACCTTTGGT	240
ATCTTTTGTG	AGACTCTACT	CATAGTGTGA	TAAGCACTGG	GTTGGTAAGG	CAAGAGGAGC	300

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GCTCTCTTG	CCTTACCAAC	TCACCCAGTA	TGTCAGCAAT	TTTATCRGCT	TTACCTACGA	60
AACAGCCTGT	ATCCAAACAC	TTAACACACT	CACCTGAAAA	GTTTCAGGCA	CAATCGCCTT	120
CTCATGGGTC	TCTCTGCTCC	AGTTCTGAAC	CTTTCTCTTT	TCCTAGAACA	TGCATTTARG	180
TCGATAGAAG	TTCCTCTCAG	TGC				203

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

TACGGGGACC	CCTGCATTGA	GAAAGCGAGA	CTCACTCTGA	AGCTGAAATG	CTGTTGCCCT	60
TGCAGTGCTG	GTAGCAGGAG	TTCTGTGCTT	TGTGGGCTAA	GGCTCCTGGA	TGACCCCTGA	120
CATGGAGAAG	GCAGAGTTGT	GTGCCCCCTC	TCATGGCCTC	GTCAAGGCAT	CATGGACTGC	180
CACACACAAA	ATGCCGTTTT	TATTAACGAC	ATGAAATTGA	AGGAGAGAAC	ACAATTCACT	240
GATGTGGCTC	GTAACCATGG	ATATGGTCAC	ATACAGAGGT	GTGATTATGT	AAAGGTTAAT	300
TCCACCCACC	TCATGTGGAA	ACTAGCCTCA	ATGCAGGGGT	CCCA		344

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GCACTGAGAG	GAACTTCGTA	GGGAGGTTGA	ACTGGCTGCT	GAGGAGGGGG	AACAACAGGG	60
TAACCAGACT	GATAGCCATT	GGATGGATAA	TATGGTGGTT	GAGGAGGGAC	ACTACTTATA	120
GCAGAGGGTT	GTGTATAGCC	TGAGGAGGCA	TCACCCG			157

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```
GCACTGAGAG GAAGTCTCTAG AAAGTGAAAG TCTAGACATA AAATAAAATA AAAATTTAAA 60
ACTCAGGAGA GACAGCCCAG CACGGTGGCT CACGCCTGTA ATCCCAGAAC TTTGGGAGCC 120
TGAGGAGGCA TCACCCG 137
```

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```
CGGGTGATGC CTCCTCAGGC TGTATTTTGA AGACTATCGA CTGGACTTCT TATCAACTGA 60
AGAATCCGTT AAAAATACCA GTTGTATTAT TTCTACCTGT CAAAATCCAT TTCAAATGTT 120
GAAGTTCCTC TCAGTGC 137
```

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 220 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```
AGCATGTTGA GCCCAGACAC GCAATCTGAA TGAGTGTGCA CCTCAAGTAA ATGTCTACAC 60
GCTGCCTGGT CTGACATGGC ACACCATCNC GTGGAGGGCA CASCTCTGCT CNGCCTACWA 120
CGAGGGCANT CTCATWGACA GGTTCCACCC ACCAACTGC AAGAGGCTCA NNAAGTACTR 180
CCAGGGTMYA SGGACMASGG TGGGAYTYCA YCACWCATCT 220
```

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CGTTAGGGTC TCTATCCACT GCTAAACCAT ACACCTGGGT AACAGGGAC CATTTAACAT	60
TCCCANCTAA ATATGCCAAG TGACTTCACA TGTTTATCTT AAAGATGTCC AAAACGCAAC	120
TGATTTTCTC CCCTAAACCT GTGATGGTGG GATGATTAAAN CCTGAGTGGT CTACAGCAAG	180
TTAAGTGCAA GGTGCTAAAT GAANGTGACC TGAGATACAG CATCTACAAG GCAGTACCTC	240
TCAACNCAGG GCAACTTTGC TTCTCANAGG GCATT'TAGCA GTGTCTGAAG TAATTTCTGT	300
ATTACAACTC ACGGGGCGGG GGGTGAATAT CTANTGGANA GNAGACCCTA ACG	353

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GCACTGAGAG GAACTTCCAA TACYATKATC AGAGTGAACA RGCARCCYAC AGAACAGGAG	60
AAAATGTTYG CAATCTCTCC ATCTGACAAA AGGCTAATAT CCAGAWTCTA AWAGGAACTT	120
AAACAAATTT ATGAGAAAAG AACARACAAC CTCAWCAAAA AGTGGGTGAA GGAWATGCTS	180
AAARGAAGAC ATYTATTTCAG CCAGTAAACA YATGAAAAAA AGGCTCATSA TCACTGAWCA	240
TTAGAGAAAT GCAAATCAAA ACCACAATGA GATACCATCT YAYRCCAGTT AGAAYGGTGA	300
TCATTAAAAAR STCAGGAAAC AACAGATGCT GGACAAGGTG TCA	343

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCACTGAGAG GAACTTCAGA GAGAGAGAGA GAGTTCACC CTGTACTTGG GGAGAGAAAC	60
AGAAGGTGAG AAAGTCTTTG GTTCTGAAGC AGCTTCTAAG ATCTTTTCAT TTGCTTCATT	120
TCAAAGTTCC CATGCTGCCA AAGTGCCATC CTTTGGGGTA CTGTTTCTG AGCTCCAGTG	180
ATAACTCATT TATACAAGGG AGATACCCAG AAAAAAGTG AGCAAATCTT AAAAAGGTGG	240
CTTGAGTTCA GCCTTAAATA CCATCTTGAA ATGACACAGA GAAAGAANGA TGTTGGGTGG	300
GAGTGGATAG AGACCCTAAC G	321

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

GCACTGAGAG GAACTTCAGA GAGAGAGAGA GAGTTCCACC CTGTACTTGG GGAGAGAAAC      60
AGAAGGTGAG AAAGTCTTTG GTTCTGAAGC AGCTTCTAAG ATCTTTTCAT TTGCTTCATT      120
TCAAAGTTCC CATGCTGCCA AAGTGCCATC CTTTGGGGTA CTGTTTCTG AGCTCCAGTG      180
ATAACTCATT TATACAAGGG AGATACCCAG AAAAAAAGTG AGCAAATCTT AAAAAGGTGG      240
CTTGAGTTCA GYCTTAAATA CCATCTTGAA ATGAMACAGA GAAAGAAGGA TGTTGGGTGG      300
GAGTGGATAG AGACCCTAAC G                                     321

```

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```

GCACTGAGAG GAACTTCCAC ATGCACTGAG AAATGCATGT TCACAAGGAC TGAAGTCTGG      60
AACTCAGTTT CTCAGTTCCA ATCCTGATTC AGGTGTTTAC CAGCTACACA ACCTTAAGCA      120
AGTCAGATAA CCTTAGCTTC CTCATATGCA AAATGAGAAT GAAAAGTACT CATCGCTGAA      180
TTGTTTTGAG GATTAGAAAA ACATCTGGCA TGCAGTAGAA ATTCAATTAG TATTCATTTT      240
CATTCTTCTA AATTAAACAA ATAGGATTTT TAGTGGTGGA ACTTCAGACA CCAGAAATGG      300
GAGTGGATAG AGACCCT                                     317

```

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

CGTTAGGGTC TCTATCCACT CCCACTACTG ATCAAACCTCT ATTTATTTAA TTATTTTAT      60
CATACTTTAA GTTCTGGGAT ACACGTGCAG CATGCGCAGG TTTGTTGCAT AGGTATACAC      120
TTGCCATGGT GGTTCGTGTC ACCCATCAGT CCATCATCTA CATTAGGTAT TTCTCCTAAT      180
GCTATCCCTC CCCTAGCCCC TTACACCCCC AACAGGCTCT AGTGTGTGAA GTTCCTCTCA      240
GTGC                                     244

```

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```

CGTTAGGGTC TCTATCCACT GAAATCTGAA GCACAGGAGG AAGAGAAGCA GTYCTAGTGA      60

```

GATGGCAAGT TCWTTTACCA CACTCTTTAA CATTTYGTTT AGTTTTAACC TTTATTTATG	120
GATAATAAAG GTTAATATTA ATAATGATTT ATTTTAAGGC ATTCCCRAT TTGCATAATT	180
CTCCTTTTGG AGATACCCTT TTATCTCCAG TGCAAGTCTG GATCAAAGTG ATASAMAGAA	240
GTTCTCTCA GTGC	254

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

TTCGATACAG GCAAACATGA ACTGCAGGAG GGTGGTGACG ATCATGATGT TGCCGATGGT	60
CCGGATGGNC ACGAAGACGC ACTGGANAC GTGCTTACGT CCTTTTGCTC TGTGATGGC	120
CCTGAGGGGA CGCAGGACCC TTATGACCCT CAGAATCTTC ACAACGGGAG ATGGCACTGG	180
ATTGANTCCC ANTGACACCA GAGACACCCC AACCACCAGN ATATCANTAT ATTGATGTAG	240
TTCCTGTAGA NGGCCCCCTT GTGGAGGAAA GCTCCATNAG TTGGTCATCT TCAACAGGAT	300
CTCAACAGTT TCCGATGGCT GTGATGGGCA TAGTCATANT TAACNTGTN TCGAA	355

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TAAGAGGCTA CCAGCAGAAA GGTTAGTATC ATCAGATAGC ATCTTATACG AGTAATATGC	60
CTGCTATTTG AAGTGTAATT GAGAAGGAAA ATTTTAGCGT GCTCACTGAC CTGCCTGTAG	120
CCCCAGTGAC AGCTAGGATG TGCAATCTCC AGCCATCAAG AGACTGAGTC AAGTTGTTCC	180
TTAAGTCAGA ACAGCAGACT CAGCTCTGAC ATTCTGATTC GAATGACACT GTTCAGGAAT	240
CGGAATCCTG TCGATTAGAC TGGACAGCTT GTGGCAAGTG AATTGCGCTG TAACAAGCCA	300
GATTTTTTAA AATTTATATT GTAAATAATG TGTGTGTGTG TGTGTGTATA TATATATATA	360
TGTACAGTTA TCTAAGTTAA TTTAAAAGTT GTTTGGTACC CTCTTA	406

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TTTTTTTTTT TTTACTCGGC TCAGTCTAAT CCTTTTGTGTA GTCCTCATA GGCCAGACTT	60
AGGGCTAGGA TGATGATTAA TAAGAGGGAT GACATAACTA TTAGTGGCAG GTTAGTTGTT	120


```

TGTAGGGCTC ATGGTAGGGG TAAAAGGAGG GCAATTTCTA GATCAAATAA TAAGAAGGTA      180
ATAGCTACTA AGAAGAATTT TATGGAGAAA GGGACGCGGG CGGGGGATAT AGGGTCGAAG      240
CCGCACTCGT AAGGGGTGGA TTTTCTATG TAGCCGTTGA GTTGTGGTAG TCAAAATGTA      300
ATAATTATTA GTAGTAAGCC TAGGAGA                                     327

```

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```

TAGTCTATGC GGTTGATTCG GCAATCCATT APTTGCTGGA TTTTGTCTG TGTTTTGCCA      60
ATTGCATTCA TAATTTATTA TGCATTTATG CTTGTATCTC CTAAGTCATG GTATATAATC      120
CATGCTTTTT ATGTTTTGTC TGACATAAAC TCTTATCAGA GCCCTTTGCA CACAGGGATT      180
CAATAAATAT TAACACAGTC TACATTTATT TGGTGAATAT TGCATATCTG CTGTACTGAA      240
AGCACATTAA GTAACAAAGG CAAGTGAGAA GAATGAAAAG CACTACTCAC AACAGTTATC      300
ATGATTGCGC ATAGACTA                                     318

```

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```

TCTTCAACCT CTACTIONCAC TAATAGCTTT TTGATGACTT CTAGCAAGCC TCGCTAACCT      60
CGCCTTACCC CCCACTATTA ACCTACTGGG AGAACTCTCT GTGCTAGTAA CCACGTTCTC      120
CTGATCAAAT ATCACTCTCC TACTTACAGG ACTCAACATA CTAGTCACAG CCCTATACTC      180
CCTCTACATA TTTACCACAA CACAATGGGG CTCACTCACC CACCACATTA ACAACATAAA      240
ACCCTCATTC ACACGAGAAA ACACCCTCAT GTTCATACAC CTATCCCCCA TTCTCCTCCT      300
ATCCCTCAAC CCCGACATCA TTACCGGGTT TTCTCTTT                                     338

```

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```

AGCCATTTAC CACCCATCCA CAAAAAAAAA AAAAAAAAAA AAAAAATATCA AGGAATAAAA      60
ATAGACTTTG AACAAAAAGG AACATTTGCT GGCCTGAGGA GGCATCACCC G                                     111

```

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TCGGGTGATG CCTCCTCAGG CCAAGAAGAT AAAGCTTCAG ACCCCTAACA CATTTCCAAA	60
AAGGAAGAAA GGAGAAAAAA GGGCATCATC CCCGTTCCGA AGGGTCAGGG AGGAGGAAAT	120
TGAGGTGGAT TCACGAGTTG CGGACAACCTC CTTTGATGCC AAGCGAGGTG CAGCCGGAGA	180
CTGGGGAGAG CGAGCCAATC AGGTTTTGAA GTTCCTCTCA GTGC	224

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GCACTGAGAG GAACTTCGTT GGAAACGGGT TTTTTCATG TAAGGCTAGA CAGAAGAATT	60
CTCAGTAACT TCCTTGTGTT GTGTGTATTC AACTCACASA GTTGAACGAT CCTTTACACA	120
GAGCAGACTT GTAACACTCT TWTGTGGAA TTTGCAAGTG GAGATTCAG SCGCTTTGAA	180
GTSAAAGGTA GAAAAGGAAA TATCTTCCTA TAAAAACTAG ACAGAATGAT TCTCAGAAAC	240
TCCTTTGTGA TGTGTGCGTT CAACTCACAG AGTTTAACTT TTCWTTTCAT AGAAGCAGTT	300
AGGAAACACT CTGTTTGTAAGTCTGCAAG TGGATAGAGA CCCTAACG	348

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GCACTGAGAG GAACTTCYTT GTGWTGKTG YATTCAACTC ACAGAGTTGA ASSWTSMTT	60
ACABAGWKCA GGCTTKCAA CACTCTTTT GTMGAATYTG CAAGWGGAKA TTTSRRCCRC	120
TTTGWGGYCW WYSKTMGA AW MGGRWATATC TTCWYATMRA AMCTAGACAG AAKSATTCTC	180
AKAAWSTYYY YTGTAAGWS TGCRTTCAAC TCACAGAGKT KAACMWTYCT KYTSATRGAG	240
CAGTTWKGA ACTCTMTTTC TTTGGATTCT GCAAGTGGAT AGAGACCCTA ACG	293

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CTCCTAGGCT

10

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AGTACTTGCC

10

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TTCCGTTATG C

11

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TGGTAAAGGG

10

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCGGTCATAG

10

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TACAACGAGG

10

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TGGATTGGTC

10

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CTTTCTACCC

10

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TTTTGGCTCC

10

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GGAACCAATC

10

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TCGATACAGG

10

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GGTACTAAGG

10

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:99:

AGTCTATGCG

10

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CTATCCATGG

10

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCTGTCCACA

10

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

AAGAGGGTAC

10

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CTTCAACCTC

10

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GCTCCTCTTG CCTTACCAAC

20

(2) INFORMATION FOR SEQ ID NO:105:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTAAGTCGAG CAGTGTGATG

20

(2) INFORMATION FOR SEQ ID NO:106:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GTAAGTCGAG CAGTCTGATG

20

(2) INFORMATION FOR SEQ ID NO:107:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GACTTAGTGG AAAGAATGTA

20

(2) INFORMATION FOR SEQ ID NO:108:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GTAATTCCGC CAACCGTAGT

20

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ATCCTTGATC GATAGTGGAA

20

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

ACGGGGACCC CTGCATTGAG

20

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TATTCTAGAC CATTGCTAC

20

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

ACATAACCAC TTTAGCGTTC

20

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CGGGTGATGC CTCCTCAC³C

20

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

AGCATGTTGA GCCCAGACAC

20

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GACACCTTGT CCAGCATCTG

20

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

TACGCTGCAA CACTGTGGAG

20

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CGTTAGGGTC TCTATCCACT

20

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

AGACTGACTC ATGTCCCCTA

20

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TCATCGCTCG GTGACTCAAG

20

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

CAAGATTCCA TAGGCTGACC

20

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

ACGTACTGGT CTTGAAGGTC

20

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GACGCTTGGC CACTTGACAC

20

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GTATCGACGT AGTGGTCTCC

20

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

TAGTGACATT ACGACGCTGG

20

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CGGGTGATGC CTCCTCAGGC

20

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ATGGCTATTT TCGGGGCTG ACA

23

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

CCGGTATCTC CTCGTGGGTA TT

22

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CTGCCTGAGC CACAAATG

18

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

CCGGAGGAGG AAGCTAGAGG AATA

24

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TTTTTTTTTT TTAG

14

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Ser Ser Gly Gly Arg Thr Phe Asp Asp Phe His Arg Tyr Leu Leu Val
1 5 10 15
Gly Ile

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Gln Gly Ala Ala Gln Lys Pro Ile Asn Leu Ser Lys Xaa Ile Glu Val
1 5 10 15
Val Gln Gly His Asp Glu
 20

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Ser Pro Gly Val Phe Leu Glu His Leu Gln Glu Ala Tyr Arg Ile Tyr
1 5 10 15
Thr Pro Phe Asp Leu Ser Ala
20

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Tyr Leu Leu Val Gly Ile Gln Gly Ala
1 5

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Gly Ala Ala Gln Lys Pro Ile Asn Leu
1 5

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Asn Leu Ser Lys Xaa Ile Glu Val Val
1 5

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Glu Val Val Gln Gly His Asp Glu Ser
1 5

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

His Leu Gln Glu Ala Tyr Arg Ile Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Asn Leu Ala Phe Val Ala Gln Ala Ala
1 5

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Phe Val Ala Gln Ala Ala Pro Asp Ser
1 5

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9388 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GCTCGCGGCC	GCGAGCTCAA	TTAACCTCA	CTAAAGGGAG	TCGACTCGAT	CAGACTGTTA	60
CTGTGTCTAT	GTAGAAAGAA	GTAGACATAA	GAGATTCCAT	TTTGTCTGT	ACTAAGAAAA	120
ATTCTTCTGC	CTTGAGATGC	TGTTAATCTG	TAACCCTAGC	CCCAACCCTG	TGCTCACAGA	180
GACATGTGCT	GTGTTGACTC	AAGGTTCAAT	GGATTTAGGG	CTATGCTTTG	TTAAAAAAGT	240
GCTTGAAGAT	AATATGCTTG	TTAAAAGTCA	TCACCATCT	CTAATCTCAA	GTACCCAGGG	300
ACACAATACA	CTGCGGAAGG	CCGCAGGGAC	CTCTGTCTAG	GAAAGGCCAGG	TATTGTCCAA	360
GATTTCTCCC	CATGTGATAG	CCTGAGATAT	GGCCTCATGG	GAAGGGTAAG	ACCTGACTGT	420
CCCCCAGCCC	GACATCCCCC	AGCCCGACAT	CCCCCAGCCC	GACACCCGAA	AAGGGTCTGT	480
GCTGAGGAGG	ATTAGTAAAA	GAGGAAGGCC	TCTTTGCAGT	TGAGGTAAGA	GGAAGGCATC	540
TGTCTCCTGC	TCGTCCCTGG	GCAATAGAAT	GTCTTGGTGT	AAAACCCGAT	TGTATGTTCT	600
ACTTACTGAG	ATAGGAGAAA	ACATCCTTAG	GGCTGGAGGT	GAGACACGCT	GGCGGCAATA	660
CTGCTCTTTA	ATGCACCGAG	ATGTTTGTAT	AAGTGCACAT	CAAGGCACAG	CACCTTTCCT	720
TAAACTTATT	TATGACACAG	AGACCTTTGT	TCACGTTTTC	CTGCTGACCC	TCTCCCCACT	780
ATTACCCTAT	TGGCCTGCCA	CATCCCCCTC	TCCGAGATGG	TAGAGATAAT	GATCAATAAA	840
TACTGAGGGA	ACTCAGAGAC	CAGTGTCCCT	GTAGGTCCCTC	CGTGTGCTGA	GCGCCCGTCC	900
CTTGGGCTCA	CTTTTCTTTC	TCTATACTTT	GTCTCTGTGT	CTCTTCTTTT	TCTCAGTCTC	960
TCGTTCCACC	TGACGAGAAA	TACCCACAGG	TGTGGAGGGG	CAGGCCACCC	CTTCAATAAT	1020
TTACTAGCCT	GTTTCGTGAC	AACAAGACTG	GTGGTGCAGA	AGGTTGGGTC	TTGGTGTTC	1080
CCGGGTGGCA	GGCATGGGCC	AGGTGGGAGG	GTCTCCAGCG	CCTGGTGCAA	ATCTCCAAGA	1140
AAGTGCAGGA	AACAGCACCA	AGGTGATTG	TAAATTTTGA	TTTGGCGCGG	CAGGTAGCCA	1200
TCCAGCGCA	AAAATGCGCA	GGAAAGCTTT	TGCTGTGCTT	GTAGGCAGGT	AGGCCCAAG	1260
CACCTCTTAT	TGGCTAATGT	GGAGGGAACC	TGCACATCCA	TTGGCTGAAA	TCTCCGTCTA	1320
TTTGAGGCTG	ACTGAGCGCG	TTCTTTTCTT	CTGTGTTGCC	TGGAAACGGA	CTGTCTGCCT	1380
AGTAACATCT	GATCACGTTT	CCCATTGGCC	GCCGTTTCCG	GAAGCCCGCC	CTCCCATTTC	1440
CGGAAGCCTG	GCGCAAGGTT	GGTCTGCAGG	TGGCCTCCAG	GTGCAAAGTG	GGAAGTGTGA	1500
GTCTCTAGTC	TTGGGCTATT	CGGCCACGTG	CCTGCCGGAC	ATGGGACGCT	GGAGGGTCAG	1560
CAGCGTGGAG	TCCTGGCCTT	TTGCGTCCAC	GGGTGGGAAA	TTGGCCATTG	CCACGGCGGG	1620
AACTGGGACT	CAGGCTGCCC	CCCGGCCGTT	TCTCATCCGT	CCACCGGACT	CGTGGGCGCT	1680
CGCACTGGCG	CTGATGTAGT	TTCTTGACCT	CTGACCCGTA	TTGTCTCCAG	ATTAAAGGTA	1740
AAAACGGGGC	TTTTTCAGCC	CACCTCGGGTA	AAACGCCTTT	TGATTCTAG	GCAGGTGTTT	1800
TGTTGCACGC	CTGGGAGGGA	GTGACCCGCA	GGTTGAGGTT	TATTAAAATA	CATTCTGCTG	1860
TTATGTTATG	TTTATAATAA	AGCACCCCAA	CCTTTACAAA	ATCTCACTTT	TTGCCAGTTG	1920
TATTATTTAG	TGGACTGTCT	CTGATAAGGA	CAGCCAGTTA	AAATGGAATT	TTGTTGTTGC	1980
TAATTAAACC	AATTTTFAGT	TTTGGTGTTC	GTCCTAATAG	CAACAACTTC	TCAGGCTTTA	2040
TAAACCATA	TTTCTGGGGG	GAAATTTCTG	TGTAAGGCAC	AGCGAGTTAG	TTTGGAATTG	2100
TTTTAAAGGA	AGTAAGTTCC	TGGTTTTGAT	ATCTTAGTAG	TGTAATGCCC	AACCTGGTTT	2160
TTACTAACCC	TGTTTTTAGA	CTCTCCCTTT	CCTTAAATCA	CCTAGCCTTG	TTTCCACCTG	2220
AATTGACTCT	CCCTTAGCTA	AGAGCGCCAG	ATGGACTCCA	TCTTGGCTCT	TTCCTGGCA	2280
GGCCCTTCTT	CAAGGACTTA	ACTTGTGCAA	GCTGACTCCC	AGCACATCCA	AGAATGCAAT	2340
TAACTGTAA	GATCTGTGG	CAAGCTATAT	CCGAGTTCC	GAGGAATTCA	TCCGATTGAT	2400
TATGCCCCAA	AGCCCGCGT	CTATCACCTT	GTAATAATCT	TAAAGCCCTT	GCACCTGGAA	2460
CTATTAACTT	TCCTGTAACC	ATTTATCCTT	TTAACTTTTT	TGCTTACTTT	ATTTCTGTAA	2520
AATTGTTTTA	ACTAGACCTC	CCCTCCCTTT	TCTAAACCAA	AGTATAAAAG	AAGATCTAGC	2580
CCCTTCTTCA	GAGCGGAGAG	AATTTTGAGC	ATTAGCCATC	TCTTGGCGGC	CAGCTAAATA	2640
AATGGACTTT	TAATTTGTCT	CAAAGTGTGG	CGTTTTCTCT	AACTCGCTCA	GGTACGACAT	2700

TTGGAGGCCC	CAGCGAGAAA	CGTCACCGGG	AGAAACGTCA	CCGGGCGAGA	GCCGGGCCCCG	2760
CTGTGTGCTC	CCCCGGAAGG	ACAGCCAGCT	TGTAGGGGGG	AGTGCCACCT	GAAAAAAAAA	2820
TTTCCAGGTC	CCCAAAGGGT	GACCGTCTTC	CGGAGGACAG	CGGATCGACT	ACCATGC3GG	2880
TGCCCCACAA	AATTCCACCT	CTGAGTCCTC	AACTGCTGAC	CCCGGGGTCA	GGTAGGTCAG	2940
ATTTGACTTT	GGTTCTGGCA	GAGGGAAGCG	ACCCTGATGA	GGGTGTCCCT	CTTTGACTC	3000
TGCCCCATTTC	TCTAGGATGC	TAGAGGGTAG	AGCCCTGGTT	TTCTGTTAGA	CGCCTCTGTG	3060
TCTCTGTCTG	GGAGGGAAGT	GGCCCTGACA	GGGGCCATCC	CTTGAGTCAG	TCCACATCCC	3120
AGGATGCTGG	GGGACTGAGT	CCTGGTTTCT	GGCAGACTGG	TCTCTCTCTC	TCTCTTTTTC	3180
TATCTCTAAT	CTTTCCTTGT	TCAGGTTTCT	TGGAGAATCT	CTGGGAAAGA	AAAAAGAAAA	3240
ACTGTTATAA	ACTCTGTGTG	AATGGTGAAT	GAATGGGGGA	GGACAAGGGC	TTGCGCTTGT	3300
CCTCCAGTTT	GTAGCTCCAC	GGCGAAAGCT	ACGGAGTTCA	AGTGGGCCCT	CACCTGCGGT	3360
TCCGTGGCGA	CCTCATAAGG	CTTAAGGCAG	CATCCGGCAT	AGCTCGATCC	GAGCCGGGGG	3420
TTTATACCGG	CCTGTCAATG	CTAAGAGGAG	CCCAAGTCCC	CTAAGGGGGA	GCGGCCAGGC	3480
GGGCATCTGA	CTGATCCCAT	CACGGGACCC	CCTCCCCTTG	TTTGTCTAAA	AAAAAAAAAA	3540
GAAGAACTG	TCATAACTGT	TTACATGCCC	TAGGGTCAAC	TGTTTGTTTT	ATGTTTATTG	3600
TTCTGTTCTG	TGTCTATTGT	CTTGTTTAGT	GGTGTCAAG	GTTTTGCATG	TCAGGACGTC	3660
GATATTGCC	AAGACGTCTG	GGTAAGAACT	TCTGCAAGGT	CCTTAGTGCT	GATTTTTTGT	3720
CACAGGAGGT	TAAATTTCTC	ATCAATCATT	TAGGCTGGCC	ACCACAGTCC	TGTCTTTTCT	3780
GCCAGAAGCA	AGTCAGGTGT	TGTTACGGGA	ATGAGTGTA	AAAAACATTC	GCCTGATTGG	3840
GATTTCTGGC	ACCATGATGG	TTGTATTTAG	ATTGTCATAC	CCCACATCCA	GGTTGATTGG	3900
ACCTCCTCTA	AACTAACTG	GTGGTGGGTT	CAAAACAGCC	ACCCTGCAGA	TTTCCTTGCT	3960
CACCTCTTTG	GTCAATCTGT	AACTTTTCTT	GTCCTTTAA	ATAGCACACT	GTGTAGGGAA	4020
ACCTACCCTC	GTACTGCTTT	ACTTCGTTTA	GATTCTTACT	CTGTTCTCTT	GTGGCTACTC	4080
TCCCATCTTA	AAAACGATCC	AAGTGGTCCT	TTTCTCTCTC	CCTGCCCCCT	ACCCACACA	4140
TCTCGTTTTC	CAGTGCAGCA	GCAAGTTCAG	CGTCTCCAGG	ACTTGGCTCT	GCTCTCACTC	4200
CTTGAACCTT	TAAAAGAAAA	AGCTGGGTTT	GAGCTATTTG	CCTTTGAGTC	ATGGAGACAC	4260
AAAAGGTATT	TAGGGTACAG	ATCTAGAAGA	AGAGAGAGAA	CACCTAGATC	CAACTGACCC	4320
AGGAGATCTC	GGGCTGGCCT	CTAGTCTCTC	TCCCTCAATC	TTAAAGCTAC	AGTGATGTGG	4380
CAAGTGGTAT	TTAGCTGTTG	TGGTTTTTCT	GCTCTTTCTG	GTCTGTGTTA	TTCTGTTCTT	4440
TCGATACTCC	AGCCCCCAG	GGAGTGAGTT	TCTCTGTCTG	TGCTGGGTTT	GATATCTATG	4500
TTCAAATCTT	ATTAAATTGC	CTTCAAAAAA	AAAAAAAAAA	GGGAAACACT	TCCTCCGAGC	4560
CTTGTAAGGG	TTGGAGCCCT	CTCCAGTATA	TGCTGCAGAA	TTTTTCTCTC	GGTTTCTCAG	4620
AGGATTATGG	AGTCCGCCTT	AAAAAAGGCA	AGCTCTGGAC	ACTCTGCAAA	GTAAGATGGC	4680
CAAAGTTTGG	AGTTGAGTGG	CCCCTTGAAG	GGTCACTGAA	CCTCACAATT	GTTCAGCTG	4740
TGTGGCGGGT	TGTTACTGAA	ACTCCCGGCC	TCCCTGATCA	GTTTCCCTAC	ATTGATCAAT	4800
GGCTGAGTTT	GGTCAGGAGC	ACCCCTTCCA	TGGCTCCACT	CATGCACCAT	TCATAATTTT	4860
ACCTCCAAGG	TCCTCCTGAG	CCAGACCGTG	TTTTCGCCTC	GACCCTCAGC	CGGTTGAGCT	4920
CGCCCTGTAC	TGCCTCTCTC	TGAAGAAGAG	GAGAGTCTCC	CTCACCAGT	CCCACCGCCT	4980
TAAAACCAGC	CTACTCCCTT	AGGGTCATCC	CATGTCTCCT	CGGCTATGTC	CCCTGTAGGC	5040
TCATCACCCA	TTGCCTCTTG	GTTGCAACCG	TGGTGGGAGG	AAGTAGCCCC	TCTACTACCA	5100
CTGAGAGAGG	CACAAGTCCC	TCTGGGTGAT	GAGTGCTCCA	CCCCCTTCCT	GGTTTATGTC	5160
CCTTCTTTCT	ACTTCTGACT	TGTATAATTG	GAAAACCCAT	AATCCTCCCT	TCTCTGAAAA	5220
GCCCCAGGCT	TTGACCTCAC	TGATGGAGTC	TGTACTCTGG	ACACATTGGC	CCACCTGGGA	5280
TGACTGTCAA	CAGCTCCTTT	TGACCTTTT	CACCTCTGAA	GAGAGGGAAA	GTATCCAAAG	5340
AGAGGCCAAA	AAGTACAACC	TCACATCAAC	CAATAGGCCG	GAGGAGGAAG	CTAGAGGAAT	5400
AGTGATTAGA	GACCCAATTG	GGACCTAATT	GGGACCCAAA	TTTCTCAAGT	GGAGGGAGAA	5460
CTTTTGACGA	TTTCCACCGG	TATCTCCTCG	TGGGTATTCA	GGGAGCTGCT	CAGAAACCTA	5520
TAAACTTGTC	TAAGGCGACT	GAAGTCGTCC	AGGGGCATGA	TGAGTCACCA	GGAGTGTTTT	5580
TAGAGCACCT	CCAGGAGGCT	TATCGGATTT	ACACCCCTTT	TGACCTGGCA	GCCCCGAAA	5640
ATAGCCATGC	TCTTAATTTG	GCATTTGTGG	CTCAGGCAGC	CCCAGATAGT	AAAAGGAAAC	5700
TCCAAAAACT	AGAGGGATTT	TGCTGGAATG	AATACCAGTC	AGCTTTTAGA	GATAGCCTAA	5760
AAGGTTTTTG	ACAGTCAAGA	GGTTGAAAAA	CAAAAACAAG	CAGCTCAGGC	AGCTGAAAAA	5820
AGCCACTGAT	AAAGCATCCT	GGAGTATCAG	AGTTTACTGT	TAGATCAGCC	TCATTTGACT	5880
TCCCCTCCCA	TATGGTGTTC	AAATCCAGCT	ACACTACTTC	CTGACTCAAA	CTCCACTATT	5940
CCTGTTTCATG	ACTGTCAGGA	ACTGTTGGAA	ACTACTGAAA	CTGGCCGACC	TGATCTTCAA	6000

AATGTGCCCC	TAGGAAAGGT	GGATGCCACC	GTGTTACAG	ACAGTAGCAG	CTTCCTCGAG	6060
AAGGGACTAC	GAAAGGCCGG	TGCAGCTGTT	ACCATGGAGA	CAGATGTGTT	GTGGGCTCAG	6120
GCTTTACCAG	CAAACACCTC	AGCACAAAAG	GCTGAATTGA	TCGCCCTCAC	TCAGGCTCTC	6180
CGATGGGGTA	AGGATATTAA	CGTTAACT	GACAGCAGGT	ACGCCTTTGC	TACTGTGCAT	6240
GTACGTGGAG	CCATCTACCA	GGAGCGTGGG	CTACTCACCT	CAGCAGGTGG	CTGTAATCCA	6300
CTGTAAGGA	CATCAAAAGG	AAAACACGGC	TGTTGCCCGT	GGTAACCAGA	AAGCTGATT	6360
AGCAGCTCAA	GATGCAGTGT	GACTTTTCAGT	CACGCCTCTA	AACTTGCTGC	CCACAGTCTC	6420
CTTTCCACAG	CCAGATCTGC	CTGACAATCC	CGCATACTCA	ACAGAAGAAG	AAAAGTGGCC	6480
TCAGAACTCA	GAGCCAATAA	AAATCAGGAA	GGTTGGTGGA	TTCTTCCTGA	CTCTAGAATC	6540
TTCATACCCC	GAAGTCTTGG	GAAAACCTTA	ATCAGTCAAC	TACAGTCTAC	CACCCATTTA	6600
GGAGGAGCAA	AGCTACCTCA	GCTCCTCCGG	AGCCGTTTGA	AGATCCCCCA	TCTTCAAAGC	6660
CTAACAGATC	AAGCAGCTCT	CCGGTGCACA	ACCTGCGCCC	AGGTAAATGC	CAAAAAAGGT	6720
CCTAAACCCA	GCCCAGGCCA	CCGTCTCCAA	GAAAACCTCAC	CAGGAGAAAA	GTGGGAAATT	6780
GACTTTACAG	AAGTAAACC	ACACCGGGCT	GGGTACAAAT	ACCTTCTAGT	ACTGGTAGAC	6840
ACCTTCTCTG	GATGGACTGA	AGCATTTGCT	ACCAAAAAACG	AACTGTCAA	TATGGTAGTT	6900
AAGTTTTTAC	TCAATGAAAT	CATCCCTCGA	CGTGGGCTGC	CTGTTGCCAT	AGGGTCTGAT	6960
AATGGACCGG	CCTTCGCCCT	GTCTATAGTT	TAGTCAGTCA	GTAAGGCGTT	AAACATTCAA	7020
TGGAAGCTCC	ATTGTGCCTA	TCGACCCAG	AGCTCTGGGC	AAGTAGAACG	CATGAAGTGC	7080
ACCCTAAAA	ACACTCTTAC	AAAATTAATC	TTAGAAACCG	GTGTAAATTG	TGTAAGTCTC	7140
CTTCCTTTAG	CCCTACTTAG	AGTAAGGTGC	ACCCCTTACT	GGGCTGGGTT	CTTACCTTTT	7200
GAAATCATGT	ATGGGAGGGC	GCTGCCTATC	TTGCCTAAGC	TAAGAGATGC	CCAATTGGCA	7260
AAAATATCAC	AAACTAATTT	ATTACAGTAC	CTACAGTCTC	CCCAACAGGT	ACAAGATATC	7320
ATCCTGCCAC	TTGTTGAGG	AACCCATCCC	AATCCAATTC	CTGAACAGAC	AGGGCCCTGC	7380
CATTCAATTC	CGCCAGGTGA	CCTGTTGTTT	GTTAAAAAGT	TCCAGAGAGA	AGGACTCCCT	7440
CCTGCTTGGA	AGAGACCTCA	CACCGTCATC	ACGATGCCAA	CGGCTCTGAA	GGTGGATGGC	7500
ATTCTGCGT	GGATTCAATCA	CTCCCGCATC	AAAAAGGCCA	ACGGAGCCCA	ACTAGAAACA	7560
TGGGTCCCCA	GGGCTGGGTC	AGGCCCTTA	AACTGCACC	TAAGTTGGGT	GAAGCCATTA	7620
GATTAATTCT	TTTTCTTAAT	TTTGTAAC	AATGCATAGC	TTCTGTCAA	CTTATGTATC	7680
TTAAGACTCA	ATATAACCCC	CTTGTTATAA	CTGAGGAATC	AATGATTGTA	TTCCCCAAAA	7740
ACACAAGTGG	GGAAATGTAGT	GTCCAACCTG	GTTTTTACTA	ACCCTGTTTT	TAGACTCTCC	7800
CTTTCCTTTA	ATCACTCAGC	CTTGTTTCCA	CCTGAATTGA	CTCTCCCTTA	GCTAAGAGCG	7860
CCAGATGGAC	TCCATCTTGG	CTCTTTCACT	GGCAGCCGCT	TCCTCAAGGA	CTTAACCTGT	7920
GCAAGCTGAC	TCCCAGCACA	TCCAAGAATG	CAATTAACCTG	ATAAGATACT	GTGGCAAGCT	7980
ATATCCGCAG	TCCCAGGAA	TTCTGTTCAAT	TGATTACACC	CAAAAGCCCC	GCGTCTATCA	8040
CCTTGTAATA	ATCTTAAAGC	CCCTGCACCT	GGAACTATTA	ACGTTCCCTGT	AACCATTTAT	8100
CCTTTTAACT	TTTTTGCCCTA	CTTTATTTCT	GTAAATTGTT	TTTAACTAGA	CCCCCCTCT	8160
CCTTTCTAAA	CCAAAGTATA	AAAGCAAATC	TAGCCCTTTC	TTCAGGCCGA	GAGAATTTTCG	8220
AGCGTTAGCC	GTCTCTTGGC	CACCAGCTAA	ATAAACGGAT	TCTTCATGTG	TCTCAAAGTG	8280
TGGCGTTTTT	TCTAACTCGC	TCAGGTACGA	CCGTGGTAGT	ATTTTCCCCA	ACGTCTTATT	8340
TTTAGGGCAC	GTATGTAGAG	TAACTTTAT	GAAAGAAACC	AGTTAAGGAG	GTTTTGGGAT	8400
TTCTTTTATC	AACTGTAATA	CTGGTTTTGA	TTATTTATTT	ATTTATTTAT	TTTTTTTGAG	8460
AAGGAGTTTC	ACTCTTGTTG	CCCAGGCTGG	AGTGCAATGG	TGCGATCTTG	GCTCACTGCA	8520
ACTTCCGCCT	CCCAGGTTCA	AGCGATTCTC	CTGCCTCAGC	CTCGAGAGTA	GCTGGGATTA	8580
TAGGCATGCG	CCACCACACC	CAGCTAATTT	TGTATTTTTA	GTAAAGATGG	GGTTTCTTCA	8640
TGTTGGTCAA	GCTGGTCTGG	AACTCCCCGC	CTCGGGTGAT	CTGCCCCCCT	CGGCCCTCCGA	8700
AAGTGCTGGG	ATTACAGGTG	TGATCCACCA	CACCCAGCCG	ATTTATATGT	ATATAAATCA	8760
CATTCTCTTA	ACCAAAATGT	AGTGTTCCT	TCCATCTTGA	ATATAGGCTG	TAGACCCCGT	8820
GGGTATGGGA	CATTGTTAAG	AGTGAGACCA	CAGCAGTTTT	TATGTCACT	GACAGCATCT	8880
CCAAATAGCC	TTCATGGTTG	TCACTGCTTC	CCAAGACAAT	TCCAAATAAC	ACTTCCCAGT	8940
GATGACTTGC	TACTTGCTAT	TGTTACTTAA	TGTGTTAAGG	TGGCTGTTAC	AGACACTATT	9000
AGTATGTCAG	GAATTACACC	AAAATTTAGT	GGCTCAAACA	ATCATTTTAT	TATGTATGTG	9060
GATTCTCATG	GTCAGGTCAG	GATTTTCAGAC	AGGGCACAAG	GGTAGCCAC	TTGTCTCTGT	9120
CTATGATGTC	TGGCCTCAGC	ACAGGAGACT	CAACAGCTGG	GGTCTGGGAC	CATTTGGAGG	9180
CTTGTTCCCT	CACATCTGAT	ACCTGGCTTG	GGATGTTGGA	AGAGGGGGTG	AGCTGAGACT	9240
GAGTGCCTAT	ATGTAGTGT	TCCATATGGC	CTTGACTTCC	TTACAGCCTG	GCAGCCTCAG	9300

GGTAGTCAGA ATTCTTAGGA GGCACAGGGC TCCAGGGCAG ATGCTGAGGG GTCTTTTATG 9360
 AGGTAGCACA GCAAATCCAC CCAGGATC 9388

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TGTAAGTCGA	GCAGTGTGAT	GGAAGGAATG	GTCTTTGGAG	AGAGCATATC	CATCTCCTCC	60
TCACTGCCTC	CTAATGTCAT	GAGGTACACT	GAGCAGAATT	AAACAGGGTA	GTCTTAACCA	120
CACTATTTTT	AGCTACCTTG	TCAAGCTAAT	GGTTAAAGAA	CACTTTTGGT	TTACACTTGT	180
TGGGTCATAG	AAGTTGCTTT	CCGCCATCAC	GCAATAAGTT	TGTGTGTAAT	CAGAAGGAGT	240
TACCTTATGG	TTTCAGTGTC	ATTCTTTAGT	TAAGTTGGGA	GCTGTGTAAT	TTAGGCTTTG	300
CGTATTATTT	CACTTCTGTT	CTCCACTTAT	GAAGTGATTG	TGTGTTGCGG	TGTGTGTGCG	360
TGCGCATGTG	CTTCCGGCAG	TTAACATAAG	CAAATACCCA	ACATCACACT	GCTCGACTT	419

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TGTAAGTCGA	GCAGTGTGAT	GTCCACTGCA	GTGTGTTGCT	GGGAACAGTT	AATGAGCAAA	60
TTGTATACAA	TGGCTAGTAC	ATTGACCGGG	ATTTGTTGAA	GCTGGTGAGT	GTTATGACTT	120
AGCCTGTTAG	ACTAGTCTAT	GCACATGGCT	CTGGTCAACT	ACCGCTCTCT	CATTCTCCA	180
GATAAATCCC	CCATGCTTTA	TATTCTCTTC	CAAACATACT	ATCCTCATCA	CCACATAGTT	240
CCTTTGTTAA	TGCTTTGTTT	TAGACTTTCC	CTTTTCTGTT	TTCTTATTCA	AACCTATATC	300
TCTTTGCATA	GATTGTAAAT	TCAAATGCC	TCAGGGTGCA	GGCAGTTCAT	GTAAGGGAGG	360
GAGGCTAGCC	AGTGAGATCT	GCATCACACT	GCTCGACTTA	CA		402

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TCGGGTGATG	CCTCCTCAGG	CCAAGAAGAT	AAAGCTTCAG	ACCCCTAACA	CATTTCCAAA	60
AAGGAAGAAA	GGAGAAAAAA	GGGCATCATC	CCCGTTCCGA	AGGGTCAGGG	AGGAUGAAAT	120
TGAGGTGGAT	TCACGAGTTG	CGGACAACCTC	CTTTGATGCC	AAGCGAGGTG	CAGCCGGAGA	180

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(D) TC Y: linear

) SEQUENC CRIPTION: D NO:160:

CGA GCAGT	GGGTGGAA	TTGTAAG C	TGC PAACT
TAA TAATA	TAGCATTT	GCACTTT A	CAA AGTAC
YCT AATTA	CCTCTCTG	AATCTGG A	TGC ACTTA
GGT CATGA	GTATGCAT	AGTTGGT G	ATG CTTTA
TATG ATGGG	TAGAGTTC	CTGTTGG A	TTG TGCAT
TTGA TGGCA	AGATCATA	ACTCGAT G	CTT CATAA
TATC TGAGT	TCATCACA	CGACTTA C	

FORMATION EQ ID NO:

) SEQUENC RACTERIST
(A) LE 193 base
(B) TY ucleic ac
(C) SI DNES: si
(D) TC Y: linear

) SEQUENC CRIPTION: D NO:161:

TTGA CCCCC	TGACCAGG	AACCAAC C	TAC ACGCC
TAGG AGAAA	ACCAATAA	TGCCCCG A	ACA AATAA
TACA AGGAC	AACAGCTA	AGAGCGG A	TGT GTGTG
TATG TTA			

FORMATION EQ ID NO:

) SEQUENC RACTERIST
(A) LE 147 base
(B) TY ucleic ac
(C) SI DNES: si
(D) TC Y: linear

) SEQUENC CRIPTION: D NO:162:

CA CAGCTA	IGATTTATC	GGACTA ATT	GG TATTTT
TA TCTCCCT	TTATCTTCA	TATTTT TG	TA TCCCAG
TT TTATGTT	AAATCACAT	TCTCAA AAT	TC ACCCAC
TC TGGGTG	GTGTGTCTG	TGTCTG GGC	AT GCTA

RMATION FC ID NO:16

SEQUENCE	CTERISTIC
(A) LEN	12 base p
(B) TYP	leic acid
(C) STR	ESS: sing
(L) TOP	linear

SEQUENCE IPTION: S NO:164:

GC TTTGAG	GATGCTGCC	ACCGCA CCC	GG AACAGA
TG CAAGTG	GAGCGCCCC	TACGTG CTC	GG GCTGGG
CC ACCGCC	GGAAGCCCA	ACCGGA TAC	CG ACAAGA
GG TGGGCC	GGAGCCCGA	CGTGAC GTC	AG GCGCCA
CG CTGGCT	CGGCTACGC	CAGTCC AAC	CC ATGACA
TG CACGAC	CCAGGGCAC	CCCAAA GAC	GG GCTCGG
GC GCGCTG	CCAGATGCT	AAGGTG TCA	TA AT

RMATION FC ID NO:16

SEQUENCE	CTERISTIC
(A) LEN	61 base p
(B) TYP	leic acid
(C) STR	ESS: sing
(D) TOP	linear

SEQUENCE IPTION: S NO:165:

TT GTCCAG	GCATCTGAT	TCCTCA CAT	CC ACTAAT
AG GAGAAC	TTGTATGGC	AAGGAA GAA	GA GCGAG
TT CTTTTC	CTTGTTCTT	CAACTG AGA	AG CTCFAG
GA CTCCAA	ATCCCAAC	TAGTTC C	AG GCTCAX

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

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TWGACTGACT CATGTCCCCT ACACCCAACT ATCTTCTCCA GGTGGCCAGG CAIGATAGAA      60
TCTGATCCTG ACTTAGGGGA ATATTTTCTT TTTACTTCCC ATCTTGATTC CCTGCCGGTG      120
AGTTTCCTGG TTCAGGGTAA GAAAGGAGCT CAGGCCAAAG TAATGAACAA ATCCATCCTC      180
ACAGACGTAC AGAATAAGAG AACWTGGACW TAGCCAGCAG AACMCAAKTG AAAMCAGAAC      240
MCTTAMCTAG GATRACAAMC MCRRARATAR KTGCCYCMCMC WTATAATAGA AACCAAACTT      300
GTATCTAATT AAATATTTAT CCACYGTCAG GGCATTAGTG GTTTTGATAA ATACGCTTTG      360
GCTAGGATTC CTGAGGTTAG AATGGAARAA CAATTGCAMC GAGGGTAGGG GACATGAGTC      420
AKTCTAA                                           427

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(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic
- (C) STRANDEDNESS
- (D) TOPOLOGY: circular

(x) SEQUENCE DESCRIPTION: SEQ ID NO:167:

```

--      f GCTCCCGGCC GC      GGAT      TGAATCATGT CCCCTAAL      0
A      ACA CCTGCTAGGT GTAA      GATGCTAGG TCTACGGAGG CTCCAGGGT      120
GGAGTAGTTC CCTGCTAAGG GAGGGTAGAC TGTTCACCT GTTCCTGCTC CGGCCTCCAC      180
TATAGCAGAT GCGAGCAGGA GTAGGAGAGA GGGAGGTAAG AGTCAGAAGC TTATGTTGTT      240
TATGCGGGGA AACCCCTAT CGGGGGCAGC CRAGTTATTA GGGGACANTR TAGWYARTCW      300
AGNTAGCATC CAAAGCGNGG GAGTTNTCCC ATATGGTTTG ACCTGCAGGC GGCCGCATTA      360
GTGATTAGCA TGTGAGCCCC AGACACGCAT AGCAACAAGG ACCTAAACTC AGATCCTGTG      420
CTGATTACTT AACATGAATT ATTGTATTTA TTTAACAAC TTAGATTATG AGGCATATTA      480
TTAGGTCCAT ATTACCTGGA                                           500

```

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

```

TTCATCGCTC GGTGACTCAA GCCTGTAATC CCAGAACTTT GGGAGGCCGA GGGGAGCAGA      60
TCACCTGAGG TTGGGAGTTT GAGACCAGCC TGGCCAACAT GGTGACAACC CGTCTCTGCT      120
AAAAATACAA AAATTAGCCA AGCATGGTGG CATGCACTTG TAATCCCAGC TACTCGGGAG      180
GCTGAGGCAG GAGAATCACT TGAGGCCAGG AGGCAGAGGT TGCAGTGAGG CAGAGGTTGA      240
GATCATGCCA CTGCACTCCA GCCTGGGCAA CAGAGTAAGA CTCCATCTCA AAAAAAAAAA      300
AAAAAAAGAA TGATCAGAGC CACAAATACA GAAAACCTTG AGTCACCGAG CGATGAAA      358

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(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

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TTCTGTCCAC ACCAATCTTA GAGCTCTGAA AGAATTTGTC TTAAATATC TTTTAATAGT      60
AACATGTATT TTATGGACCA AATTGACATT TTCGACTATT TTTCCCAAA AAAAGTCAGG      120
TGAATTTTCAG CACACTGAGT TGGGAATTC TTATCCGAGA AGWCGGCACG AGCAATTTCA      180
TATTTATTTA AGATTGATTC CATACTCCGT TTTCAAGGAG AATCCCTGCA GTCTCCTTAA      240
AGGTAGAACA AATAC TTCT ATTTTTTTTT CACCATTGTG GGATTGGACT TTAAGAGGTG      300
ACTCTAAAAA AAC/      ATATC CAGT ATT /      CCATATTATC      360
ATATTCACCTT AAA/      ... ..TCCTC CCT GGC /      TTCAATGTAG      420
GGAAAAACTT AGT/      TG AAAACCC VAT PAA /      GT/      GTGGGCAGA      480
ARGTTTGGGG GTG/      TG TATGTGT TT CCC /      CAC GAAGCTGTT      540
GTATGGGTCA GAG/      GA ATGCTTA G ACA /      AAG AGAAGCAAA      600
CCACATGTCT CAG/      TTATTI      CAT /      GAA ITTCTTCTG      660
TATTAATTTT CAA/      .. .ACCCTC      TTT /      AAC GCATTGACA      720
ATGGGTTGAT ATT/      TT AAAAGAA T.      ATG /      CAA AATCTGAAG      780
CCTGTTTTAT TTT/      TT TTTATGT GT      ATG /      TGT TTTGTTTCT      840
ATTTTGTTGG TTT/      TT TGTTTTT TT/      TGT /      TTT JATACTACAT      900
GCAGTTTCTT TAA/      TTTTG AAT/      PTA /      TTTATATGAG      960
TGCATTTCAA CTA/      TTTCT TATT TGT C      TTTAC TGGTAATTT      1020
TTTATTTACA ATATGTTTAA AGAGATAACA GTTTGATATG TTTTCATGTG TTTATAGCAG      1080
AAGTTATTTA TTTCTATGGC ATTCCAGCGG ATATTTTGGT GTTTGCGAGG CATGCACTCA      1140
ATATTTTGTA CAGTTAGTGG ACAGTATTCA GCAACGCCTG ATAGCTTCTT TGGCCTTATG      1200
TTAAATAAAA AGACCTGTTT GGGATGTAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA      1260
AAAAA                                         1265

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(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

```

TGTAAGTCGA GCAGTGTGAT GACGATATTC TTCTTATTAA TGTGGTAATT GAACAAATGA      60
TCTGTGATAC TGATCCTGAG CTAGGAGGCG CTGTTCAGTT AATGGGACTT CTTCGTACTC      120
TAATTGATCC AGAGAACATG CTGGCTACAA CTAATAAAAC CGAAAAAAGT GAATTTCTAA      180
ATTTTTTCTA CACCATTGT ATGCATGTTT TCACAGCACC ACTTTTGACC AATACTTCAG      240
AAGACAAATG TGAAAAGGAT AATATAGTTG GATCAAACAA AAACAACACA ATTTGTCCCG      300
ATAATTATCA AACAGCACAG CTAATTGCCT TAATTTTAGA GTTACTCACA TTTTGTGTGG      360
AACATCACAC TGCTCGACTT ACA                                         383

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(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

TGGGCACCTT CAATATCGCA AGTTAAAAAT AATGTTGACT TTATTATACT TTTGACCTGT	60
TTAGCTCAAC AGGGTGAAGG CATGTAAAGA ATGTGGACTT CTGAGGAATT TTCTTTTAAA	120
AAGAACATAA TGAAGTAAAC TTTTAATTAC TCAAGGACTA CTTTGGTTG AAGTTTATAA	180
TCTAGATACC TCTACTTTT GTTTTGTCTG TTCGACAGTT CACAAAGACC TTCAGCAATT	240
TACAGGGTAA AATCGTTGAA GTAGTGGAGG TGAAACTGAA ATTTAAAATT ATTCTGTAAA	300
TACTATAGGG AAAGAGGCTG AGCTTAGAAT CTTTGGTTG TTCATGTGTT CTGTGCTCTT	360
ATCATCACAC TGCTCGACTT ACA	383

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

TCGGGTGATG CCTCCTCAGG CTTGTCGTTA GTGTACACAG AGCTGCTCAT GAAGCGACAG	60
CGGCTGCCCC TGGCACTTCA GAACCTCTTC CTCTACACTT TTGGTGCGCT TCTGAATCTA	120
GGTCTGCATG CTGGCGGCGG CTCTGGCCCA GGCCTCCTGG AAAGTTTCTC AGGATGGGCA	180
GCACTCGTGG TGCTGAGCCA GGCATAAAT GGAAGTCTCA TGTCTGCTGT CATGGAGCAT	240
GGCAGCAGCA TCACACGCCT CTTTGTGGTG TCCTGCTCGC TGGTGGTCAA CGCCGTGCTC	300
TCAGCAGTCC TGCTACGGCT GCAGCTCACA GCGCCTTCT TCCTGGCCAC ATTGCTCATT	360
GGCCTGGCCA TGCGCTGTA CTATGGCAGC CGCTAGTCCC TGACAACTTC CACCCTGATT	420
CCGGACCCTG TAGATTGGGC GCCACCACCA GATCCCCCTC CCAGGCCTTC CTCCCTCTCC	480
CATCAGCGGC CCTGTAACAA GTGCCTTGTG AGAAAAGCTG GAGAAGTGAG GGCAGCCAGG	540
TTATTCTCTG GAGGTTGGTG GATGAAGGGG TACCCCTAGG AGATGTGAAG TGTGGGTTTG	600
GTTAAGGAAA TGCTTACCAT CCCCACCCC CAACCAAGTT NTTCCAGACT AAAGAATTAA	660
GGTAACATCA ATACCTAGGC CTGAGGAGGC ATCACCCGA	699

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 701 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

TCGGGTGATG CCTCCTCAGG CCAGATCAAA CTTGGGGTTG AAAACTGTGC AAAGAAATCA	60
ATGTCGGAGA AAGAATTTTG CAAAAGAAAA ATGCCTAATC AGTACTAATT TAATAGGTCA	120

CATTAGCAGT	GGAAGAAGAA	ATGTTGATAT	TTTATGTCAG	CTATTTTATA	ATCACCAGAG	180
TGCTTAGCTT	CATCTAAGCC	ATCTCGTATT	CATTAGAAAT	AAGAACAATT	TTATTCGTCT	240
GAAAGAACTT	TTCAATTTAT	AGCATCTTAA	TTGCTCAGGA	TTTTAAATTT	TGATAAAGAA	300
AGCTCCACTT	TTGGCAGUAG	TAGGGGGCAG	GGAGAGAGGA	GGCTCCATCC	ACAAGGACAG	360
AGACACCAGG	GCCAGTAGGG	TAGCTGGTGG	CTGGATCAGT	CACAACGGAC	TGACTTATGC	420
CATGAGAAGA	AACAACCTCC	AAATCTCAGT	TGCTTAATAC	AACACAAGCT	CATTTCTTGC	480
TCACGTTACA	TGTCCTATGT	AGATCAACAG	CAGGTGACTC	AGGGACCCAG	GCTCCATCTC	540
CATATGAGCT	TCCATAGTCA	CCAGGACACG	GGCTCTGAAA	GTGTCCTCCA	TGCAGGGACA	600
CATGCCCTTT	CCTTTTCATTG	GGCAGAGCAA	GTCACCTTATG	GCCAGAAGTC	AACTGCAGG	660
GCAGTGCCAT	CCTGCTGTAT	GCCTGAGGAG	GCATCACCCG	A		701

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

TCGGGTGATG	CCTCCTCANG	CCCCTAAATC	AGAGTCCAGG	GTCAGAGCCA	CAGGAGACAG	60
GGAAAGACAT	AGATTTTAAAC	CGGCCCCCTT	CAGGAGATTTC	TGAGGCTCAG	TTCACTTTGT	120
TGCAGTTTGA	ACAGAGGCAG	CAAGGCTAGT	GGTTAGGGGC	ACGGTCTCTA	AAGCTGCACT	180
GCCTGGATCT	GCCTCCCAGC	TCTGCCAGGA	ACCAGCTGCG	TGGCCTTGAG	CTGCTGACAC	240
GCAGAAAGCC	CCCTGTGGAC	CCAGTCTCCT	CGTCTGTAAG	ATGAGGACAG	GACTCTAGGA	300
ACCTTTTCCC	TTGGTTTGGC	CTCACTTTCA	CAGGCTCCCA	TCTTGAAGTC	TATCTACTCT	360
TTTCCTGAAA	CCTTGTAATA	GAAAAAAGTG	CTAGCCTGGG	CAACATGGCA	AAACCTGTG	420
TCTACAAAAA	ATACAAAAAT	TAGTTGGGTG	TGGTGGCATG	TGCCTGTAGT	CCCAGCCACT	480
TGGGAGGTGC	TGAGGTGGGA	GGATCACTTG	AGCCCGGGAG	GTGGAGGTTG	CAGTGAGCCA	540
AGATCATGCC	ACTGCACTCC	AGCCTGAGTA	ATAGAGTAAG	ACTCTGTCTC	AAAAACAACA	600
ACAACAACAG	TGAGTGTGCC	TCTGTTTCCG	GCTTGGATGG	GGCACCACAT	TTATGCATCT	660
CTCAGATTTG	GACGCTGCAG	CCTGAGGAGG	CATCACCCGA			700

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

TATAGGGCGA	ATTGGGCCCG	AGTTGCATGN	TCCCGGCCGC	CATGGCCGCG	GGATTCCGGT	60
GATGCCTCCT	CAGGCTTGTC	TGCCACAAGC	TACTTCTCTG	AGCTCAGAAA	GTGCCCCCTG	120
ATGAGGGA	ATGTCCTACT	GCACTGCGAA	TTTCTCAGTT	CCATTTTACC	TCCCAGTCCT	180
CCTTCTAAAC	CAGTTAATAA	ATTCATTCCA	CAAGTATTTA	CTGATTACCT	GCTTGTGCCA	240
GGGACTATTC	TCAGGCTGAA	GAAGGTGGGA	GGGGAGGGCG	GAACCTGAGG	AGCCACCTGA	300
GCCAGCTTTA	TATTTCAACC	ATGGCTGGCC	CATCTGAGAG	CATCTCCCCA	CTCTCGCCAA	360
CCTATCGGGG	CATAGCCCAG	GGATGCCCCC	AGGCGGCCCA	GGTTAGATGC	GTCCCTTTGG	420
CTTGTCAGTG	ATGACATACA	CCTTAGCTGC	TTAGCTGGTG	CTGGCCTGAG	GAGGCATCAC	480
CCGA						484

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

```
TCGGGTGATG CCTCCTCAGG GCTCAAGGGA TGAGAAGTGA CTTCTTTCTG GAGGGACCGT      60
TCATGCCACC CAGGATGAAA ATGGATAGGG ACCCACTTGG AGGACTTGCT GATATGTTTG      120
GACAAATGCC AGGTAGCGGA ATTGGTACTG GTCCAGGAGT TATCCAGGAT AGATTTTCAC      180
CCACCATGGG ACGTCATCGT TCAAATCAAC TCTTCAATGG CCATGGGGGA CACATCATGC      240
CTCCACACA ATCGCAGTTT GGAGAGATGG GAGGCAAGTT TATGAAAAGC CAGGGGCTAA      300
GCCAGCTCTA CCATAACCAG AGTCAGGGAC TCTTATCCCA GCTGCAAGGA CAGTCGAAGG      360
ATATGCCACC TCGGTTTCTT AAGAAAGGAC AGCTTAATGC AGATGAGATT AGCCTGAGGA      420
GGCATCACCC GA                                     432
```

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 788 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

```
TAGCATGTTG AGCCCAGACA CAGTAGCATT TGTGCCAATT TCTGTTGGA ATGGTGACAA      60
CATGCTGGAG CCAAGTGCTA ACATGCCTTG GTTCAAGGGA TGGAAAGTCA CCCGTAAGGA      120
TGGCAATGCC AGTGAACCA CGCTGCTTGA GGCTCTGGAC TGCATCCTAC CACCAACTCG      180
CCCAACTGAC AAGCCCTTGC GCCTGCCTCT CCAGGATGTC TACAAAATTG GTGGTATTGG      240
TACTGTTTCT GTTGCCGAG TGGAGACTGG TGTTCTCAA CCCGGTATGG TGGTCACCTT      300
TGCTCCAGTC AACGTTACAA CGGAAGTAAA ATCTGTGCGA ATGCACCATG AAGCTTTGAG      360
TGAAGCTCTT CCTGGGGACA ATGTGGGCTT CAATGTCAAG AATGTGTCTG TCAAGGATGT      420
TCGTCGTGGC AACGTTGCTG GTGACAGCAA AAATGACCCA CCAATGGAAG CAGCTGGCTT      480
CACTGCTCAG GTGATTATCC TGAACCATCC AGGCCAAATA AGTGCCGGCT ATGCCCCCTGT      540
ATTGGATTGC CACACGGCTC ACATTGCATG CAAGTTTGCT GAGCTGAAGG AAAAGATTGA      600
TCGCCGTTCT GGTAAGAGC TGGAAGATGG CCCTAAATTC TTGAAGTCTG GTGATGCTGC      660
CATTGTTGAT ATGGTTCCTG GCAAGCCCAT GTGTGTTGAG AGCTTCTCAG ACTATCCACC      720
TTTGGGTCGC TTTGCTGTTC GTGATATGAG ACAGACAGTT GCGGTGGGTG TCTGGGCTCA      780
ACATGCTA
```

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

TAGCATGTTG	AGCCCAGACA	CCTGTGTTTC	TGGGAGCTCT	GGCAGTGGCG	GATTCATAGG	60
CACTTGGGCT	GCACTTTGAA	TGACACACTT	GGCTTTATTA	GATTCACTAG	TTTTTAAAAA	120
ATTGTTGTTC	GTTTCTTTTC	ATTAAAGGTT	TAATCAGACA	GATCAGACAG	CATAATTTTG	180
TATTTAATGA	CAGAAACGTT	GGTACATTTT	TTCATGAATG	AGCTTGCAAT	CTGAAGCAAG	240
AGCCTACAAA	AGGCACTTGT	TATAAATGAA	AGTTCTGGCT	CTAGAGGCCA	GTACTCTGGA	300
GTTTCAGAGC	AGCCAGTGAT	TGTTCCAGTC	AGTGATGCCT	AGTTATATAG	AGGAGGAGTA	360
CACTGTGCAC	TCTTCTAGGT	GTAAGGGTAT	GCAACTTTGG	ATCTTAAAAAT	TCTGTACACA	420
TACACACTTT	ATATATATGT	ATGTATGTAT	GAAAACATGA	AATTAGTTTG	TCAAATATGT	480
GTGTGTTTAG	TATTTTAGCT	TAGTGCAACT	ATTTCCACAT	TATTTATTAA	ATTGATCTAA	540
GACACTTTCT	TGTTGACACC	TTGAATATTA	ATGTTCAAGG	GTGCAATGTG	TATTCCTTTA	600
GATTGTAAAA	GCTTAATTAC	TATGATTTGT	AGTAAATTAA	CTTTTAAAAAT	GTATTTGAGC	660
CCTTCTGTAG	TGTCGTAGGG	CTCTTACAGG	GTGGGAAAGA	TTTTAATTTT	CCAGTTGCTA	720
ATTGAACAGT	ATGGCCTCAT	TATATATTTT	GATTTATAGG	AGTTTGTGTC	TGGGCTCAAC	780
ATGCTA						786

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

TAGCATGTTG	AGCCCAGACA	CTGGTTACAA	GACCAGACCT	GCTTCCTCCA	TATGTAAACA	60
GCTTTTAAAA	AGCCAGTGAA	CCTTTTAAAT	ACTTTGGCAA	CCTTCTTTCA	CAGGCAAAGA	120
ACACCCCCAT	CCGCCCCTTG	TTTGGAGTGC	AGAGTTTGGC	TTTGGTTCTT	TGCCTTGCCT	180
GGAGTATACT	TCTAATTCCT	GTTGTCCTGC	ACAAGCTGAA	TACCGAGCTA	CCCACCGCCA	240
CCCAGGCCAG	GTTTCCACTC	ATTTATTACT	TTATGTTTCT	GTTCCATTGC	TGGTCCACAG	300
AAATAAGTTT	TCCTTTGGAG	GAATGTGATT	ATACCCCTTT	AATTCCTCC	TTTTGCTTTT	360
TTTTAATATC	ATTGGTATGT	GTTTGGCCCA	GAGGAAACTG	AAATTCACCA	TCATCTTGAC	420
TGGCAATCCC	ATTACCATGC	TTTTTTTAAA	AAACGTAATT	TTTCTTGCCT	TACATTGGCA	480
GAGTAGCCCT	TCCTGGCTAC	TGGCTTAATG	TAGTCACTCA	GTTTCTAGGT	GGCATTAGGC	540
ATGAGACCTG	AAGCACAGAC	TGTCTTACCA	CAAAAGGTGA	CAAGATCTCA	AACCTTAGCC	600
AAAGGGCTAT	GTCAAGTTTC	AATGCTATCT	GCTTCTGTTC	CTGCTCACTG	TTCTGGATTT	660
TGTCCTTCTT	CATCCCTAGC	ACCAGAATTT	CCCAGTCTCC	CTCCCTACCT	TCCCTTGTTT	720
TAATTCTAAT	CTATCAGCAA	AATAACTTTT	CAAATGTTTT	AACCGGTATC	TCCATGTGTC	780
TGGGCTCAAC	ATGCTA					796

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:


```

GGATGTGCTG CAAGGCGATT AAGTTGGGTA ACGCCAGGGT TTTCCCAGTC ACGACGTTGT      60
AAAACGACGG CCAGTGAATT GTAATACGAC TCACTATAGG GCGAATTGGG CCCGACGTCG      120
CATGCTCCCC GCGGCCATGG CCGCGGGATA GCATGTTGAG CCCAGACACC TGCAGGTCAT      180
TTGGAGAGAT TTTTCACGTT ACCAGCTTGA TGGTCTTTT CAGGAGGAGA GACACTGAGC      240
ACTCCCAAGG TGAGGTTGAA GATTTCTCT AGATAGCCGG ATAAGAAGAC TAGGAGGGAT      300
GCCTAGAAAA TGATTAGCAT GCAAATTTCT ACCTGCCATT TCAGAACTGT GTGTCAGCCC      360
ACATTCAGCT GCTTCTTGTT AACTGAAAAG AGAGAGGTAT TGAGACTTTT CTGATGGCCG      420
CTCTAACATT GTAACACAGT AATCTGTGTG TGTGTGGGTG TGTGTGTGTG TCTGGGCTCA      480
ACATGCTA                                     488

```

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

```

TAGCATGTTG AGCCCAGACA CGGCGACGGT ACCTGATGAG TGGGGTGATG GCACCTGTGA      60
AAAGGAGGAA CGTCATCCCC CATGATATTG GGGAGCCAGA TGATGAACCA TGGCTCCGCG      120
TCAATGCATA TTTAATCCAT GATACTGCTG ATTGGAAGGA CCTGAACCTG AAGTTTGTGC      180
TGCAGGTTTA TCGGGACTAT TACCTCACGG GTGATCAAAA CTTCTGAAG GACATGTGGC      240
CTGTGTGTCT AGTAAGGGAT GCACATGCAG TGGCCAGTGT GCCAGGGGTA TGGTTGGTGT      300
CTGGGCTCAA CATGCTA                                     317

```

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

```

TAGCATGTTG AGCCCAGACA CTGGCTGTTA GCCAAATCCT CTCTCAGCTG CTCCCTGTGG      60
TTTGGTGACT CAGGATTACA GAGGCATCCT GTTTCAGGGA AAAAAAGAT TTTAGCTGCC      120
AGCAGAGAGC ACCACATACA TTAGAATGGT AAGGACTGCC ACCTCCTTCA AGAACAGGAG      180
TGAGGGTGGT GGTGAATGGG AATGGAAGCC TGCATTCCCT GATGCATTTG TGCTCTCTCA      240
AATCCTGTCT TAGTCTTAGG AAAGGAAGTA AAGTTTCAAG GACGGTTCCG AACTGCTTTT      300
TGTGTCTGGG CTCAACATGC TATCCGCGCG CCATGGCGGC CGGAGCATG CGACGTCGGG      360
CCCAATTCGC CCTATAGTGA GTCGTATTAC AATTCCTGG CCGTCGTTTT ACAACGTCGT      420
GACTGGGAAA ACCCTGGCGT TACCCAACTT AATCGCCTTG CAGCACATCC CCCTTTCCCA      480
GCTGGCGTAA TANCAGAAAAG GCCCGCA                                     507

```

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GATTTACGCT GCAACACTGT GGAGGTAGCC CTGGAGCAAG GCAGGCATGG ATGCTTCTGC	60
AATCCCCAAA TGGAGCCTGG TATTTAGCC AGGAATCTGA GCAGAGCCCC CTCTAATTGT	120
AGCAATGATA AGTTATTCTC TTTGTTCTTC AACCTTCCAA TAGCCTTGAG CTTCCAGGGG	180
AGTGTGCTTA ATCATTACAG CCTGGTCTCC ACAGTGTTCG AGCGTAA	227

(2) INFORMATION FOR SEQ ID NO:184:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

TTACGCTGCA AACTGTGGA GCAGATTAAC ATCAGACTTT TCTATCAACA TGACTGGGGT	60
TACTAAAAAG ACAACAAATC AATGGCTTCA AAAGTCTAAG GAATAATTTC GATACTTCAA	120
CTTTATAAAA CCGACAAAA CTATCAATCA AGCATAAACA CAGATGAAGA ACATTTCCAG	180
ATTTTGCCCA ATCAGATATT TTACCTCCAC AGTGTTCGAG CGTAA	225

(2) INFORMATION FOR SEQ ID NO:185:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GGCCCGACGT CGCATGCTCC CGGCCGCCAT GGCCGCGGGA TTCGTTAGGG TCTCTATCCA	60
CTGGGACCCA TAGGCTAGTC AGAGTATTTA GAGTTGAGTT CCTTCTCCT TCCCAGAATT	120
TGAAAGAAAA GGAGTGAGGT GATAGAGCTG AGAGATCAGA TTGCGCTCTG AAGCCTGTTC	180
AAGATGTATG TGCTCAGACC CCACCACTGG GGCCTGTGGG TGAGGTCTTG GGCATCTATT	240
TGAATGAATT GCTGAAGGGG AGCACTATGC CAAGGAAGGG GAACCCATCC TGGCACTGGC	300
ACAGGGGTCA CTTATCCAG TGCTCAGTGC TTCTTTGCTG CTACCTGGTT TTCTCTCATA	360
TGTGAGGGGC ACGTAAGAAG AAGTGCCCRG TGTGTGCGA GTTTTAGAAC ATCTACCACT	420
AAGTGGGGAA GTTTCACAAA GCAGCAGCTT TGTTTGTGT ATTTTCACCT TCAGTTAGAA	480
GAGGAAGGCT GTGAGATGAA GTTAGTTGA GTGGAAAAGA CGGGTAAGCT TAGTGGATAG	540
AGACCCTAAC GAATCACTAG TGCGGCCGCC TTGCAGGTCG ACCATATGGG AGAGCTC	597

(2) INFORMATION FOR SEQ ID NO:186:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GGCCCGAAGT TGCATGTTCC CGGCCGCCAT GGCCGCGGGA TTCGTTAGGG TCTCTATCCA	60
CTACCTAAAA AATCCCAAAC ATATAACTGA ACTCCTCACA CCCAATTGGA CCAATCCATC	120
ACCCAGAGG CCTACAGATC CTCCTTTGAT ACATAAGAAA ATTTCCCCAA ACTACCTAAC	180
TATATCATTT TGCAAGATTT GTTTACCAA ATTTTGATGG CCTTCTGAG CTTGTCAGTG	240
TGAACCACTA TTACGAACGA TCGGATATTA ACTGCCCCCTC ACCGTCCAGG TGTAGCTGGC	300
AACATCAA GCAGTAAATA TTCATTAAGT TTTCACCTAC TAAGGTGCTT AAACACCCTA	360
GGGTGCCA TCGGTAGCAG ATCTTTTGAT TTGTTTTTAT TTCCCATAAG GGTCCGTGTC	420
AAGGTCAATC ATACATGTAG TGTGAGCAGC TAGTCACTAT CGCATGACTT GGAGGGTGAT	480
AATAGAGGCC TCCTTTGCTG TTAAAGAACT CTTGTCCCAG CCTGTCAAAG TGGATAGAGA	540
CCCTAACGAA TCACTAGTGC GGCCGCCTGC AGGTCGACCA TATGGGAGAG CTCCCAA	597

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

TCGTTAGGGT CTCTATCCAC TTGCAGGTAA AATCCAATCC TGTGTATATC TTATAGTCTT	60
CCATATGTAG TGGTTCAAGA GACTGCAGTT CCAGAAAGAC TAGCCGAGCC CATCCATGTC	120
TTCCACTTAA CCCTGCTTTG GGTACACAT CTTAACTTTT CTGTTCAAGT TTCTCTGTGT	180
AGTTTATAGC ATGAGTATTG GGAWAATGCC CTGAAACCTG ACATGAGATC TGGGAAACAC	240
AACTTACTC AATAAGAATT TCTCCCATAT TTTTATGATG GAAAAATTTC ACATGCACAG	300
AGGAGTGGAT AGAGACCCTA ACGA	324

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GCGCGGGGAT TCGGGGTGAT ACCTCCTCAT GCCAAAATAC AACGTNTAAT TTCACAACCTT	60
GCCTTCCAAT TTACGCATTT TCAATTTGCT CTCCCCATTT GTTGAGTCAC AACAAACACC	120
ATTGCCCAGA AACATGTATT ACCTAACATG CACATACTCT TAAAACTACT CATCCCTT	178

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TGACACCTTG TCCAGCATCT GACACAGTCT TGGCTCTTGG AAAATATTGG ATAAATGAAA	60
ATGAATTTCT TTAGCAAGTG GTATAAGCTG AGAATATACG TATCACATAT CCTCATTCTA	120
AGACACATTC AGTGTCCCTG AAATTAGAAT AGGACTTACA ATAAGTGTGT TCACTTTCTC	180
AATAGCTGTT ATTCAATTGA TGGTAGGCCT TAAAAGTCAA AGAAATGAGA GGGCATGTGA	240
AAAAAGCTC AACATCACTG ATCATTAGAA AACTTCCATT CAAACCCCA ATGAGATACC	300
ATCTCATACC AGTCAGAATG GCTATTATTA AAAAGTCAAA AAATAACAGA TGCTGGACAA	360
GGTGTC	369

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

GACACCTTGT CCAGCATCTG ACAACGCTAA CAGCCTGAGG AGATCTTTAT TTATTTATTT	60
AGTTTTTACT CTGGCTAGGC AGATGGTGGC TAAACATTC ATTTACCCAT TTATTCATTT	120
AATTGTTTCT GCAAGGCTA TGGATAGAGT ATTCTCCAGC ACTGCTCTGG AAGCTAGGAG	180
CATGGGGATG AACAAGATAG GCTACATCCT GTTCCACAG AACTTCCACT TTAGTCTGGG	240
AAACAGATGA TATATACAAA TATATAAATG AATTCAGGTA GTTTTAAGTA CGAAAAGAAT	300
AAGAAAGCAG AGTCATGATT TANAATGCTG GAAACAGGGG CTATTGCTTG AGATATTGAA	360
GGTGCCCAA	369

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

TGACACCTTG TCCAGCATCT GCACAGGGAA AAGAACTAT TATCAGAGTG AACAGGCAAC	60
CTACAGAATG GGAGAAAATT TTTGCAATCT ATCCATCTGA CAAAGGGCTA ATATCCAGAA	120
TCTACAAAGA ACTTATACAA ATTTACAAGA AACAAACAAA CAAACAACCTC CTCAAAAAGT	180
GGGTGAAGGA TGTAACAGA CACTTCTCAA AAGAAGACAT TTATGGGGCC AACAAACATA	240
TGAAAAAAG CTCATCATCA CTGGTCACTA GATAAATGCA AATCAAAACC ACAATGAGAT	300
ACCATCTCAT TCCAGTTAGA ATGGCAATCA TTAAAAAGTC AGGAAACAAC AGATGCTGGA	360
CAAGGTGTC	369

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid

100

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

TGACGCTTGG	CCACTTGACA	CTTCATCTTT	GCACAGAAAA	ACTTCTTTAC	AGATTTAATT	60
CAAGACTGGT	CTAGTGACAG	TCCTCCAGAC	ATTTTTTCAT	TTGTTCCATA	TACGTGGAAT	120
TTTAAATCA	TGTTTCATCA	GTTTGAAATG	ATTTGGGCTG	CTAATCAACA	CAATTGGATC	180
GACTGTTCTA	CTAAACAACA	GGAAAATGTG	TATCTGGCAG	CCTGTGGAGA	AACACTAAAC	240
ATTGATTTTT	CTTGCCTTT	TACGGACTTT	GTTCCAGCTA	CATGTAATAC	CAAGTTCTCT	300
TTAAGAGGAG	AAGATGTTGA	TCTTCATTTG	TTTCTACCAG	ACTGCCACCC	TAGTAAATAT	360
TCTTTATTTA	TGCTGGTAAA	AAATGCCAT	CCAAATAAGA	TGATTCATGA	TACTGGTATT	420
CCTGCTGAGT	GTCAAGTGGC	CAAGCGTCA				449

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

TGACGCTTGG	CCACTTGACA	CCAGGGATGT	AKCAGTTGAA	TATAATCCTG	CAATTGTACA	60
TATTGGCAAT	TTCCCATCAA	ACATTCTAGA	AAGAGACAAC	CAGGATTGCT	AGGCCATAAA	120
AGCTGCAATA	AATAACTGGT	AATTGCAGTA	ATCATTTTCAG	GCCAATTCAA	TCCAGTTTGG	180
CTCAGAGGTG	CCTTTGGCTG	AGAGAAGAGG	TGAGATATAA	TGTGTTTCT	TGCAACTTCT	240
TGGAAGAATA	ACTCCACAAT	AGTCTGAGGA	CTAGATACAA	ACCTATTTGC	CATTAAAGCA	300
CCAGAGTCTG	TTAATTCCAG	TACTGATAAG	TGTTGGAJAT	TAGACTCCAG	TGTGTCAAGT	360
GGCCAAGCGT	CA					372

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

TGACGCTTGG	CCACTTGACA	CTTATGTAGA	ATCCATCGTG	GGCTGATGCA	AGCCCTTTAT	60
TTAGGCTTAG	TGTTGTGGGC	ACCTTCAATA	TCACACTAGA	GACAAACGCC	ACAAGATCTG	120
CAGAAACATT	CAGTTCTGAN	CACTCGAATG	GCAGGATAAC	TTTTTGTGTT	GTAATCCTTC	180
ACATATACAA	AAACAACTC	TGCANTCTCA	CGTTACAAAA	AAACGTACTG	CTGTAAAATA	240
TTAAGAAGGG	GTAAGGATA	CCATCTATAA	CAAAGTAACT	TACAACTAGT	GTCAAGTGGC	300
CAAGCGTCA						309

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

101

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

TGACGCTTGG CCACTTGACA CCAATCTCG CACTTCATCC TCCCAGCACC TGATGAAGTA	60
GGACTGCAAC TATCCCCACT TCCCAGATGA GGGGACCAAN GTACACATTA GGACCCGGAT	120
GGGAGCACAG ATTTGTCCGA TCCCAGACTC CAAGCACTCA GCGTCACTCC AGGACAGCGG	180
CTTTCAGATA AGGTCACAAA CATGAATGGC TCCGACAACC GGAGTCAGTC CGTGCTGACT	240
TAAGGCAATG GTGACACGGA TGCACGTGTN ACCTGTAATG GTTCATCGTA AGTGTC AAGT	300
GGCCAAGCGT CA	312

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

TGTATCGACG TAGTGCTCTC CTCAGCCATG CAGAACTGTG ACTCAATTAA ACCTCTTTCC	60
TTTATGAATT ACCCAATCTC GGGTAGTGTC TTTATAGTAG TGTGAGAATG GACTAATACA	120
AGTACATTTT ACTTAGTAAT AATAATAAAC AAATATATTA CATTTTTGTG TATTACTAC	180
ACCATATTTT TTATTGTTAT TGTAGTGTA ACCTTCTACT TATTAAAAGA AATAGGCCCCG	240
AGGCGGGCAG ATCACCAGGT CAGGAGATGG AGACCACTAC GTCGATAC	288

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTGGGCACCT TCAATATCAT GACAGGTGAT GTGATAACCA AGAAGGCTAC TAAGTGATTA	60
ATGGGTGGGT AATGTATACA GACTAGGTAC ACTGGACAGA GGGGTAATTC ATAGCCAAGG	120
CAGGAGAAGC AGAATGGCAA AACATTTTCAT CACACTACTC AGGATAGCAT GCAGTTTAAA	180
ACCATATAAGT AGTTTATTTT TGGAATTTTC CACTTAATAT TTTCAGACTG CAGGTAAC TA	240
AACTGTGGAA CACAAGAACA TAGATAAGGG GAGACCACTA CGTCGATAC	289

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GTATCGACCT AGTGGTCTCC CAAGCAGTGG GAAGAAAACG TGAACCAATT AAAATGTATC	60
AGATACCCCA AAGAAAGGCG CTTGAGTAAA GATTCCAAGT GGGTCACAAT CTCAGATCTT	120
AAAATTCAGG CTGTCAAAGA GATTTGCTAT GAGGTTGCTC TCAATGACTT CAGGCACAGT	180
CGGCAGGAGA TTGAAGCCCT GGCCATTGTC AAGATGAAGG AGCTTTGTGC CATGTATGGC	240
AAGAAAGACC CCAATGAGCG GGACTCCTGJ AGACCACTAC GTCGATAC	288

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GCTTTTGGG AAAACNCAA NTGGGGGAAA GGGGNTTNN TNGCAAGGGG ATAAAGGGGG	60
AANCCAGGG TTTCCCATTT CAGGGAGGTG TAAAAAGNCG GCCAGGGGAT TGTAANAGGA	120
TTCAATAATA GGGGAATGG GCCNGAAGT TGCAAGGTC CNCCCCGCA TGNCCGCGGG	180
ATTTAGTGAC ATTACGACGS TGGTAATAAA GTGGGSCCAA WAAATATTG TGATGTGATT	240
TTTSGACCAG TGAACCCATT GWACAGGACC TCATTTCCTY TGAGATGRTA GCCATAATCA	300
GATAAAAGRT TAGAAGTYTT TCTGCACGTT AACAGCATCA TTAAATGGAG TGGCATCACC	360
AATTTACCC TTTGTTAGCC GATACCTTCC CCTTGAAGGC ATTCAATTAA GTGACCAATC	420
GTCATACGAG AGGGGATGGC ATGGGGATTG ATGATGATAT CAGGGGTGAT ACCTTCACAG	480
GTGAAAGGCA TATCCTCTTG TCTATACTGA ATACCACAAG TACCCTTTT ACCATGTCGA	540
CTAGCAAATT TGTCTCCAAT CTGTGTWATC CCTAACAGAG CGTACCCFTA TTTTACAAAA	600
TTTATATCCT TCCTGATTGA GAGTTACCAT AACCTGATCC ACAATGCCC TCTCGCTWGT	660
TCTGAGAAAA GTGCTACAGT CTCTCTTGGT ATAGCGTCTA TTGGTGCTCT CCAATTCATC	720
TTCAATTTTC AGGCAAGGTG AACTGTTTTG CCTATAATAA CMTCATCTCC TGATACMCGA	780
AACCCCKGGA RCTATCAAAC CATCATCATC CAGCGTTCKT WATGYMCTA AATCCCTATT	840
GCGGCCGCCT GCAGGTCAAC ATATNGGAAA ACCCCCCACC CCTTNGGAGC NTACCTTGAA	900
TTTTCCATAT GTCCCNATAA TTANCTNGNC TTANCCTGGC CNTAACCTNT TCCGGTTTAA	960
ATTGTTTCCG CCCCNTTCC CCNCCTTNA ACCGGAAACC TTAATTTTNA ACCNGGGGTT	1020
CCTATCC	1027

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

AGTGACATTA CGACGCTGGC CATCTTGAAT CCTAGGGCAT GAAGTTGCC CAAAGTTCAG	60
CACTTGGTTA AGCCTGATCC CTCTGGTTTA TCACAAAGAA TAGGATGGGA TAAAGAAAGT	120
GGACACTTAA ATAAGCTATA AATTATATGG TCCTTGTCTA GCAGGAGACA ACTGCACAGG	180

TATACTACCA GCGTCGTAAT GTCACTA

207

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TGGGCACCTT CAATATCTAT TAAAAGCACA AATACTGAAG AACACACCAA GACTATCAAT	60
GAGGTTACAT CTGGAGTCCT CGATATATCA GGAAAAAATG AAGTGAACAT TCACAGAGTT	120
TTACTTCTTT GGGAAGTCAA ATGCTAGAAA AGAAAAGCGT GCCCTCTTTC TCTGGCTTCC	180
TGGTCCTATC CAGCGTCGTA ATGTCACTA	209

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

NTACGCTGCA AACTGTGGA GCCACTGGTT TTTATTCCCG GCAGGTTATC CAGCAAACAG	60
TCACTGAACA CACCGAAGAC CGTGGTATGG TAACCGTTCA CAGTAATCGT TCCAGTCGTC	120
TGCGGGACCC CGACGAGCGT CACTGGGTAC AGACCAGATT CAGCCGGAAG AGAAAGCGCC	180
GCAGGGAGAG ACTCGAACTC CACTCCGCTG GTGAGCAGCC CCATGTTTTT AACTCGAAGT	240
TCAAACGGCA TTGGGTATATA TACCATCAGC TGAACCTCAC ACACATCTCC TTGAACCCAC	300
TGGAAATCTA TTTTCTTGTT CCGCTCTTCT CCACAGTGTT GCAGCGTAA	349

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TGCTCCTCTT GCCTTACCAA CCCAAAGCCC ACTGTGAAAT ATGAAGTGAA TGACAAAATT	60
CAGTTTTTCAA CGCAATATAG TATAGTTTAT CTGATTCTTT TGATCTCCAG GACACTTTAA	120
ACAACTGCTA CCACCACCAC CAACCTAGGG ATTTAGGATT CTCCACAGAC CAGAAATTAT	180
TTCTCCTTTG AGTTTCAGGC TCCTCTGGGA CTCCTGTTCA TCAATGGGTG GTAAATGGCT	240
A	241

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TAGCCATTTA CCACCCATCT GCAAACCSWG ACMWWCARGR CYWGWACKYA GGCGATTTGA	60
AGTACTGGTA ATGCTCTGAT CATGTTAGTT ACATAAGTGT GGTCAGTTTA CAAAAATTCA	120
CAGAACTAAA TACTCAATGC TATGTGTTCA TGTCTGTGTT TATGTGTGTG TAATGTTTCA	180
ATTAAGTTTT TTTAAAAAAA AGAGATGATT TCCAAATAAG AAAGCCGTGT TGGTAAGGCA	240
AGAGGAGC	248

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TACGCTGCAA CACTGTGGAG CCATTCATAC AGGTCCCTAA TTAAGGAACA AGTGATTATG	60
CTACCTTTGC ACGGTTAGGG TACCGCGGCC GTTAAACATG TGTCACTGGG CAGGCGGTGC	120
CTCTAATACT GGTGATGCTA GAGGTGATGT TTTTGGTAAA CAGGCGGGGT AAGATTTGCC	180
GAGTTCCTTT TACTTTTTTT AACCTTTCCT TATGAGCATG CCTGTGTTGG GTTGACAGTG	240
GGGGTAATAA TGACTTGTTG GTTGATTGTA GATATTGGGC TGTTAATTGT CAGTTCAGTG	300
TTTTAATCTG ACGCAGGCTT ATGCGGAGGA GAATGTTTTT ATGTTACTTA TACTAACATT	360
AGTTCTTCTA TAGGGTGATA GATTGGTCCA ATTGGGTGTG AGGAGTTCAG TTATATGTTT	420
GGGATTTTTT AGGTAGTGGG TGTTGANCTT GAACGCTTTC TTAATTGGTG GCTGCTTTTA	480
RGCCTACTAT GGGTGGTAAA TGGCT	505

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TAGACTGACT CATGTCCCCT ACCAAAGCCC ATGTAAGGAG CTGAGTTCTT AAAGACTGAA	60
GACAGACTAT TCTCTGGAGA AAAATAAAAT GGAAATTGTA CTTTAAAAAA AAAAAAATC	120
GGCCGGGCAT GGTAGCACAC ACCTGTAATC CCAGCTACTA GGGGACATGA GTCAGTCTA	179

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs

105

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

```
AGACTGACTC ATGTCCCCTA CCCACCTTC TGCTGTGCTG CCGTGTTTCCT AACAGGTCAC      60
AGACTGGTAC TGGTCAGTGG CCTGGGGGTT GGGGACCTCT ATTATATGGG ATACAAATTT      120
AGGAGTTGGA ATTGACACGA TTTAGTGAAT GATGGGATAT GGGTGGTAA TGGCTA          176
```

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

```
AGACTGACTC ATGTCCCCTA TTTAACAGGG TCTCTAGTGC TGTGAAAAAA AAAAATGCTG      60
AACATTGCAT ATAACCTATA TTGTAAGAAA TACTGTACAA TGACTTTATT GCATCTGGGT      120
AGCTGTAAGG CATGAAGGAT GCCAAGAAGT TTAAGGAATA TGGGTGGTAA ATGGCTAGGG      180
GACATGAGTC AGTCTA                                196
```

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

```
GACGCTTGGC CACTTGACAC CTTTTATTTT TTAAGGATTC TTAAGTCATT TANGTNACTT      60
TGTAAGTTTT TCCTGTGCCC CCATAAGAAT GATAGCTTTA AAAATTATGC TGGGGTAGCA      120
AAGAAGATAC TTCTAGCTTT AGAATGTGTA GGTATAGCCA GGATTCTTGT GAGGAGGGGT      180
GATTTAGAGC AAATTTCTTA TTCTCCTTGC CTCATCTGTA ACATGGGGAT AATAATAGAA      240
CTGGCTTGAC AAGGTTGGAA TTAGTATTAC ATGGTAAATA CATGTAAAAT GTTTAGAATG      300
GTGCCAAGTA TCTAGGAAGT ACTTGGGCAT GGGTGGTAAA TGGCT                          345
```

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 178 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GACGCTTGCC	CACTTGACAC	TAGAGTAGGG	TTTGGCCAAC	TTTTTCTATA	AAGGACCAGA	60
GAGTAAATAT	TTCAGGCTTT	GTGGGTTGTG	CAGTCTCTCT	TGCAACTACT	CAGCTCTGCC	120
ATTGTAGCAT	AGAAATCAGC	CATAGACAGG	ACAGAAATGA	ATGGGTGGTA	AATGGCTA	178

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

TGGGCACCTT	CAATATCTAT	CCAGCGCATC	TAAATTCGCT	TTTTTCTTGA	TTAAAAATTT	60
CACCACTTGC	TGTTTTTGCT	CATGTATACC	AAGTAGCAGT	GGTGTGAGGC	CATGCTTGTT	120
TTTTGATTCG	ATATCAGCAC	CGTATAAGAG	CAGTGCTTTG	GCCATTAATT	TATCTTCATT	180
GTAGACAGCA	TAGTGTAGAG	TGGTATCTCC	ATACTCATCT	GGAATATTTG	GATCAGTGCC	240
ATGTTCCAGC	AACATTAACG	CACATTCATC	TTCCTGGCAT	TGTACGGCCT	TTGTCAGAGC	300
TGTCCTCTTT	TTGTTGTCAA	GGACATTAAG	TTGACATCGT	CTGTCCAGCA	CGAGTTTTAC	360
TACTTCTGAA	TTCCCATTTG	CAGAGGCCAG	ATGTAGAGCA	GTCTCTTTTT	GCTTGTCCCT	420
CTTGTTTACA	TCAGTGTCCC	TGAGCATAAC	GGAA			454

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

TCCGTTATGC	CACCCAGAAA	ACCTACTGGA	GTTACTTATT	AACATCAAGG	CTGGAACCTA	60
TTTGCCCTCAG	TCCTATCTGA	TTCATGAGCA	CATGGTTATT	ACTGATCGCA	TTGAAAACAT	120
TGATCACCTG	GGTTTCTTTA	TTTATCGACT	GTGTCA TGAC	AAGGAACTT	ACAAACTGCA	180
ACGCAGAGAA	ACTATTAAAG	GTATTCAGAA	ACGTGAAGCC	AGCAATTGTT	TCGCAATTCTG	240
GCATTTTGAA	AACAAATTTG	CCGTGGAAAC	TTTAATTTGT	TCTTGAACAG	TCAAGAAAAA	300
CATTATTGAG	GAAAATTAAT	ATCACAGCAT	AACGGAA			337

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

TCGGGTGATG	CCTCCTCAGG	CATCTTCCAT	CCATCTCTTC	AAGATTAGCT	GTCCCAAATG	60
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TTTTTCCTTC TCTTCTTTAC TGATAAATTT GGA CTCCTTC TTGACACTGA TGACAGCTTT 120
AGTATCCTTC TTGTCACCTT GCAGACTTTA AACATAAAAA TACTCATTGG TTTTAAAAGG 180
AAAAAAGTAT ACATTAGCAC TATTAAGCTT GGCCTTGAAA CATTTTCTAT CTTTATTAA 240
ATGTCGGTTA GCTGAACAGA ATTCATTTTA CAATGCAGAG TGAGAAAAGA AGGGAGCTAT 300
ATGCATTTGA GAATGCAAGC ATTGTCAAAT AACATTTTA AATGCTTCT TAAAGTGAGC 360
ACATACAGAA ATACATTAAG ATATTAGAAA GTGTTTTTGC TTGTGTACTA CTAATTAGGG 420
AAGCACCTTG TATAGTTCCT CTTCTAAAT TGAAGTAGAT TTTAAAACC CATGTAATTT 480
AATTGAGCTC TCAGTTCAGA TTTTAGGAGA ATTTTAACAG GGATTGGTT TTGTCTAAAT 540
TTTGTCAATT TNNTTACTTA ATCTGTATAA TTTTATAAAT GTCAAACGT ATTTAGTCCG 600
TTTTCATGCT GCTATGAAAG AAATACCCAN GACAGGGTTA TTTATAAANG GAAAGANGTT 660
AATTTGACTC CCAGTTCACA GGCCTGAGGA NGNATCNCCC GAAATCCTTA TTGCG 715

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(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```

GGTAANGNGC ATACNTCGGT GCTCCGGCCG CCGGAGTCGG GGGATTCGGG TGATGCCTCC 60
TCAGGCCAC TTGGGCCCTGC TTTTCCCAA TGGCAGCTCC TCTGGACATC CCATTCCTTC 120
TCCCACCTGC CTGATTCCTC ATATGTTGGG TGTCCTTGTT TTTCTGGTGC TATTCCTGA 180
CTGCTGTTCA GCTGCCACTG TCCTGCAAAG CCTGCCTTTT TAAATGCCTC ACCATTCCTT 240
CATTTGTTTC TTAAATATGG GAAGTGAAAG TGCCACCTGA GGCCGGGCAC AGTGGCTCAC 300
GCCTGTAATC CCAGCACTTT GGGAGCCTGA GGAGGCATCA CCCGA 345

```

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```

GGTGATGCCT CCTCAGGCGA AGCTCAGGGA GGACAGAAAC CTCCCGTGGA GCAGAAGGGC 60
AAAAGCTCGC TTGATCTTGA TTTTCAGTAC GAATACAGAC CGTGAAAGCG GGGCCTCACG 120
ATCCTTCTGA CTTTTTGGGT TTTAAGCAGG AGGTGTCAGA AAAGTTACCA CAGGGATAAC 180
TGGCTTGTGG CGGCCAAGCG TTCATAGCGA CGTCGCTTTT TGATCCTTCG ATGTCGGCTC 240
TTCCTATCAT TGTGAAGCAG AATTCACCAA GCGTTGGATT GTTCACCCAC TAATAGGGAA 300
CGTGAGCTGG GTTTAGACCG TCGTGAGACA GGTTAGTTTT ACCCTACTGA TGATGTGTTG 360
TTGCCATGGT AATCCTGCTC AGTACGAGAG GAACCGCAGG TTCAJACATT TGGTGTATGT 420
GCTTGCCTT 429

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(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TGACACCTAT	GTCGNGCATC	TGTTACAGT	TTCCACAAAT	AGCCAGCCTT	TGGCCACCTC	60
TCTGTCTGA	GGTATACAAG	TATATCAGGA	GGTGTATACC	TTCTCTTCTC	TTCCCCACCA	120
AAGAGAACAT	GCAGGCTCTG	GAAGCTGTCT	TAGGAGCCTT	TGGGCTCAGA	ATTTCAGAGT	180
CTTGGGTACC	TTGGATGTGG	TCTGGAAGGA	GAAACATTGG	CTCTGGATAA	GGAGTACAGC	240
CGGAGGAGGG	TCACAGAGCC	CTCAGCTCAA	GCCCCGTGTC	CTTAGTCTAA	AAGCAGCTTT	300
GGATGAGGAA	GCAGGTAAAG	TAACATACGT	AAGCGTACAC	AGGTAGAAAG	TGCTGGGAGT	360
CAGAATTGCA	CAGTGTGTAG	GAGTAGTACC	TCAATCAATG	AGGGCAAATC	AACTGAAAGA	420
AGAAGACCNA	TTAATGAATT	GCTTANGGGG	AAGGATCAAG	GCTATCATGG	AGATCTTTCT	480
AGGAAGATTA	TTGTTTANAA	TTATGAAAGG	ANTAGGGCAG	GGACAGGGCC	AGAAGTANAA	540
GANAAACATTG	CCTATANCCC	TTGTCTTGCA	CCCAGATGCT	GGACAAGGTG	TCA	593

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 335 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

TGACACCTTG	TCCAGCATCT	GACGTGAAGA	TGAGCAGCTC	AGAGGAGGTG	TCCTGGATTT	60
CCTGGTTCTG	TGGGCTCCGT	GGCAATGAAT	TCTTCTGTGA	AGTGGATGAA	GACTACATCC	120
AGGACAAATT	TAATCTTACT	GGACTCAATG	AGCAGGTCCC	TCACTATCGA	CAAGCTCTAG	180
ACATGATCTT	GGACCTGGAG	CCTGATGAAG	AACTGGAAGA	CAACCCCAAC	CAGAGTGACC	240
TGATTGAGCA	GGCAGCCGAG	ATGCTTTATG	GATTGATCCA	CGCCCGCTAC	ATCCTTACCA	300
ACCGTGGCAT	CGCCCAGATG	CTGGACAAGG	TGTCA			335

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

TACGTACTGG	TCTTGAAGGT	CTTAGGTAGA	GAAAAAATGT	GAATATTTAA	TCAAAGACTA	60
TGTATGAAAT	GGGACTGTAA	GTACAGAGGG	AAGGGTGGCC	CTTATCGCCA	GAAGTTGGTA	120
GATGCGTCCC	CGTCATGAAA	TGTTGTGTCA	CTGCCCGACA	TTTGCCGAAT	TACTGAAATT	180
CCGTAGAATT	AGTGCAAATT	CTAACGTTGT	TCATCTAAGA	TTATGGTTCC	ATGTTTCTAG	240
TACTTTTA						248

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TGACGCTTGG CCACTTGACA CAAGTAGGGG ATAAGGACAA AGACCCATNA GGTGGCCTGT	60
CAGCCTTTTG TTACTGTTGC TTCCCTGTCA CCACGGCCCC CTCTGTAGGG GTGTGCTGTG	120
CTCTGTGGAC ATTGGTGCA TTTACACAT ACCATTCTCT TTCTGCTTCA CAGCAGTCCT	180
GAGGCGGGAG CACACAGGAC TACCTTGTC GATGANGATA ATGATGTCTG GCCAACTCAC	240
CCCCAACCT TCTACTAGT TATANGAAGA GCCANGCCTA NAACCTTCTA TCCTGNCCCC	300
TTGCCCTATG ACCTCATCCC TGTTCATGC CCTATTCTGA TTTCTGGTGA ACTTTGGAGC	360
AGCCTGGTTT NTCCTCCTCA CTCCAGCCTC TCTCCATACC ATGGTANGGG GGTGCTGTTC	420
CACNCAAANG GTCAGGTGTG TCTGGGGAAT CCTNANANCT GCCNGGAGTT TCCNANGCAT	480
TCTTAAAAAC CTTCTTGCTT AATCANATNG TGTCCAGTGG CCAACCNTCN	530

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

TGACGCTTGG CCACTTGACA CTAAATAGCA TCTTCTAAAG GCCTGATTCA GAGTTGTGGA	60
AAATTCTCCC AGTGTCAGGG ATTGTCAGGA ACAGGGCTGC TCCTGTGCTC ACTTTACCTG	120
CTGTGTTTCT GCTGGAAAAG GAGGGAAGAG GAATGGCTGA TTTTACCTA ATGTCTCCCA	180
GTTTTTCATA TTCTTCTTGG ATCCTCTTCT CTGACAAC TGAGAAAGGA GAATGAGCAA ATGATTAAAG	240
TCTTGCTCAG AGAGCAGGTC TCTTTAAAAAC TGAGAAGGGA GAATGAGCAA ATGATTAAAG	300
AAAACACACT TCTGAGGCCC AGAGATCAAA TATTAGGTAA AACTAAACC GCTTGCCTGC	360
TGTGGTCACT TTTCTCTCT TTCACATGCT CTATCCCTCT ATCCCCACC TATTCATATG	420
GCTTTTATCT GCCAAGTTAT CCGGCCTCTC ATCAACCTTC TCCCCTAGCC TACTGGGGGA	480
TATCCATCTG GGTCTGTCTC TGGTGTATTG GTGTCAAGTG GCCAAGCGTC A	531

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

ATTGACGCTT GGCCACTTGA CACCCGCCTG CCTGCAATAC TGGGGCAAGG GCCTTCACTG	60
CTTTCCTGCC ACCAGCTGCC ACTGCACACA GAGATCAGAA ATGCTACCAA CCAAGACTGT	120
TGGTCCTCAG CCTCTCTGAG GAGAAAGAGC AGAAGCCTGG AAGTCAGAAG AGAAGCTAGA	180
TCGGCTACGG CCTTGGCAGC CAGCTTCCCC ACCTGTGGCA ATAAAGTCGT GCATGGCTTA	240
ACAATGGGGG CACCTCTGTA GAAACACATT GTTAGGCAAT TCGGCGTGTG TTCATCAGAG	300

CATATTTACA	CAAACCTCGA	TAGTGCAGCC	TACTATCCAC	TATTGCTCCT	ACGCTGCAAA	360
CCTGAACAGC	ATGGGACTGT	ACTGAATACT	GGAAGCAGCT	GGTGATGGTA	CTTATTTGTG	420
TATCTAAACA	CAGAGAAGGT	ACACTAAGAA	TATGGTATCA	TAAACTTACA	GGGACCGCCA	480
TCCTATATGC	AGTCTGTTGT	GACCAAAATG	TGTCAAGTGG	CCAAGCGTCA		530

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

TGTATCGACG	TAGTGGTCTC	CGGGCTACTA	GGCCGTGTG	TCCTGGTAGT	ACCTGGTTCA	60
CTGAAAGGCG	CATCTCCCTC	CCCGCGTCGC	CCTGAAGCAG	GGGGAGGACT	TCGCCCAGCC	120
AAGGCAGTTG	TATGAGTTT	AGCTGCGGCA	CTTCGAGACC	TCTGAGCCCA	CCTCCTTCAG	180
GAGCCTTCCC	CGATTAAAGG	AGCCAGGGTA	AGGATTCCCT	CCTCCCCCAG	ACACCACGAA	240
CAAACCACCA	CCCCCCTAT	TCTGGCAGCC	CATATACATC	AGAACGAAAC	AAAAATAACA	300
AATAAACNAA	AACCAAAAAA	AAAAGAGAAG	GGGAAATGTA	TATGCTGTGC	CATCCTGTTG	360
CTTTAGCCTG	TCAGCTCCTA	NAGGGCAGGG	ACCGTGTCTT	CCGAATGGTC	TGTGCAGCGC	420
CGACTGCGGG	AAGTATCGGA	GGAGGAAGCA	GAGTCAGCAG	AAGTTGAACG	GTGGGCCCCG	480
CGGCTCTTGG	GGGCTGGTGT	TGTACTTCGA	GACCCGCTTC	GCTTTTGTGC	TTAGATTTAC	540
GTTTGCTCTT	TGGAGTGGGA	NACCACTACN	TCNATACA			578

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

TGTATCGACG	TAGTGGTCTC	CTCTTGCAAA	GGACTGGCTG	GTGAATGGTT	TCCCTGAATT	60
ATGGACTTAC	CCTAAACATA	TCTTATCATC	ATTACCAGTT	GCAAAATATT	AGAATGTGTT	120
GTCAGTGT	CATTTGATTC	CTAGAAGGTT	AGTCTTAGAT	ATGTTACTTT	AACCTGTATG	180
CTGTAGTGCT	TTGAATGCAT	TTTTTGTTTG	CATTTTGTG	TGCCCAACCT	GTCAATTATA	240
GCTGCTTAGG	TCTGGACTGT	CCTGGATAAA	GCTGTAAAAA	TATTCACCAG	TCCAGCCATC	300
TTACAAGCTA	ATTAAGTCAA	CTAAATGCTT	CCTTGTTTTG	CCAGACTTGT	TATGTCAATC	360
CTCAATTTCT	GGGTTCAATT	TGGGTGCCCT	AAATCTTAGG	GTGTGACTTT	CTTAGCATCC	420
TGTAACATCC	ATTCCCAAGC	AAGCACAAC	TCACATAATA	CTTCCAGAA	GTTTATTGCT	480
GAAGCCTTTC	CTTCACCCAG	CGGAGCAACT	TGATTTTCTA	CAACTTCCCT	CATCAGAGCC	540
ACAAGAGTAT	GGGATATGGA	GACCACTACG	TCGATACA			578

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

TGTATCGACG TANTGGTCTC CCAAGGTGCT GGGATTGCAG GCATGAGCCA CCACTCCCAG	60
GTGGATCTTT TTCTTTATAC TTACTTCATT ACGTTTCTGT TATTCAAGAA GTGTAGTGGT	120
AAAAGTCTTT TCAATCTACA TGGTTAAATA ATGATAGCCT GGGAAATAAA TAGAAATTTT	180
TTCTTTTCATC TTTAGGTTGA ATAAAGAAAC AGAAAAAATA GAACATACTG AAAATAATCT	240
AAGTTCCAAC CATAGAAGAA CTGCAGAAGA AATGAAGAAA GTGATGATGA TTTAGATTTT	300
GATATTGATT TAGAAGACAC AGGAGGAGAC CACTACGTCG ATACA	345

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

TGTATCGACG TAGTGGTCTC CAAACTGAGG TATGTGTGCC ACTAGCACAC AAAGCCTTCC	60
AACAGGGACG CAGGCACAGG CAGTTTAAAG GGAATCTGTT TCTAAATTAA TTTCCACCTT	120
CTCTAAGTAT TCTTTCCTAA AACTGATCAA GGTGTGAAGC CTGTGCTCTT TCCCAACTCC	180
CCTTTGACAA CAGCCTTCAA CTAACACAAG AAAAGGCATG TCTGACACTC TTCCTGAGTC	240
TGACTCTGAT ACGTTGTTCT GATGTCTAAA GAGCTCCAGA ACACCAAAGG GACAATTCAG	300
AATGCTGGTG TATAACAGAC TCCAATGGAG ACCACTACGT CGATACA	347

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

AGGNGNGGGA NTGTATCGAC GTAGTGGTCT CCCAACAGTC TGTCATTTCAG TCTGCAGGTG	60
TCAGTGTTTT GGACAATGAG GCACCATTTGT CACTTATTGA CTCCTCAGCT CTAAATGCTG	120
AAATTAATATC TTGTCATGAC AAGTCTGGAA TTCCTGATGA GGTTTTACAA AGTATTTTGG	180
ATCAATACTC CAACAAATCA GAAAGCCAGA AAGAGGATCC TTTCAATATT GCAGAACCAC	240
GAGTGGATTT ACACACCTCA GGAGACCACT ACGTCGATAC A	281

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3646 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

GGGAAACACT TCCTCCCAGC CTTGTAAGGG TTGGAGCCCT CTCCAGTATA TGCTGCAGAA	60
TTTTTCTCTC GGTTCCTCAG AGGATTATGG AGTCCGCCTT AAAAAGGCA AGCTCTGGAC	120
ACTCTGCAAA GTAGAATGGC CAAAGTTTGG AGTTGAGTGG CCCCTTGAAG GGTCAC TGAA	180

CCTCACAAATT	GTTCAAGCTG	TGTGGCGGGT	TGTTACTGAA	ACTCCCGGCC	TCCCTGATCA	240
GTTTCCCTAC	ATTGATCAAT	GGCTGAGTTT	GGTCAGGAGC	ACCCCTTCCG	TGGCTCCACT	300
CATGCACCAT	TCATAATTTT	ACCTCCAAGG	TCCTCCTGAG	CCAGACCGTG	TTTTTCGCCTC	360
GACCCTCAGC	CGGTTTCGGCT	CGCCCTGTAC	TGCCTCTCTC	TGAAGAAGAG	GAGAGTCTCC	420
CTCACCCAGT	CCCACCGCCT	TAAAACCAGC	CTACTCCCTT	AGGGTCATCC	CATGTCTCCT	480
CGGCTATGTC	CCCTGTAGGC	TCATCACCCA	TTGCCTCTTG	GTTGCAACCG	TGGTGGGAGG	540
AAGTAGCCCC	TCTACTACCA	CTGAGAGAGG	CACAAGTCCC	TCTGGGTGAT	GAGTGCTCCA	600
CCCCCTTCCCT	GGTTTATGTC	CCTTCTTTCT	ACTTCTGACT	TGTATAATTG	GAAAACCCAT	660
AATCCTCCCT	TCTCTGAAAA	GCCCCAGGCT	TTGACCTCAC	TGATGGAGTC	TGTACTCTGG	720
ACACATTGGC	CCACCTGGGA	TGACTGTCAA	CAGCTCCTTT	TGACCCTTTT	CACCTCTGAA	780
GAGAGGGAAA	GTATCCAAAG	AGAGGCCAAA	AAGTACAACC	TCACATCAAC	CAATAGGCCG	840
GAGGAGGAAG	CTAGAGGAAT	AGTGATTAGA	GACCCAATTG	GGACCTAATT	GGGACCCAAA	900
TTTCTCAAGT	GGAGGGAGAA	CTTTTGACGA	TTTCCACCGG	TATCTCCTCG	TGGGTATTCA	960
GGGAGCTGCT	CAGAAACCTA	TAAACTTGTC	TAAGGCGACT	GAAGTCGTCC	AGGGGCATGA	1020
TGAGTCACCA	GGAGTGTTTT	TAGAGCACCT	CCAGGAGGCT	TATCAGATTT	ACACCCCTTT	1080
TGACCTGGCA	GGCCCCGAAA	ATAGCCATGC	TCTTAATTTG	GCATTTGTGG	CTCAGGCAGC	1140
CCCAGATAGT	AAAGGAAAC	TCCAAAAACT	AGAGGGATT	TGCTGGAATG	AATACCAGTC	1200
AGCTTTTAGA	GATAGCCTAA	AAGGTTTTTG	ACAGTCAAGA	GGTTGAAAAA	CAAAAAACAAG	1260
CAGCTCAGGC	AGCTGAAAAA	AGCCACTGAT	AAAGCATCCT	GGAGTATCAG	AGTTTACTGT	1320
TAGATCAGCC	TCATTTGACT	TCCCTCCCA	CATGGTGTTT	AAATCCAGCT	ACAC'ACTTC	1380
CTGACTCAAA	CTCCACTATT	CCTGTTTCATG	ACTGTCAGGA	ACTGTTGGAA	ACTACTGAAA	1440
CTGGCCGACC	TGATCTTCAA	AATGTGCCCC	TAGGAAAGGT	GGATGCCACC	ATGTTACACAG	1500
ACAGTAGCAG	CTTCCTCGAG	AAGGGACTAC	GAAAGGCCGG	TGCAGCTGTT	ACCATGGAGA	1560
CAGATGTGTT	GTGGGCTCAG	GCTTTACCAG	CAAACACCTC	AGCACAAAAG	GCTGAATTGA	1620
TCGCCCCAC	TCAGGCTCTC	CGATGGGGTA	AGGATATTAA	CGTTAACACT	GACAGCAGGT	1680
ACGCCCTTGC	TACTGTGCAT	GTACGTGGAG	CCATCTACCA	GGAGCGTGGG	CTACTCACCT	1740
CAGCAGGTGG	CTGTAATCCA	CTGTAAAGGA	CATCAAAAGG	AAAACACGGC	TCTTGCCCGT	1800
GGTAACCAGA	AAGCTGATTC	AGCAGCTCAA	GATGCAGTGT	GACTTTCAGT	CACGCCTCTA	1860
AACTTGCTGC	CCACAGTCTC	CTTTCCACAG	CCAGATCTGC	CTGACAATCC	CGCATACTCA	1920
ACAGAAGAAG	AAGACTGGCC	TCAGAACTCA	GAGCCAATAA	AAATCAGGAA	GGTTGGTGGA	1980
TTCTTCCTGA	CTCTAGAATC	TTCATACCCC	GAACCTTTGG	GAAAACTTTA	ATCAGTCACC	2040
TACAGTCTAC	CACCCATTTA	GGAGGAGCAA	AGCTACCTCA	GCTCCTCCGG	AGCCGTTTTTA	2100
AGATCCCCCA	TCTTCAAAGC	CTAACAGATC	AAGCAGCTCT	CCGGTGCACA	ACCTGCGCCC	2160
AGGTAAATGC	CAGAAAAGGT	CCTAAACCCA	GCCCCAGCCA	CCGTCTCCAA	GAAAACTCAC	2220
CAGGAGAAAA	GTGGGAAATT	GACTTTACAG	AAGTAAAACC	ACACCGGGCT	GGGTACAAAT	2280
ACCTTCTAGT	ACTGGTAGAC	ACCTTCTCTG	GATGGACTGA	AGCATTTGCT	ACCAAAAACG	2340
AAACTGTCAA	TATGGTAGTT	AAGTTTTTAC	TCAATGAAAT	CATCCCTCGA	CATGGGCTGC	2400
CTGTTTGCCA	TAGGGTCTGA	TAATGGACCG	GCCTTCGCCT	TGTCTATAGT	TTAGTCAGTC	2460
AGTAAGGCGT	TAAACATTCA	ATGGAAGCTC	CATTGTGCCT	ATCGACCCCA	GAGCTCTGGG	2520
CAAGTAGAAC	GCATGAACTG	CACCCTAAAA	AACACTCTTA	CAAAATTAAT	CTTAGAAACC	2580
GGTGTAATT	GTGTAAGTCT	CCTTCC'TTTA	GCCCTACTTA	GAGTAAGGTC	CACCCCTTAC	2640
TGGGCTGGGT	TCTTACCTTT	TGAAATCATG	TATGGGAGGG	TGCTGCCTAT	CTTGCCCTAAG	2700
CTAAGAGATG	CCCAATTGGC	AAAAATATCA	CAAACTAATT	TATTACAGTA	CCTACAGTCT	2760
CCCCAACAGG	TACAAGATAT	CATCCTGCCA	CTTGTTTCGAG	GAACCCATCC	CATACCAATT	2820
CCTGAACAGA	CAGGGCCCTG	CCATTCAATC	CCGCCAGGTG	ACCTGTTGTT	TGTTAAAAAG	2880
TTCCAGAGAG	AAGGACTCCC	TCCTGCTTGG	AAGAGACCTC	ACACCGTCAT	CACGATGCCA	2940
ACGGCTCTGA	AGGTGGATGG	CATTCTTGCG	TGGATTTCATC	ACTCCCGCAT	CAAAAAGGCC	3000
AACAGAGCCC	AAGTAGAAAC	ATGGGTCCCC	AGGGCTGGGT	CAGGCCCTTT	AAAACCTGCAC	3060
CTAAGTTGGG	TGAGCCATT	AGATTAATTC	TTTTTCTTAA	TTTTGTAAAA	CAATGCATAG	3120
CTTCTGTCAA	ACTTATGTAT	CTTAAGACTC	AATATAACCC	CCTTGTTTATA	ACTGAGGAAT	3180
CAATGATTTG	ATCCCCCAA	AAACACAAGT	GGGGAATGTA	GTGTCCAACC	TGGTTTTTAC	3240
TAACCCGTGT	TTTAGACTCT	CCCTTTCCTT	TAATCACTCA	GCTTGTTTCC	ACCTGAATTG	3300
ACTCTCCCTT	AGCTAAGAGC	GCCAGATGGA	CTCCATCTTG	GCTCTTTCAC	TGGCAGCCGC	3360
TTCTCTAAGG	ACTTAACTTG	TGCAAGCTGA	CTCCCAGCAC	ATCCAAGAAT	GCAATTAACT	3420
GATAAGATAC	TGTGGCAAGC	TATATCCGCA	GTTCCAGGA	ATTCTGCCAA	TTGATCACAG	3480

CCCCCTCTACC CTTTCAGCAAC CACCACCCTG ATCAGTCAGC AGCCATCAGC ACCGAGGCAA	3540
GGCCCTCCAC CAGCAAAAAG ATTCTGACTC ACTGAAGACT TGGATGATCA TTAGTATTTT	3600
TAGCAGTAAA GTTTTTTTTT CTTTTTCTTT CTTTTTTTCT CGTGCC	3645

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

TAAGAGGGTA CAAGATCTAA GCACAGCCGT CAATGCAGAA CACAGAACGT AGCCTGGTAA	60
GTGTGTTAAG AGTGGGAATT TTTGGAGTAC AGAGTAAGGC ACCTAACCTT AGCTGGGGTT	120
TGCTGACGGT CCCAGATGGC TTACAGAAGA AAGTGTCTTG AGATGAGTTT TTAAGAAATGA	180
ATAAGGATAG ACACAAGTGA GGACTGACTT GGCAGTGGTG AATGGTGGGT CGCAAAAAAC	240
TTCGCATGTA TGGAAACTGC ACGTACAGGA ATGAAGAATG AGACTGTGTG GTGTTTAATG	300
AGCTGCAAAT ACTAATTTTA TCCTGAAAGT TTTGAAGAGT TAACTAAAAA GTATTTTSTA	360
GTAAGGAAAT AACCTTACAT TTCAGGGTTA TTGTTTGTTC ANATATTGAA GGTGCCCAA	419

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

AAGAGGGTAC CTGTATGTAG CCATGGTGGC AATGAGAGAC TGATTACTAC CTGCTGGAGA	60
TTGTTTAAAGT GAGTTAATAT ATTAAGGATA AAGGGAGCCA GGTTTTTTGA CTGTTGGAGA	120
AGGAAATTAC AGATATTGAA GGTCCCAA	148

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

TAAGAGGGTA CMAAAAAAAAA AAAATAGAAC GAATGAGTAA GACCTACTAT TTGATAGTAC	60
AACAGGGTGA CTATAGTCAA TGATAACTTA ATTATACATT TAACATAGAG TGTAATTGGA	120
TTGTTTGTA CTCGAAGGAT AAATGCTTCA GAGGATGGAT ACCCATTTCT CCATGATGTA	180
CTTATTTTAC ATTACATGCC TGTATCAAAG CATCTCATAT ACCCTATAAA TATGTACACC	240
TACTATGTAC CCTCTTA	257

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

TAAGAGGGTA CGGGTATTTG CTGATGGGAT TTTTTTTTCT TTCTTTTCT TTGGAAAACA	60
AAATGAAAGC CAGAACAAAA TTATTGAACA AAAGACAGGG ACTAAATCTG GAGAAATGAA	120
GTCCCCTCAC CTGACTGCCA TTTCATTCTA TGTGACCTTC CAGTCTAGGT TAGGAGAATA	180
GGGGGTGGAG GGGATTAATC TGATACAGGT ATATTTAAAG CAACTCTGCA TGTGTGCCAG	240
AAGTCCATGG TACCCTCTTA	260

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

TGCTCCTCTT GCCTTACCAA CCACAAATTA GAACCATAAT GAGATGTCAC CTCATACCTG	60
GTGGGATTAA CATTATTTAA AAAATCAGAA GTATTGACAA GGATGTGAAG AAATTAGAAC	120
ATCTGTGCAC TGTTGGTGGG AATGTAAAAA AGGTGTGGCC ACTATGGGTA ACAGCATGAA	180
GGTTCCTCAA AAAAAATTTT TTTAATCTA CTCTATGATC GATCTTGAGG TTGTTTATGC	240
AAAAGAACTG AAATCAGGAT TTTGAGGAAA TATTCACATT CCCACATCCA TTTCTGCTTT	300
ATTATAATA CTCAAGAGAT GGAAACAACC TAAATGTCCA TCCCAGGATG AATGGATAAA	360
CACAGTGTGG TATATGCATA CAATGGAATA TTATTTAGTC TTTAAAAGA AAAATTCTAT	420

CATATACTAC AACTTANATN AACCTTGAGG ACACAATGCT NAGTGAAATA AGCCACGGAA	480
GGACGAATAC TGCATTATTC CCTTATATGA AGTATCTAAA GTGGTCAAAC TCTTANAGCA	540
NAAAGTAAAA ATGGGTGGTT GCCANACAGT TGCTTAGGCN AGAAGANAAN CCTANT	596

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

TCTTCTGAAG ACCTTTCGCG ACTCTTAAGC TCGTGGTTGG TAAGGCAAGA GGAGCGTTGG	60
TAAGGCAAGA GGAGCGTTGG TAAGGCAAGA GGAGCA	96

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

TGTAAGTCGA GCACTGTGAT GATAAACTT GAATGGATCA ATAGTTGCTT CTTATGGATG	60
AGCAAAGAAA GTAGTTTCTT GTGATGGAAT CTGCTCCTGG CAAAATGCT GTGAACGTTG	120
TTGAAAAGAC AACAAAGAGT TTAGAGTAGT ACATAAATTT AGAATAGTAC ATAACTTAG	180
AATAGTACAT AAACCTTAGTA CATAAATAAT GCACGAAGCA GGGGCAGGGC TTGAGAGAAT	240
TGACTTCAAT TTGGAAAGAG TATCTACTGT AGGTTAGATG CTCTCAAACA GCATCACACT	300
GCTCGACTTA CAA	313

(2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 550 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

AACGAGGACA GATCCTTAAA AAGAATGTTG ACTGAAAAAA GTAGAAAATA AGATAATCTC	60
CAAAGTCCAG TAGCATTATT TAAACATTTT TAAAAAATAC ACTGATAAAA ATTTTGTACA	120
TTTCCCAAAA ATACATATGG AAGCACAGCA GCATGAATGC CTATGGGRTT GAGGATAGGG	180
GTTGGGAGTA GGGATGGGGA TAAAGGGGGA AAATAAAACC AGAGAGGAGT CTTACACATT	240
TCATGAACCA AGGAGTATAA TTATTTCAAC TATTTGTACC WGAAGTCCAG AAAGAGTGGA	300
GGCAGAAGGG GGAGAAGAGG GCGAAGAAAC GTTTTTGGGA GAGCGGTCCC ASAAGAGAGA	360
TTTTCGCGAT GTGGCGCTAC ATACGTTTTT CCAGGATGCC TTAAGCTCTG CACCCATTAT	420
TTCTCATCAC TAATATTAGA TTAAACCCCT TGAAGACAGC GTCTGTGGTT TCTCTACTTC	480
AGCTTTCCTT CCCTGTCTTG CACACAGTAG CTGTTTTACA AGGGTTGAAC TGAAGTGAAGT	540
GAGATTATTC	550

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

TAGACTGACT CATGTCCCCT ACCAGAGTAG CTAGAATTAA TAGCACAAGC CTCTACACCC	60
AGGAATCAC TATTGAATAC ATAAATGGAA TTTATTCAGC CTTAAAAAGT TTGGAAGGAA	120
ATTCTGACAT ATGCTAAAAC ATGGATGAAC CTTGAAGACT TTATGATAAG TAAAAGAAGC	180
CAGTCATAAA AGGAAAAATA TTGCATGATT CCACTTATAT GAGGTACCTA GAGTAGTCAA	240
TTTCATAGAA ACACAAAATA GAATGGTGTT TGCCAGGGCT TTTGAGGAAA AGGGAATGAC	300
AAGTTAGGGG ACATGAGTCA GTCTA	325

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

TAGACTGACT CATGTCCCCT ATCTACTCAA CATTTCCTACT TGAAGTCTGA TAGGCATCTC	60
AGACTTATCT TGTCCCAAAG CAAACTCTTT ATTTCTTTTC ATCCTAGTCT TTATTTCTTG	120
TGCTGTCTTA CCCATCTCAA AAGAGTGCCA AAATCCACCA AGTTGCTGAA ACAGAAATCT	180

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AAGAAATATC	CTTGATTCTT	CTTTTCCCA	TC'TACTTCAC	TTCTAATTCA	TTAGTAAATA	240
ATCTGTTTCA	GAAAACCAAA	CACCTCATGT	TCTCACTCAT	AAGGGGGAGT	TGAACAATGA	300
GAACACACAG	ACACAGGGAG	GGGAACATCA	CACACCACGG	CCCGTCAGGG	ACTANGGGAC	360
ATGAGTCAGT	CTA					373

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

TAGACTGACT	CATGTCCCCT	ATAATGCTCC	CAGGCATCAG	AAAGCATCTC	AAACTGGAGC	60
TGACACCATG	GCAGAGGTTT	CAGGTAAGTC	ACAAAAGGGG	TCCTAAAGAA	TTTGCCCTCA	120
ATATCAGAGT	GATTAGAAGA	AGTGGACAGA	GCTACCCAAG	TTAAACATAT	GCGAGATAAA	180
AAAAATATGG	CACCTGTGAA	CACACACTAC	AGGAGGAAAA	TAAGGAACAT	AATAGCATAT	240
TGTGCTATTA	TGATGATGAA	GAACCTCTCT	ANAAGAAAAC	ATAACCAAAG	AAACAAAGAA	300
AATTCCTGCN	AATGTTTAAT	GCTATAGAAG	AAATTAACAA	AAACATATAT	TCAATGAATT	360
CAGAAAAGTT	AGCAGGTCAN	AAGAAAACAA	ATCAAAGACC	AGAATAATCC	CATTTTAGAT	420
TGTCGAGTAA	ACTANAACAG	AAAGAATACC	ACTGGAAATT	GAATTCCTAC	GTANGGGACA	480
TGANTCANTC	TA					492

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

TGGAAAGTAT	TTAATGATGG	GCAACTTGCT	GTTTACTTCC	TACATATCCC	ATCATCTTCT	60
GTATTTTTTT	AAATAACTTT	TTTTTGGATT	TTTAAAGTAA	CCTTATTCTG	AGAGGTAACA	120
TGGATTACAT	ACTTCTAAGC	CATTAGGAGA	CTCTATGTTA	AACCAAAAGG	AAATGTTACT	180
AGATCTTCAT	TTGATCAATA	GGATGTGATA	ATCATCATCT	TTCTGCTCTA	ATGGAAAAGT	240
ACTANAAACA	TGGAACCATA	ATCTTAGATG	AACAACGTTA	GAATTTGCAC	TAATTTCTACG	300
GAATTTTCACT	AATTCGGCAA	ATGTCGGGCA	GTGACACAAC	ATTCATGAC	GGGCACGCAT	360
CTACCAACTT	CTGGCGATAA	GGGCCACCTT	TCCCTCTGTA	CTTACAGTCC	CATTTTCATAC	420
ACAGTCTTTG	ATTAAATATT	CACATTTTTT	CTCTACCTAA	AGACCTTCAA	GACCAGTACC	480
TA						482

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 519 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

TGTATCGACG TAGTGGTCTC CCCATGTGAT AGTCTGAAAT ATAGCCTCAT GGCATGAGAG	60
GCTGTGCCCC AGCCCCGACAC CCGTAAAGGG TCTGTGCTGA GGTGGATTAG TAAAAGAGGA	120
AAGCCTTGCA GTTGAGATAG AGGAAGGGCA CTGTCTCCTG CCTGCCCCCTG GGAAGTGAAT	180
GTCTCGGTAT AAAACCCGAT TGTACATTTG TTCAATTCTG AGATAGGAGA AAAACCACCC	240
TATGGCGGGA GGCGAGACAT GTTGGCAGCA ATGCTGCCTT GTTATGCTTT ACTCCACAGA	300
TGTTTGGGCG GAGGGAACA TAAATCTGGC CTACGTGCAC ATCCAGGCAT AGTACCTCCC	360
TTTGAAGTTA ATTATGACAC AGATTCTCTT GCTCACATGT TTTTGTGCTG ACCTTCTCCT	420
TATTATCACC CTGCTCTCCT ACCGCATTCC TTGTGCTGAG ATAATGAAAA TAATATCAAT	480
AAAAACTTGA NGGAACTCGG AGACCACTAC GTCGATACA	519

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 771 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

TGTATCGACG TAGTGGTCTC CACTCCCGCC TTGACGGGGC TGCTATCTGC CTTCCAGGCC	60
ACTGTCACGG CTCCCGGGTA GAAGTCACTT ATGAGACACA CCAGTGTTGGC CTTGTTGGCT	120
TGAAGCTCCT CAGAGGAGGG TGGGAACAGA GTGACCGAGG GGGCAGCCTT GGGCTGACCT	180
AGGACGGTCA GCTTGGTCCC TCCGCCAAAC ACGAGAGTGC TGCTGCTTGT ATATGAGCTG	240
CAGTAATAAT CAGCCTCGTC CTCAGCCTGG AGCCCAGAGA TGCTCAGGGA GGCCGTGTTG	300
CCANACTTGG AGCCAGAGAA GCGATTAGAA ACCCCTGAGG GCCGATTACC GACCTCATAA	360
ATCATGAATT TGGGGGCTTT GCCTGGGTGC TGTTGGTACC ANGAGACATT ATTATAACCA	420
CCAACGTCAC TGCTGGTTCC ANTGCAGGGA AAATGGTTGA TCNAACTGTC CAGAGAAAACC	480
ACTACGTCCA TACCAATCCA CTAATTGCCN GCCGCCTGCA GGTCAACCA TATTGGGGAA	540
NAACTCCCCN CCGCCGTTTG GGATTGNCAT NAACCTTTGA AATTTTTCCT TATTANTTGT	600
CCCCCTAAAA TAAACNTTG GGCNTTAATC CATTGGGTCC ATANCTTNTT TNCCCGTTT	660
TTAAANTTGT TTTATCCCGC CNCCCNATTT CCCCCCAAC TTCCAAAAC CGAAACCNT	720
TNAAATTTNT TNAAACCCTG GGGGTTCCC NNAATTNNAN TTNAANCTNC C	771

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

TGGGCACCTT CAATATCGGG CTCATCGATA ACATCACGCT GCTGATGCTG CTGTTGCTGG	60
TCCTCTCTAG GAACCTCTGG ATTTTCAAAT TCTTTGAGGA ATTCATCCAA ATTATCTGCC	120
TCTCCTCCTT TCCTCCTTTT TCTAAGGTCT TCTGGTACAA GCGGTCA	167

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

TTGGGCACCT TCAATATCTA CTGATCTAAA TAGTGTGGTT TGAGGCCTCT TGTCCTGGC	60
TAAAAATCCT TGGCAAGAGT CAATCTCCAC TTTACAATAG AGGTAAAAAT CTTACAATGG	120
ATATTCTTGA CAAAGCTAGC ATAGAGACAG CAATTTTACA CAAGGTATTT TTCACCTGTT	180
TAATAACAGT GGTTTTCTTA CACCCATAGG GTGCCACCAA GGGAGGAGTG CACAGTTGCA	240
GAAACAAATT AAGATACTGA AGACAACACT ACTTACCATT TCCCGTATAG CTAACCACCA	300
GTTCAACTGT ACATGTATGT TCTTATGGGC AATCAAGA	338

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

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TTTTTGGCTC CCATACAGCA CACTCTCATG GGAAATGTCT GTTCTAAGGT CAACCCATAA      60
TGCAAAAATC ATCAATATAC TTGAAGATCC CCGTGTAAGG TACAATGTAT TTAATATTAT      120
CACTGATACA ATTGATCCAA TACCAGTTTT AGTCTGGCAT TGAATCAAAT CACTGTTTTT      180
GTTGTATAAA AAGAGAAATA TTTAGCTTAT ATTTAAGTAC CATATTGTAA GAAAAAAGAT      240
GCTTATCTTT ACATGCTAAA ATCATGATCT GTACATTGGT GCAGTGAATA TTAGTGTAAG      300
AGGGAAGAAG GAATGAAGAC GAGCTAAGGA TATTGAAGGT GCCCAA      346

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(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

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ACCAATCCCA CACGGATACT GAGGGACAAG TATATCATCC CATTTCATCC CTACAGCAGC      60
AACTTCATGA GGCAGGAGTT ATTAGTCCCA TTTTACAGAA GAGGAAACTG AGACTTAGGG      120
AGATCAAGTA ATTTGCCAGC GTCGCACAAT TAGTGATAGA GCCAGGGCTT GAAGCGACGT      180
CTGTCTTAAG CCAATGACCC CTGCAGATTA TTAGAGCAAC TGTTCTCCAC AACAGTGTAA      240
GCCTCTTGCT ANAAGCTCAG GTCCACAAGG GCAGAGATTT TTGTCTGTTT TGCTCATTGC      300
TCCTTCCCCA TTGCTTAGAG CAGGGTCTGC CACGAANCAG GTTCTCAATG CATAGTTATT      360
AAATGTATAT AAGAGCAAAC ATATGTTACA GAGAACTTTC TGTATGCTTG TCACTTACAT      420
GAATCACCTG TGANATGGGT ATGCTTGTTT CCCANTGTTG CAGATNAAGA TATTGAANGT      480
GCCCAAATCA CTANTTGCGG GCGCCTGCAN GTCCANCATA T      521

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(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

```

TGGAACCAAT CCAAATACCC ATCAATGATA GACTGGATAA AGAAAATTTG GCACATGTTC      60
ACCATGAAAT ACTATGCAGC CATAAAAAAG GATGAGTTCA TATCCTTTGC AGGGACATGG      120
ATGAAGCTGG AGACCATCAT TCTCAGCAAA CTAACAAGGG AACAGAAAAC CAAACACTGC      180
ATGTTCTCAC TCTTAAGTGG GAGCTGAACA ATGGAACAC ATGGACACAG GGAGGGGAAC      240
ATCACACAGT GGGGCTGCT GGTGGGTAGG GGTCTAGGGG AGGGATAGCA TTAGGAGAAA      300
TACCTAATGT AGATGACGGG TTGATGGGTG CAGCAAACCA CCATGACACG TGTATACCTA      360
TGTAACAAAC CTGCATGTTC TGCACATGTA CCCCAGAACT TAAAGTGTTA ATAAAAAAT      420
TAAGAAAAAA GTTAAGTATG TCATAGATAC ATAAATATT GTANATATTG AAGGTGCCCA      480

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AA

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(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

TTCGATACAG GCACAGAGTA AGCAGAAAAA TGGCTGTGGT TTAACCAAGT GAGTACACTT	60
AAGTGAGAGA GGGGCAGAGA AGACAAGGGC ATATGCAGGG GGTGATTATA ACAGGTGGTT	120
GTGCTGGGAA GTGAGGGTAC TCGGGGATGA GGAACAGTGA AAAAGTGGCA AAAAGTGGTA	180
AGATCAGTGA ATTGTACTTC TCCAGAATTT GATTTCTGN GGAGTCAAAT AACTATCCAG	240
TTTGGGGTAT CATANGGCAA CAGTTGAGGT ATAGGAGGTA GAAGTCNCAG TGGGATAATT	300
GAGGTTATGA ANGGTTTGGT ACTGACTGGT ACTGACAANG TCTGGGTAT GACCATGGGA	360
ATGAATGACT GTANAAGCGT ANAGGATGAA ACTATTCCAC GANAAAGGGG TCCNAAAAC	420
AAAAANNNA GNNNNNGGG AATATTATTT ATCTGGATAT TGAANGTGCC CAAA	474

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

TTCGATACAG GCAAACATGA ACTGCAGGAG GGTGGTGACG ATCATGATGT TGCCGATGGT	60
CCGGATGGNC ACGAAGACGC ACTGGANCAC GTGCTTACGT CCTTTTGCTC TGTTGATGGC	120
CCTGAGGGGA CGCAGGACCC TTATGACCT CAGAATCTTC ACAACGGGAG ATGGCACTGG	180
ATTGANTCCC ANTGACACCA GAGACACCCC AACCACCAGN ATATCANTAT ATTGATGTAG	240
TTCTGTAGA NGGCCCCCTT GTGGAGGAAA GCTCCATNAG TTGGTCATCT TCAACAGGAT	300
CTCAACAGTT TCCGATGGCT GTGATGGGCA TAGTCATANT TAACCNTGTN TCGAA	355

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

TTGGATTGGT CCTCCAGGAG AACAAAGGGGA AAAAGGTGAC CGAGGGCTCC CTGGAAC	60
AGGATCTCCA GGAGCAAAAG GGGATGGGG AATTCCTGGT CCTGCTGGTC CCTTAGGTCC	120

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ACCTGGTCCT CCAGGCTTAC CAGGTCCTCA AGGCCCAAAG GGTAACAAAG GCTCTACTGG	180
ACCCGCTGGC CAGAAAGGTG ACAGTGGTCT TCCAGGGCCT CCTGGGCCTC CAGGTCCACC	240
TGGTGAAGTC ATTCAGCCTT TACCAATCTT GTCCTCCAAA AAAACGAGAA GACATACTGA	300
AGGCATGCAA GCAGATGCAG ATGATAATAT TCTTGATTAC TCGGATGGAA TGGAAAGAAAT	360
ATTTGGTTCC CTCAATTCCC TGAAACAAGA CATCGAGCAT ATGAAATTTT CAATGGGTAC	420
TCAGACCAAT CCAA	434

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

TGGATTGGTC ACATGGCAGA GACAGGATTC CAAGGCAGTG AGAGGAGGAT ACAATGCTTC	60
TCACTAGTTA TTATTATTTA TTTTATTTTT GAGATGAAGT CTCGCTTTGT CTCCCAGGCT	120
GGAGAGCGGT GGTGCGATCT TGGCTCTCTG CAACCCCGC CTCAAGCAAT TCTCCTGTCT	180
TAGCCTCGCG GGTAGATGGA ATTACAGGCG CCCACCGCCA TGCCCAACTA ATTTTTTTGT	240
GTCTTCAGTA GAGACAGGGT TTCGCCATGT TGGGCAGGCT GGTCTTGAAC TCCTGACCTC	300
NAGTGATCTG CCCTCCTCGG CCTCACAAAG TGCTGGAATT ACAGGCATGG GCTGCTGCAC	360
CCAGTCAACT TCTCACTAGT TATGGCCTTA TCATTTCAC CACATTCTAT TGGCCCAAAA	420
AAAAAAAAAN	430

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

TGGTACTCCA CCATYATGGG GTCAACCGCC ATCCTCGCCC TCCTCCTGGC TGTTCTCCAA	60
GGAGTCTGTG CCGAGGTGCA GCTGRTGCAG TCTGGAGCAG AGGTGAAAAA GTCCGGGGAG	120
TCTCTGAAGA TCTCCTGTAA GGGTTCTGGA TACACCTTTA AGATCTACTG GATCGCCTGG	180
GTGCGCCAGT TGCCCGGGAA AGGCCTGGAG TGGATGGGGC TCATCTTTCC TGATGACTCT	240
GATACCAGAT ACAGCCCGTC CTTCCAAGGC CAGGTCACCA TCTCAGTCGA TAAGTCCATC	300
AGCACCGCCT ATCTGCAGTG GAGTACCAA	329

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

TGGTACTCCA CTCAGCCCAA CCTTAATTAA GAATTAAGAG GGAACCTATT ACTATTCTCC	60
CAGGCTCCTC TGCTCTAACC AGGCTTCTGG GACAGTATTA GAAAAGGATG TCTCAACAAG	120

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TATGTAGATC CTGTACTGGC CTAAGAAGTT AACTGAGAA TAGCATAAAT CAGACCAAAC	180
TTAATGGTCC TTGAGACTTG TGTCCTGGAG CAGCTGGGAT AGGAAAACCTT TTGGGCAGCA	240
AGAGGAAGAA CTGCCTGGAA GGGGGCATCA TGTTAAAAAT TACAAGGGGA ACCCACACCA	300
GGCCCCCTTC CCAGCTCTCA GCCTAGAGTA TTAGCATTTT TCAGCTAGAG ACTCACAAC	360
TCCTTGCTTA GAATGTGCCA CCGGGGGGAG TCCCTGTGGG TGATGAGGCT CTCAAGAGTG	420
AGAGTGGCAT CCTATCTTCT GTGTGCCAC AGGAGCCTGG CCCGAGACTT AGCAGGTGAA	480
GTTTCTGGTC CAGGCTTTGC CCTTGACTCA CTATGTGACC TCTGGTGGAG TACCAA	536

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

NTGTTGCGAT CCCAGTAACT CGGGAAGCTG AGGCGGGAGG ATCACCTGAG CTCAGGAGGT	60
TGAGGCCGCA GTGAGCCGGG ACCACGCCAC TACTCTCCAG CCTGGGGCAT AGAGTGAGAC	120
CCTCCAAGAC AGAAAAGAAA AGAAAGGAAG GGAAAGGGAA AGGGAAAAGG AAAAGGAAAA	180
GGAAAAGGAA AAGGAAAAGA CAAGACAAAA CAAGACTTGA ATTTGGATCT CCTGACTTCA	240
ATTTTATGTT CTTTCTACAC CACAATTCCT CTGCTTACTA AGATGATAAT TTAGAAACCC	300
CTCGTTCCAT TCTTTACAGC AAGCTGGAAG TTTGGTCAAG TAATTACAAT AATAGTAACA	360
AATTTGAATA TTATATGCCA GGTGTTTTTC ATTCTGCTC TCACTTAATT CTCACCACTC	420
TGATATAAAT ACAATTGCTG CCGGGTGTGG TGGCTCATGC CTGTAATCCC GGCACTTTGG	480
GAGACCGAGG TGGGCGGATS GCAACAA	507

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

TTGGATTGGT CACTGTGAGG AAGCCAAATC GGATCCGAGA GTCTTTTTCT AAAGGCCAGT	60
ACTGGCCACA CTTTCTCCTG CCGCTTCCT CAAAGCTGAA GACACACAGA GCAAGGCGCT	120
TCTGTTTTAC TCCCAATGG TAACTCCAAA CCATAGATGG TTAGCTNCCC TGCTCATCTT	180
TCCACATCCC TGCTATTGAG TATAGTCCGT GGACCAATCC AA	222

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

TGTTGCGATC CATAAATGCT GAAATGGAAA TAAACAACAT GATGAGGGAG GATTAAGTTG	60
GGGAGGGAGC ACATTAAGGT GGCCATGAAG TTTGTTGGAA GAAGTGACTT TTGAACAAGG	120

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CCTTGGTGT	T AAGAGCTGAT	GAGAGTGTCC	CAGACAGAGG	GGCCACTGGT	ACAATAGACG	180
AGATGGGAGA	GGGCTTGGA	GGTGTGCGAA	ATAGGAAGGA	GTTTGTCTG	GTATGAGTCT	240
AGTGAACACA	GAGGCGAGAG	GCCCTGGTGG	GTGCAGCTGG	AGAGTTATGC	AGAATAACAT	300
TAGGCCCTGT	GGGGGACTGT	AGACTGTCAG	CAATAATCCA	CAGTTTGGAT	TTTATTCTAA	360
GAGTGATGGG	AAGCCGTGGA	AAGGGGGTTA	AGCAAGGAGT	GAAATTATCA	GATTTACAGT	420
GATAAAAATA	AATTGGTCTG	GCTACTGGGG	AAAAAAAAAA	AAA		463

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

TTGGATTGGT	CAACCTGCTC	AACTCTACYT	TTCCTCCTTC	TTCCTAAAA	ATTAATGAAT	60
CCAATACATT	AATGCCAAAA	CCCTTGGGTT	TTATCAATAT	TTCTGTAAAA	AAGTATTATC	120
CAGAACTGGA	CATAATACTA	CATAATAATA	CATAACAACC	CCTTCATCTG	GATGCAAACA	180
TCTATTAATA	TAGCTTAAGA	TCACCTTCAC	TTTACAGAAG	CAACATCCTG	TTGATGTTAT	240
TTTGATGTTT	GGACCAATCC	AA				262

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GNNGNNNNNN	NNNCAATTCG	ACTCNGTTCC	CNTGGTANCC	GGTCGACATG	GCCGCGGGAT	60
TACCGCTTGT	NNCTGGGGGT	GTATGGGGGA	CTATGACCGC	TTGTAGCTGG	GGGTGTATGG	120
GGGACTATGA	CCGCTTGTAG	MTGGKGGTGT	ATGGGGGACT	ATGACCGCTT	GTCGGGTGGT	180
CGGATAAACC	GACGCAAGGG	ACGTGATCGA	AGCTGCGTTC	CCGCTCTTTC	GCATCGGTAG	240
GGATCATGGA	CAGCAATATC	CGCATTCGYC	TGAAGGCGTT	CGACCATCGC	GTGCTCGATC	300
AGGCGACCGG	CGACATCGCC	GACACCGCAC	GCCGTACCGG	CGCGCTCATC	CGCGGTCCGA	360
TCCCGCTTCC	CACGCGCATC	GAGAAGTTCA	CGGTCAACCG	TGGCCCCGAC	GTCGACAAGA	420
AGTCGCGCGA	GCAGTTCGAG	GTGCGTACCT	ACAAGCGGTC	A		461

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

TGACCGCTTG	TAGCTGGGGG	TGTATGGGGG	ACTACGACCG	CTTGTAGCTG	GGGGTGTATG	60
GGGGACTATG	ACCGCTTGTA	GCTGGGGGTG	TATGGGGGAC	TATGACCGCT	TGTAGCTGGG	120
GGTGTATGGG	GGACTAGGAC	CGCTTGTAGC	TGGGGGTGTA	TGGGGGACTA	TGACCGCTTG	180

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TAGCTGGGGG TGTATGGGGG ACTACGACCG C TGTAGCTG TGGGTGTATG GGGGACTATG      240
ACCGCTTGTA NCTGGGGGTG TATGGGGGAC TATGACCC' TGTGCTGCCT GGGGGATGGG      300
AGGAGAGTTG TGGTGGGGA AAAAAAAAAA AA                                     332

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(2) INFORMATION FOR SEQ ID NO:259:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:259:

```

TACCGCTTGT GACCGCTTGT GACCGCTTGT GACCGCTTGT GACCGCTTGT GACCGCTTGT      60
GACCGCTTGT GACCGCTTGT GACCGCTTGT GACCGCTTGT GACCGCTTGT GACCGCTTGT      120
GACCGCTTGT GACCGCTTGT NACNGGGGGT GTCTGGGGGA CTATGANNGA NTGTNACTGG      180
GGGTGTCTGG GGGNCTATCA NNGANTGTNA CNGGGGGTGT CTGGGGGACT ATGANNGACT      240
GTGNNNCTG GGGGATCNGA GGAGANTNGN GGNTAGNGAT CGTTNCGGAN A               291

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(2) INFORMATION FOR SEQ ID NO:260:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:260:

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TAAGAGGSTA CTGGTTAAAA TACAGGAAAT CTGGGGTAAT GAGGCAGAGA ACCAGGATAC      60
TTTGAGGTCA GGGATGAAAA CTAGAATTTT TTTCTTTTTT TTTGCCTGAG AAACCTGCTG      120
CTCTGAAGAG CCCCATGTAT TAATTGCTTT GATCTTCCTT TTCTTACAGC CCTTCAAGG      180
GCAGAGCCCT CTTTATCCTG AAGGAATCTT ATCCTTAGCT ATAGTATGTA CCCTCTTA       238

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(2) INFORMATION FOR SEQ ID NO:261:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 746 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:261:

```

TTGGGCACCT TCAATATCAA TAGCTAACAT TTATTGAGTG TTTATCGTAT CATAAAACAC      60
TGTTCTAAGC CTTTAAACGT ACTAATTCAT TTAATGCTCA TAATCACTTT AGAAGGTGGG      120
TACTAGTATT AGTCAACATT ACAGATGCAA CATGCAGGCA CAGAGAGGTT AATTAACTTG      180
CCCAAGGTAA CACAGCTAAG AAATAGAAAA AATATGAAT CTGGAAAGTT GGGCTTCTGG      240
GTAACCCACA GAGTCTTCAA TGAGCCTGGG GCCTCACTCA GTTTGCTTTT ACAAGCGGAA      300
TGAGTAACAT CACTTAATTC AGTGAGTAGG CCAAATGGAG GTCAGCTACG AGTTTCTGCT      360
GTTCTTGCA G TGGACTGACA GATGTTTACA ACGTCTGGCC ATCAGTWAAT GGA CTGATTA      420
TCATTGGGAW GTGGGTGGGC TGAATGTTGG CCAGTGAAGT TTATTCAWGC CATATTTTTA      480
TGTTTAGGAT GACTTTTGGC TGCTCCTAGG GCAAGCTCTG TCTGSCACGG AACACAGAAT      540
WACACAGGGA CCCCCTCAAT TTCTGGTGTG GCTAGAACCA TGAACCACTG GTTGGGGGAA      600

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CAAGCGGTCA AAACCTAAGT GCGGCCGGCT GGCAGGGTCC ACCCATATGG GGAAAACTCC	660
CNACGCGTTT GGAATCCCTN AGCTNGAATT ATTCTAANAG TTGTCCNCNT AAAATTAGCC	720
TGGGCGTTAA TCANGGTCN NAAGCC	746

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

TGACCGCTTC TCATCTCACA TGGGGTCCTG CACGCTTTTG CCTTGTAGG AAACCTGACA	60
TTTGTCTGTT TCTTCTTCT CTTTTCCTTC CCATATCCTC CTAATTTACG TTTGACTTGT	120
TTGCTGAGGA GGCAGGAGCT AGAGACTGCT GTGAGCTCAT AGGGGTGGGA AGTTTATCCT	180
TCAAGTCCCG CCCACTCATC ACTGCTTCTC ACCTTCCCT GACCAGGCTT ACAAGTGGGT	240
TCTTGCCTGC TTTCCTTTG GACCCAACAA TCCCCTGTAA TGAGTGTGCA TGA CTCTGAC	300
AGCTGTGGAC TCAGGGTCCT TGGCTACAGC TGCCATGTAA AATATCTCAT CCAGTTCTCG	360
CAAATTGTTA AAATAACCAC ATTTCTTAGA TTCCAGTACC CAAATCATGT CTTTACGAAC	420
TGCTCCTCAC ACCCAGAAAGT GGCACAATAA TTCTTGGGGA ATTATTACTT TTTTTTTTCT	480
CTCTNTTNNC GNNNGNNNNG GNNNGNCCAG GAATTACCAC NTTGGAAGAC CTGGCCNGAA	540
TTTATTATAN AGGGGAGCCG ATTN'TTTTTC CTAACACAAA GCGGGTCA	588

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

TTTTTTTTTT TTTGGCCTGA GCAACTGAAA TTATGAAATT TCCATATACT CAAAAGAGTA	60
AGACTGCAAA AAGATTAAAT GTAAAAGTTG TCTTGTATAC AGTAATGTTT AAGATACCTA	120
TTANATTAT AAATGGAAAA TTAGGGCATT TGGATATACA AGTTGAAAT TCAGGAGTGA	180
GGTTGGGCTG GCTGGGTATA TACTGAAAAC TGTCAGTACA CAGATGACAT CTAACCAC	240
AAATCTGCTT TTATTTTAGC AGTGATATGT GTCACCTCCA CAAAAGCCTT CCCAATTGGC	300
CTCAGCATAC ACAACAAGTC ACCTCCCCAC AGCCCTCTAC ACATAAACAA ATTCCTTAGT	360
TTAGTTCAGG AGGAAATGCG CCCTTTTCCT TCCGCTCTAG GTGACCGCAA GGCCCACTTC	420
TCGTACCAA GATGTAAAGG GAAGTCTGCC AAAGAGGCAT CTGAAAGGAA ATAAGGGGAA	480
TGGGAGTGAC CACAAAGGAA AGCCAAGGAN AAAC'TTGGGA GACCGTTTCT AGANCCCTGG	540
CATTTACAA CAAAACCTNG GAACAAACCT TGTCTCATCA ATCATTAAAG CCCTTCGTTT	600
GGANNAGACT TTCTGAACTG GGCGCTGAAC ATAANCCTCA TTGAATGTCT TCACAGTCTC	660
CCAGCTGAAG GCACACCTTG GGCCAGAAGG GGAATCTTCC AGGTCTCTCA NACAGGGCTC	720
GCCCTTTGNC	730

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

TTTTTTTTTT	TTTGGCCAGT	ATGATAGTCT	CTACCACTAT	ATTGAAGCTC	TTAGGTCATT	60
TACACTTAAT	GTGGTTATAG	ATGCTGTTGA	GCTTACTTCT	ACCACCTTGC	TATTTCTCCC	120
GTCTCTTTTT	TGTTCCTTTT	CTCTTCTTTT	CCTCCCTTAT	TTTATAATTG	AATTTTTTTAG	180
GATTCTATTT	TATATAGATT	TATCAGCTAT	AACACTTTGT	ATTCTTTTGT	TTTGTGGTTC	240
TTCTGTCATT	TCAATGTGCA	TCTTAACTC	ATCACAATCT	ATTTTCAAAT	AATATCATAT	300
AACCTTACAT	ATAATGTAAG	AATCTACCAC	CATATATTTT	CATTTCTCCC	TTCCATCCTA	360
TGTNTGTCAT	ATTTTTTCCT	TTATATATCT	TTTAAAGACA	TAATAGTATA	TGGGAGGTTT	420
TTGCTTAAAA	TGTGATCAAT	ATTCCTTCAA	NGAAACGTAA	AAATTCAAAA	TAAATNTCTG	480
TTTATTCTCA	AAATNNACCTA	ATATTTCCTA	CCATNTCTNA	TACNTTTCAA	GAATCTGAAG	540
GCATTGGTTT	TTTCCGGCTT	AAGAACCTCC	TCTAAAGCAC	TCTAAGCACA	ATTAAGTCTT	600
CTGGGAGAGG	AATTCTCCCA	AGCTTGGGCC	TTNANNTGTA	CTCCNTNANG	GTTAAANTTT	660
GGCCGGGAAA	TAGAAATTCC	AAGTTAACAG	GNTANTTTTT	NTTTTTNTTN	TCNCC	715

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

TTTTTTTTTT	TTTCCCAACA	CAAAGCACCA	TTATCTTTCC	TCACAATTTT	CAACATAGTT	60
TGATTCCCAT	GAAGAGGTTA	TGATTTCTAA	AGAAAACATG	GCTACTATAC	TATCAATCAG	120
GGTTAAATCT	TTTTTTTTTT	AGACGGAGTT	TA			152

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

TAAACTCCGT	CCCCTTCTTA	ATCAATATGG	AGGCTACCCA	CTCCACATTA	CCTTCTTTTC	60
AAGGGACTGT	TTCCGTAACT	GTGTGGGTA	TTCACGACCA	GGCTTCTAAA	CCTCTTAAAA	120
CTCCCCAATT	CTGGTGCCAA	CTTGACAAC	ATGCTTTTTT	TTTTTTTTTT	TTTTTTTTTN	180
GAGACGGAGT	TTA					193

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

128

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TGTTCGCATC CCTTAAGCAT GGGTGCTATT AAAAAAATGG TGGAGAAGAA AATACCTGGA      60
ATTTACGTCT TATCTTTAGA GATTGGGAAG ACCCTGATGG AGGACGTGGA GAACAGCTTC      120
TTCTTGAATG TCAATTCCTCA AGTAACAACA GTGTGTCAGG CACTTGCTAA GCATCCTAAA      180
TTGCAGCAAG GCTACAATGC TATGGGATTC TCCCAGGGAG GCCAATTTCT GAGGGCACTG      240
GCTCAGAGAT GCCCTTCACC TCCCATGATC AATCTGATCT CGGTTGGGGG ACAACATCAA      300
GGTGTTTTTG GACTCCCTCG ATGCCCAGGA GAGAGCTCTC ACATCTGTGA CTTTCATCCGA      360
AAAACACTGA ATGCTGGGGC GTACTCCAAA GTTGTTCAGG AACGCCTCGT GCAAGCCGAA      420
TACTGGCATG ACCCATAAAA GGAGGATGTG GATCGCAACA      460

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(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

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TGTTCGCATC CGTTGATAGA ATAGCGACGT GGTAATGAGT GCATGGCACG CCTCCGACTT      60
ACCTTCGCCC GTGGGGACCC CGAGTACGTC TACGGCGTCG TCACTTAGAG TACCCTCTGG      120
ACGCCCCGGG GCGTTTCGATT TACCGGAAGC GCGAGCTGCA GTGGGCTTGC GCCCCCGGCC      180
AAATTCTTTG GGGGGTTTAA GGCCGCGGGG AATTGTGAGT ATCTCTATCA GTATGTAGCC      240
AAGTTGGAAC AGTCGCCATT CCCGAAATCG CTTTCTTTGA ATCCGCACCG CCTCCAGCAT      300
TGCCTCATTC ATCAACCTGA AGGCACGCAT AAGTGACGGT TGTGTCTTCA GCAGCTCCAC      360
TCCATAACTA GCGCGCTCGA CCTCGTCTTC GTACGCGCCA GGTCCGTGCG TCGCAATTCC      420
CAACTCCGGT GAGTTGCGCA TTTCAAGTTN CGAAACTGTT CGCCTCCACN ATTTGGCATG      480
TTCACGCATG ACACGGAATA AACTCGTCCA GTACCGGGAA TGGGATCGCA ACA      533

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(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

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TTTTTTTTTT TTCGCCTGAA TTAGCTACAG ATCCTCCTCA CAAGCGGTCA      50

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(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

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TGTTCGCATC CAAATAACCC ACCAGCTTCT TGCACACTTC GCAGAAGCCA CCGTCCTTTG      60
GCTGAGTCAC GTGAACGGTC AGTGCAAGCA GCCGCGTGCC AGAGCAGAGG TGCAGCATGC      120
TGCACACCAG CTCAGGGCTG ACCTCCTCCA GCAGGATGGA CAGGATGGAG CTGCCGTACG      180

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TGTCCACCAC	CTCCTGGCAC	TCTTCCGACA	GGGACTTCGG	CAGCTTCGAG	CACATTTTGT	240
CAAAAGCGTC	GAGTATTTCT	TTCTCAGTCT	TGTTGTTGTC	AATCAGCTTC	GTCACCTCCT	300
TCACCAGGAA	TTACACACACC	TCACAGTAAA	CATCAGACTT	TGCTGGGACC	TCGTGCTTCT	360
TAATGGGCTC	CACCAATTCC	AGGGCAGGGA	TGACATTCTT	GGAGGCCACT	TTGGCGGGGA	420
CCAGAGTCTG	CATGGGCATC	TCTTTCACCT	CATCACAGAA	CCCAACCAGC	GCACAGATCT	480
CCTTGGGTTG	CATGTGCATC	ATCATCTGGG	ATCGCAACA			519

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

TTTTTTTTTT	TTGGGGCGGC	GACCGGACGT	GCACTCC'TCC	AGTAGCGGCT	GCACGTCGTG	60
CCAATGGCCC	GCTATGAGGA	GGTGAGCCTG	TCCGGCTTCG	AGGAGTTCCA	CCGGGCCGTC	120
GAACAGCACA	ATGGCAAGAC	CATTTTCGCC	TACTTTACGG	GTTCTAAGGA	CGCCGGGGGG	180
AAAAGCTGGT	CCCCGACTG	CCTGCAGGCT	GAACCAGTCG	TACGAGAGGG	GCTGAAGCAC	240
ATTAGTCAAG	GATGTGTGTT	CATCTACTGC	CAAGTAGGAG	AAGAGCCTTA	TTGGAAAGAT	300
CCAAATAATG	ACTTCAGAAA	AAACTTGAAA	GTAACAGCAG	TGCCTACACT	ACTTAAGTAT	360
GGAACACCTC	AAAAACTGGT	AGAATCTGAG	TGTCTTCAGG	CCAACCTGGT	GGAAATGTTG	420
TTCTCTGAAG	ATTAAGATTT	TAGGATGGCA	ATCAAGA			457

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

TTTTTTTTTT	TTGGGCAACA	ACCTGAATAC	CTTTTCAAGG	CTCTGGCTTG	GGCTCAAGCC	60
CGCAGGGGAA	ATGCAACTGG	CCAGGTCACA	GGGCAATCAA	GA		102

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

TTTTTTTTTT	TTGGCAATCA	ACAGGTTTAA	GTCTTCGGCC	GAAGTTAATC	TCGTGTTTTT	60
GGCAATCAAC	AGGTTTAAAGT	CTTCGGCCGA	AGTTAATCTC	GTGTTTTTGG	CAATCAACAG	120
GTTTAAAGTCT	TCGGCCGAAG	TTAATCTCGT	GTTTTTGGCA	ATCAACAGGT	TTAAGTCTTC	180
GGCCGAAGTT	AATCTCGTGT	TTTTGGCAAT	CAACAGGTTT	AAGTCTTCGG	CCGAAGTTAA	240
TCTCGTGTTT	TTGGCAATCA	ACAGGTTTAA	GTCTTCGGCC	GAAGTTAATC	TCGTGTTTTT	300
GGCAATCAAG	AGGTTTAAAGT	CTTCGGCCGA	AGTTAATCTC	GTGTTTTTGG	CAATCAACAG	360

GTTTAAGTCT TCGGCCGAAN TTAATCTCGT GTTTTGGCA ATCAACAGGT TTAANTCTTC	420
GGCCGAAGTT AATCTCGTGT TTTTGGCAAT CAANA	455

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

TTTTTTTTTIT TTGGCCAATA CCCTTGATGA ACATCAATGT GAAAATCCTC GGTAATAATAC	60
TGGCAAACCA AATCCAGCAG CACATCAAAA AGCTTATCCA CCATGATCAA GTGGGCTTCA	120
TCCCTGGGAT GCAAGGCTGG TTCAACATAA GAAAATCAAT AAATGTAATC CATCACATAA	180
ACAGAACCAA AGACAAAAAC CACATGATTA TCTCAATAGA TGCAGAAAAG GCCTTGACAA	240
AATTCAACAG CCCTTCATGC TAAACACTCT TAATAAACTA GATATTGATG GAATGTATCT	300
CAAAATAATA AGAGCTATTT ATGACAAACC CACAGCCAAT ATCATACTGA ATGGGCAAAG	360
ACTGGAAGCA TTCCCTTTGA AAAGTGGCAC AAGACAAGGA TGCCCTCTCT CACCGCTCCT	420
ATTCAACATA GTATTGGAAG TTCTGGCCAG GGCAATCAAG A	461

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

TTTTTTTTTT TTGGCCAACA CCAAGTCTTC CACGTGGGAG GTTTTATTAT GTTTTACAAC	60
CATGAAAACA TAGGAAGGTG GCTGTTACAG CAAACATTTC AGATAGACGA ATCGGCCAAG	120
CTCCCCAAAC CCCACCTTCA CAGCCTCTTC CACACGTCTC CCANAGATTG TTGTCCTTCA	180
CTTGCAAATT CANGGATGTT GGAAGTNGAC ATTTNNAGTN GCNGGAACCC CATCAGTGAA	240
NCANTAAGCA GAANTACGAT GACTTTGANA NACANCTGAT GAAGAACACN CTACNGANAA	300
CCCTTTCTNT CGTGTTANGA TCTCNNGTCC NTCCTAATG CGGCCCCCTG CNGGTCCACC	360
ATTTGGGAGA ACTCCCCCN CGTTGGATCC CCCCTTGAGT NTCCCATTCT NGTCCCCCAN	420
ACCNGNCTTG NGNGNCANTN CNNCCTCNCA CCNTGTTTCC CTGNNGTNAA AATNNGTTTT	480
NCCGCCNCCC NAATTCCCAC CCNAATCACA GCGAANCCNG AAGGCCTTCN NAAGTGTTTA	540
ANGCCNGNG GTTTCCTCNT NTANTTGCAG CCTACCCTCC CNCTTNNNT TNCNGTTGG	600
TCGCGCCCTG GNCNCGCCTN GTTCCTCTTT NNGGNNACAA CCTNGNTCN NGGCNCNTCN	660
NNNCTNTTCC TNNNACTAGC TNGCCTNTCC NCNCCGNGGN NCANNGCACA TTNCNCNNAC	720
TNTGTNNCC	729

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

TGACCTGACA	TGTAGTAGAT	ACTTAATAAA	TATTTGTGGA	ATGAATGGAT	GAAGTGAGT	60
TACAGAGAAA	AATAGAAAAG	TACAAATTGT	TGTCAGTGT	TTGAAGGAAA	ATTATGATCT	120
TTCCCAAAGT	TCTGACTTCA	TTCTAAGACA	GGGTTAGTAT	CTCCATACAT	AATTTTACTT	180
GCTTTTGAAA	ATCAAATGAG	ATAATCTATT	TAGATTGATA	ATTTATTTAG	ACTGGCTATA	240
AACTATTAAAG	TGCTAGCAAA	TATACATTTT	AATCTCATTT	TCCACCTCTT	GTGATATAGC	300
TATGTAGGTG	TTGACTTTAA	TGGATGTCAG	GTCAATCCC			339

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

TGACCTGACA	TCCATAACAA	AATCTTTCTC	CATTATATTC	TTCTAGGGGA	ATTTCTTGAA	60
AAGCATCCAA	AGGAAACAAA	TGATGGTAAG	ACCGTGCCAA	GTGGGGAGCA	GACACCAAAG	120
TAAGACCACA	GATTTTACAT	TCAACAGGTA	GCTCACAGTA	CTTTGCCCGA	CACTGTGGGC	180
AGAAATAGCC	TCCTAATGTA	AGCCCTGGCT	CAGTATTGCC	ATCCAAATGC	GCCATGCTGA	240
AAGAGGGTTT	TGCATCCTGG	TCAGATNAAG	AAGCAATGGT	GTGCTGAGGA	AATCCCATAC	300
GAATAAGTGA	GCATTTCAGAA	CTTGAGCTAG	CAGGAGGAGG	ACTAAGATGA	TGTGTGAGCA	360
ACTCTTTGTA	ATGGCTTTCA	TCTAAAATAA	CATGGTACGT	GCCACCAGTT	TCACGAGCAA	420
GTACAGTGCA	AACCCGAAC	TCTGCAGACA	ATCCAATAAC	AGATACTCTA	ATTTTAGCTG	480
CCTTTAGGGT	CTTGATTAAA	TCATAAATAT	TAGATGGATC	GCAAGTTGTA	AGGNTGCTAA	540
AAGATGATTA	GTACTTCTCG	ACTTGTATGT	CCAGGCATGT	TGTTTTAAAN	TCTGCCTTAG	600
NCCCTGCTTA	GGGGAATTTT	TAAAGAAGAT	GGCTCTCCAT	GTTCANGGTC	AATCACNAAT	660
TGCC						664

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

TGACCTGACA	TTGAGGAAGA	GCACACACCT	CTGAAATTC	TTAGGTTTCA	AAGGGCATTT	60
GACACAGAGT	GGGCCTCTGA	TAATTCATGA	AATGCATTCT	GAAGTCATCC	AGAATGGAGG	120
CTGCAATCTG	CTGTGCTTTG	GGGGTTGCCT	CACTGTGCTC	CTGGATATCA	CACAAAAGCT	180
GCAATCCTTC	TTCTTCAACT	AACATTTTGC	AGTATTTGCT	GGGATTTTTA	CTGCAGACAT	240
GATACATAGC	CCATAGTGCC	CAGAGCTGAA	CCTCTGGTTG	AGAGAAGTTG	CCAAGGAGCG	300
GGAAAAATGT	CTTGAAAGAT	CTATAGGTCA	CCAATGCTGT	CATCTTACAA	CTTGAAGTTG	360
GCCAAATCTG	TATGGTTGCA	TGCAGATCTT	GGAGAAGAGT	ACGCCTCTGG	AAGTCACGGG	420
ATATCCAAAN	CTGTCTGTCA	GATGTCAGGT	CA			452

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

TTTTTTTTTTT TTCGGCAAGG CAAATTTACT TCTGCAAAAG GGTGCTGCTT GCACTTTTGG	60
CCACTGCGAG AGCACACCAA ACAAAGTAGG GAAGGGGTTT TTATCCCTAA CGCGGTATT	120
CCCTGGTTCT GTGTCGTGTC CCCATTGGCT GGAGTCAGAC TGCACAATCT ACACTGACCC	180
AACTGGCTAC TGTTTAAAT TGAATATGAA TAATTAGGTA GGAAGGGGA GGCTGTTGT	240
TACGGTACAA GACGTGTTTG GGCATGTCAG GTCA	274

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

TACCTGACAT GGAGAAATAA CTTGTAGTAT TTTGCGTGCA ATGGAATACT ATATGAGGGT	60
GAAAATGAAT GAACTAGCAA TCGGTGTATC AACATGAATA AATCCCCAA ACATAATAAT	120
GTTGAATGGA AAAGGTGAGT TTCAGAAGGA TATATATGCC CTCTAAATCC ATTTATGTAA	180
ACCTTTAAAA AACTACATTA TTTATGGTCA TAAGTCCATC CAGAAAATAT TTAACACCT	240
ACATGGGATT GATAACTACT GATGTCAGGT CA	272

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

TTTTTTTTTT TTGGCCAATA GCATGATTTA AACATTGGAA AAAGTCAAAT GAGCAATGCG	60
AATTTTATG TTCTCTTGAA TAATCAAAAG AGTAGGCAAC ATTGGTTCCT CATTCTTGAA	120
TAGCATTAAT CAGAAAATAT TGCATAGCCT CTAGCCTCCT TAGAGTAGGT GTGCTCTCTC	180
AAATATATCA TAGTCCCACA GTTTATTTCA TGTATATTTT CTGCCTGAAT CACATAGACA	240
TTTGAATTTG CAACGCCTGA TGTAATATA TAAATCTTA CCAATCAGAA ACATAGCAAG	300
AAATTCAGGG ACTTGGTCAT YATCAGGGTA TGACAGCANA TCCCTGTARA AACACTGATA	360
CACACTCACA CACGTATGCA ACGTGGAGAT GTCGCTTWW KKKTWYWCWM RMRYCRWCGN	420
AATCACTTAN N	431

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

ATTCGATTCTG ATGCTTGAGC CCAGGAGTTC AAGACTGCAG TGAGCCACTG CACTTCAGGC 60
 TGGACAACAG AGCGAGTCCC TGTGCCAAAA AAAAAAAA 98

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

TTTTTTTTTT TTCGCAAGCA CGTGCACTTT ATTGAATGAC ACTGTAGACA GGTGTGTGGG 60
 TATAAACTGC TGTATCTAGG GGCAGGACCA AGGGGGCAGG GGCAACAGCC CCAGCGTGCA 120
 GGGCCASCAT TGCACAGTGG ASTGCAAAGG TTGCAGGCTA TGGGCGGCTA CTAVTAACCC 180
 CGTTTTTCCT GTATTATCTG TAACATAATA TGGTAGACTG TCACAGAGCC GAATWCCART 240
 HACASGATGA ATCCAAGGT CAYGAGGATG CCCASAATCA GGGCCASAT STTCAGGCAC 300
 TTGGCGGTGG GGGCATASGC CTGKGCCCGG GTCACGTCSC CAACCWTCTY CCTGTCCCTA 360
 CMCTTGAWTC CNCNCCTTNN NNTNCCNTNA TNTGCCCGCC CNCCTCCTNG NGTCAACCNG 420
 NATCTGCACT ANCTCCCTCN CCCCTTNTGG ANTCTCNTCC TTCAANTAAN NTTATCCTTN 480
 ACNCCCCCT CNCCTTTCCC CTNCCNCCCN TNATCCCNNG NCCNCTATCA NTCNTNCCCT 540
 CNCTNTNCTN CNMATCGTTC CNCCTNNTAA CTACNCTTNN NACNANNCCCT CACTNATNCC 600
 NGNNANTTCT TTCCTTCCCT CCCNACGCNN TGCGTGCGCC CGTCTNGCCT NNNCTNCGNA 660
 CCCNNACTTT ATTTACCTTT NCACCCTAGC NCTCTACTTN ACCCANCCNC TCCTACCTCC 720
 NGGNCCACCC NNCCCTNATC NCTNNCTCTN TCNNCTCNTT CCCC 764

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

CAAGTGTAGG CACAGTGATG AAAGCCTGGA GCAAACACAA TCTGTGGGTA ATTAACGTTT 60
 ATTTCTCCCC TTCCAGGAAC GTCTTGCATG GATGATCAAA GATCAGCTCC TGGTCAACAT 120
 AAATAAGCTA GTTTAAGATA CGTTCCCCTA CACTTGA 157

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

ATTCGATTGT ACTCAGACAA CAATATGCTA AGTGGAAGAA GTCAGTCACA AAAGACCACA 60
 TACTGTATGA CTTCAATTTAC ATTAAGTGTC CAGAATAGGC AAATCCGTAG AGACAGAAAG 120
 TAGATGAGCA GCTGCCTAGG TCTGAGTACA 150

(2) INFORMATION FOR SEQ ID NO:286:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

ATTCGATTTT TTTTTTTTTG GCCATGATGA AATTCTTACT CCCTCAGATT TTTTGTCTGG	60
ATAAATGCAA GTCTCACCAC CAGATGTGAA ATTACAGTAA ACTTTGAAGG AATCTCCTGA	120
GCAACCTTGG TTAGGATCAA TCCAATATTC ACCATCTGGG AAGTCAGGAT GGCTGAGTTG	180
CAGGTCTTTA CAAGTTCGGG CTGGATTGGT CTGAGTACA	219

(2) INFORMATION FOR SEQ ID NO:287:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

ATTCGATTCT TGAGGCTACC AGGAGCTAGG AGAAGAGGCA TGGAACAAAT TTTCCCTCAT	60
ATCCATACTC AGAAGGAACC AACCTGCTG ACACCTTAAT TTCAGCTTCT GGCCTCTAGA	120
ACTGTGAGAG AGTACATTTC TCTTGTTTA AGCCAAGAGA ATCTGTCTTT TGGTACTTTA	180
TATCATAGCC TCAAGA	196

(2) INFORMATION FOR SEQ ID NO:288:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 199 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

ATTCGATTTT AGTCCAGTCC CAGAACCCAC ATTGTCAATT ACTACTCTGT ARAAGATTCA	60
TTTGTTGAAA TTCATTGAGT AAAACATTTA TGATCCCTTA ATATATGCCA ATTACCATGC	120
TAGGTACTGA AGATTCAAGT GACCGAGATG CTAGCCCTTG GGTTCAAGTG ATCCCTCTCC	180
CAGAGTGCAC TGGACTGAA	199

(2) INFORMATION FOR SEQ ID NO:289:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 182 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

ATTTCGATTCT TGAGGCTACA AACCTGTACA GTATGTTACT CTA CTGAATA CTGTAGGCAA	60
TAGTAATACA GAAGCAAGTA TCTGTATATG TAAACATTAA AAAGGTACAG TGAAACTTCA	120
GTATTATAAT CTTAGGGACC ACCATTATAT ATGTGGTCCA TCATTGGCCA AAAAAAAAAA	180
AA	182

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1646 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

GGCACGAGGA GAAATGTAAT TCCATATTTT ATTTGAAACT TATTCCATAT TTTAATTGGA	60
TATTGAGTGA TTGGGTATC AAACACCCAC AAACTTTAAT TTTGTTAAAT TTATATGGCT	120
TTGAAATAGA AGTATAAGTT GCTACCATT TTTGATAACA TTGAAAGATA GTATTTTACC	180
ATCTTTAATC ATCTTGGAAT ATACAAGTCC TCTGAACAAC CACTCTTTCA CCTAGCAGCA	240
TGAGGCCAAA AGTAAAGGCT TTAAATTATA ACATATGGGA TTCTTAGTAG TATGTTTTTT	300
TCTTGAAACT CAGTGGCTCT ATCTAACCTT ACTATCTCCT CACTCTTTCT CTAAGACTAA	360
ACTCTAGGCT CTTAAAAATC TGCCACACC AATCTTAGAA GCTCTGAAA GAATTTGTCT	420
TTAAATATCT TTTAATAGTA ACATGTATTT TATGGACCAA ATTGACATTT TCGACTATTT	480
TTTCCAAAA AGTCAGGTGA ATTTGAGCAC ACTGAGTTGG GAATTTCTTA TCCCAGAAAG	540
CCAACCAATT TCATATTTAT TTAAGATTGA TTCCATACTC CGTTTTCAAG GAGAATCCCT	600
GCAGTCTCCT TAAAGGTAGA ACAAATACTT TCTATTTTTT TTTCACCATT GTGGGATTGG	660
ACTTTAAGAG GTGACTCTAA AAAACAGAG AACAAATATG TCTCAGTTGT ATTAAGCACC	720
GACCCATATT ATCATATTCA CTTAAAAAAA TGATTTCTTG TGCACCTTTT GGCAACTTCT	780
CTTTTCAATG TAGGGAAAAA CTTAGTCACC CTGAAAACCC ACAAATAAAA TAAACTTGT	840
AGATGTGGGC AGAAGGTTT GGGGTGGACA TTGTATGTGT TTAAATTAAA CCCTGTATCA	900
CTGAGAAGCT GTTGTATGGG TCAGAGAAAA TGAATGCTTA GAAGCTGTT ACATCTTCAA	960
GAGCAGAAGC AAACCACATG TCTCAGCTAT ATTATTATTT ATTTTTTATG CATAAAGTGA	1020
ATCATTCTCT CTGTATTAAT TTCCAAAGGG TTTTACCTC TATTTAAATG CTTTGAAAAA	1080
CAGTGCATTG ACAATGGGTT GATATTTTTT TTTAAAAGAA AAATATAATT ATGAAAGCCA	1140
AGATAATCTG AAGCCTGTTT TATTTTAAAA CTTTTTATGT TCTGTGGTTG ATGTTGTTTG	1200
TTTGTGTTGT TCTATTTTGT TGGTTTTTTA CTTTGTTTTT TGTGTTGTTT TGTGTTGTTT	1260
KGCATACTAC ATGCAGTTCT TTAACCAATG TCTGTTTGGC TAATGTAATT AAAGTTGTTA	1320
ATTTATATGA GTGCATTCA ACTATGTCAA TGGTTTCTTA ATATTTATTG TGTAGAAGTA	1380
CTGGTAATTT TTTTATTTAC AATATGTTTA AAGAGATAAC AGTTTGATAT GTTTTCATGT	1440
GTTTATAGCA GAAGTTATTT ATTTCTATG CATTCCAGCG GATATTTTGG TGTGCGAG	1500
GCATGCAGTC AATATTTTGT ACAGTTAGTG GACAGTATTC AGCAACGCCT GATAGCTTCT	1560
TTGGCCTTAT GTTAAATAAA AAGACCTGTT TGGGATGTAT TTTTATTTT TAAAAAAA	1620
AAAAAAAAA AAAAAAAAAA AAAAAA	1646

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

TCATCACCAT	TGCCAGCAGC	GGCACCGTTA	GTCAGGTTTT	CTGGGAATCC	CACATGAGTA	60
CTTCCGTGTT	CTTCATTCTT	CTTCAATAGC	CATAAATCTT	CTAGCTCTGG	CTGGCTGTTT	120
TCACTTCCTT	TAAGCCTTTG	TGACTCTTCC	TCTGATGTCA	GCTTTAAGTC	TTGTTCTGGA	180
TTGCTGTTTT	CAGAAGAGAT	TTTTAACATC	TGTTTTTCTT	TGTAGTCAGA	AAGTAACTGG	240
CAAATTACAT	GATGATGACT	AGAAACAGCA	TACTCTCTGG	CCGTCTTTCC	AGATCTTGAG	300
AAGATACATC	AACATTTTGC	TCAAGTAGAG	GGCTGACTAT	ACTTGCTGAT	CCACAACATA	360
CAGCAAGTAT	GAGAGCAGTT	CTTCCATATC	TATCCAGCGC	ATTTAAATTC	GCTTTTTTCT	420
TGATTAAAAA	TTTCACCACT	TGCTGTTTTT	GCTCATGTAT	ACCAAGTAGC	AGTGGTGTGA	480
GGCCATGCTT	GTTTTTTGAT	TCGATATCAG	CACCGTATAA	GAGCAGTGCT	TTGGCCATTA	540
ATTTATCTTC	ATTGTAGACA	GCATAGTGTA	GAGTGGTATT	TCCATACTCA	TCTGGAATAT	600
TTGGATCAGT	GCCATGTTCC	AGCAACATTA	ACGCACATTC	ATCTTCCTGG	CATTGTACGG	660
CCTTTGTCAG	AGCTGTCCTC	TTTTTGTTGT	CAAGGACATT	AAGTTGACAT	CGTCTGTCCA	720
GCACGAGTTT	TACTACTTCT	GAATTCCCAT	TGGCAGAGGC	CAGATGTAGA	GCAGTCCTCT	780
TTTGCTTGTC	CCTCTTGTTT	ACATCCGTGT	CCCTGAGCAT	GACGATGAGA	TCCTTTCTGG	840
GGACTTTACC	CCACCAGGCA	GCTCTGTGGA	GCTTGTCAG	ATCTTCTCCA	TGGACGTGGT	900
ACCTGGGATC	CATGAAGGCG	CTGTCATCGT	AGTCTCCCA	AGCGACCACG	TTGCTCTTGC	960
CGCTCCCCTG	CAGCAGGGGA	AGCAGTGGCA	GCACCACTTG	CACCTCTTGC	TCCCAAGCGT	1020
CTTCACAGAG	GAGTCGTTGT	GGTCTCCAGA	AGTGCCACG	TTGCTCTTGC	CGCTCCCCCT	1080
GTCCATCCAG	GGAGGAAGAA	ATGCAGGAAA	TGAAAGATGC	ATGCACGATG	GTATACTCCT	1140
CAGCCATCAA	ACTTCTGGAC	AGCAGGTCAC	TTCCAGCAAG	GTGGAGAAAG	CTGTCCACCC	1200
ACAGAGGATG	AGATCCAGAA	ACCACAATAT	CCATTACAAA	ACAAACACTT	TTCAGCCAGA	1260
CACAGGTACT	GAAATCATGT	CATCTGCGGC	AACATGGTGG	AACCTACCCA	ATCACACATC	1320
AAGAGATGAA	GACACTGCAG	TATATCTGCA	CAACGTAATA	CTCTTCATCC	ATAACAAAAT	1380
AATATAATTT	TCCTCTGGAG	CCATATGGAT	GAACATAGAA	GGAAGAACTC	CCCGAAGAAG	1440
CCAGTCGCAG	AGAAGCCACA	CTGAAGCTCT	GTCTCAGCC	ATCAGCCCA	CGGACAGGAR	1500
TGTGTTTCTT	CCCCAGTGAT	GCAGCCTCAA	GTTATCCCGA	AGCTGCCGCA	GCACACGGTG	1560
GCTCCTGAGA	AACACCCAG	CTCTTCCGGT	CTAACACAGG	CAAGTCAATA	AATGTGATAA	1620
TCACATAAAC	AGAATTAAAA	GCAAAGTCAC	ATAAGCATCT	CAACAGACAC	AGAAAAGGCA	1680
TTTGACAAAA	TCCAGCATCC	TTGTATTTAT	TGTTGCAGTT	CTCAGAGGAA	ATGTTCTTAA	1740
CTTTTCCCCA	TTTAGTATTA	TGTTGGCTGT	GGGCTTGTC	TAGGTGGTTT	TATTACTTTT	1800
AAGGTATGTC	CCTTCTATGC	CTGTTTTGCT	GAGGGTTTTA	ATTCTCGTGC	C	1851

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

TCATCACCAT	TGCCAGCAGC	GGCACCGTTA	GTCAGGTTTT	CTGGGAATCC	CACATGAGTA	60
CTTCCGTGTT	CTTCATTCTT	CTTCAATAGC	CATAAATCTT	CTAGCTCTGG	CTGGCTGTTT	120
TCACTTCCTT	TAAGCCTTTG	TGACTCTTCC	TCTGATGTCA	GCTTTAAGTC	TTGTTCTGGA	180
TTGCTGTTTT	CAGAAGAGAT	TTTTAACATC	TGTTTTTCTT	TGTAGTCAGA	AAGTAACTGG	240
CAAATTACAT	GATGATGACT	AGAAACAGCA	TACTCTCTGG	CCGTCTTTCC	AGATCTTGAG	300
AAGATACATC	AACATTTTGC	TCAAGTAGAG	GGCTGACTAT	ACTTGCTGAT	CCACAACATA	360
CAGCAAGTAT	GAGAGCAGTT	CTTCCATATC	TATCCAGCGC	ATTTAAATTC	GCTTTTTTCT	420
TGATTAAAAA	TTTCACCACT	TGCTGTTTTT	GCTCATGTAT	ACCAAGTAGC	AGTGGTGTGA	480
GGCCATGCTT	GTTTTTTGAT	TCGATATCAG	CACCGTATAA	GAGCAGTGCT	TTGGCCATTA	540
ATTTATCTTC	ATTGTAGACA	GCATAGTGTA	GAGTGGTATT	TCCATACTCA	TCTGGAATAT	600
TTGGATCAGT	GCCATGTTCC	AGCAACATTA	ACGCACATTC	ATCTTCCTGG	CATTGTACGG	660
CCTTTGTCAG	AGCTGTCCTC	TTTTTGTTGT	CAAGGACATT	AAGTTGACAT	CGTCTGTCCA	720
GCACGAGTTT	TACTACTTCT	GAATTCCCAT	TGGCAGAGGC	CAGATGTAGA	GCAGTCCTCT	780

TTTGCTTGTC	CCTCTTG TTC	ACATCCGTGT	CCCTGAGCAT	GACGATGAGA	TCCTTTCTGG	840
GGACTTTACC	CCACCAGGCA	GCTCTGTGGA	GCTTGTC CAG	ATCTTCTCCA	TGGACGTGGT	900
ACCTGGGATC	CATGAAGGCG	CTGTCA TC GT	AGTCTCCCCA	AGCGACCACG	TTGCTCTTGC	960
CGCTCCCC TG	CAGCAGGGGA	AGCAGTGGCA	GCACCACTTG	CACCTCTTGC	TCCCAAGCGT	1020
CTTCACAGAG	GAGTCGTTGT	GGTCTCCAGA	AGTGCC CACG	TTGCTCTTGC	CGCTCCCCCT	1080
GTCCATCCAG	GGAGGAAGAA	ATGCAGGAAA	TGAAAGATGC	ATGCACGATG	GTATACTCCT	1140
CAGCCATCAA	ACTTCTGGAC	AGCAGGTCAC	TTCCAGCAAG	GTGGAGAAAG	CTGTCCACCC	1200
ACAGAGGATG	AGATCCAGAA	ACCACAATAT	CCATT CACAA	ACAAACACTT	TTCAGCCAGA	1260
CACAGGTACT	GAAATCATGT	CATCTGCGGC	AACATGGTGG	AACCTACCCA	ATCACACATC	1320
AAGAGATGAA	GACACTGCAG	TATATCTGCA	CAACGTAATA	CTCTTCATCC	ATAACAAAAT	1380
AATATAATTT	TCCTCTGGAG	CCATATGGAT	GAACATAGAA	GGAAGAACTC	CCCGAAGAAG	1440
CCAGTCGCAG	AGAAGCCACA	CTGAAGCTCT	GTCCTCAGCC	ATCAGCGCCA	CGGACAGGAR	1500
TGTGTTTCTT	CCCCAGTGAT	GCAGCCTCAA	GTTATCCCGA	AGCTGCCGCA	GCACACGGTG	1560
GCTCCTGAGA	AACACCCCAG	CTCTTCCGGT	CTAACACAGG	CAAGTCAATA	AATGTGATAA	1620
TCACATAAAC	AGAATTAAAA	GCAAAGTCAC	ATAAGCATCT	CAACAGACAC	AGAAAAGGCA	1680
TTTGACAAAA	TCCAGCATCC	TTGTATTTAT	TGTTGCAGTT	CTCAGAGGAA	ATGCTTCTAA	1740
CTTTTCCCCA	TTTAGTATTA	TGTTGGCTGT	GGGCTTG TCA	TAGGTGGTTT	TTATTACTTT	1800
AAGGTATGTC	CCTTCTATGC	CTGTTTGCT	GAGGGTTTTA	ATTCTCGTGC	C	1851

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

CTTGAGCTTC	CAAATAYGGA	AGACTGGCCC	TTACACASGT	CAATGTTAAA	ATGAATGCAT	60
TTCAGTATTT	TGAAGATAAA	ATTRGTAGAT	CTATACCTTG	TTTTTTGATT	CGATATCAGC	120
ACCR TATAAG	AGCAGTGCTT	TGGCCATTAA	TTTATCTTTC	ATTRTAGACA	GCRTAGTGYA	180
GAGTGGTATT	TCCATACTCA	TCTGGAATAT	TTGGATCAGT	GCCATGTTCC	AGCAACATTA	240
ACGCACATTC	ATCTTCTCTG	CATTGTACGG	CCTGTCAGTA	TTAGACCCAA	AAACAAATTA	300
CATATCTTAG	GAATTCAAAA	TAACATTCCA	CAGCTTTCAC	CAACTAGTTA	TATTTAAAGG	360
AGAAA ACTCA	TTTTTATGCC	ATGTATTGAA	ATCAAACCCA	CCTCATGCTG	ATATACTTGG	420
CTACTGCATA	CCTTTATCAG	AGCTGTCCTC	TTTTTGT TGT	CAAGGACATT	AAGTTGACAT	480
CGTCTGTCCA	GCAGGAGTTT	TACTACTTCT	GAATTCCCAT	TGGCAGAGGC	CAGATGTAGA	540
GCAGTCCTAT	GAGAGTGAGA	AGACTTTTTA	GGAAATTGTA	GTGCACTAGC	TACAGCCATA	600
GCAATGATTC	ATGTA ACTGC	AAACACTGAA	TAGCCTGCTA	TTACTCTGCC	TTCAAAAAAA	660
AAAAAAA						668

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

GGGTCGCCCC	GGGGSGCGT	GGGCTTTCCT	CGGGTGGGTG	TGGGTTTTCC	CTGGGTGGGG	60
TGGGCTGGGC	TRGAATCCCC	TGCTGGGGTT	GGCAGGTTTT	GGCTGGGATT	GACTTTTYTC	120
TTCAAACAGA	TTGGAAACCC	GGAGTTACCT	GCTAGTTGGT	GAAACTGGTT	GGTAGACCGC	180

ATCTGTTGGC	TACTACTGGC	TTCTCCTGGC	TGTTAAAAGC	AGATGGTGGT	TGAGGTTGAT	240
TCCATGCCCG	CTGCTTCTTC	TGTGAAGAAG	CCATTTGGTC	TCAGGAGCAA	GATGGGCAAG	300
TGGTGCTGCC	GTGCTTCCC	CTGCTGCAGG	GAGAGCGGCA	AGAGCAACGT	GGGCACCTCT	360
GGAGACCACG	ACGACTCTGC	TATGAAGACA	CTCAGGAGCA	AGATGGGCAA	GTGGTGCCGC	420
CACTGCTTCC	CCTGCTGCAG	GGGGAGTGGC	AAGAGCAACG	TGGGCGCTTC	TGGAGACCAC	480
GACGAYTCTG	CTATGAAGAC	ACTCAGGAAC	AAGATGGGCA	AGTGGTGCTG	CCACTGCTTC	540
CCCTGCTGCA	GGGGGAGCRG	CAAGAGCAAG	GTGGGCGCTT	GGGGAGACTA	CGATGACAGT	600
GCCTTCATGG	AGCCCAGGTA	CCACGTCCGT	GGAGAAGATC	TGGACAAGCT	CCACAGAGCT	660
GCCTGGTGGG	GTAAAGTCCC	CAGAAAGGAT	CTCATCGTCA	TGCTCAGGTA	CACTGACGTG	720
AACAAGAAGG	ACAAGCAAAA	GAGGACTGCT	CTACATCTGG	CCTCTGCCAA	TGGGAATTCA	780
GAAGTAGTAA	AACTCSTGCT	GGACAGACGA	TGTCAACTTA	ATGTCCTTGA	CAACAAAAAG	840
AGGACAGCTC	TGAYAAAGGC	CGTACAATGC	CAGGAAGATG	AATGTGCGTT	AATGTTGCTG	900
GAACATGGCA	CTGATCCAAA	TATTCCAGAT	GAGTATGGAA	ATACCACTCT	RCACTAYGCT	960
RTCTAYAATG	AAGATAAATT	AATGGCCAAA	GCCTGCTCT	TATAYGGTGC	TGATATCGAA	1020
TCAAAAAACA	AGGTATAGAT	CTACTAATTT	TATCTTCAAA	ATACTGAAAT	GCATTCAATT	1080
TAACATTGAC	GTGTGTAAGG	GCCAGTCTTC	CGTATTTGGA	AGCTCAAGCA	TAAGTTGAAT	1140
GAAAATATTT	TGAAATGACC	TAATTATCTM	AGACTTTATT	TTAAATATTG	TTATTTTCAA	1200
AGAAGCATT	GAGGGTACAG	TTTTTTTTTT	TAAATGCAC	TTCTGGTAAA	TACTTTTGTT	1260
GAAAACACTG	AATTTGTAAA	AGGTAATACT	TACTATTTTT	CAATTTTCC	CTCCTAGGAT	1320
TTTTTTCCCC	TAATGAATGT	AAGATGGCAA	AATTTGCCCT	GAAATAGGTT	TTACATGAAA	1380
ACTCCAAGAA	AAGTTAAACA	TGTTTCAGTG	AATAGAGATC	CTGCTCCTTT	GGCAAGTTCC	1440
TAAAAACAG	TAATAGATAC	GAGGTGATGC	GCCTGTCAGT	GGCAAGGTTT	AAGATATTTT	1500
TGATCTCGTG	CC					1512

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1853 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GGGTCGCCCCA	GGGGGSGCGT	GGGCTTTCCT	CGGGTGGGTG	TGGGTTTTTCC	CTGGGTGGGG	60
TGGGCTGGGC	TRGAATCCCC	TGCTGGGGTT	GGCAGGTTTT	GGCTGGGATT	GACTTTTTYTC	120
TTCAAACAGA	TTGGAAACCC	GGAGTTACCT	GCTAGTTGGT	GAAACTGGTT	GGTAGACGCG	180
ATCTGTTGGC	TACTACTGGC	TTCTCCTGGC	TGTTAAAAGC	AGATGGTGGT	TGAGGTTGAT	240
TCCATGCCCG	CTGCTTCTTC	TGTGAAGAAG	CCATTTGGTC	TCAGGAGCAA	GATGGGCAAG	300
TGGTGCTGCC	GTGCTTCCC	CTGCTGCAGG	GAGAGCGGCA	AGAGCAACGT	GGGCACCTCT	360
GGAGACCACG	ACGACTCTGC	TATGAAGACA	CTCAGGAGCA	AGATGGGCAA	GTGGTGCCGC	420
CACTGCTTCC	CCTGCTGCAG	GGGGAGTGGC	AAGAGCAACG	TGGGCGCTTC	TGGAGACCAC	480
GACGAYTCTG	CTATGAAGAC	ACTCAGGAAC	AAGATGGGCA	AGTGGTGCTG	CCACTGCTTC	540
CCCTGCTGCA	GGGGGAGCRG	CAAGAGCAAG	GTGGGCGCTT	GGGGAGACTA	CGATGACAGY	600
GCCTTCATGG	AKCCCAGGTA	CCACGTCCRT	GGAGAAGATC	TGGACAAGCT	CCACAGAGCT	660
GCCTGGTGGG	GTAAAGTCCC	CAGAAAGGAT	CTCATCGTCA	TGCTCAGGGA	CAKGAAGTG	720
AACAAGARGG	ACAAGCAAAA	GAGGACTGCT	CTACATCTGG	CCTCTGCCAA	TGGGAATTCA	780
GAAGTAGTAA	AACTCSTGCT	GGACAGACGA	TGTCAACTTA	ATGTCCTTGA	CAACAAAAAG	840
AGGACAGCTC	TGAYAAAGGC	CGTACAATGC	CAGGAAGATG	AATGTGCGTT	AATGTTGCTG	900
GAACATGGCA	CTGATCCAAA	TATTCCAGAT	GAGTATGGAA	ATACCACTCT	RCACTAYGCT	960
RTCTAYAATG	AAGATAAATT	AATGGCCAAA	GCCTGCTCT	TATAYGGTGC	TGATATCGAA	1020
TCAAAAAACA	AGCATGGCCT	CACACCACTG	YTAAGTTGGT	TACATGAGCA	AAAACAGCAA	1080
GTSGTGAAAT	TTTTAATYAA	GAAAAAAGCG	AATTTAAAAT	GCRCTGGATA	GATATGGAAG	1140
RACTGCTCTC	ATACTTGCTG	TATGTTGTGG	ATCAGCAAGT	ATAGTCAGCC	YTCTACTTGA	1200
GCAAAATRTT	GATGTATCTT	CTCAAGATCT	GGAAAGACGG	CCAGAGAGTA	TGCTGTTTCT	1260

AGTCATCATC	ATGTAATTTG	CCAGTTACTT	TCTGACTACA	AAGAAAAACA	GATGTTAAAA	1320
ATCTCTTCTG	AAAACAGCAA	TCCAGAACAA	GACTTAAAGC	TGACATCAGA	GGAAGAGTCA	1380
CAAAGGCTTA	AAGGAAGTGA	AAACAGCCAG	CCAGAGGCAT	GGAAACTTTT	AAATTTAAAC	1440
TTTGGGTTAA	ATGTTTTTTT	TTTTTGCCCT	AATAATATTA	GATAGTCCCA	AATGAAATWA	1500
CCTATGAGAC	TAGGCTTTGA	GAATCAATAG	ATTCTTTTTT	TAAGAATCTT	TTGGCTAGGA	1560
GCGGTGTCTC	ACGCCTGTAA	TTCCAGCACC	TTGAGAGGCT	GAGGTGGGCA	GATCACGAGA	1620
TCAGGAGATC	GAGACCATCC	TGGCTAACAC	GGTGAAACCC	CATCTCTACT	AAAAATACAA	1680
AAACTTAGCT	GGGTGIGGTG	GCGGGTGCCT	GTAGTCCCAG	CTACTCAGGA	RGCTGAGGCA	1740
GGAGAATGGC	ATGAACCCGG	GAGGTGGAGG	TTGCAGTGAG	CCGAGATCCG	CCACTACACT	1800
CCAGCCTGGG	TGACAGAGCA	AGACTCTGTC	TCAAAAAAAA	AAAAAAAAAA	AAA	1853

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x) SEQUENCE DESCRIPTION: SEQ ID NO:296:

JGCACGAGAA	TTAAAACCCCT	CAGCAAAACA	GGCATAGAAG	GGACATACCT	TAAAGTAATA	60
AAAACCACCT	ATGACAAGCC	CACAGCCAAC	ATAATACTAA	ATGGGGAAAA	GTTAGAAGCA	120
TTTCTCTCTG	GAAGTGAAC	AATAAATACA	AGGATGCTCG	ATTTTGTCAA	ATGCCCTTTC	180
TGTGTCTGTT	GAGATGCTTA	TGTGACTTTG	CTTTTAATTC	TGTTTATGTG	ATTATCATAT	240
TTATTGACTT	GCCTGTGTTA	GACCGGAAGA	GCTGGGGTGT	TTCTCAGGAG	CCACCCGTGTG	300
CTGCGGCAGC	TTCCGGGATAA	CTTGAGSCTG	CATCACTGGG	GAAGAAACAC	AYTCCTGTCC	360
GTGCGGCTGA	TGGCTGAGGA	CAGAGCTTCA	GTGTGGCTTC	TCTGCGACTG	GCTTCTTCGG	420
GGAGTTCTTC	CTTCATAGTT	CATCCATATG	GCTCCAGAGG	AAAAATTATAT	TATTTTGTTA	480
TGGATGAAGA	GTATTACGTT	GTGCAGATAT	ACTGCAGTGT	CTTCATCTCT	TGATGTGTGA	540
TTGGCTAGGT	TCCACCATGT	TGCCGCAGAT	GACATGATTT	CAGTACCTGT	GTCTGGCTGA	600
AAAGTGTTTG	TTTGTGAATG	GATATTGTGG	TTTCTGGATC	TCATCCTCTG	TGGGTGGACA	660
GCTTTCTCCA	CCTTGCTTGA	AGTGACCTGC	TGTCCAGAAG	TTTGATGGCT	GAGGAGTATA	720
CCATCGTGCA	TGCATCTTTC	ATTTCCCTGCA	TTTCTTCCTC	CCTGGATGGA	CAGGGGGAGC	780
GGCAAGAGCA	ACGTGGGCAC	TTCTGGAGAC	CACAACGACT	CCTCTGTGAA	GACGTTGGGG	840
AGCAAGAGGT	GCAAGTGGTG	CTGCCACTGC	TTCCCCTGCT	GCAGGGGAGC	GGCAAGAGCA	900
ACGTGGTCCG	TTGGGGAGAC	TACGATGACA	GCGCCTTCAT	GGATCCCAGG	TACCACGTCC	960
ATGGAGAAGA	TCTGGACAAG	CTCCACAGAG	CTGCCCTGGT	GGGTAAAGTC	CCCAGAAAGG	1020
ATCTCATCGT	CATGCTCAGG	GACACGGATG	TGAACAAGAG	GGACAAGCAA	AAGAGGACTG	1080
CTCTACATCT	GGCCTCTGCC	AATGGGAATT	CAGAAGTAGT	AAAACCTCGT	CTGGACAGAC	1140
GATGTCAACT	TAATGTCCTT	GACAACAAAA	AGAGGACAGC	TCTGACAAAG	GCCGTACAAT	1200
GCCAGGAAGA	TGAATGTGCG	TTAATGTTGC	TGGAACATGG	CACTGATCCA	AATATTCAG	1260
ATGAGTAIGG	AAATACCACT	CTACACTATG	CTGTCTACAA	TGAAGATAAA	TTAATGGCCA	1320
AAGCACTGCT	CTTATACGGT	GCTGATATCG	AATCAAAAAA	CAAGCATGGC	CTCACACCAC	1380
TGCTACTTGG	TATACATGAG	CAAAAACAGC	AAGTGGTGAA	ATTTTAAATC	AAGAAAAAAG	1440
CGAATTTAAA	TGCGCTGGAT	AGATATGGAA	GAAGTGTCTT	CATACTTGCT	GTATGTTGTG	1500
GATCAGCAAG	TATAGTCAGC	CCTCTACTTG	AGCAAAATGT	TGATGTATCT	TCTCAAGATC	1560
TGGAAGAGCG	GCCAGAGAGT	ATGCTGTTTC	TAGTCATCAT	CATGTAATTT	GCCAGTTACT	1620
TTCTGACTAC	AAAGAAAAAC	AGATGTTAAA	AATCTCTTCT	GAAAACAGCA	ATCCAGAACA	1680
AGACTTAAAC	CTGACATCAG	AGGAAGAGTC	ACAAAGGCTT	AAAGGAAGTG	AAAACAGCCA	1740
GCCAGAGGCA	TGGAAGCTTT	TAAATTTAAA	CTTTTGGTTT	AATGTTTTTT	TTTTTTGCCT	1800
TAATAATATT	AGATAGTCCC	AAATGAAATW	ACCTATGAGA	CTAGGCTTTG	AGAATCAATA	1860
GATTCTTTTT	TTAAGAAATCT	TTTGGCTAGG	AGCGGTGTCT	CACGCCTGTA	ATTCCAGCAC	1920
CTTGAGAGGC	TGAGGTGGGC	AGATCACGAG	ATCAGGAGAT	CGAGACCATC	CTGGCTAACA	1980
CGGTGAAACC	CCATCTCTAC	TAAAAATACA	AAAACCTAGC	TGGGTGTGGT	GCGGGGTGCC	2040

140

TGTAGTCCCA GCTACTCAGG ARGCTGAGGC AGGAGAATGG CATGAACCCG GGAGGTGGAG	2100
GTTGCAGTGA GCCGAGATCC GCCACTACAC TCCAGCCTGG GTGACAGAGC AAGACTCTGT	2160
CTCAAAAAAA AAAAAA AAAA	2184

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

TGCACGCATC GGCCAGTGTC TGTGCCACGT ACACTGACGC CCCCTGAGAT GTGCACGCCG	60
CACGCGCACG TTGCACGCGC GGCAGCGGCT TGGCTGGCTT GTAACGGCTT GCACGCGCAC	120
GCCGCCCCCG CATAACCGTC AGACTGGCCT GTAACGGCTT GCAGGCGCAC GCCGACGCG	180
CGTAACGGCT TGGCTGCCCT GTAACGGCTT GCACGTGCAT GCTGCACGCG CCGTAACGGC	240
TTGGCTGGCA TGTAGCCGCT TGGCTTGGCT TTGCATTYTT TGCTKGGCTK GCGGTGKTY	300
TCTTGATTG ACGCTTCCTC CTTGGATKGA CGTTTCCTCC TTGGATKGAC GTTTCYTYTY	360
TCGCGTTCCT TTGCTGGACT TGACCTTTYT TCTGCTGGGT TTGGCATTCC TTTGGGGTGG	420
GCTGGGTGTT TTCTCCGGGG GGGKTKGCCC TTCTGGGGT GGGCGTGGGK CGCCCCCAGG	480
GGGCGTGGGC TTTCCCCGGG TGGGTGTGGG TTTTCCTGGG GTGGGCTGGG CTGTGCTGGG	540
ATCCCCCTGC TGGGGTTGGC AGGGATTGAC TTTTTCTTC AACAGATTG GAAACCCGGA	600
GTAACNTGCT AGTTGGTGAA ACTGGTTGGT AGACGCGATC TGCTGGTACT ACTGTTTCTC	660
CTGGCTGTTA AAAGCAGATG GTGGCTGAGG TTGATTCAAT GCCGGCTGCT TCTTCTGTGA	720
AGAAGCCATT TGGTCTCAGG AGCAAGATGG GCAAGTGGTG CCCCACTGCT TCCCCTGCTG	780
CAGGGGGAGC GGCAAGAGCA ACGTGGGCAC TTCTGGAGAC CACAACGACT CCTCTGTGAA	840
GACGCTTGGG AGCAAGAGGT GCAAGTGGTG CTGCCCCACTG CTTCCCCCTGC TGCAGGGGAG	900
CGGCAAGAGC AACGTGGKCG CTTGGGGAGA CTACGATGAC AGCGCCTTCA TGGAKCCCAG	960
GTACCACGTC CRTGGAGAAG ATCTGGACAA GCTCCACAGA GCTGCCTGGT GGGGTAAAGT	1020
CCCCAGAAAG GATCTCATCG TCATGCTCAG GGACACTGAY GTGAACAAGA RGGACAAGCA	1080
AAAGAGGACT GCTCTACATC TGGCCTCTGC CAATGGGAAT TCAGAAGTAG TAAAACTCGT	1140
GCTGGACAGA CGATGTCAAC TTAATGTCTT TGACAACAAA AAGAGGACAG CTCTGACAAA	1200
GGCCGTACAA TGCCAGGAAG ATGAATGTGC GTTAATGTTG CTGGAACATG GCACTGATCC	1260
AAATATTCCA GATGAGTATG GAAATACCAC TCTACACTAT GCTGTCTACA ATGAAGATAA	1320
TTTAATGGCC AAAGCACTGC TCTTATACGG TGCTGATATC GAATCAAAAA ACAAGGTATA	1380
GATCTACTAA TTTTATCTTC AAAATACTGA AATGCATTCA TTTTAACATT GACGTGTGTA	1440
AGGGCCAGTC TTCCGTATTT GGAAGCTCAA GCATAACTTG AATGAAAATA TTTTGAAATG	1500
ACCTAATTAT CTAAGACTTT ATTTTAAATA TTGTTATTTT CAAAGAAGCA TTAGAGGGTA	1560
CAGTTTTTTT TTTTTAAATG CACTTCTGGT AAATACTTTT GTTGAAAACA CTGAATTTGT	1620
AAAAGGTAAT ACTTACTATT TTTCAATTTT TCCCTCCTAG GATTTTTTTC CCCTAATGAA	1680
TGTAAGATGG CAAAATTTGC CCTGAAATAG GTTTTACATG AAAACTCCAA GAAAAGTTAA	1740
ACATGTTTCA GTGAATAGAG ATCCTGCTCC TTTGGCAAGT TCCTAAAAAA CAGTAATAGA	1800
TACGAGGTGA TGCGCCTGTC AGTGGCAAGG TTTAAGATAT TTCTGATCTC GTGCC	1855

CLAIMS

1. An isolated DNA molecule, comprising:

(a) a nucleotide sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297;

(b) a variant of said nucleotide sequence that contains one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide positions, such that the antigenic and/or immunogenic properties of the polypeptide encoded by the nucleotide sequence are retained; or

(c) a nucleotide sequence encoding an epitope of a polypeptide encoded by at least one sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297.

2. An isolated DNA molecule encoding an epitope of a polypeptide, wherein said polypeptide is encoded by a nucleotide sequence that:

(a) hybridizes to a sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297 under stringent conditions; and

(b) is at least 80% identical to a sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297.

3. An isolated DNA molecule encoding an epitope of a polypeptide, wherein said polypeptide is encoded by:

(a) a nucleotide sequence transcribed from the sequence of SEQ ID NO: 141; or

(b) a variant of said nucleotide sequence that contains one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide positions, such that the antigenic and/or immunogenic properties of the polypeptide encoded by the nucleotide sequence are retained.

4. An isolated DNA or RNA molecule comprising a nucleotide sequence complementary to a DNA molecule according to any one of claims 1-3.

5. A recombinant expression vector comprising a DNA molecule according to any one of claims 1-3.

6. A host cell transformed or transfected with an expression vector according to claim 5.

7. A polypeptide comprising an amino acid sequence encoded by a DNA molecule according to any one of claims 1-3.

8. A polypeptide according to claim 7 wherein said polypeptide comprises an epitope of an amino acid sequence encoded by at least one nucleotide sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297.

9. A monoclonal antibody that binds to a polypeptide according to claim 7.

10. A method for determining the presence of breast cancer in a patient comprising detecting, within a biological sample, at least one polypeptide according to claim 7, and therefrom determining the presence of breast cancer in the patient.

11. A method for determining the presence of breast cancer in a patient comprising detecting within a biological sample, at least one polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

12. The method of claims 10 or 11 wherein the biological sample is a portion of a breast tumor.

13. The method of claim 10 wherein the step of detecting comprises contacting the biological sample with a monoclonal antibody according to claim 9.

14. The method of claim 11 wherein the step of detecting comprises contacting the biological sample with a monoclonal antibody that binds to a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

15. A method for determining the presence of breast cancer in a patient comprising detecting, within a biological sample, an RNA molecule encoding at least one polypeptide according to claim 7, and therefrom determining the presence of breast cancer in the patient.

16. A method for determining the presence of breast cancer in a patient comprising detecting, within a biological sample, at least one RNA molecule encoding a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions; and therefrom determining the presence of breast cancer in the patient.

17. The method of claims 15 or 16 wherein the biological sample is a portion of a breast tumor.

18. The method of claim 15 wherein the step of detecting comprises:

(a) preparing cDNA from RNA molecules within the biological sample;

and

(b) specifically amplifying cDNA molecules that are capable of encoding at least a portion of a polypeptide according to claim 7, and therefrom determining the presence of breast cancer in the patient.

19. The method of claim 16 wherein the step of detecting comprises:

(a) preparing cDNA from RNA molecules within the biological sample;

and

(b) specifically amplifying cDNA molecules that are capable of encoding at least a portion of a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions; and therefrom determining the presence of breast cancer in the patient.

20. A method for monitoring the progression of breast cancer in a patient, comprising:

(a) detecting an amount, in a biological sample, of at least one polypeptide according to claim 7 at a first point in time;

(b) repeating step (a) at a subsequent point in time; and

(c) comparing the amounts of polypeptide detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient.

21. A method for monitoring the progression of breast cancer in a patient, comprising:

(a) detecting in a biological sample an amount of at least one polypeptide at a first point in time, the polypeptide being encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions;

(b) repeating step (a) at a subsequent point in time; and

(c) comparing the amounts of polypeptide detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient.

22. The method of claims 20 or 21 wherein the biological sample is a portion of a breast tumor.

23. The method of claim 20 wherein the step of detecting comprises contacting a portion of the biological sample with a monoclonal antibody according to claim 9.

24. The method of claim 21 wherein the step of detecting comprises contacting the biological sample with a monoclonal antibody that binds to a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252,

256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

25. The method of claim 20 wherein said polypeptide comprises an epitope of an amino acid sequence encoded by at least one nucleotide sequence selected from the group consisting of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291-297.

26. A method for monitoring the progression of breast cancer in a patient, comprising:

- (a) detecting an amount, within a biological sample, of at least one RNA molecule encoding a polypeptide according to claim 7 at a first point in time;
- (b) repeating step (a) at a subsequent point in time; and
- (c) comparing the amounts of RNA molecules detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient.

27. The method of claim 26 wherein the step of detecting comprises:

- (a) preparing cDNA from RNA molecules within the biological sample;
- and
- (b) specifically amplifying cDNA molecules that are capable of encoding at least a portion of a polypeptide according to claim 7.

28. A method for monitoring the progression of breast cancer in a patient, comprising:

- (a) detecting an amount, within a biological sample, of at least one RNA molecule at a first point in time, the RNA molecule encoding a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270,

274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions;

- (b) repeating step (a) at a subsequent point in time; and
- (c) comparing the amounts of RNA molecules detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient.

29. A pharmaceutical composition, comprising a polypeptide according to claim 7 and a physiologically acceptable carrier.

30. A pharmaceutical composition for inhibiting the development of breast cancer, comprising a polypeptide and a physiologically acceptable carrier, the polypeptide being encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

31. A vaccine, comprising a polypeptide according to claim 7 and an immune response enhancer.

32. A vaccine, comprising a DNA molecule according to any one of claims 1-3.

33. A vaccine, comprising a recombinant expression vector comprising a DNA molecule according to any one of claims 1-3.

34. A vaccine for inhibiting the development of breast cancer, comprising a polypeptide and an immune response enhancer, the polypeptide being encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270,

274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

35. A pharmaceutical composition according to either of claims 29 or 30, for use in the manufacture of a medicament for inhibiting the development of breast cancer in a patient, comprising administering to a patient.

36. A vaccine according to any one of claims 31-34, for use in the manufacture of a medicament for inhibiting the development of breast cancer in a patient.

37. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies according to claim 9; and
- (b) a detection reagent.

38. A diagnostic kit comprising:

- (a) one or more monoclonal antibodies that bind to a polypeptide encoded by a nucleotide sequence selected from the group consisting of sequences provided in SEQ ID 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 and 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290; and
- (b) a detection reagent.

39. The kit of any one of claims 37 or 38 wherein the monoclonal antibody(s) are immobilized on a solid support.

40. A diagnostic kit comprising two polymerase chain reaction primers, at least one of the primers being specific for an RNA molecule according to claim 4.

41. The kit of claim 40, wherein at least one of the polymerase chain reaction primers comprises at least about 10 contiguous nucleotides of an RNA molecule according to claim 4.

42. A diagnostic kit comprising two polymerase chain reaction primers, at least one of the primers being specific for an RNA molecule encoding a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

43. The kit of claim 42, wherein at least one of the polymerase chain reaction primers comprises at least about 10 contiguous nucleotides of an RNA molecule encoding a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

44. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe containing at least about 15 contiguous nucleotides of a DNA molecule according to claim 4.

45. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe comprising at least about 15 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NOS:78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

46. A diagnostic kit comprising at least one oligonucleotide probe specific for a DNA molecule according to claim 4.

47. The kit of claim 46, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule according to claim 4.

48. A diagnostic kit comprising at least one oligonucleotide probe specific for a DNA sequence selected from the group consisting of SEQ ID NOS:78-86, 144, 145,

153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

49. The kit of claim 48, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NOS:78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

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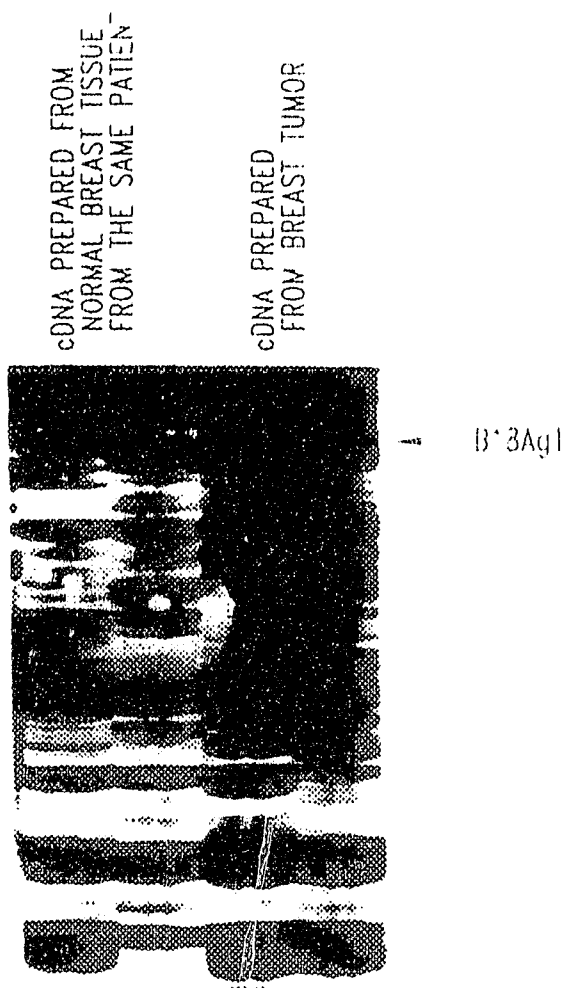


Fig. 1

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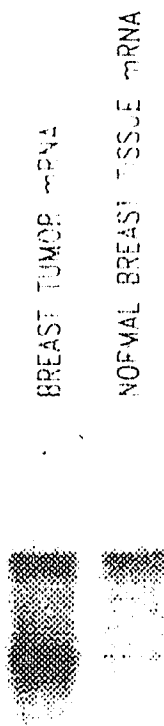
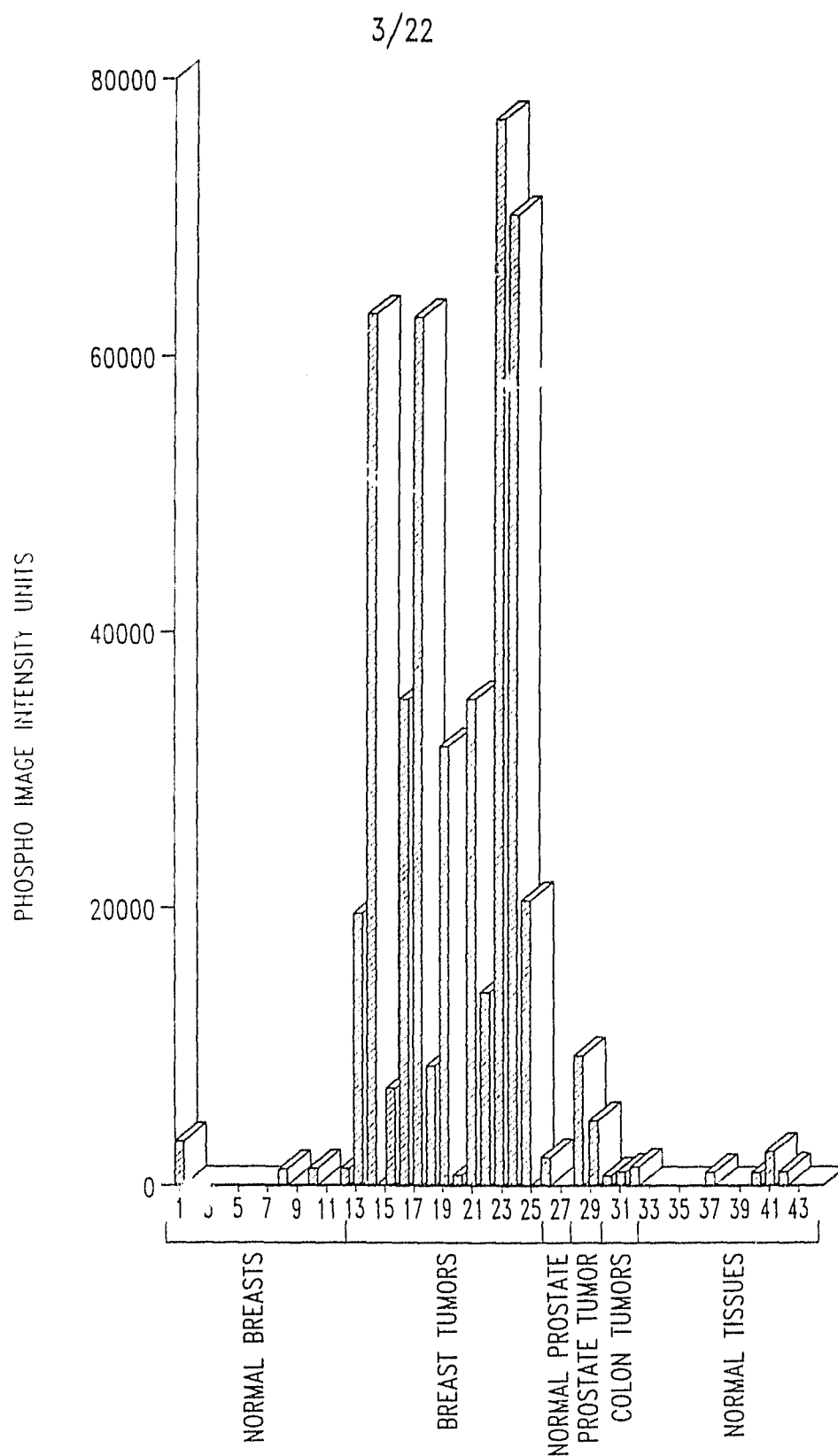
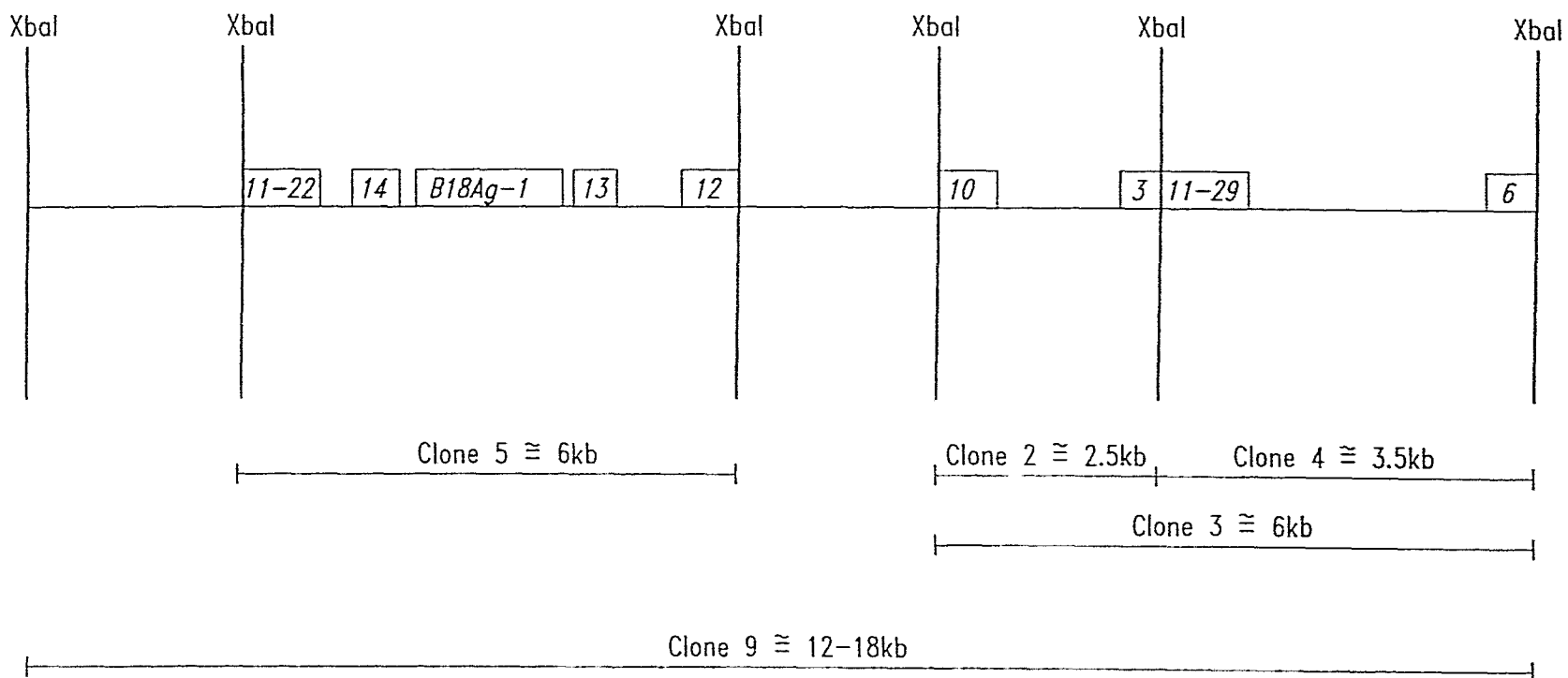


Fig. 2

*Fig. 3*

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GENOMIC CLONE MAP*Fig. 4*

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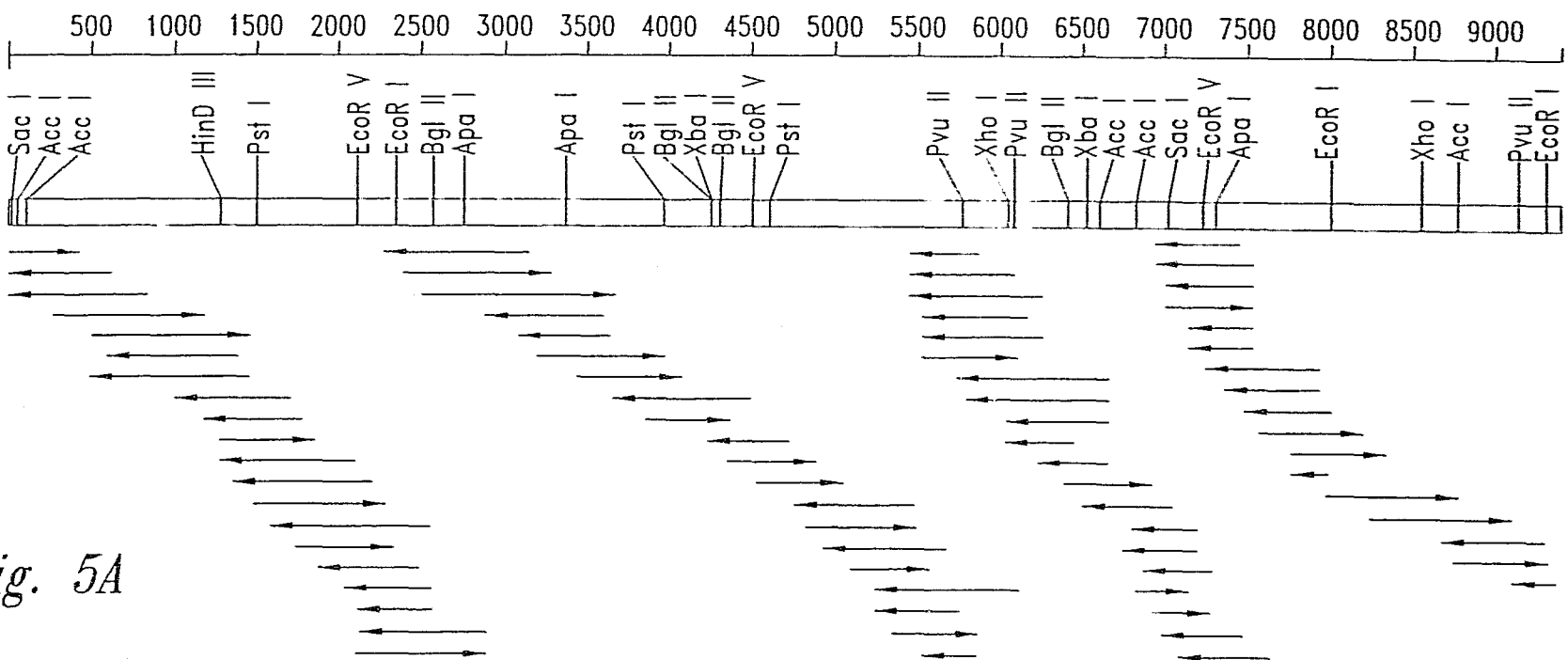


Fig. 5A

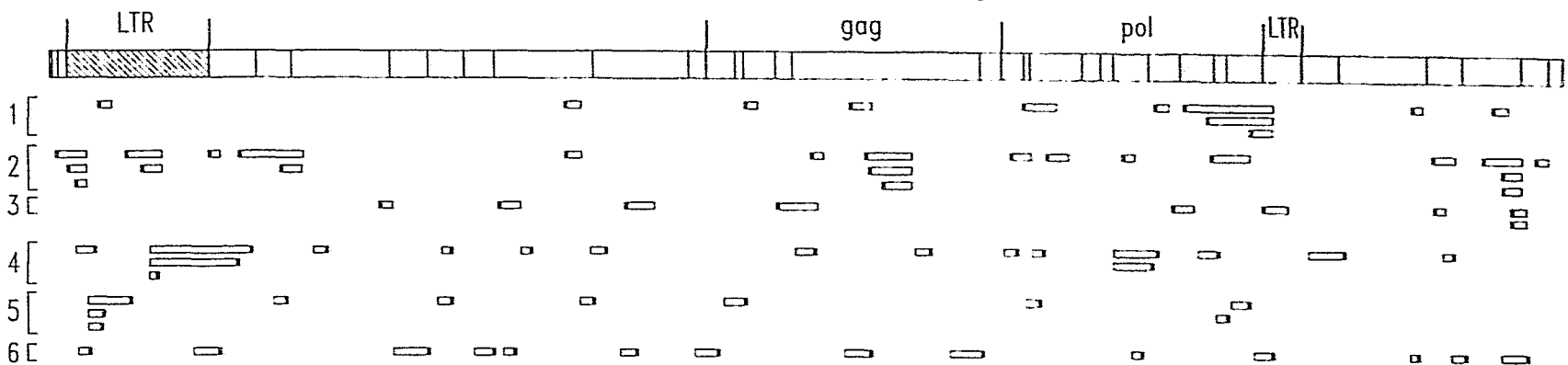


Fig. 5B

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B18Ag1

TTA	GAG	ACC	CAA	TTG	GGA	CCT	AAT	TGG	GAC	CCA	AAT	TTC	TCA	AGT	GGA	48
Leu	Glu	Thr	Gln	Leu	Gly	Pro	Asn	Trp	Asp	Pro	Asn	Phe	Ser	Ser	Gly	
1				5				10					15			
GGG	AGA	ACT	TTT	GAC	GAT	TTC	CAC	CGG	TAT	CTC	CTC	GTG	GGT	ATT	CAG	96
Gly	Arg	Thr	Phe	Asp	Asp	Phe	His	Arg	Tyr	Leu	Leu	Val	Gly	Ile	Gln	
			20					25				30				
GGA	GCT	GCC	CAG	AAA	CCT	ATA	AAC	TTG	TCT	AAG	GCG	ATT	GAA	GTC	GTC	144
Gly	Ala	Ala	Gln	Lys	Pro	Ile	Asn	Leu	Ser	Lys	Ala	Ile	Glu	Val	Val	
			35				40					45				
CAG	GGG	CAT	GAT	GAG	TCA	CCA	GGA	GTG	TTT	TTA	GAG	CAC	CTC	CAG	GAG	192
Gln	Gly	His	Asp	Glu	Ser	Pro	Gly	Val	Phe	Leu	Glu	His	Leu	Gln	Glu	
	50					55					60					
GCT	TAT	CGG	ATT	TAC	ACC	CCT	TTT	GAC	CTG	GCA	GCC	CCC	GAA	AAT	AGC	240
Ala	Tyr	Arg	Ile	Tyr	Thr	Pro	Phe	Asp	Leu	Ala	Ala	Pro	Glu	Asn	Ser	
65				70				75							80	
CAT	GCT	CTT	AAT	TTG	GCA	TTT	GTG	GCT	CAG	GCA	GCC	CCA	GAT	AGT	AAA	288
His	Ala	Leu	Asn	Leu	Ala	Phe	Val	Ala	Gln	Ala	Ala	Pro	Asp	Ser	Lys	
				85				90						95		
AGG	AAA	CTC	CAA	AAA	CTA	GAG	GGA	TTT	TGC	TGG	AAT	GAA	TAC	CAG	TCA	336
Arg	Lys	Leu	Gln	Lys	Leu	Glu	Gly	Phe	Cys	Trp	Asn	Glu	Tyr	Gln	Ser	
			100				105					110				
GCT	TTT	AGA	GAT	AGC	CTA	AAA	GGT	TTT								363
Ala	Phe	Arg	Asp	Ser	Leu	Lys	Gly	Phe								
		115					120									

Fig. 6

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B17Ag1

GC TGGGCACAGT GGCTCATACC TGTAATCCTG ACCGTTTCAG AGGCTCAGGT	60
CG CTTGAGCCCA AGATTTCAAG ACTAGTCTGG GTAACATAGT GAGACCCTAT	120
AA AAATAAAAAA ATGAGCCTGG TGTAGTGGCA CACACCAGCT GAGGAGGGAG	180
CT AGGAGA	196

Fig. 7

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B17Ag2

GC TTGGGGGCTC TGACTAGAAA TTCAAGGAAC CTGGGATTCA AGTCCAAC TG	60
AC TTACACTGTG GNCTCCAATA AACTGCTTCT TTCCTATTCC CTCTCTATTA	120
AA GGAAAACGAT GTCTGTGTAT AGCCAAGTCA GNTATCCTAA AAGGAGATAC	180
AT TAAATATCAG AATGTAAAAC CTGGGAACCA GGTTC CCAGC CTGGGATTAA	240
CA AGAAGACTGA ACAGTACTAC TGTGAAAAGC CCGAAGNGGC AATATGTTCA	300
TT GAAGGATGGC TGGGAGAATG AATGCTCTGT CCCCAGTCC CAAGCTCACT	360
CT CCTTTATAGC CTAGGAGA	388

Fig. 8

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B13Ag2a

GC CTATAATCAT GTTTCTCATT ATTTTCACAT TTTATTAACC AATTTCTGTT	60
AA AATATGAGGG AAATATATGA AACAGGGAGG CAATGTTTCAG ATAATTGATC	120
TG ATTTCTACAT CAGATGCTCT TTCCTTTTCTT GTTTATTTCC TTTTATTTT	180
GG TCGAATGTAA TAGCTTTGTT TCAAGAGAGA GTTTTGGCAG TTTCTGTAGC	240
CT GCTCATGTCT CCAGGCATCT ATTTGCACTT TAGGAGGTGT CGTGGGAGAC	300
CT ATTTTTTCCA TATTTGGGCA ACTACTA	337

Fig. 9

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B13Ag1b

GC CATACAGTGC CTTTCCATTT ATTTAACCCC CACCTGAACG GCATAAACTG	60
GC TGGTGTTTTT TACTGTAAAC AATAAGGAGA CTTTGCTCTT CATTTAAACC	120
AT TTCATATTTT ACGCTCGAGG GTTTTTACCG GTTCCTTTTT ACACTCCTTA	180
TT TAAGTCGTTT GGAACAAGAT ATTTTTTCTT TCCTGGCAGC TTTTAACATT	240
TT TGTGTCTGGG GGACTGCTGG TCACTGTTTC TCACAGTTGC AAATCAAGGC	300
CC AAGAAAAAAA AATTTTTTTG TTTTATTTGA AACTGGACCG GATAAACGGT	360
CG GCTGCTGTAT ATAGTTTTAA ATGGTTTATT GCACCTCCTT AAGTTGCACT	420
GG GGGGNTTTTG NATAGAAAGT NTTTANTCAC ANAGTCACAG GGACTTTTNT	480
NA CTGAGCTAAA AAGGGCTGNT TTTCGGGTGG GGGCAGATGA AGGCTCACAG	540
TC TCTTAGAGGG GGGAACTNCT A	571

Fig. 10

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B13Ag1a

TA ATAACTTAAA TATATTTTGA TCACCCACTG GGGTGATAAG ACAATAGATA	60
TT TCCAAAAAGC ATAAAACCAA AGTATCATAC CAAACCAAAT TCATACTGCT	120
CC GCACTGAAAC TTCACCTTCT AACTGTCTAC CTAACCAAAT TCTACCCTTC	180
GG TGC GTGCTCA CTACTCTTTT TTTTTTTTTT TTTNTTTTGG AGATGGAGTC	240
CA GCCCAGGGGT GGAGTACAAT GGCACAACCT CAGCTCACTG NAACCTCCGC	300
TT CATGAGATTC TCCTGNTTCA GCCTTCCCAG TAGCTGGGAC TACAGGTGTG	360
TG CCTGGNTAAT CTTTTTTNGT TTTNGGGTAG AGATGGGGGT TTTACATGTT	420
TG GTNTCGAACT CCTGACCTCA AGTGATCCAC CCACCTCAGG CTCCCAAAGT	480
TA CAGACATGAG CCACTGNGCC CAGNCCTGGT GCATGCTCAC TTCTCTAGGC	540
	548

Fig. 11

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B11Ag1

TG CACATGCAGA ATATTCTATC GGTACTTCAG CTATTACTCA TTTTGATGGC	60
AG CCTATCCTCA AGATGAGTAT TTAGAAAGAA TTGATTTAGC GATAGACCAA	120
GC ACTCTGACTA CACGAAATTG TTCAGATGTG ATGGATTTAT GACAGTTGAT	180
GA GATTATTAAG TGATTATTTT AAAGGGAATC CATTAAATTCC AGAATATCTT	240
TC AAGATGATAT AGAAATAGAA CAGAAAGAGA CTACAAATGA AGATGTATCA	300
TA TTGAAGAGCC TATAGTAGAA AATGAATTAG CTGCATTTAT TAGCCTTACA	360
TT TTCCTGATGA ATCTTATATT CAGCCATCGA CATAGCATTG CCTGATGGGC	420
GA ATAATAGAAA CTGGGTGCGG GGCTATTGAT GAATTCATCC NCAGTAAATT	480
AC AAAATATAAC TCGATTGCAT TTGGATGATG GAATACTAAA TCTGGCAAAA	540
GG AGCTACTAGT AACCTCTCTT TTTGAGATGC AAAATTTTCT TTTAGGGTTT	600
CT ACTTTACGGA TATTGGAGCA TAACGGGA	638

Fig. 12

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA3c

ACTGATGGAT GTCGCCGGAG GCGAGGGGCC TTATCTGATG CTCGGCTGCC TGTTTCGTGAT 60
GTGCGCGGCG ATTGGGCTGT TTATCTCAAA CACCGCCACG GCGGTGCTGA TGGCGCCTAT 120
TGCCTTAGCG GCGGCGAAGT CAATGGGCGT CTCACCCTAT CCTTTTGCCA TGGTGGTGGC 180
GATGGCGGCT TCGGCGGCGT TTATGACCCC GGTCTCCTCG CCGGTTAACA CCCTGGTGCT 240
TGGCCCTGGC AAGTACTCAT TTAGCGATTT TGTCAAATA GGCGTG 286

Fig. 13

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B9CG1

AG CAGCCCCTTC TTCTCAATTT CATCTGTCAC TACCCTGGTG TAGTATCTCA	60
CA TTTTATAGC CTCCTCCCTG GTCTGTCTTT TGATTTTCCT GCCTGTAATC	120
AC ATAAGTGCAA GTAAACATTT CTAAAGTGTG GTTATGCTCA TGTCACCTCCT	180
AA ATAGTTTCCA TTACCGTCTT AATAAAATTC GGATTTGTTC TTTNCTATTN	240
CA CCTATGACCG AA	262

Fig. 14

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B9CG3

AG CAAAGCCAGT GGTGGAGCT CTCTACTGTG TAAACTCCTA AACCAAGGCC	60
TA AATGGTGGCA GGATTTTAT TATAACATG TACCCATGCA AATTCCTAT	120
GA TATATTCTTC TACATTTAAA CAATAAAAAT AATCTATTTT TAAAAGCCTA	180
AG TTAGGTAAGA GTGTTTAATG AGAGGGTATA AGGTATAAAT CACCAGTCAA	240
TG CCTATGACCG A	261

Fig. 15

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B2CA2

GG GCATGGACGC AGACGCCTGA CGTTTGGCTG AAAATCTTTC ATTGATTCGT	60
AT AGGAAAATTC CCAAAGAGGG AATGTCCTGT TGCTCGCCAG TTTTNTGTT	120
GG ANAAGGCAAN TAGCTCTTCA GACTATTGGN ATTNTCGTTC GGTCTTCTGC	180
CG NCTTGCNANG ATCTTCAT	208

Fig. 16

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NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA1

GG GCATGGACGC AGACGCCTGA CGTTTGGCTG AAAATCTTTC ATTGATTCGT	60
AT AGGAAAATTC CCAAAGAGGG AATGTCCTGT TGCTCGCCAG TTTTNTGTT	120
GG ANAAGGCAAN GAGCTCTTCA GACTATTGGN ATTNTCGTTC GGTCTTCTGC	180
CG NCTTGCAANG ATCTTCAT	208

Fig. 17

18/22

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA2

GG GCATGGACGC AGACGCCTGA CGTTTGCTG AAAATCTTTC ATTGATTCTG	60
AT AGGAAAATTC CCAAAGAGGG AATGTCCTGT TGCTCGCCAG TTTTNTGTT	120
GG ANAAGGCAAN GAGCTCTTCA GACTATTGGN ATTNTCGTTC GGTCTTCTGC	180
CG NCTTGCAANG ATCTTCAT	208

Fig. 18

19/22

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA3

AG GGAGCAAGGA GAAGGCATGG AGAGGCTCAN GCTGGTCCTG GCCTACGACT	60
CT GTCGCCGGGG ATGGTGGAGA ACTGAAGCGG GACCTCCTCG AGGTCCTCCG	120
TC NCCGTCCAGG AGGAGGGTCT TTCCGTGGTC TNGGAGGAGC GGGGGGAGAA	180
TC ATGGTCNACA TCCC	204

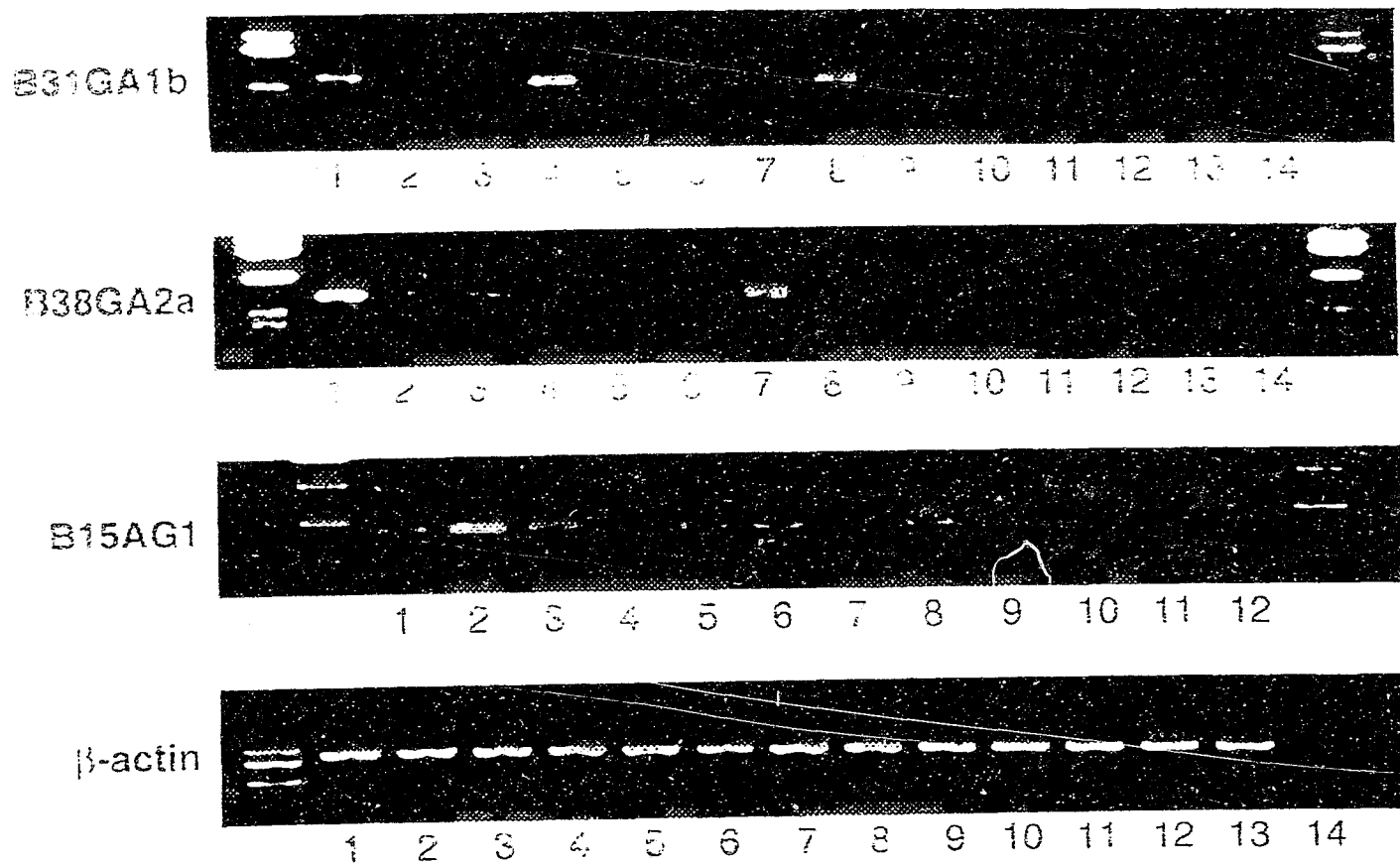
Fig. 19

20/22

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B4CA1

TC AGGAGCGGGT AGAGTGGCAC CATTGAGGGG ATATTCAAAA ATATTATTTT	60
TG ATAGTTGCTG AGTTTTTCTT TGACCCATGA GTTATATTGG AGTTTATTTT	120
CC AATCGCATGG ACATGTTAGA CTTATTTTCT GTTAATGATT NCTATTTTTA	180
GA TTTGAGAAAT TGGTTNTTAT TATATCAATT TTTGGTATTT GTTGAGTTTG	240
GC TTAGTATGTG ACCA	264

Fig. 20

*Fig. 21A*

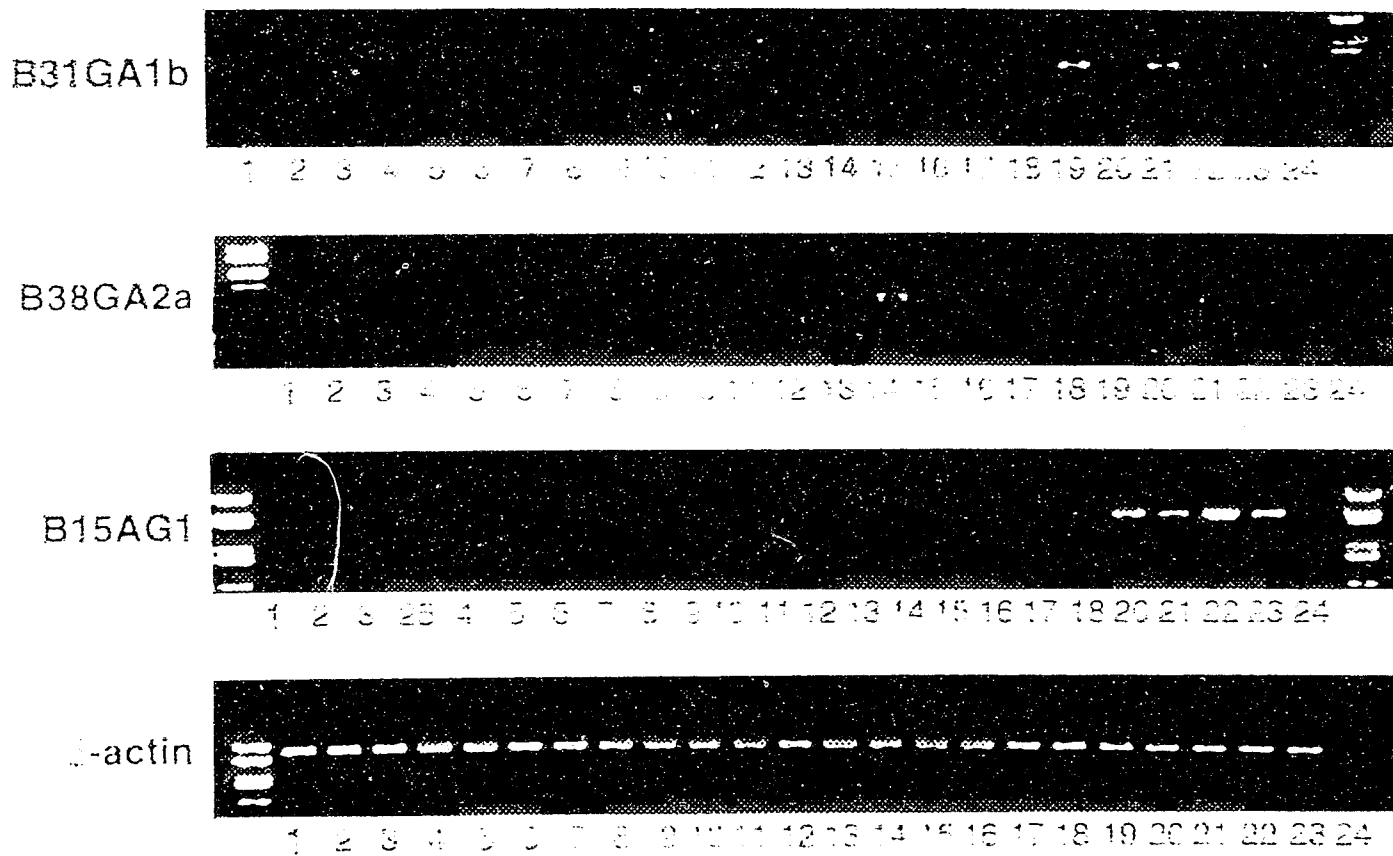


Fig. 21B