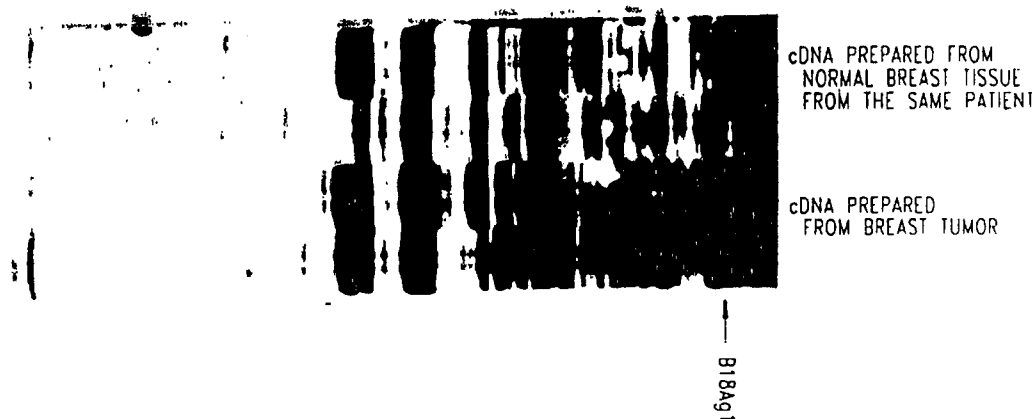




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(54) Title: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER



(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 in a patient.

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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 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 polynucleotides are provided, comprising (a) a nucleotide sequence preferentially expressed in breast cancer tissue, relative to normal tissue; (b) a variant of such a sequence, as defined below; or (c) a nucleotide sequence encoding an epitope of a polypeptide encoded by at least one of the above sequences. In one embodiment, the isolated polynucleotide comprises a human endogenous retroviral sequence recited in SEQ ID NO:1. In other embodiments, the isolated polynucleotide comprises a 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, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317.

In related embodiments, the isolated polynucleotide 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, 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, 291-298, 301-303, 307, 313, 314, 316 and 317 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, 291-298, 301-303, 307, 313, 314, 316 and 317.

In another embodiment, the present invention provides an isolated polynucleotide 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 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 polynucleotide as described above are also provided.

10 In related aspects, the present invention provides recombinant expression vectors comprising a polynucleotide 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 polynucleotide as described above, and monoclonal antibodies that bind to such polypeptides are provided. In certain embodiments, the inventive polypeptides 15 comprise an amino acid sequence selected from the group consisting of SEQ ID NO: 299, 300, 304-306, 308 and 315, and variants thereof as defined below.

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 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 25 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 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 30 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.

Diagnostic kits are also provided that comprise a first polymerase chain reaction primer and a second polymerase chain reaction primer, at least one of the primers being specific for a polynucleotide described herein. In one embodiment, at least one of the primers comprises at least about 10 contiguous nucleotides of a polynucleotide as described above, or a polynucleotide encoding a polypeptide encoded by a 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 polynucleotide described herein. In one embodiment, the probe comprises at least about 15 contiguous nucleotides of a polynucleotide as described above, or a polynucleotide 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 immunostimulant 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.

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
5 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 NO:3 - SEQ ID NO:10) relative to B18Ag1.

Figures 5A and 5B show the sequencing strategy, genomic organization
10 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.

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

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

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

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

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

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

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

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

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

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

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

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

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

10 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 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).

20 Figure 22 shows the recognition of a B11Ag1 peptide (referred to as B11-8) by an anti-B11-8 CTL line.

Figure 23 shows the recognition of a cell line transduced with the antigen B11Ag1 by the B11-8 specific clone A1.

25 Figure 24 shows recognition of a lung adenocarcinoma line (LT-140-22) and a breast adenocarcinoma line (CAMA-1) by the B11-8 specific clone A1.

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. The compositions described herein include polypeptides, polynucleotides 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. Polynucleotides 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. 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.

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). 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 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, 291-298, 301-303, 307, 313, 314, 316 and 317.

As used herein, the term "polypeptide" encompasses amino acid chains of any length, including 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.

5 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
10 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,
15 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.

20 The term "polynucleotide(s)," as used herein, means a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases and includes DNA and corresponding RNA molecules, including HnRNA and mRNA molecules, both sense and anti-sense strands, and comprehends cDNA, genomic DNA and recombinant DNA, as well as wholly or partially synthesized polynucleotides. An HnRNA molecule contains
25 introns and corresponds to a DNA molecule in a generally one-to-one manner. An mRNA molecule corresponds to an HnRNA and DNA molecule from which the introns have been excised. A polynucleotide may consist of an entire gene, or any portion thereof. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes
30 all such operable anti-sense fragments.

The compositions and methods of the present invention also encompass variants of the above polypeptides and polynucleotides.

A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the antigenic properties of the polypeptide are retained. In a preferred embodiment, variant polypeptides differ from an identified sequence by substitution, deletion or addition of five amino acids or fewer. Such variants may generally be identified by modifying one of the above polypeptide sequences, and evaluating the antigenic properties of the modified polypeptide using, for example, the representative procedures described herein. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity (determined as described below) to the identified polypeptides.

As used herein, 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; (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, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydrophobic nature of the polypeptide. For 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 polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or

additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity (determined as described below) to the recited sequence.

The breast tumor antigens provided by the present invention include variants that are encoded by DNA sequences which are substantially homologous to one or more of the DNA sequences specifically recited herein. "Substantial homology," as used herein, refers to DNA sequences that are capable of hybridizing under moderately stringent conditions. Suitable moderately stringent conditions include prewashing in a solution of 5X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5X SSC, overnight or, in the event of cross-species homology, at 45°C with 0.5X SSC; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS. Such hybridizing DNA sequences are also within the scope of this invention, as are nucleotide sequences that, due to code degeneracy, encode an immunogenic polypeptide that is encoded by a hybridizing DNA sequence.

Two nucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acid residues in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment

schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) Fast and sensitive multiple sequence alignments on a microcomputer *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) Optimal alignments in linear space *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) The neighbor joining method. A new method for reconstructing phylogenetic trees *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) Rapid similarity searches of nucleic acid and protein data banks *Proc. Natl. Acad., Sci. USA* 80:726-730.

Preferably, the “percentage of sequence identity” is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e. gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (i.e. the window size) and multiplying the results by 100 to yield the percentage of sequence identity. In general, polynucleotides 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 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 vector (e.g., the T-vector, Novagen, Madison, WI).

- 5 Polynucleotides 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 polynucleotide encoding a polypeptide as described herein (or a portion thereof) may be amplified from human genomic DNA, or from breast
10 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'CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO:127). An amplified portion of
15 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 the retroviral genome of which B18Ag1 is a part may be similarly prepared by screening
20 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 promoter, such as T7. The resulting constructs can be employed in a translation reaction, using techniques
25 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:11-86, 142-298, 301-303, 307, 313, 314, 316 and 317.

Recombinant polypeptides encoded by the DNA sequences described
30 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. 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
5 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 invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a polynucleotide that
10 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.

Such techniques may also be used to prepare polypeptides comprising epitopes or variants of the native polypeptides. For example, variants of a native
15 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 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
20 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 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
25 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 encompass amino acid sequences encoded by a polynucleotide 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,
30 200-204, 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, 291-298, 301-303, 307, 313, 314, 316 and 317, and variants of such polypeptides. Polypeptides within the scope of the present invention also include polypeptides (and epitopes thereof) encoded by DNA sequences that hybridize 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, 291-298, 301-303, 307, 313, 314, 316 and 317 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 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. Polynucleotides according to the present invention include molecules that encode any of the 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 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 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.

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 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 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 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 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 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.

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
5 preparation from the biological sample is submitted to gel electrophoresis, 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
10 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
15 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
20 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.

25 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
30 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
5 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 with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody,
10 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 methods known to those of ordinary skill in the art.

15 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 and bound second antibody is detected using the reporter group. The method employed
20 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 reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter
25 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 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
30 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 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
5 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 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
10 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 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
15 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 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
20 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 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
25 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 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,
30 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 the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 1 μ g. 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 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 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, 142-298 301-303, 307, 313, 314, 316 and 317, 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. 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 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 polynucleotide" 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 polynucleotide in question, or an oligonucleotide sequence that is anti-sense to a sequence that has at least about 80% identity, preferably at least about 90% and more preferably at least about 95%, identity to the polynucleotide 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 polynucleotide that encodes one of the polypeptides disclosed herein or that is anti-sense to a sequence that encodes one of the polypeptides disclosed herein. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a polynucleotide that encodes one of the polypeptides disclosed herein or that is anti-sense to a sequence that encodes 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 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 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.

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 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
5 measured at least 48 hours after injection, more preferably 48-72 hours.

The DTH reaction is a cell-mediated immune response, which is greater 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,
10 preferably greater than about 5.0 cm in diameter, is a positive response, indicative of breast cancer.

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
15 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 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 80™.

20 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 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
25 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, 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
30 herein may be used for the immunotherapy of breast cancer. In these aspects, the

compounds (which may be polypeptides, antibodies or polynucleotides) are 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 such compounds in combination with an immunostimulant, such as an adjuvant or a liposome (into which the compound is incorporated). An immunostimulant may be any substance that enhances or potentiates an immune response (antibody and/or cell-mediated) to an exogenous antigen. Examples of immunostimulants include adjuvants, biodegradable microspheres (*e.g.*, polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

Alternatively, a vaccine may contain DNA encoding one or more of the 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 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 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 cells.

While any suitable carrier known to those of ordinary skill in the art may
5 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 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,
10 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 immunostimulants may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a
15 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,
20 Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or
25 -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (*e.g.*, IFN- γ , TNF α , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast,
30 high levels of Th2-type cytokines (*e.g.*, IL-4, IL-5, IL-6 and IL-10) tend to favor the

induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Corixa Corporation (Seattle, WA; *see* US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555 and WO 99/33488. Immunostimulatory DNA sequences are also described, for example, by Sato et al., *Science* 273:352, 1996. Another preferred adjuvant is a saponin, preferably QS21 (Aquila Biopharmaceuticals Inc., Framingham, MA), which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

Other preferred adjuvants include Montanide ISA 720 (Seppic, France), SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series of adjuvants (*e.g.*, SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart, Belgium), Detox (Ribi ImmunoChem Research Inc., Hamilton, MT), RC-529 (Ribi ImmunoChem Research Inc., Hamilton, MT) and Aminoalkyl glucosaminide 4-phosphates (AGPs).

Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immunostimulant and a suitable carrier or excipient. The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule, sponge or gel (composed of polysaccharides, for example) that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology (*see, e.g.*, Coombes et al., *Vaccine* 14:1429-1438, 1996) and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane.

Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. Such carriers include microparticles of poly(lactide-co-glycolide), as well as polyacrylate, latex, starch, cellulose and dextran. Other delayed-release carriers include supramolecular biovectors, which comprise a non-liquid hydrophilic core (*e.g.*, a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (*see e.g.*, U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA

haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (see Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (see Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible

intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide encoding a polypeptide of the present invention (or portion or other variant thereof) such that the polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

Vaccines and pharmaceutical compositions may be presented in unit-dose or multi-dose containers, such as sealed ampoules or vials. Such containers are preferably hermetically sealed to preserve sterility of the formulation until use. In general, formulations may be stored as suspensions, solutions or emulsions in oily or aqueous vehicles. Alternatively, a vaccine or pharmaceutical composition may be stored in a freeze-dried condition requiring only the addition of a sterile liquid carrier

immediately prior to use.

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. In a preferred embodiment, the compounds are administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs. To prevent or slow 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 polynucleotides 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*. 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 100 µg 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.

5 Polypeptides disclosed herein may also be employed in adoptive immunotherapy for the treatment of cancer. Adoptive immunotherapy may be broadly classified into either active or passive immunotherapy. In active immunotherapy, treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (for
10 example, tumor vaccines, bacterial adjuvants, and/or cytokines).

In passive immunotherapy, treatment involves the delivery of biologic reagents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T lymphocytes (for
15 example, CD8+ cytotoxic T-lymphocyte, CD4+ T-helper, tumor-infiltrating lymphocytes), killer cells (Natural Killer cells, lymphokine-activated killer cells), B cells, or antigen presenting cells (such as dendritic cells and macrophages) expressing the disclosed antigens. The polypeptides disclosed herein may also be used to generate antibodies or anti-idiotypic antibodies (as in U.S. Patent No. 4,918,164), for passive
20 immunotherapy.

The predominant method of procuring adequate numbers of T-cells for adoptive immunotherapy is to grow immune T-cells *in vitro*. Culture conditions for expanding single antigen-specific T-cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. These *in vitro* culture conditions
25 typically utilize intermittent stimulation with antigen, often in the presence of cytokines, such as IL-2, and non-dividing feeder cells. As noted above, the immunoreactive polypeptides described herein may be used to rapidly expand antigen-specific T cell cultures in order to generate sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage or B-cells, may be pulsed with
30 immunoreactive polypeptides or transfected with a polynucleotide sequence(s), using

standard techniques well known in the art. For cultured T-cells to be effective in therapy, the cultured T-cells must be able to grow and distribute widely and to survive long term *in vivo*. Studies have demonstrated that cultured T-cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation
5 with antigen supplemented with IL-2 (see, for example, Cheever et al. *Ibid*).

The polypeptides disclosed herein may also be employed to generate and/or isolate tumor-reactive T-cells, which can then be administered to the patient. In one technique, antigen-specific T-cell lines may be generated by *in vivo* immunization with short peptides corresponding to immunogenic portions of the disclosed
10 polypeptides. The resulting antigen specific CD8+ CTL clones may be isolated from the patient, expanded using standard tissue culture techniques, and returned to the patient.

Alternatively, peptides corresponding to immunogenic portions of the polypeptides may be employed to generate tumor reactive T cell subsets by selective *in vitro* stimulation and expansion of autologous T cells to provide antigen-specific T cells
15 which may be subsequently transferred to the patient as described, for example, by Chang et al. (*Crit. Rev. Oncol. Hematol.*, 22(3), 213, 1996).

In another embodiment, syngeneic or autologous dendritic cells may be pulsed with peptides corresponding to at least an immunogenic portion of a polypeptide disclosed herein. The resulting antigen-specific dendritic cells may either be transferred
20 into a patient, or employed to stimulate T cells to provide antigen-specific T cells which may, in turn, be administered to a patient. The use of peptide-pulsed dendritic cells to generate antigen-specific T cells and the subsequent use of such antigen-specific T cells to eradicate tumors in a murine model has been demonstrated by Cheever et al. ("Therapy With Cultured T Cells: Principles Revisited," *Immunological Reviews*,
25 157:177, 1997).

Additionally vectors expressing the disclosed polynucleotides may be introduced into stem cells taken from the patient and clonally propagated *in vitro* for autologous transplant back into the same patient. In one embodiment, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a
30 commercially available cell separation system, such as CellPro Incorporated's (Bothell,

WA) CEPRATE™ system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

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.

5 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 spans
10 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 in
20 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 experiments
25 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 B18Ag1
30 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 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 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.

5 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
10 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 obtained (SEQ ID NO:227) which contains minor nucleotide differences (less than 1%)
15 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 converted into cDNA using a (dT)₁₂AG anchored 3' primer, as described above.
20 Differential display PCR was then executed using the randomly chosen primers of 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 (Invitrogen, San Diego, CA) and sequenced. The sequences are provided in SEQ ID
25 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 further studies. Comparison of the sequence of SEQ ID NO: 290 with those in the gene
30 bank as described above, revealed homology to the known human β -A activin gene.

Further studies led to the isolation of the full-length cDNA sequence for the antigen B21GT2 (also referred to as B311D; originally identified partial cDNA sequence provided in SEQ ID NO: 56). The full-length sequence is provided in SEQ ID NO: 307, with the corresponding amino acid sequence being provided in SEQ ID NO: 308.

5 Further studies led to the isolation of a splice variant of B311D. The B311D clone of SEQ ID NO: 316 was sequenced and a XhoI/NotI fragment from this clone was gel purified and 32P-cDTP labeled by random priming for use as a probe for further screening to obtain additional B311D gene sequence. Two fractions of a human breast tumor cDNA bacterial library were screened using standard techniques. One of the
10 clones isolated in this manner yielded additional sequence which includes a poly A+ tail. The determined cDNA sequence of this clone (referred to as B311D_BT1_1A) is provided in SEQ ID NO: 317. The sequences of SEQ ID NO: 316 and 317 were found to share identity over a 464 bp region, with the sequences diverging near the poly A+ sequence of SEQ ID NO: 317.

15 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, 221-240, 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
20 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, several different splice forms of the antigen B11Ag1 (also referred to as B305D) were isolated, with each of the various splice forms containing slightly different versions of the B11Ag1 coding frame. Splice junction
25 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-, normal prostate- and normal testis-specific. The determined cDNA sequences
30 for the isolated protein coding exons are provided in SEQ ID NO: 292-298, respectively.

The predicted amino acid sequences corresponding to the sequences of SEQ ID NO: 292 and 298 are provided in SEQ ID NO: 299 and 300. Additional studies using rapid amplification of cDNA ends (RACE), a 5' specific primer to one of the splice forms of B11Ag1 provided above and a breast adenocarcinoma, led to the isolation of three additional, related, splice forms referred to as isoforms B11C-15, B11C-8 and B11C-9,16. The determined cDNA sequences for these isoforms are provided in SEQ ID NO: 301-303, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 304-306.

In subsequent studies on B305D isoform A (cDNA sequence provided in SEQ ID NO: 292), the cDNA sequence (provided in SEQ ID NO: 313) was found to contain an additional guanine residue at position 884, leading to a frameshift in the open reading frame. The determined DNA sequence of this ORF is provided in SEQ ID NO: 314. This frameshift generates a protein sequence (provided in SEQ ID NO: 315) of 293 amino acids that contains the C-terminal domain common to the other isoforms of B305D but that differs in the N-terminal region.

EXAMPLE 2

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

5 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
10 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 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
15 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) and B18Ag1-3 (5'CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO: 127) yield a single 151 bp amplification product.

20

EXAMPLE 4

IDENTIFICATION OF B-CELL AND T-CELL EPITOPES OF B18AG1

This Example illustrates the identification of B18Ag1 epitopes.

25 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. 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
30 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)).

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 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 response in animals (mice, rats, rabbits, chimps etc.) following immunization *in vivo*. Generation of a 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 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 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 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, broken down according to predicted HLA Class I MHC binding antigen, is shown below:

5

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

SSGGRTFDDFHRYLLVGI

QGAAQKPINLSKXIEVVQGHDE

SPGVFLEHLQEAYRIYTPFDLSA

10

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

YLLVGIQGA

GAAQKPINL

NLSKXIEVV

15

EVVQGHDES

HLQEAYRIY

NLAFVAQAA

FVAQAAPDS

20

EXAMPLE 5

IDENTIFICATION OF T-CELL EPITOPES OF B11AG1

This Example illustrates the identification of B11Ag1 (also referred to as B305D) epitopes. Four peptides, referred to as B11-8, B11-1, B11-5 and B11-12 (SEQ ID NO: 309-312, respectfully) were derived from the B11Ag1 gene.

25

Human CD8 T cells were primed *in vitro* to the peptide B11-8 using dendritic cells according to the protocol of Van Tsai et al. (*Critical Reviews in Immunology* 18:65-75, 1998). The resulting CD8 T cell cultures were tested for their ability to recognize the B11-8 peptide or a negative control peptide, presented by the B-LCL line, JY. Briefly, T cells were incubated with autologous monocytes in the presence of 10 ug/ml peptide, 10 ng/ml IL-7 and 10 ug/ml IL-2, and assayed for their ability to

30

specifically lyse target cells in a standard 51-Cr release assay. As shown in Fig. 22, the bulk culture line demonstrated strong recognition of the B11-8 peptide with weaker recognition of the peptide B11-1.

A clone from this CTL line was isolated following rapid expansion using the monoclonal antibody OKT3 and human IL-2. As shown in Fig. 23, this clone (referred to as A1), in addition to being able to recognize specific peptide, recognized JY LCL transduced with the B11Ag1 gene. This data demonstrates that B11-8 is a naturally processed epitope of the B11Ag1 gene. In addition these T cells were further found to recognize and lyse, in an HLA-A2 restricted manner, an established tumor cell line naturally expressing B11Ag1 (Fig. 24). The T cells strongly recognize a lung adenocarcinoma (LT-140-22) naturally expressing B11Ag1 transduced with HLA-A2, as well as an A2+ breast carcinoma (CAMA-1) transduced with B11Ag1, but not untransduced lines or another negative tumor line (SW620).

These data clearly demonstrate that these human T cells recognize not only B11-specific peptides but also transduced cells, as well as naturally expressing tumor lines.

CTL lines raised against the antigens B11-5 and B11-12, using the procedures described above, were found to recognize corresponding peptide-coated targets.

Example 6

CHARACTERIZATION OF BREAST TUMOR GENES DISCOVERED BY
DIFFERENTIAL DISPLAY PCR

5 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 a variety of tissues were examined, including 8 breast tumors, 5 normal breasts, 2 prostate
10 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 as internal control for each of the tissues examined. Serial dilutions of the first strand
15 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 transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and
20 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
25 (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

5	Breast Tissues	Over-expressed in Breast Tumors	84%
		Equally Expressed in Normals and Tumor	16%
10	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%
15		Over-expressed in Breast Tumors but Equally Expressed in All Other Tissues	61%

20 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.

CLAIMS

1. An isolated polypeptide, comprising at least an immunogenic portion of a protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:
- (a) sequences recited in SEQ ID NOs: 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, 291-298, 301-303, 307, 313, 314, 316 and 317;
 - (b) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 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, 291-298, 301-303, 307, 313, 314, 316 and 317 under moderately stringent conditions; and
 - (c) complements of sequences of (a) or (b).
2. An isolated polypeptide according to claim 1, wherein the polypeptide comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 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, 291-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing polynucleotide sequences.
3. An isolated polypeptide comprising a sequence recited in any one of SEQ ID NOs: 299, 300, 304-306, 308 and 315.
4. An isolated polynucleotide encoding at least 15 amino acid

residues of a protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with antigen-specific antisera is not substantially diminished, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs: 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, 291-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing sequences.

10

5. An isolated polynucleotide encoding a protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs: 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, 291-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing sequences.

6. An isolated polynucleotide, comprising a sequence recited in any one of SEQ ID Nos: 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, 291-298, 301-303, 307, 313, 314, 316 and 317.

7. An isolated polynucleotide, comprising a sequence that hybridizes to a sequence recited in any one of SEQ ID NOs: 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, 291-298, 301-303, 307, 313, 314, 316 and 317 under moderately stringent conditions.

30

8. An isolated polynucleotide complementary to a polynucleotide according to any one of claims 4-7.

9. An expression vector, comprising a polynucleotide according to
5 any one of claims claim 4-8.

10. A host cell transformed or transfected with an expression vector according to claim 9.

10 11. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a protein that comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 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,
15 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing polynucleotide sequences.

12. A fusion protein, comprising at least one polypeptide according to claim 1.

20

13. A fusion protein according to claim 12, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.

25 14. A fusion protein according to claim 12, wherein the fusion protein comprises a T helper epitope that is not present within the polypeptide of claim 1.

15. A fusion protein according to claim 12, wherein the fusion
30 protein comprises an affinity tag.

16. An isolated polynucleotide encoding a fusion protein according to claim 12.

17. A pharmaceutical composition, comprising a physiologically acceptable carrier and at least one component selected from the group consisting of:

- (a) a polypeptide according to claim 1;
- (b) a polynucleotide according to claim 4;
- (c) an antibody according to claim 11;
- (d) a fusion protein according to claim 12; and
- (e) a polynucleotide according to claim 16.

18. A vaccine comprising an immunostimulant and at least one component selected from the group consisting of:

- (a) a polypeptide according to claim 1;
- (b) a polynucleotide according to claim 4;
- (c) an antibody according to claim 11;
- (d) a fusion protein according to claim 12; and
- (e) a polynucleotide according to claim 16.

19. A vaccine according to claim 18, wherein the immunostimulant is an adjuvant.

20. A vaccine according to any claim 18, wherein the immunostimulant induces a predominantly Type I response.

21. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a pharmaceutical composition according to claim 17.

22. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a vaccine according to

claim 18.

23. A pharmaceutical composition comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a
5 pharmaceutically acceptable carrier or excipient.

24. A pharmaceutical composition according to claim 23, wherein the antigen presenting cell is a dendritic cell or a macrophage.

10 25. A vaccine comprising an antigen-presenting cell that expresses a polypeptide comprising at least an immunogenic portion of a protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(a) sequences recited in SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-
15 298, 301-303, 307, 313, 314, 316 and 317;

(b) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 under moderately stringent conditions; and

(c) complements of sequences of (i) or (ii);
20 in combination with an immunostimulant.

26. A vaccine according to claim 25, wherein the immunostimulant is an adjuvant.

25 27. A vaccine according to claim 25, wherein the immunostimulant induces a predominantly Type I response.

28. A vaccine according to claim 25, wherein the antigen-presenting cell is a dendritic cell.

30

29. A method for inhibiting the development of a cancer in a patient,

comprising administering to a patient an effective amount of an antigen-presenting cell that expresses a polypeptide comprising at least an immunogenic portion of a protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

- 5 (a) sequences recited in SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317;
- (b) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 under moderately stringent conditions; and
- 10 (c) complements of sequences encoded by a polynucleotide recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317;

and thereby inhibiting the development of a cancer in the patient.

- 15 30. A method according to claim 29, wherein the antigen-presenting cell is a dendritic cell.

31. A method according to any one of claims 21, 22 and 29, wherein the cancer is breast cancer.

20

32. A method for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

- 25 (i) polynucleotides recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317; and
- (ii) complements of the foregoing polynucleotides;

wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the antigen from the sample.

30

33. A method according to claim 32, wherein the biological sample is

blood or a fraction thereof.

34. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated according to the
5 method of claim 32.

35. A method for stimulating and/or expanding T cells specific for a protein, comprising contacting T cells with at least one component selected from the group consisting of:

- 10 (a) polypeptides comprising at least an immunogenic portion of a protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:
- (i) sequences recited in SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317;
 - 15 (ii) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 under moderately stringent conditions; and
 - (iii) complements of sequences of (i) or (ii);
- (b) polynucleotides encoding a polypeptide of (a); and
- 20 (c) antigen presenting cells that express a polypeptide of (a);
- under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

36. An isolated T cell population, comprising T cells prepared
25 according to the method of claim 35.

37. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population according to claim 36.

30

38. A method for inhibiting the development of a cancer in a patient,

comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

5 (i) polypeptides comprising at least an immunogenic portion of a protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(1) sequences recited in SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317;

10 (2) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 under moderately stringent conditions; and

(3) complements of sequences of (1) or (2);

(ii) polynucleotides encoding a polypeptide of (i); and

15 (iii) antigen presenting cells that expresses a polypeptide of (i);

such that T cells proliferate; and

(b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

20

39. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

25 (i) polypeptides comprising at least an immunogenic portion of a protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(1) sequences recited in SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317;

30

(2) sequences that hybridize to a sequence recited in

any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 under moderately stringent conditions; and

(3) complements of sequences of (1) or (2);

(ii) polynucleotides encoding a polypeptide of (i); and

5 (iii) antigen presenting cells that express a polypeptide of (i);

such that T cells proliferate;

(b) cloning at least one proliferated cell to provide cloned T cells;

and

10 (c) administering to the patient an effective amount of the cloned T cells, and thereby inhibiting the development of a cancer in the patient.

40. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

15 (a) contacting a biological sample obtained from a patient with a binding agent that binds to a protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing polynucleotide sequences;

20 (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and

(c) comparing the amount of polypeptide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

25 41. A method according to claim 40, wherein the binding agent is an antibody.

42. A method according to claim 43, wherein the antibody is a monoclonal antibody.

30

43. A method according to claim 40, wherein the cancer is breast

cancer.

44. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

- 5 (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing polynucleotide sequences;
- 10 (b) detecting in the sample an amount of polypeptide that binds to the binding agent;
- (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and
- (d) comparing the amount of polypeptide detected in step (c) to the
15 amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

45. A method according to claim 44, wherein the binding agent is an antibody.

20

46. A method according to claim 45, wherein the antibody is a monoclonal antibody.

47. A method according to claim 44, wherein the cancer is a breast
25 cancer.

48. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

- 30 (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence

recited in any one of SEQ ID NO: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing polynucleotide sequences;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

5 (c) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

49. A method according to claim 48, wherein the amount of
10 polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

50. A method according to claim 48, wherein the amount of
15 polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

51. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with an
20 oligonucleotide that hybridizes to a polynucleotide that encodes a protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NO: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing polynucleotide sequences;

(b) detecting in the sample an amount of a polynucleotide that
25 hybridizes to the oligonucleotide;

(c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and

(d) comparing the amount of polynucleotide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer
30 in the patient.

52. A method according to claim 51, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

5 53. A method according to claim 51, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

54. A diagnostic kit, comprising:
10 (a) one or more antibodies according to claim 11; and
(b) a detection reagent comprising a reporter group.

55. A kit according to claim 54, wherein the antibodies are immobilized on a solid support.

15 56. A kit according to claim 54, wherein the detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin.

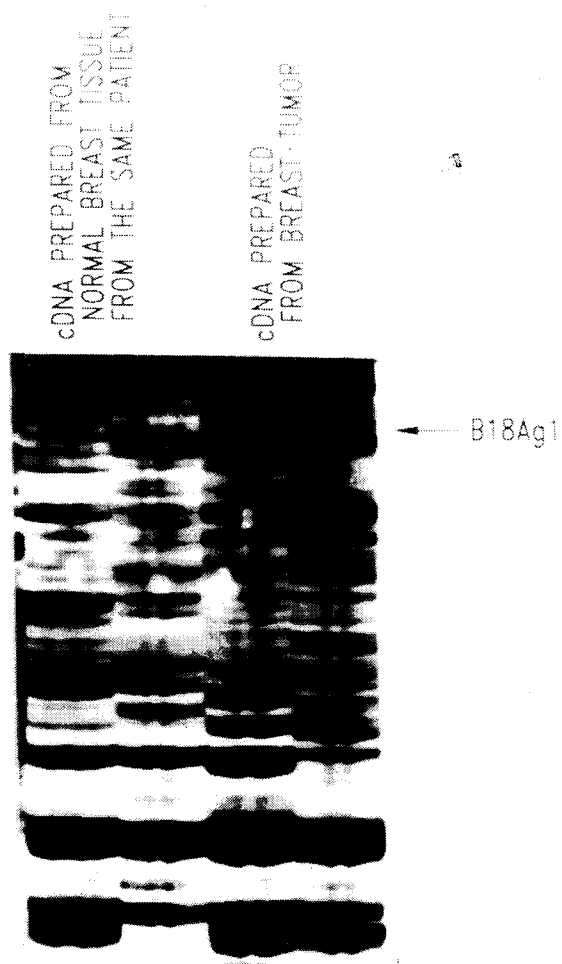
57. A kit according to claim 54, wherein the reporter group is
20 selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

58. An oligonucleotide comprising 10 to 40 contiguous nucleotides that hybridize under moderately stringent conditions to a polynucleotide that encodes a
25 protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 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, 291-298, 301-303, 307, 313, 314, 316 and 317 or a
30 complement of any of the foregoing polynucleotides.

59. A oligonucleotide according to claim 58, wherein the oligonucleotide comprises 10-40 contiguous nucleotides recited in any one of SEQ ID Nos: 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,
5 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317.

60. A diagnostic kit, comprising:
(a) an oligonucleotide according to claim 59; and
10 (b) a diagnostic reagent for use in a polymerase chain reaction or hybridization assay.

1/25

*Fig. 1*

2/25

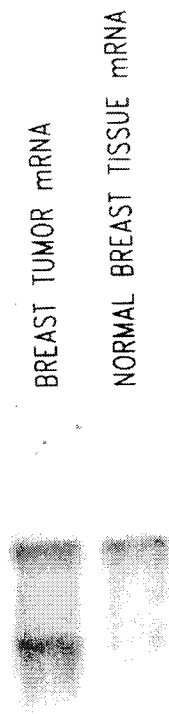
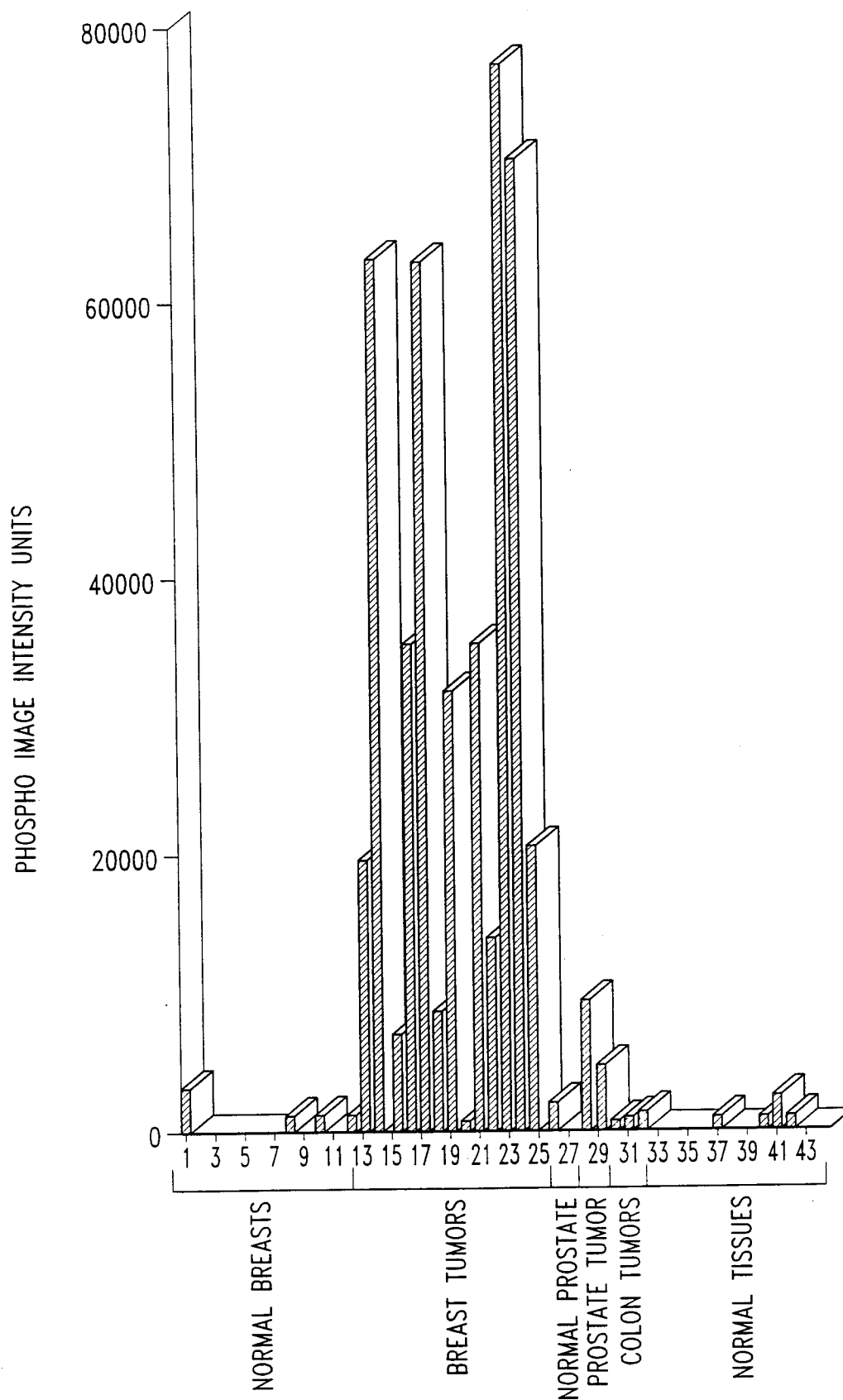


Fig. 2

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*Fig. 3*

GENOMIC CLONE MAP

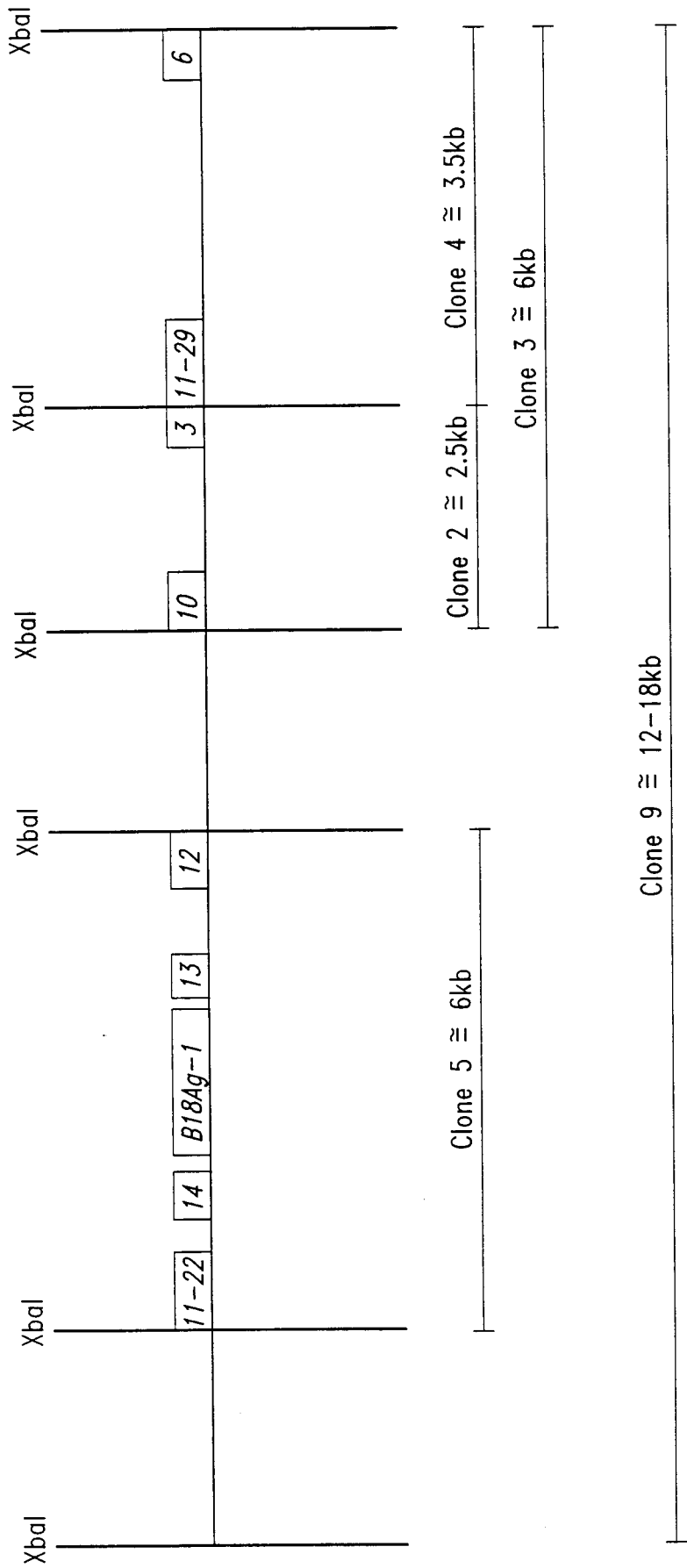


Fig. 4

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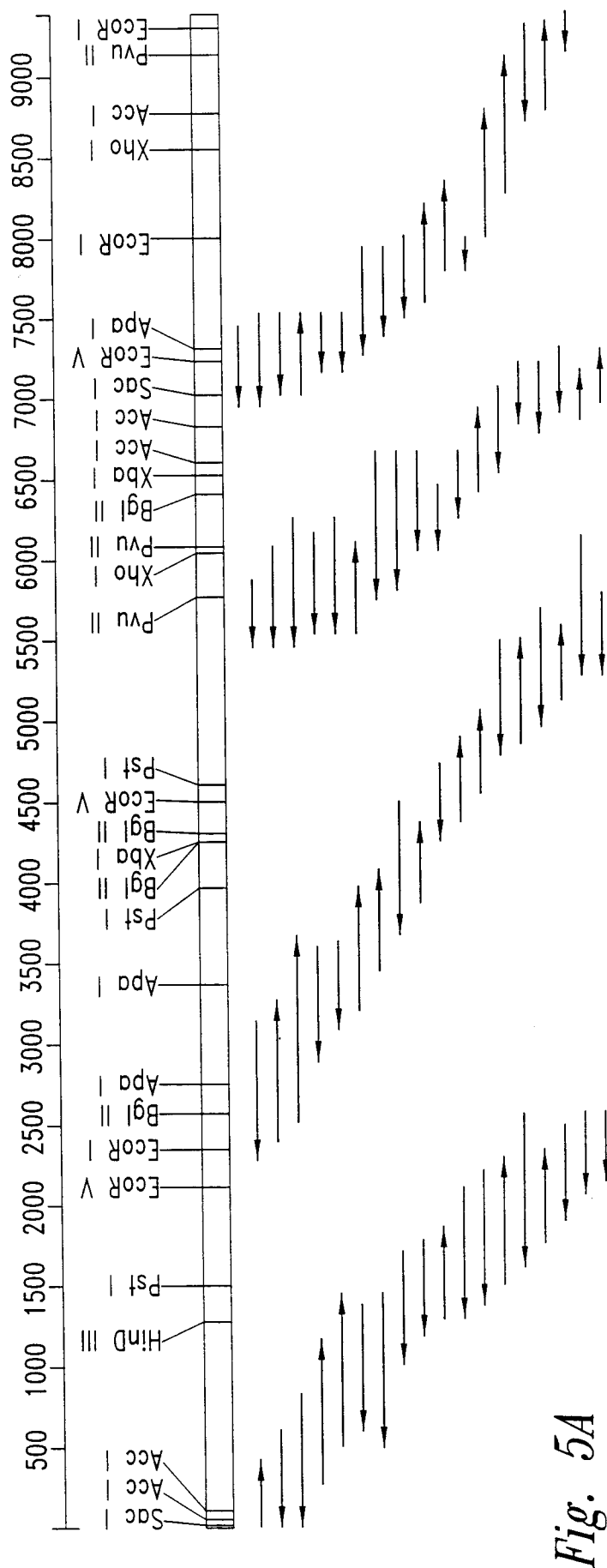


Fig. 5A

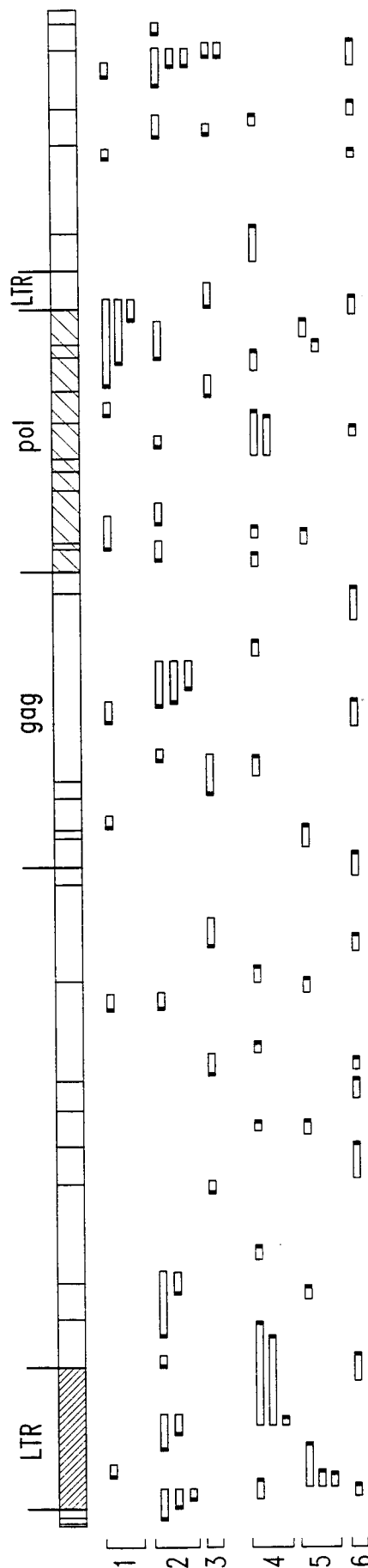


Fig. 5B

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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

7/25

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B17Ag1

GC TGGGCACAGT GGCTCATACC TGTAATCCTG ACCGTTTCAG AGGCTCAGGT	60
CG CTTGAGCCCA AGATTTC AAG 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 AGTCCAACTG	60
AC TTACACTGTG GNCTCCAATA AACTGCTTCT TTCCTATTCC CTCTCTATTA	120
AA GGAAAACGAT GTCTGTGTAT AGCCAAGTCA GNTATCCTAA AAGGAGATAC	180
AT TAAATATCAG AATGTAAAAC CTGGGAACCA GGTTCCTCAGC 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 GTTCTCATT ATTTTCACAT TTTATTAACC AATTTCTGTT	60
AA AATATGAGGG AAATATATGA AACAGGGAGG CAATGTTTCAG ATAATTGATC	120
TG ATTTCTACAT CAGATGCTCT TTCCTTTCCT GTTTATTTCC TTTTATTTTC	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 ATTAAACCCC CACCTGAACG GCATAAACTG	60
GC TGGTGTTTTT TACTGTAAAC AATAAGGAGA CTTTGCTCTT CATTTAAACC	120
AT TTCATATTTT ACGCTCGAGG GTTTTTACCG GTTCCTTTTT AACTCCTTA	180
TT TAAGTCGTTT GGAACAAGAT ATTTTTTCTT TCCTGGCAGC TTTTAACATT	240
TT TGTGTCTGGG GGAAGTCTGG 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 GGGAACNCT A	571

Fig. 10

11/25

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B13Ag1a

TA ATAACTTAAA TATATTTTGA TCACCCACTG GGGTGATAAG ACAATAGATA	60
TT TCCAAAAAGC ATAAACCAA AGTATCATAC CAAACCAAAT TCATACTGCT	120
CC GCACTGAAAC TTCACCTTCT AACTGTCTAC CTAACCAAAT TCTACCCTTC	180
GG TCGTGCTCA CTA CTCTTTTT 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 ATGGATTAT GACAGTTGAT	180
GA GATTATTAAG TGATTATTTT AAAGGGAATC CATTAATTCC AGAATATCTT	240
TC AAGATGATAT AGAAATAGAA CAGAAAGAGA CTACAAATGA AGATGTATCA	300
TA TTGAAGAGCC TATAGTAGAA AATGAATTAG CTGCATTAT 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 TGTTCTGTGAT   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 GGCCTG                               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

15/25

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B9CG3

AG CAAAGCCAGT GGTTCGAGCT 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

16/25

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B2CA2

GG GCATGGACGC AGACGCCTGA CGTTTGGCTG AAAATCTTTC ATTGATTCGT	60
AT AGGAAAATTC CCAAAGAGGG AATGTCCTGT TGCTCGCCAG TTTTNTGT	120
GG ANAAGGCAAN GAGCTCTTCA GACTATTGGN ATTNTCGTTC GGTCTTCTGC	180
CG NCTTGCAANG ATCTTCAT	208

Fig. 16

17/25

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA1

GG GCATGGACGC AGACGCCTGA CGTTTGGCTG AAAATCTTTC ATTGATTCTG	60
AT AGGAAAATTC CCAAAGAGGG AATGTCCTGT TGCTCGCCAG TTTTNTGTT	120
GG ANAAGGCAAN GAGCTCTTCA GACTATTGGN ATTNTCGTTC GGTCTTCTGC	180
CG NCTTGCAANG ATCTTCAT	208

Fig. 17

18/25

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA2

GG GCATGGACGC AGACGCCTGA CGTTTGGCTG AAAATCTTTC ATTGATTCGT	60
AT AGGAAAATTC CCAAAGAGGG AATGTCCTGT TGCTCGCCAG TTTTNTGTT	120
GG ANAAGGCAAN GAGCTCTTCA GACTATTGGN ATTNTCGTTC GGTCTTCTGC	180
CG NCTTGCNANG ATCTTCAT	208

Fig. 18

19/25

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

20/25

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 NCTATTTTAA	180
GA TTTGAGAAAT TGGTTNTTAT TATATCAATT TTTGGTATTT GTTGAGTTTG	240
GC TTAGTATGTG ACCA	264

Fig. 20

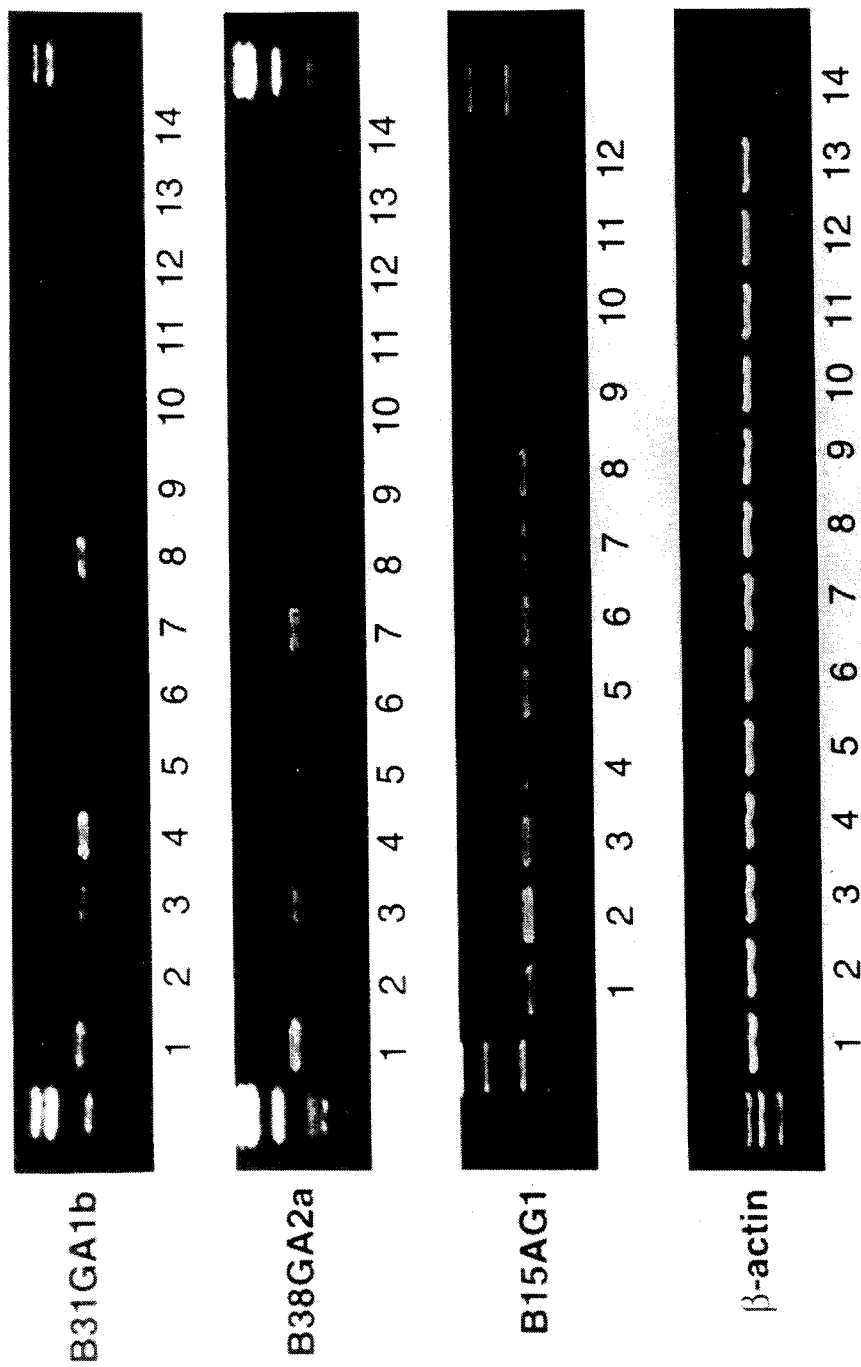


Fig. 21A

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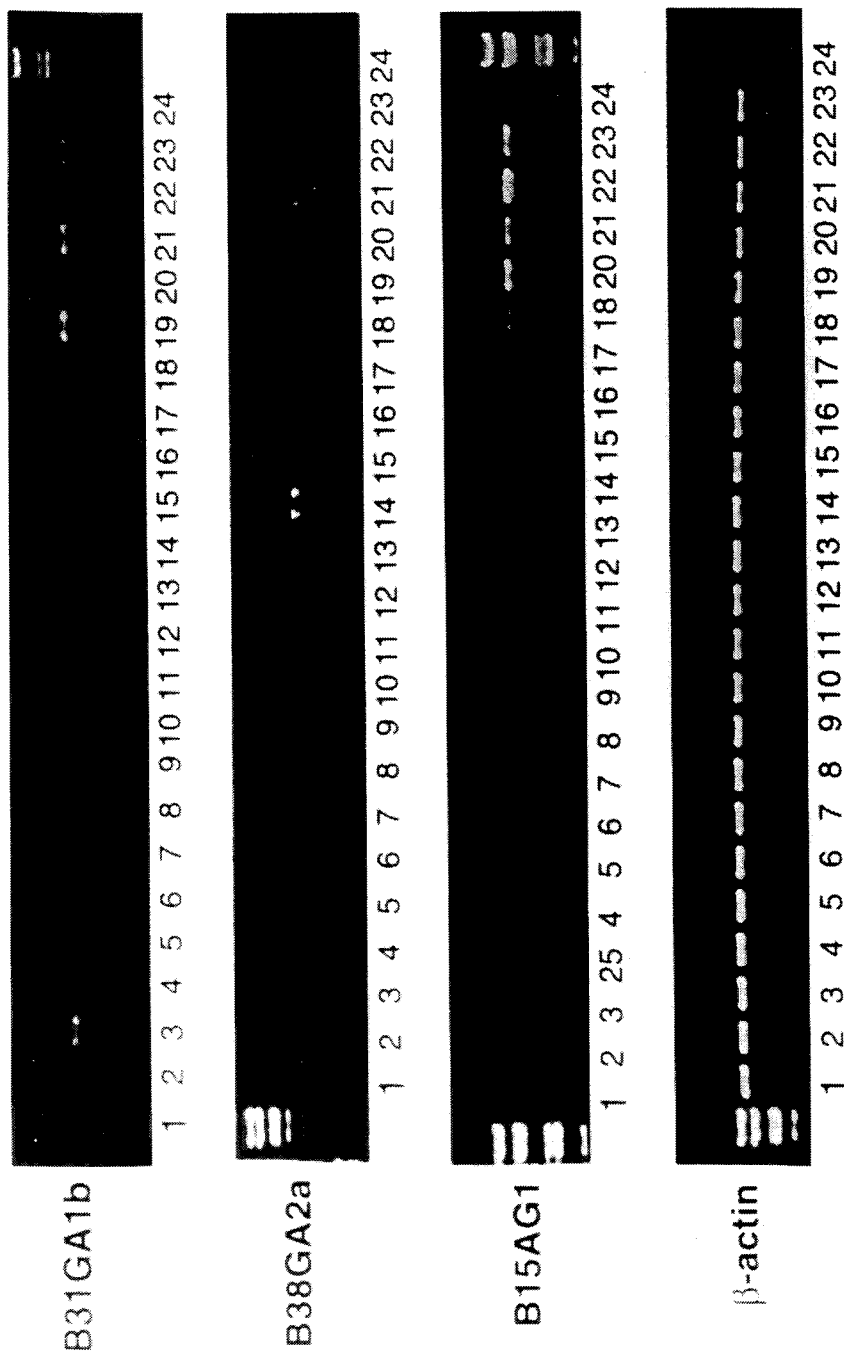
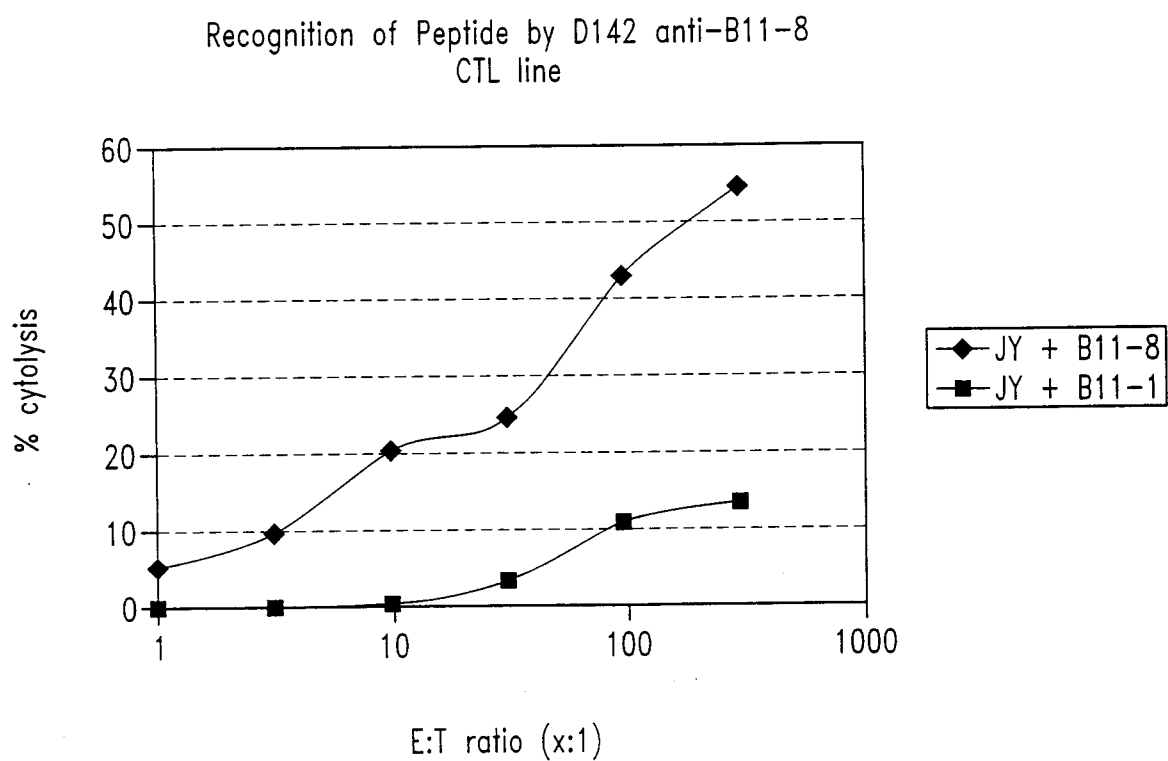
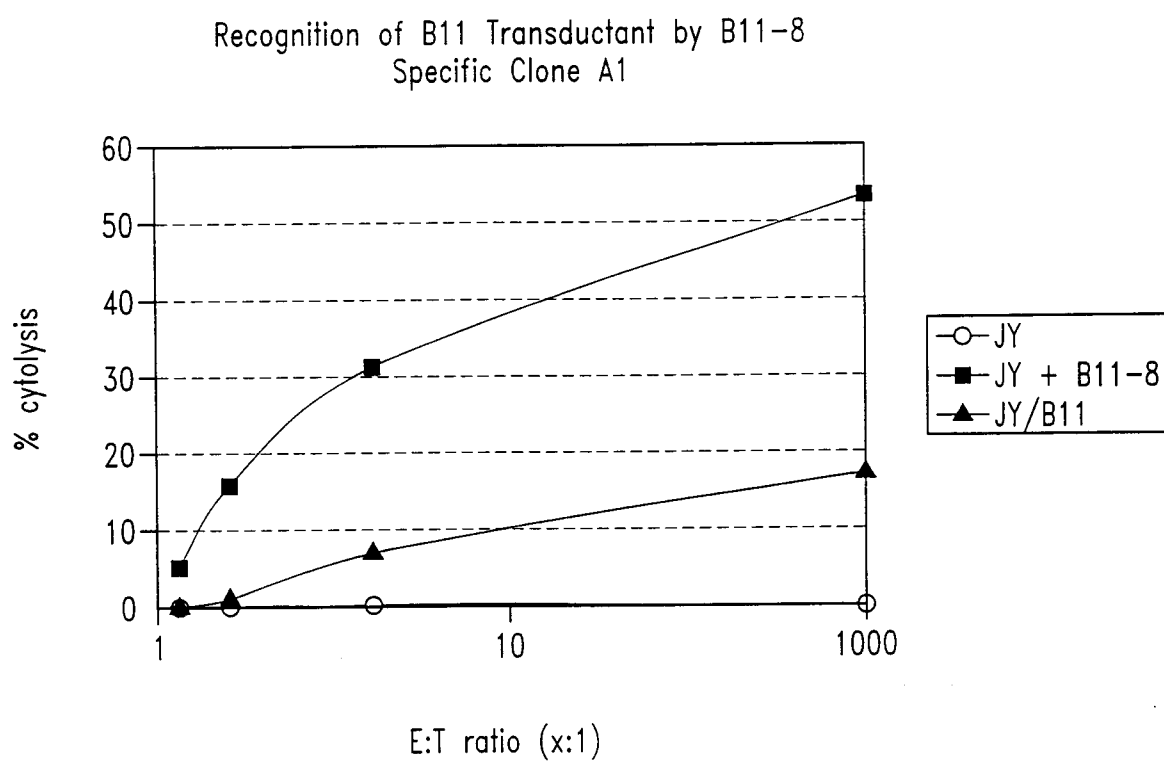


Fig. 21B

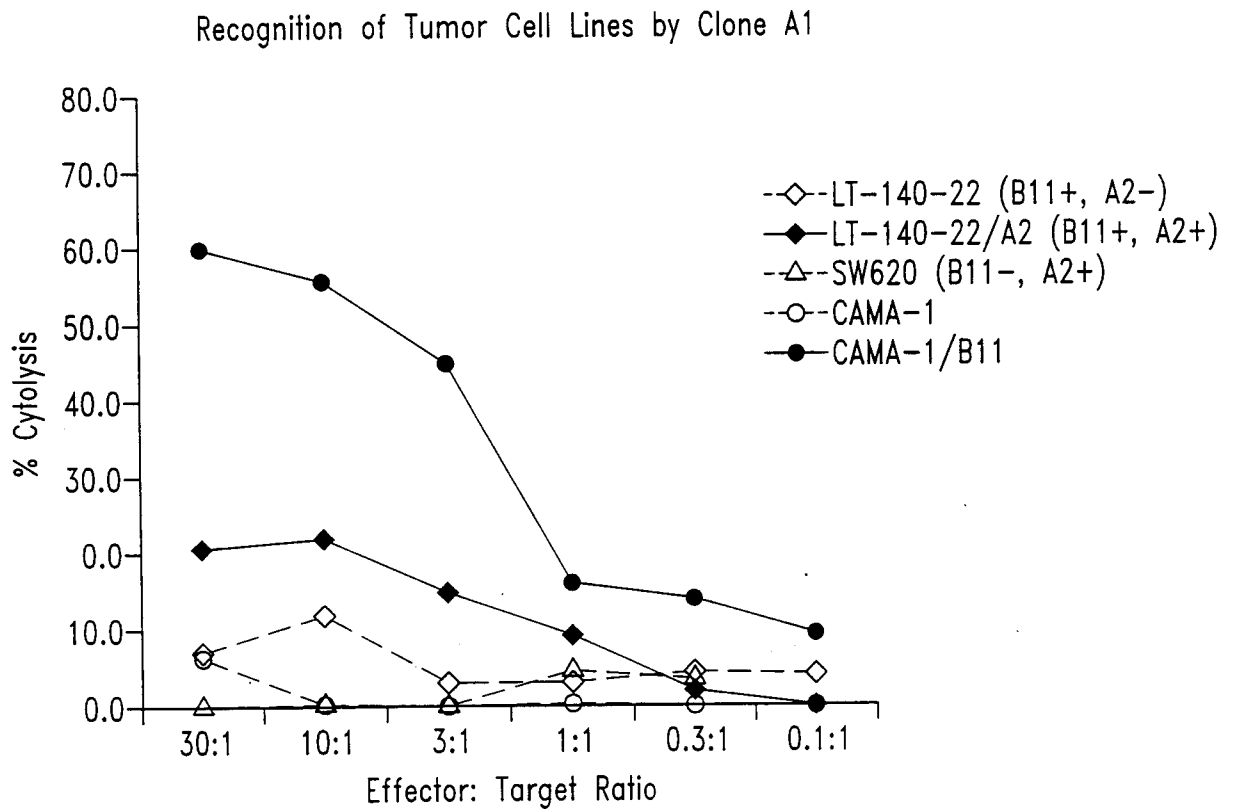
23/25

*Fig. 22*

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*Fig. 23*

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*Fig. 24*

SUBSTITUTE SHEET (RULE 26)

SEQUENCE LISTING

<110> Corixa Corporation

<120> COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER

<130> 210121.41926PC

<140> PCT

<141> 2000-04-07

<160> 317

<170> FastSEQ for Windows Version 3.0

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catgctctta atttggcatt tgtggctcag gcagccccag atagtaaaag gaaactccaa	300
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<211> 121

<212> PRT

<213> Homo sapien

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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	
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Arg Lys Leu Gln Lys Leu Glu Gly Phe Cys Trp Asn Glu Tyr Gln Ser	
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115 120	

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gctttaaagt	actgttagtg	agaaattaaa	attccttcag	gaggattaaa	ctgccatttc	480
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acctggaatt	anaggccccc	ncccccccc	cggctaattt	gtttttgttt	ttagtaaaaa	780
acgggtttcc	tgtttttagtt	aggatggccc	anntctgacc	ccntnatcnt	ccccctcngc	840
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aggatcactg gctctaata caatgacatg aggtcaccac caaaccatca agcgctaaac      240
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ttcctaaaat taaaaaatan ccggttnng nnggcctct tccctceng gngggngng      900
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<210> 6

<211> 950

<212> DNA

<213> Homo sapien

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gttttccctt gttggccann atggtctcna acccctgacc tcnngtgatc ccccncccn      240
nganctenna ctgctgggga tnnccgnnnn nnnccctecn ncnennnnnn ncnennnccn      300
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<212> DNA

<213> Homo sapien

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ggtagatggc	tccacgtaca	tgcacagtag	caaaggcgta	cctgctgtca	gtgttaacgt	420
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<211> 196

<212> DNA

<213> Homo sapien

<400> 11

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actgacagca	agaagactga	acagtactac	tgtgaaaagc	ccgaagnngc	aatatgttca	300
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<211> 337

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<213> Homo sapien

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acaagatatg	atctctacat	cagatgctct	ttcctttcct	gtttatttcc	tttttatttc	180
ggttgtgggg	tcgaatgtaa	tagctttgtt	tcaagagaga	gttttggcag	tttctgtagc	240
ttctgacact	gctcatgtct	ccaggcatct	atctgcactt	taggaggtgt	cgtgggagac	300
tgagaggtct	attttttcca	tatttgggca	actacta			337

<210> 14

<211> 571

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(571)

<223> n = A,T,C or G

<400> 14

tagtagttgc	catacagtgc	ctttccattt	atttaacccc	cacctgaacg	gcataaactg	60
agtgttcagc	tggtgttttt	tactgtaaac	aataaggaga	ctttgctctt	catttaaacc	120
aaaatcatat	ttcatatttt	acgctcgagg	gtttttaccg	gttccttttt	acactcctta	180
aaacagtttt	taagtcgttt	ggaacaagat	atTTTTtctt	tcctggcagc	ttttaacatt	240
atagcaaatt	tgtgtctggg	ggactgctgg	tcactgtttc	tcacagttgc	aaatcaaggc	300
atTTgcaacc	aagaaaaaaa	aatttttttg	ttttatttga	aactggaccg	gataaacggt	360
gtttggagcg	gctgctgtat	atagttttta	atggttttatt	gcacctcctt	aagttgcact	420
tatgtggggg	ggggnttttg	natagaaagt	ntttantcac	anagtcacag	ggacttttnt	480
cttttggnna	ctgagctaaa	aagggtgnt	tttcgggtgg	gggcagatga	aggctcacag	540
gaggcctttc	tcttagaggg	gggaactnct	a			571

<210> 15

<211> 548

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(548)

<223> n = A,T,C or G

<400> 15

tatatatttta	ataacttaaa	tatatTTttga	tcacccactg	gggtgataag	acaatagata	60
taaaagtatt	tccaaaaagc	ataaaaccaa	agtatcatat	caaaccaaat	tcatactgct	120
tccccacccc	gcactgaaac	ttcaccttct	aactgtctac	ctaaccaaat	tctacccttc	180
aagtcttttg	tgctgtctca	ctactctttt	TTTTTTTTTT	ttnttttttg	agatggagtc	240
tggctgtgca	gccaggggt	ggagtacaat	ggcacaacct	cagctcactg	naacctccgc	300
ctcccagggt	catgagattc	tcctgnttca	gccttcccag	tagctgggac	tacagggtgtg	360
catcaccatg	cctggntaat	cttttttngt	tttngggtag	agatgggggt	tttacctgtt	420
ggccaggntg	gtntcgaact	cctgacctca	agtgatccac	ccacctcagg	ctcccaaagt	480
gctaggatta	cagacatgag	ccactgngcc	cagnccgtgt	gcatgctcac	ttctctaggc	540
aactacta						548

<210> 16

<211> 638

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(638)

<223> n = A,T,C or G

<400> 16

ttccgttatg	cacatgcaga	atattctatc	ggtacttcag	ctattactca	ttttgatggc	60
gcaatccgag	cctatcctca	agatgagtat	ttagaaagaa	ttgatttagc	gatagaccaa	120
gctggtaagc	actctgacta	cacgaaattg	ttcagatgtg	atggatttat	gacagttgat	180

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ctttggaaga gattattaag tgattatattt aaaggggaatc cattaattcc agaatatctt 240
ggtttagctc aagatgatat agaaatagaa cagaaagaga ctacaaatga agatgtatca 300
ccaactgata ttgaagagcc tatagtagaa aatgaattag ctgcatttat tagccttaca 360
catagcgatt ttcctgatga atccttatatt cagccatcga catagcatta cctgatgggc 420
aaccttacga ataatagaaa ctgggtgcgg ggctattgat gaattcatcc ncagtaaatt 480
tggaatnac aaaatataac tcgattgcat ttggatgatg gaatactaaa tctggcaaaa 540
gtaactttgg agctactagt aacctctctt tttgagatgc aaaattttct tttagggttt 600
cttattctct actttacgga tattggagca taacggga 638

```

<210> 17

<211> 286

<212> DNA

<213> Homo sapien

<400> 17

```

actgatggat gtcgccggag gcgaggggccc ttatctgatg ctcggtgccc tgttcgtgat 60
gtgcgcggcg attgggctgt ttatctcaaa caccgccacg gcggtgctga tggcgccctat 120
tgccttagcg gcggcggaagt caatgggcgt ctcaccctat ccttttgcca tgggtggtggc 180
gatggcgggt tcggcgggcg ttatgacccc ggtctcctcg ccggttaaca ccctggtgct 240
tggccctggc aagtactcat ttagcgattt tgtcaaaata ggcgtg 286

```

<210> 18

<211> 262

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (262)

<223> n = A,T,C or G

<400> 18

```

tcggtcatag cagccccttc ttctcaattt catctgtcac taccctgggtg tagtatctca 60
tagccttaca tttttatagc ctctccctg gtctgtcttt tgattttcct gcctgtaatc 120
catatcacac ataactgcaa gtaaacattt ctaaagtgtg gttatgctca tgctactcct 180
gtgncaagaa atagttttcca ttaccgtctt aataaaaattc ggatttgttc ttttctattn 240
tcactcttca cctatgaccg aa 262

```

<210> 19

<211> 261

<212> DNA

<213> Homo sapien

<400> 19

```

tcggtcatag caaagccagt ggtttgagct ctctactgtg taaactccta aaccaaggcc 60
atztatgata aatgggtggc ggatttttat tataaacatg taccatgca aatttcctat 120
aactctgaga tatattcttc tacatttaaa caataaaaaat aatctatttt taaaagccta 180
atttgcgtag ttaggtaaga gtgtttaatg agagggtata aggtataaat caccagtcaa 240
cgtttctctg cctatgaccg a 261

```

<210> 20

<211> 294

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(294)

<223> n = A,T,C or G

<400> 20

tacaacgagg	cgacgtcggg	aaaatcggac	atgaagccac	cgctgggtctt	ttcgtccgag	60
cgataggcgc	cggccagcca	gcggaacggg	tgcccggatg	gcgaagcgag	ccggagttct	120
tcggactgag	tatgaatctt	gttgtagaaa	tactcgccgc	cttcgttcga	cgacgtcgcg	180
tcgaaatctt	cganctcctt	acgatcgaag	tcttcgtggg	cgacgatcgc	ggtcagttcc	240
gccccaccga	aatcatgggt	gagccggatg	ctgnccccga	agnccctcgtt	tgtn	294

<210> 21

<211> 208

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(208)

<223> n = A,T,C or G

<400> 21

ttggtaaagg	gcatggacgc	agacgcctga	cgtttggtctg	aaaatctttc	attgattcgt	60
atcaatgaat	aggaaaattc	ccaaagaggg	aatgtcctgt	tgctcgccag	ttttntgtgt	120
gttctcatgg	anaaggcaan	gagctcttca	gactattggn	attntcgttc	ggctctctgc	180
caactagtcg	ncttgcnang	atcttcat				208

<210> 22

<211> 287

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(287)

<223> n = A,T,C or G

<400> 22

nccnttgagc	tgagtgattg	agatntgtaa	tggttgtaag	ggtgattcag	gcggattagg	60
gtggcggggtc	acccggcagt	gggtctcccg	acaggccagc	aggatttggg	gcagggtacgg	120
ngtgcgcatc	gctcgactat	atgctatggc	aggcgagccg	tggaaaggngg	atcagggtcac	180
ggcgctggag	ctttccacgg	tccatgnatt	gngatggctg	ttctaggcgg	ctgttgccaa	240
gcgtgatggt	acgctggctg	gagcattgat	ttctgggtgcc	aaggtgg		287

<210> 23

<211> 204

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(204)

<223> n = A,T,C or G

<400> 23
ttgggttaaag ggagcaagga gaaggcatgg agaggctcan gctggtcctg gcctacgact 60
gggccaaagct gtcgccgggg atgggtggaga actgaagcgg gacctcctcg aggtcctccg 120
ncgttacttc nccgtccagg aggaggggtct ttccgtggtc tnggaggagc ggggggagaa 180
gatnctcttc atggtcnaca tccc 204

<210> 24
<211> 264
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(264)
<223> n = A,T,C or G

<400> 24
tggattggtc aggagcgggt agagtggcac cattgagggg atattcaaaa atattatttt 60
gtcctaaatg atagtgtctg agtttttctt tgacccatga gttatattgg agttttatttt 120
ttaactttcc aatcgcatgg acatgttaga cttattttct gttaatgatt nctattttta 180
ttaaattgga tttgagaaat tggttnttat tatatcaatt tttggtattt gttgagtttg 240
acattatagc ttagtatgtg acca 264

<210> 25
<211> 376
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(376)
<223> n = A,T,C or G

<400> 25
ttacaacgag gggaaactcc gtctctacaa aaattaaaaa attagccagg tgtgggtggtg 60
tgcacccgca atcccagcta cttgggaggt tgagacacaa gantcaccta natgtgggag 120
gtcaagggtg catgagtcac gattgtgcca ctgcactcca gcctgggtga cagaccgaga 180
ccctgcctca anaganaang aataggaagt tcagaaatcn tggntgtggn gccagcaat 240
ctgcatctat ncaaccctg caggcaangc tgatgcagcc tangttcaag agctgctgtt 300
tctggaggca gcagttnggg cttccatcca gtatcacggc cacactcgca cnagccatct 360
gtcctccgtn tgnac 376

<210> 26
<211> 372
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(372)
<223> n = A,T,C or G

<400> 26
ttacaacgag gggaaactcc gtctctacaa aaattaaaaa attagccagg tgtgggtggtg 60
tgcacctgta atcccagcta cttgggcggc tgagacacaa gaaccaccta aatgtgggag 120

```

ggccaagggtt 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

```

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<210> 27
<211> 477
<212> DNA
<213> Homo sapien

```

```

<400> 27
ttctgtccac atctacaagt tttatatttatt ttgtgggttt tcagggtgac taagtttttc 60
cctacattga aaagagaagt tgctaaaagg tgcacaggaa atcatttttt taagtgaata 120
tgataatatg ggtccgtgct taatacaact gagacatatt tgttctctgt ttttttagag 180
tcacctctta aagtccaatc ccacaatggg gaaaaaaaaa tagaaagtat ttgttctacc 240
tttaaggaga ctgcagggat tctccttgaa aacggagtat ggaatcaatc ttaaataaat 300
atgaaattgg ttggtcttct gggataagaa attcccaact cagtgtgctg aaattcacct 360
gacttttttt gggaaaaaat agtcgaaaat gtcaatttgg tccataaaat acatgttact 420
attaaaagat atttaaagac aaattctttc agagctctaa gattgggtgtg gacagaa 477

```

```

<210> 28
<211> 438
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(438)
<223> n = A,T,C or G

```

```

<400> 28
tctncaacct cttgantgtc aaaaaccttn taggctatct ctaaaagctg actggtattc 60
attccagcaa aatccctcta gtttttggag tttcctttta ctatctgggg ctgcctgagc 120
cacaaatgcc aaattaagag catggctatt ttcgggggct gacagggtcaa aaggggtgta 180
aatccgataa gcctcctgga ggtgctctaa aaacactcct ggtgactcat catgcccctg 240
gacgacttca atcgncttag acaagtttat aggtttctgg gcagctccct gaatacccac 300
gaggagatac cgggtggaat cgtcaaaagt tctccctcca cttgagaaat ttgggtccca 360
attaggtccc aattgggtct ctaatcacta ttctcttagc ttctcctcc ggnctattgg 420
ttgatgtgag gttgaaga 438

```

```

<210> 29
<211> 620
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(620)
<223> n = A,T,C or G

```

```

<400> 29
aagagggtac cagccccaag ccttgacaac ttccataggg tgtcaagcct gtgggtgcac 60
agaagtcaaa aattgagttt tgggatcctc agcctagatt tcagaggata taaagaaaca 120
cctaacacct agatattcag acaaaagttt actacaggga tgaagctttc acggaaaacc 180

```

tctactagga	aagtacagaa	gagaaatgtg	ggtttggagc	ccccaacag	aatccccctct	240
agaacactgc	ctaataaaac	tgtgagaaga	tggccactgt	catccagaca	ccagaatgat	300
agacccacca	aaaactttatg	ccatattgcc	tataaaacct	acagacactc	aatgccagcc	360
ccatgaaaaa	aaaactgaga	agaagactgt	nccctacaat	gccaccggag	cagaactgcc	420
ccaggccatg	gaagcacagc	tcttatatca	atgtgacctg	gatgttgaga	catggaatcc	480
nangaaatcn	ttttaanact	tccacggtn	aatgactgcc	ctattanatt	cngaacttan	540
atccnggct	gtgacctctt	tgctttggcc	attccccctt	tttggaatgg	ctnttttttt	600
cccatgcctg	tncctcttta					620

<210> 30

<211> 100

<212> DNA

<213> Homo sapien

<400> 30

ttacaacgag	gggggtcaatg	tcataaatgt	cacaataaaa	caatctcttc	tttttttttt	60
tttttttttt	tttttttttt	tttttttttt	tttttttttt			100

<210> 31

<211> 762

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(762)

<223> n = A,T,C or G

<400> 31

tagtctatgc	gccggacaga	gcagaattaa	attggaagtt	gccctccgga	ctttctaccc	60
acactcttcc	tgaaaagaga	aagaaaagag	gcaggaaaaga	ggtaggatt	tcattttcaa	120
gagtcagcta	attaggagag	cagagtttag	acagcagtag	gcaccccatg	atacaaacca	180
tggacaaaagt	ccctgttttag	taactgccag	acatgatcct	gctcagggtt	tgaaatctct	240
ctgcccataa	aagatggaga	gcaggagtgc	catccacatc	aacacgtgtc	caagaaagag	300
tctcagggag	acaaggggtat	caaaaaacaa	gattcttaat	gggaaggaaa	tcaaaccaaa	360
aaattagatt	tttctctaca	tatatataat	atacagatat	ttaacacatt	attccagagg	420
tggtctcagt	ccttggggct	tgagagatgg	tgaaaacttt	tgttccacat	taacttctgc	480
tctcaaattc	tgaagtatat	cagaatggga	caggcaatgt	tttgctccac	actggggcac	540
agacccaaat	ggttctgtgc	ccgaagaaga	gaagcccga	agacatgaag	gatgcttaag	600
gggggttggg	aaagccaaat	tggtantatc	ttttctctct	gcctgtgttc	cngaagtctc	660
cnctgaagga	attcttaaaa	ccctttgtga	ggaaatgcc	ccttaccatg	acaantggtc	720
ccattgcttt	tagggngatg	gaaacaccaa	gggttttgat	cc		762

<210> 32

<211> 276

<212> DNA

<213> Homo sapien

<400> 32

tagtctatgc	gtgtattaac	ctccccctcc	tcagtaacaa	ccaaagaggc	aggagctggt	60
attaccaacc	ccattttaca	gatgcatcaa	taatgacaga	gaagtgaagt	gacttgcgca	120
cacaaccagt	aaattggcag	agtcagattt	gaatccatgg	agtctgggtc	gcactttcaa	180
tcaccgaata	ccctttctaa	gaaacgtgtg	ctgaatgagt	gcatggataa	atcagtgtct	240
actcaacatc	tttgcttaga	tatcccgcat	agacta			276

<210> 33
 <211> 477
 <212> DNA
 <213> Homo sapien

<400> 33
 tagtagttgc caaatatattg aaaatttacc cagaagtgat tgaaaacttt ttggaaacaa 60
 aaacaaataa agccaaaagg taaaataaaa atatctttgc actctcgtta ttacctatoc 120
 ataacttttt caccgtaagc tctcctgctt gttagtgtag tgtgggtata ttaaactttt 180
 tagttattat tttttattca cttttccact agaaagtcatt tattgattta gcacacatgt 240
 tgatctcatt tcattttttc tttttatagg caaaatttga tgctatgcaa caaaaatact 300
 caagcccatt atcttttttc ccccgaaat ctgaaaattg caggggacag aggggaagtta 360
 tcccattaaa aaattgtaaa tatgttcagt ttatgtttta aaatgcacaa aacataagaa 420
 aattgtgttt acttgagctg ctgattgtaa gcagttttat ctcaggggca actacta 477

<210> 34
 <211> 631
 <212> DNA
 <213> Homo sapien

<400> 34
 tagtagttgc caattcagat gatcagaaat gctgctttcc tcagcattgt cttgtttaa 60
 cgcattgccat ttggaacttt ggcagtgaga agccaaaagg aagaggtgaa tgacatatat 120
 atatatatat attcaatgaa agtaaaatgt atatgctcat atactttcta gttatcagaa 180
 tgagtttaagc tttatgccat tgggctgctg catattttta tcagaagata aaagaaaatc 240
 tgggcatttt tagaatgtga tacatgtttt tttaaaactg ttaaataatta tttcgatatt 300
 tgtctaagaa ccggaatgtt cttaaaattt actaaaacag tattgtttga ggaagagaaa 360
 actgtactgt ttgccattat tacagtcgta caagtgcatt tcaagtcacc cactctctca 420
 ggcattcagta tccacctcat agctttacac attttgacgg ggaatattgc agcatcctca 480
 ggcctgacat ctgggaaagg ctcagatcca cctactgctc cttgctcggt gatttggttt 540
 aaaatattgt gcctggtgtc acttttaagc cacagccctg cctaaaagcc agcagagaa 600
 agaacccgca ccattctata ggcaactact a 631

<210> 35
 <211> 578
 <212> DNA
 <213> Homo sapien

<400> 35
 tagtagttgc catcccatat tacagaaggc tctgtataca tgacttattt ggaagtgatc 60
 tgttttctct ccaaaccat ttatcgtaat ttcaccagtc ttggatcaat cttggtttcc 120
 actgatacca tgaaacctac ttggagcaga cattgcacag ttttctgtgg taaaaactaa 180
 aggttttatt gctaagctgt catcttatgc ttagtatttt ttttttacag tggggaattg 240
 ctgagattac attttgttat tcattagata ctttgggata acttgacact gtcttctttt 300
 tttcgctttt aattgctatc atcatgcttt tgaaacaaga acacattagt cctcaagtat 360
 tacataagct tgcttgttac gcctggtggt ttaaaggact atctttggcc tcagggtcac 420
 aagaatgggc aaagtgttct cttatgttct gtagttctca ataaaagatt gccaggggcc 480
 ggtactgtg gctcgactg taatcccagc actttgggaa gctgaggctg gcggatcatg 540
 ttagggcagg tgttcgaaac cagcctgggc aactacta 578

<210> 36
 <211> 583
 <212> DNA
 <213> Homo sapien

<400> 36

tagtagttgc	ctgtaatccc	agcaactcag	gaggctgggg	caggagaatc	agttgaacct	60
gggaggcaga	agttgtaatt	agcaaagatc	gcaccattgc	acttcagcct	gggcaacaag	120
agtgagattc	catctcaaaa	acaaaaaaaa	gaaaaagaaa	agaaaaggaa	aaaacgtata	180
aaccagcca	aaacaaaatg	atcattcttt	taataagcaa	gactaattta	atgtgtttat	240
ttaatcaaag	cagttgaatc	ttctgagtta	ttggtgaaaa	tacccatgta	gttaatttag	300
ggttcttact	tgggtgaacg	tttgatgttc	acaggttata	aaatggttaa	caaggaaaat	360
gatgcataaa	gaatcttata	aactactaaa	aataaataaa	atataaatgg	ataggtgcta	420
tggatggagt	ttttgtgtaa	tttaaaatct	tgaagtcatt	ttggatgctc	attggttgtc	480
tggtaatttc	cattaggaaa	aggttatgat	atggggaaac	tgtttctgga	aattgcggaa	540
tgtttctcat	ctgtaaaatg	ctagtatctc	agggcaacta	cta		583

<210> 37

<211> 716

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(716)

<223> n = A,T,C or G

<400> 37

gatctactag	tcatntggat	tctatccatg	gcagctaagc	ctttctgaat	ggattctact	60
gctttcttgt	tctttaatcc	agacccttat	atatgtttat	gttcacaggc	agggcaatgt	120
ttagtgaana	caattctaaa	ttttttat	tgcattttca	tgctaatttc	cgtcacactc	180
cagcaggctt	cctgggagaa	taaggagaaa	tacagctaaa	gacattgtcc	ctgcttactt	240
acagcctaat	ggtagcaaaa	accacttcaa	taaagtaaca	ggaaaagtac	taaccaggta	300
gaatggacca	aaactgatat	agaaaaatca	gaggaagaga	ggaacaaata	tttactgagt	360
cctagaatgt	acaaggcttt	ttaattacat	attttatgta	aggcctgcaa	aaaacagggtg	420
agtaatcaac	atttgtccca	ttttacatat	aaggaaactg	aagcttaaat	tgaataat	480
aatgcataga	ttttatagtt	agaccatgtt	caggctcccta	tggtataactt	actagctgta	540
tgaatatgag	aaaataat	tggtat	ttggcatcag	tattttcatc	tgcaaaaataa	600
agctaaagtt	atthagcaaa	cagtcagcat	agtgcctgat	acatagtagg	tgctccaaac	660
atgattacnc	tantatnng	tattanaaaa	atccaatata	ggcntggata	aaaccg	716

<210> 38

<211> 688

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(688)

<223> n = A,T,C or G

<400> 38

ttctgtccac	atatcatccc	actttaattg	ttaatcagca	aaactttcaa	tgaaaaatca	60
tccattttta	ccaggatcac	accaggaaac	tgaagggtgta	ttttttttta	ccttaaaaaa	120
aaaaaaaaaa	accaaacaaa	ccaaaacaga	ttaacagcaa	agagttctaa	aaaattttaca	180
tttctcttac	aactgtcatt	cagagaacaa	tagttcttaa	gtctgttaaa	tcttggcatt	240
aacagagaaa	cttgatgaan	agttgtactt	ggaatattgt	ggattttttt	ttttgtctaa	300
tctcccccta	ttgttttgcc	aacagtaatt	taagtttgtg	tggaacatcc	ccgtagttga	360
agtgtaaaca	atgtatagga	aggaatat	gataagatga	tgcatcacat	atgcattaca	420
tgtagggacc	ttcacaactt	catgcactca	gaaaacatgc	ttgaagagga	ggagaggacg	480

```

gccaggggtc accatccagg tgccttgagg acagagaatg cagaagtggc actgttgaaa 540
tttagaagac catgtgtgaa tggtttcagg cctgggatgt ttgccaccaa gaagtgcctc 600
cgagaaattt ctttccatt tggatacag ggtggcttga tgggtacggt ggtgaccca 660
acgaagaaaa tgaaattctg ccctttcc 688

```

```

<210> 39
<211> 585
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(585)
<223> n = A,T,C or G

```

```

<400> 39
tagtagttgc cgcnnaccta aaanttggaa agcatgatgt ctaggaaaca tantaaaata 60
gggtatgctt atgtgtctaca gagagatggt agcatttaaa gtgcatantt ttatgtattt 120
tgacaaatgc atatnctctt ataattccaca actgattacg aagctattac aattaaaaag 180
tttggccggg cgtggtgggc ggtggctgac gcctgtaatc ccagcacttt gggaggccga 240
ggcacgcgga tcacgaggtc gggagttcaa gaccatcctg gctaacacgg tgaaagtcca 300
tctctactaa aaatacgaaa aaattacccc ggctggtggt cgggcgcctg tagtcccagc 360
tactccggag gctgaggcag gagaatggcg tgaaccacgg acacggagct tgcagtgtgc 420
caacatcacg tcaactgcct ccagcctggg ggacaggaac aagantcccg tcctcanaaa 480
agaaaaatac tactnatant ttcnacttta ttttaantta cacagaactn cctcttggtgta 540
cccccttacc attcatctca cccacctcct atagggcacn nctaa 585

```

```

<210> 40
<211> 475
<212> DNA
<213> Homo sapien

```

```

<400> 40
tctgtccaca ccaatcttag aagctctgaa aagaatttgt ctttaaataat cttttaatag 60
taacatgtat tttatggacc aaattgacat tttcgactgt tttttccaaa aaagtcaggt 120
gaatttcagc aacttgaggt ggggaatttct tatcccagaa gaccaaccaa tttcatattt 180
atttaagatt gattccatac tccgttttca aggagaatcc ctgcagtctc cttaaaggta 240
gaacaaatac ttcctatttt tttttcacca ttgtgggatt ggactttaag aggtgactct 300
aaaaaaacag agaacaaata tgtctcagtt gtattaagca cggaccataa ttatcatatt 360
cacttaaaaa aatgatttcc tgtgcacctt ttggcaactt ctcttttcaa tgtagggaaa 420
aacttagtca ccctgaaaac ccacaaaata aataaaactt gtagatgtgg acaga 475

```

```

<210> 41
<211> 423
<212> DNA
<213> Homo sapien

```

```

<400> 41
taagagggta catcgggtaa gaacgtaggc acatctagag cttagagaag tctggggtag 60
gaaaaaaatc taagtattta taagggtata ggtaacattt aaaagtaggg ctagctgaca 120
ttatttagaa agaacacata cggagagata agggcaaagg actaagacca gaggaacact 180
aatatttagt gatcacttcc attcttggtg aaaatagtaa cttttaagtt agcttcaagg 240
aagatttttg gccatgatta gttgtcaaaa gttagttctc ttgggtttat attactaatt 300
ttgttttaag atccttggtg gtgctttaat aaagtcatgt tatatcaaac gctctaaaac 360
attgtagcat gttaaatgtc acaatatact taccatttgt tgtatatggc tgtaccctct 420

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cta

423

<210> 42
 <211> 527
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (527)
 <223> n = A,T,C or G

<400> 42
 tctcctaggc taatgtgtgt gtttctgtaa aagtaaaaag ttaaaaattt taaaaataga 60
 aaaaagctta tagaataaga atatgaagaa agaaaatatt tttgtacatt tgcacaatga 120
 gtttatgttt taagctaagt gttattacaa aagagccaaa aagggttttaa aaattaaaac 180
 gtttgtaaag ttacagtacc cttatgttaa tttataattg aagaaagaaa aacttttttt 240
 tataaatgta gtgtagccta agcatacagt atttataaag tctggcagtg ttcaataatg 300
 tcctaggcct tcacattcac tcaactgactc acccagagca acttccagtc ctgtaagctc 360
 cattcgtggg aagtgcccta tacagggtgca ccattttattt tacagtattt ttactgtacc 420
 ttctctatgt ttccatatgt ttcgatatac aaataccact gggttactatn gcccnacagg 480
 taattccagt aacacggcct gtatacgtct ggtancccta gngaaga 527

<210> 43
 <211> 331
 <212> DNA
 <213> Homo sapien

<400> 43
 tcttcaacct cgtaggacaa ctctcatatg cctgggcact attttttaggt tactaccttg 60
 gctgcccttc ttttaagaaaa aaaaaagaag aaaaaagaac ttttccacaa gtttctcttc 120
 ctctagttgg aaaattagag aaatcatgtt ttttaattttg tgttatttca gatcacaaat 180
 tcaaacactt gtaaacatta agcttctgtt caatccccctg ggaagaggat tcattctgat 240
 atttacgggt caaaaagaagt tgtaatatgt tgcttggaac acagagaacc agttattaac 300
 ttctactac tattatataa taaataataa c 331

<210> 44
 <211> 592
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (592)
 <223> n = A,T,C or G

<400> 44
 ggcttagtag ttgccaggca aaatarcgtt gattctcctc aggagccacc cccaacaccc 60
 ctgtttgctt ctagacctat acctagacta aagtcccagc agaccctag aggtgagggt 120
 cagagtgacc cttgaggaga tgtgctacac tagaaaagaa ctgcttgagt tttctaattt 180
 atataagcag aaatctggag aagagtcata ggaatggata ttaaggggtg gagataatgg 240
 cggaagggaat atagagtgtg atcaggctgg acttattgat ttgaaccac taagtagaga 300
 ttctgctttt gatgttgcag ctcagggtg taaaaaagggt tttaatgggt ctaatagttt 360
 atttgcttgg ttagctgaaa tatggataaa agatggccca ctgtgagcaa gctggaaatg 420
 cctgatctct ctcagtttaa tgtagaggaa gggatccaaa agtttaggga ganttggtg 480

ctggraktgg attggctact ttgrgacctt cccwtcccag ctggggagggg ccagaagata 540
cacccttgac caacgctttg cgaaatggat ttgtgatggc ggcaactact aa 592

<210> 45
<211> 567
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (567)
<223> n = A,T,C or G

<400> 45
ggcttagtag ttgccattgc gagtgcctgc tcaacgagcg ttgaacatgg cggattgtct 60
agattcaacg gatttgagtt ttaccagcaa agcgaaccaa gcgcggccca gagaattatg 120
ggttgggttg ctttgaaaag atggaaatcc tgtaggccta gtcagaaaag ccttcttgca 180
gaacagttgg ttctcgggcg aacgctcatc aagatgccca ttggaaaggc tagcgtgtat 240
ttgggagagc ctgatagcgt gtcttctgat gatgtttgtg cttggacagt gacaaaagat 300
atgcaaagca agtccgaact agacgtcaag ctctcgtgagc aaattattgt agactcctac 360
ttatactgtg aggaatgata gccaaaggtg gggactttta gactaagggtg gtttgtactt 420
gcgccgatga tcccaggcag aaagamctga tcgctagttt tatacgggca actactaagc 480
cgaattccag cacactggcg gccgttacta attggatccg anctcgggtac cagcttgatg 540
catascctga gttwtctata ntgtcnc 567

<210> 46
<211> 908
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (908)
<223> n = A,T,C or G

<400> 46
gagcgaaaga ccgagggcag ngnttangng cgangaagcg gagagggcca aaaagcaacc 60
gctttccccg gggggtgccg attcattaag gcaggtggag gacaggtttc ccgatggaag 120
gcggcagggg cgcaagcaat taatgtgagt aggccattca ttagcaccgc ggcttaacat 180
ttaagcttcg ggttggtatg tgggtgggaat tgtgagcgga taacaatttc acacaggaaa 240
cagctatgac catgattacg ccaagctatt taggtgacat tatagaataa ctcaagttat 300
gcatcaagct tggtagcgag ttccggatcca ctagtaacgg ccgccagtgt gtggaattcg 360
gcttagtagt tgccgaccat ggagtgtac 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 ggggtgagaaa gccagaatca gtgtccagct 660
gcagttgttg gagaagggtg tattatgtat gtctcagaag tgacaccata tgggcaacta 720
ctaagccccg attccagcac actggcgggc gttactaatg gatccgagct cggtaaccaag 780
cttgatgcat agcttgagta tctatagtgt cactaaatag cctggcggtta tcatggtcat 840
agctgtttcc tgtgtgaaat tgttatccgc tcccaattcc ccccaccata cgagccggaa 900
cataaagt 908

<210> 47
<211> 480

<212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(480)
 <223> n = A,T,C or G

<400> 47

tgccaacaag	gaaagtttta	aatttccccc	tgaggattct	tggtgatcat	caaattcagt	60
ggtttttaag	ggtgttttct	gtcaaataac	tctaacttta	agccaaacag	tatatggaag	120
cacagataka	atattacaca	gataaaagag	gagttgatct	aaagtaraga	tagttggggg	180
ctttaatttc	tggaacctag	gtctccccc	cttcttctgt	gctgaggaac	ttcttggaag	240
cggggattct	aaagttcttt	ggaagacagt	ttgaaaacca	ccatgttggt	ctcagtacct	300
ttatttttaa	aaagtaggtg	aacattttga	gagagaaaag	ggcttggttg	agatgaagtc	360
ccccccccc	cttttttttt	tttttagctg	aatagatacc	ctatgttnaa	rgaarggatt	420
attatttacc	atgccaytar	scacatgctc	tttgatgggc	nytccestac	cctccttaag	480

<210> 48
 <211> 591
 <212> DNA
 <213> Homo sapien

<400> 48

aagagggtac	cgagtggaat	ttccgcttca	ctagtctggt	gtggctagtc	ggtttcgtgg	60
tgccaacat	tacgaacttc	caactcaacc	gttcttggtg	gttcaagcgg	gagtaccggc	120
gaggatggtg	gcgtgaattc	tggcctttct	ttgccgtggg	atcggtagcc	gccatcatcg	180
gtatgtttat	caagatcttc	tttactaacc	cgacctctcc	gatttacctg	cccagaccgt	240
ggtttaacga	ggggaggggg	atccagtcac	gcgagtactg	gtcccagatc	ttcgccatcg	300
tcgtgacaat	gcctatcaac	ttcgtcgtca	ataagttgtg	gaccttccga	acgggtgaagc	360
actccgaaaa	cgtccgggtg	ctgctgtgcg	gtgactccca	aaatcttgat	aacaacaagg	420
taaccgaatc	gcgctaagga	accccgccat	ctcgggtact	ctgcatatgc	gtacccttta	480
agccgaattc	cagcacactg	gcggccgtta	ctaattggat	ccgaactccg	taaccaagcc	540
tgatgcgtaa	cttgagttat	tctatagtgt	ccctaaaata	acctggcggt	a	591

<210> 49
 <211> 454
 <212> DNA
 <213> Homo sapien

<400> 49

aagagggtac	ctgccttgaa	atttaaattgt	ctaaggaaar	tgggagatga	ttaagagttg	60
gtgtggcyta	gtcacaccaa	aatgtattta	ttacatcctg	ctccttttcta	gttgacagga	120
aagaaagctg	ctgtggggaa	aggagggata	aatactgaag	ggatttacta	aacaaatgtc	180
catcacagag	ttttcccttt	tttttttttg	agacagagtc	ttgctctgtc	acctaggctg	240
gaatgaagwg	gtatgatctc	agttgaatgc	aacctctacc	tcctagggttc	aagcgattct	300
catgcctcag	cctcctgagc	agctgggact	ataggcgcat	gctaccatgc	caggctaatt	360
tttatatttt	tattagagac	ggggtgttgc	catgttggcc	aggcaggtct	cgaactcctg	420
ggcctcagat	gatctgcccc	accgtaccct	ctta			454

<210> 50
 <211> 463
 <212> DNA
 <213> Homo sapien

<400> 50

aagagggtac	caaaaaaaaaag	aaaaaggaaa	aaaagaaaaa	caacttgtat	aaggctttct	60
gctgcataca	gctttttttt	tttaaataaa	tggtgccaac	aaatgttttt	gcattcacac	120
caattgctgg	ttttgaaatc	gtactcttca	aaggatattg	tgcagatcaa	tccaatagtg	180
atgccccgta	ggttttgtgg	actgcccacg	ttgtctacct	tctcatgtag	gagccattga	240
gagactgttt	ggacatgcct	gtgttcatgt	agccgtgatg	tccggggggc	gtgtacatca	300
tgttaccgtg	gggtgggggc	tgcattggct	gctgggcata	tggtctgggtg	cccatcatgc	360
ccatctgcat	ctgcataggg	tattggggcg	tttgatccat	atagccatga	ttgctgtggt	420
agccactggt	catcattggc	tgggacatgc	tgttaccctc	tta		463

<210> 51

<211> 399

<212> DNA

<213> Homo sapien

<400> 51

cttcaacctc	ccaaagtgct	gggattacag	gactgagcca	ccacgctcag	cctaagcctc	60
tttttcacta	ccctctaagc	gatctaccac	agtgatgagg	ggctaaagag	cagtgcattt	120
tgattacaat	aatggaactt	agatttatta	attaacaatt	tttccttagc	atgttggttc	180
cataattatt	aagagtatgg	acttacttag	aaatgagctt	tcattttaag	aatttcatct	240
ttgaccttct	ctattagtct	gagcagtatg	acactatacg	tattttattt	aactaaccta	300
ccttgagcta	ttacttttta	aaaggctata	tacatgaatg	tgtattgtca	actgtaaagc	360
cccacagtat	ttaattatat	catgatgtct	ttgagggtg			399

<210> 52

<211> 392

<212> DNA

<213> Homo sapien

<400> 52

cttcaacctc	aatcaacctt	ggtaattgat	aaaatcatca	cttaactttc	tgatataatg	60
gcaataatta	tctgagaaaa	aaaagtgggtg	aaagattaaa	cttgcatttc	tctcagaatc	120
ttgaaggata	tttgaataat	tcaaaagcgg	aatcagtagt	atcagccgaa	gaaactcact	180
tagctagaac	ggtggacca	tggatctaag	tccctgacct	tccactaacc	agctgattgg	240
ttttgtgtaa	acctcctaca	cgcttgggct	tggtcgccct	atttgtcaaa	gtaaaggctg	300
aaataggaag	ataatgaacc	gtgtcttttt	ggtctctttt	ccatccatta	ctctgatttt	360
acaaagaggg	ctgtattccc	ctgggtgaggt	tg			392

<210> 53

<211> 179

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (179)

<223> n = A,T,C or G

<400> 53

ttcgggtgat	gcctcctcag	gctacagtga	agactggatt	acagaaagg	gccagcgaga	60
tttcagattc	ctgtaaacct	ctaaagaaaa	ggagtcgcgc	ctcaactgat	gtagaaatga	120
ctagttcagc	atacngagac	acntctgact	ccgattctag	aggactgagt	gacctgcan	179

<210> 54

<211> 112

<212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(112)
 <223> n = A,T,C or G

<400> 54
 ttctgggtgat gcctcctcag gctacatcat natagaagca aagtagaana atcnngtttg 60
 tgcattttcc cacanacaaa attcaaatga ntggaagaaa ttggganagt at 112

<210> 55
 <211> 225
 <212> DNA
 <213> Homo sapien

<400> 55
 tgagcttccg cttctgacaa ctcaatagat aatcaaagga caactttaac agggattcac 60
 aaaggagtat atccaaatgc caataaacat ataaaaagga attcagcttc atcatcatca 120
 gaagwatgca aattaaaacc ataattgagaa accactatgt ccactagaa tagataaaat 180
 cttaaaagac tggtaaaacc aagtgttggg aaggcaagag gagca 225

<210> 56
 <211> 175
 <212> DNA
 <213> Homo sapien

<400> 56
 gctcctcttg cettaccaac acattctcaa aaacctgtta gagtcctaag cattctcctg 60
 ttagtattgg gattttaccc ctgtcctata aagatgttat gtacaaaaaa tgaagtggag 120
 ggccataccc tgagggaggg gagggatctc tagtgttgtc agaagcggaa gctca 175

<210> 57
 <211> 223
 <212> DNA
 <213> Homo sapien

<400> 57
 agccatttac caccatgga tgaatggatt ttgtaattct agctgttgta ttttgtgaat 60
 ttgttaattt tgttgttttt ctgtgaaaca catcattgg atatgggagg taaaggagtg 120
 tcccagttgc tcttggtcac tccctttata gccattactg tcttgtttct tgtaactcag 180
 gttaggtttt ggtctctctt gctccactgc aaaaaaaaaa aaa 223

<210> 58
 <211> 211
 <212> DNA
 <213> Homo sapien

<400> 58
 gttcgaagggt gaacgtgtag gtagcggatc tcacaactgg ggaactgtca aagacgaatt 60
 aactgacttg gatcaatcaa atgtgactga ggaaacacct gaagggtgaag aacatcatcc 120
 agtggcagac actgaaaata aggagaatga agttgaagag gtaaaagagg aggggtccaa 180
 agagatgact ttggatgggt ggtaaatggc t 211

<210> 59
 <211> 208
 <212> DNA
 <213> Homo sapien

<400> 59
 gctcctcttg ccttaccaac tttgcaccca tcatcaacca tgtggccagg tttgcagccc 60
 aggctgcaca tcaggggact gcctcgcaat acttcatgct gttgctgctg actgatgggtg
 120ctgtgacgga tgtggaagcc acacgtgagg ctgtggtgcg tgccctgaac ctgcccattgt
 180
 cagtgatcat tatgggtggt aaatggct 208

<210> 60
 <211> 171
 <212> DNA
 <213> Homo sapien

<400> 60
 agccatttac caccataact aaattctagt tcaaactcca acttcttcca taaaacatct 60
 aaccactgac accagttggc aatagcttct tccttcttta acctcttaga gtatttatgg 120
 tcaatgccac acatttctgc aactgaataa agttggtgaag gcaagaggag c 171

<210> 61
 <211> 134
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(134)
 <223> n = A,T,C or G

<400> 61
 cgggtgatgc ctccctcaggc tttggtgtgt ccaactnact cactggcctc ttctccagca 60
 actggtgaan atgtccctcan gaaaancncc acacgcngct caggggtgggg tgggaancat 120
 canaatcatc nggc 134

<210> 62
 <211> 145
 <212> DNA
 <213> Homo sapien

<400> 62
 agaggggtaca tatgcaacag tatataaagg aagaagtgca ctgagaggaa cttcatcaag 60
 gccatttaata caataagtga tagagtcaag gctcaaccca ggtgtgacgg attccaggtc 120
 ccaagctcct tactggtacc ctctt 145

<210> 63
 <211> 297
 <212> DNA
 <213> Homo sapien

<400> 63
 tgcactgaga ggaattcaaa gggtttatgc caaagaacaa accagtcctc tgcagcctaa 60
 ctcatattgtt tttgggctgc gaagccatgt agagggcgat caggcagtag atgggtccctc 120

ccacagtcag	cgccatgggtg	gtccggtaaa	gcatttggtc	aggcaggcct	cgtttcaggt	180
agacggggcac	acatcagctt	tctggaaaaa	cttttgtagc	tctggagctt	tgtttttccc	240
agcataatca	tacactgttg	aatcggaggt	cagtttagtt	ggtaaggcaa	gaggagc	297

<210> 64

<211> 300

<212> DNA

<213> Homo sapien

<400> 64

gcactgagag	gaacttccaa	tactatgttg	aataggagtg	gtgagagagg	gcatecttgt	60
cttggtgccg	ttttcaaagg	gaatgcttcc	agcttttgcc	cattcagtat	aatattaaag	120
aatgttttac	cattttctgt	cttgccgtgt	tttctgtgtt	tttggtggtc	tcttcattct	180
ccatttttag	gcctttacat	gttaggaata	tatttctttt	aatgatactt	cacctttggg	240
atcttttgtg	agactctact	catagtgtga	taagcactgg	gttggttaagg	caagaggagc	300

<210> 65

<211> 203

<212> DNA

<213> Homo sapien

<400> 65

gctcctcttg	ccttaccac	tcacccagta	tgtcagcaat	tttatcrgct	ttacctacga	60
aacagcctgt	atccaaacac	ttaacacact	cacctgaaaa	gttcaggcaa	caatcgcctt	120
ctcatgggtc	tctctgctcc	agttctgaac	ctttctcttt	tcctagaaca	tgcatattarg	180
tcgatagaag	ttcctctcag	tgc				203

<210> 66

<211> 344

<212> DNA

<213> Homo sapien

<400> 66

tacgggggacc	cctgcattga	gaaagcgaga	ctcactctga	agctgaaatg	ctgttgccct	60
tgcatgtgctg	gtagcaggag	ttctgtgctt	tgtgggctaa	ggctcctgga	tgacccttga	120
catggagaag	gcagagttgt	gtgccccttc	tcatggcctc	gtcaaggcat	catggactgc	180
cacacacaaa	atgccgtttt	tattaacgac	atgaaattga	aggagagaac	acaattcact	240
gatgtgggtc	gtaaccatgg	atatggtcac	atacagaggt	gtgattatgt	aaagggttaat	300
tccaccacc	tcatgtggaa	actagcctca	atgcaggggt	ccca		344

<210> 67

<211> 157

<212> DNA

<213> Homo sapien

<400> 67

gcactgagag	gaacttcgta	gggaggttga	actggctgct	gaggaggggg	aacaacaggg	60
taaccagact	gatagccatt	ggatggataa	tatgggtggtt	gaggaggggac	actacttata	120
gcagaggggtt	gtgtatagcc	tgaggaggca	tcacccg			157

<210> 68

<211> 137

<212> DNA

<213> Homo sapien

<400> 68
gcactgagag gaacttctag aaagtgaaag tctagacata aaataaaata aaaattttaa 60
actcaggaga gacagcccag cacggtggct cacgcctgta atcccagaac tttgggagcc 120
tgaggaggca tcacccg 137

<210> 69
<211> 137
<212> DNA
<213> Homo sapien

<400> 69
cgggtgatgc ctcctcaggc tgtatattga agactatcga ctggacttct tatcaactga 60
agaatccgtt aaaaatacca gttgtattat ttctacctgt caaaatccat ttcaaagtgt 120
gaagttcctc tcagtgc 137

<210> 70
<211> 220
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(220)
<223> n = A,T,C or G

<400> 70
agcatgttga gccagacac gcaatctgaa tgagtgtgca cctcaagtaa atgtctacac 60
gctgcctggt ctgacatggc acaccatcnc gtggagggca casctctgct cngcctacwa 120
cgagggcant ctcattwgaca ggttccaccc accaaactgc aagaggctca nnaagtactr 180
ccaggggtmya sggacmasgg tgggaytyca ycacwcatct 220

<210> 71
<211> 353
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(353)
<223> n = A,T,C or G

<400> 71
cgttaggggtc tctatccact gctaaacat acacctgggt aaacaggac catttaacat 60
tccanctaa atatgccaaag tgacttcaca tgtttatctt aaagatgtcc aaaacgcaac 120
tgattttctc ccctaaacct gtgatgggtg gatgattaan cctgagtggc ctacagcaag 180
ttaagtgcaa ggtgctaaat gaangtgacc tgagatacag catctacaag gcagtacctc 240
tcaacncagg gcaactttgc ttctcanagg gcatttagca gtgtctgaag taatttctgt 300
attacaactc acggggcgagg ggggtgaatat ctantggana gnagacccta acg 353

<210> 72
<211> 343
<212> DNA
<213> Homo sapien

<400> 72

gcactgagag	gaacttccaa	tacyatkatc	agagtgaaca	rgcarccyac	agaacaggag	60
aaaatgttyg	caatctctcc	atctgacaaa	aggctaatat	ccagawtcta	awaggaactt	120
aaacaaatth	atgagaaaag	aacaracaac	ctcawcaaaa	agtgggtgaa	ggawatgcts	180
aaargaagac	atytattcag	ccagtaaaca	yatgaaaaaa	aggctcatsa	tcactgawca	240
ttagagaaat	gcaaatcaaa	accacaatga	gataccatct	yayrccagtt	agaayggtga	300
tcattaaaar	stcaggaaac	aacagatgct	ggacaagggtg	tca		343

<210> 73

<211> 321

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(321)

<223> n = A,T,C or G

<400> 73

gcactgagag	gaacttcaga	gagagagaga	gagttccacc	ctgtacttgg	ggagagaaac	60
agaagggtgag	aaagtctttg	gttctgaagc	agcttctaag	atcttttcat	ttgcttcatt	120
tcaaagttcc	catgctgcca	aagtgccatc	ctttggggta	ctgttttctg	agctccagtg	180
ataactcatt	tatacaaggg	agatacccag	aaaaaaagtg	agcaaattctt	aaaaagggtg	240
cttgagttca	gccttaata	ccatcttgaa	atgacacaga	gaaagaanga	tggtgggtgg	300
gagtggatag	agaccctaac	g				321

<210> 74

<211> 321

<212> DNA

<213> Homo sapien

<400> 74

gcactgagag	gaacttcaga	gagagagaga	gagttccacc	ctgtacttgg	ggagagaaac	60
agaagggtgag	aaagtctttg	gttctgaagc	agcttctaag	atcttttcat	ttgcttcatt	120
tcaaagttcc	catgctgcca	aagtgccatc	ctttggggta	ctgttttctg	agctccagtg	180
ataactcatt	tatacaaggg	agatacccag	aaaaaaagtg	agcaaattctt	aaaaagggtg	240
cttgagttca	gycttaata	ccatcttgaa	atgamacaga	gaaagaagga	tggtgggtgg	300
gagtggatag	agaccctaac	g				321

<210> 75

<211> 317

<212> DNA

<213> Homo sapien

<400> 75

gcactgagag	gaacttccac	atgcactgag	aaatgcatgt	tcacaaggac	tgaagtctgg	60
aactcagttt	ctcagttcca	atcctgattc	agggtgtttac	cagctacaca	accttaagca	120
agtcagataa	ccttagcttc	ctcatatgca	aaatgagaat	gaaaagtact	catcgctgaa	180
ttgttttgag	gattagaaaa	acatctggca	tgtagtagaa	attcaattag	tattcatttt	240
cattcttcta	aattaaacaa	ataggatttt	tagtggtgga	acttcagaca	ccagaaatgg	300
gagtggatag	agaccct					317

<210> 76

<211> 244

<212> DNA

<213> Homo sapien

<400> 76

cgttaggggc	tctatccact	cccactactg	atcaaactct	at ttattttaa	ttatttttat	60
catactttta	gttctgggat	acacgtgcag	catgcgcagg	tttggtgcat	aggtatacac	120
ttgccatggg	ggtttgctgc	acccatcagt	ccatcatcta	cattaggtat	ttctccta	180
gctatccctc	ccctagcccc	ttacaccccc	aacaggctct	agtgtgtgaa	gttcctctca	240
gtgc						244

<210> 77

<211> 254

<212> DNA

<213> Homo sapien

<400> 77

cgttaggggc	tctatccact	gaaatctgaa	gcacaggagg	aagagaagca	gtyctagtga	60
gatggcaagt	tcwtttacca	cactctttta	catttygttt	agttttaacc	tttatttatg	120
gataataaag	gttaatat	ataatgattt	attttaaggc	attcccraat	ttgcataatt	180
ctccttttgg	agataccctt	ttatctccag	tgcaagtctg	gatcaaagtg	atasamagaa	240
gttcctctca	gtgc					254

<210> 78

<211> 355

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(355)

<223> n = A,T,C or G

<400> 78

ttcgatacag	gcaaacatga	actgcaggag	gggtgtgacg	atcatgatgt	tgccgatggg	60
ccggatggnc	acgaagacgc	actggancac	gtgcttacgt	ccttttgctc	tggtgatggc	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	taaccntgtn	tcgaa	355

<210> 79

<211> 406

<212> DNA

<213> Homo sapien

<400> 79

taagagggta	ccagcagaaa	ggttagtatc	atcagatagc	atccttatacg	agtaatatgc	60
ctgctatttg	aagtgttaatt	gagaaggaaa	at ttttagcgt	gctcactgac	ctgcctgtag	120
ccccagtgc	agctaggatg	tgcatctctc	agccatcaag	agactgagtc	aagttgttcc	180
ttaagtcaga	acagcagact	cagctctgac	attctgattc	gaatgacact	gttcaggaat	240
cggaaatcctg	tcgattagac	tggaacagctt	gtggcaagtg	aatttgctg	taacaagcca	300
gattttttta	aatttatatt	gtaaataatg	tgtgtgtgtg	tgtgtgtata	tatatatata	360
tgtacagtta	tctaagttaa	tttaaaagtt	gtttgggtacc	ctctta		406

<210> 80

<211> 327

<212> DNA

<213> Homo sapien

<400> 80

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agggctagga	tgatgattaa	taagagggat	gacataacta	ttagtggcag	gtagttgtt	120
tgtagggctc	atggtagggg	taaaaggagg	gcaatttcta	gatcaaataa	taagaaggta	180
atagctacta	agaagaatth	tatggagaaa	gggacgcggg	cgggggatat	agggtcgaag	240
ccgcactcgt	aaggggtgga	tttttctatg	tagccgttga	gttgtggtag	tcaaatgta	300
ataattatta	gtagtaagcc	taggaga				327

<210> 81

<211> 318

<212> DNA

<213> Homo sapien

<400> 81

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attgcattca	taatttatta	tgcatthtatg	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

<210> 82

<211> 338

<212> DNA

<213> Homo sapien

<400> 82

tcttcaacct	ctactccac	taatagcttt	ttgatgactt	ctagcaagcc	tcgctaacct	60
cgccttacct	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	cccagacatca	ttaccgggtt	ttcctctt			338

<210> 83

<211> 111

<212> DNA

<213> Homo sapien

<400> 83

agccattttac	cacccatcca	caaaaaaaaa	aaaaaaaaag	aaaaatatca	aggaataaaa	60
atagactttg	aacaaaaagg	aacatttgct	ggcctgagga	ggcatcaccc	g	111

<210> 84

<211> 224

<212> DNA

<213> Homo sapien

<400> 84

tcgggtgatg	cctcctcagg	ccaagaagat	aaagcttcag	acccctaaca	catttccaaa	60
aaggaagaaa	ggagaaaaaa	gggcatcatc	cccgttccga	agggtcaggg	aggaggaaat	120
tgaggtggat	tcacgagttg	cggacaactc	ctttgatgcc	aagcgaggtg	cagccggaga	180
ctggggagag	cgagccaatc	aggttttgaa	gttcctctca	gtgc		224

<210> 85
 <211> 348
 <212> DNA
 <213> Homo sapien

<400> 85
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 ctcaagtaact tccttggtgt gtgtgtattc aactcacasa gttgaacgat cctttacaca 120
 gagcagactt gtaacactct twttgtggaa ttgcaagtg gagatttcag scgctttgaa 180
 gtsaaaggta gaaaaggaaa tatcttccta taaaaactag acagaatgat ttcagaaac 240
 tcctttgtga tgtgtgctgt caactcacag agtttaacct ttcwtttcat agaagcagtt 300
 aggaaacact ctgtttgtaa agtctgcaag tggatagaga ccctaacg 348

<210> 86
 <211> 293
 <212> DNA
 <213> Homo sapien

<400> 86
 gcactgagag gaacttcygt gtgwtgktgt yattcaactc acagagttga asswtsmttt 60
 acabagwkca ggcttkcaaa cactcttttt gtmgaatygt caagwggaka tttsrrccrc 120
 ttgwggycw wysktmgaaw mgyrwtatc ttcwyatmra amctagacag aaksattctc 180
 akaawstyyy ytgtgawgws tgcrttcaac tcacagagkt kaacmwttyct kytsatrgag 240
 cagttwkga actctmtttc ttgggattct gcaagtggat agagacccta acg 293

<210> 87
 <211> 10
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer for amplification from breast tumor cDNA

<400> 87
 ctccctaggct 10

<210> 88
 <211> 10
 <212> DNA
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<220>
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<400> 88
 agtagttgcc 10

<210> 89
 <211> 11
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<220>
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<400> 89
ttccggttatg c 11

<210> 90
<211> 10
<212> DNA
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<220>
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<400> 90
tggtaaaggg 10

<210> 91
<211> 10
<212> DNA
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<220>
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<400> 91
tcggtcatag 10

<210> 92
<211> 10
<212> DNA
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<220>
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<400> 92
tacaacgagg 10

<210> 93
<211> 10
<212> DNA
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<220>
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<400> 93
tggattggtc 10

<210> 94
<211> 10
<212> DNA
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<220>
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<400> 94
ctttctaccc 10

<210> 95
<211> 10
<212> DNA
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<220>
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<400> 95
ttttggctcc 10

<210> 96
<211> 10
<212> DNA
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<220>
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<400> 96
ggaaccaatc 10

<210> 97
<211> 10
<212> DNA
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<220>
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<400> 97
tcgatacagg 10

<210> 98
<211> 10
<212> DNA
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<220>
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<400> 98
ggtactaagg 10

<210> 99
<211> 10
<212> DNA
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<220>
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<400> 99
agtctatgcg 10

<210> 100
<211> 10
<212> DNA
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<220>
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<400> 100
ctatccatgg 10

<210> 101
<211> 10
<212> DNA
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<220>
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<400> 101
tctgtccaca 10

<210> 102
<211> 10
<212> DNA
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<220>
<223> Primer for amplification from breast tumor cDNA

<400> 102
aagagggtac 10

<210> 103
<211> 10
<212> DNA
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<220>
<223> Primer for amplification from breast tumor cDNA

<400> 103
cttcaacctc 10

<210> 104
<211> 20
<212> DNA
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<220>
<223> Primer for amplification from breast tumor cDNA

<400> 104
gctcctcttg ccttaccaac 20

<210> 105
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 105
gtaagtcgag cagtgtgatg 20

<210> 106
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 106
gtaagtcgag cagtctgatg 20

<210> 107
<211> 20
<212> DNA
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<220>
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<400> 107
gacttagtgg aaagaatgta 20

<210> 108
<211> 20
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<220>
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<400> 108
gtaattccgc caaccgtagt 20

<210> 109
<211> 20
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<220>
<223> Primer for amplification from breast tumor cDNA

<400> 109
atggttgatc gatagtggaa 20

<210> 110
<211> 20
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<223> Primer for amplification from breast tumor cDNA

<400> 110
acggggaccc ctgcattgag 20

<210> 111
<211> 20
<212> DNA
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<220>
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<400> 111
tattctagac cattcgctac 20

<210> 112
<211> 20
<212> DNA
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<220>
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<400> 112
acataaccac ttttagcgttc 20

<210> 113
<211> 20
<212> DNA
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<220>
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<400> 113
cggtgatgc ctctcaggc 20

<210> 114
<211> 20
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<220>
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<400> 114
agcatgttga gccagacac 20

<210> 115
<211> 20
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<220>
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<400> 115
gacacctgtg ccagcatctg 20

<210> 116
<211> 20
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<220>
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<400> 116
tacgctgcaa cactgtggag 20

<210> 117
<211> 20
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<220>
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<400> 117
cgtaggggtc tctatccact 20

<210> 118
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<220>
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<400> 118
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<210> 119
<211> 20
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<220>
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<400> 119
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<210> 120
<211> 20
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<220>
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<400> 120
caagattcca taggctgacc 20

<210> 121
<211> 20
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<220>
<223> Primer for amplification from breast tumor cDNA

<400> 121
acgtactggc cttgaaggtc 20

<210> 122
<211> 20
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<220>
<223> Primer for amplification from breast tumor cDNA

<400> 122
gacgcttggc cacttgacac 20

<210> 123
<211> 20
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<220>
<223> Primer for amplification from breast tumor cDNA

<400> 123
gtatcgacgt agtggctctcc 20

<210> 124
<211> 20
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<220>
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<400> 124
tagtgacatt acgacgctgg 20

<210> 125
<211> 20
<212> DNA
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<220>
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<400> 125
cgggtgatgc ctctcaggc 20

<210> 126
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 126
atggctatatt tcgggggctg aca 23

<210> 127
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 127
ccggtatctc ctctgggta tt 22

<210> 128
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 128
ctgcctgagc cacaaatg 18

<210> 129
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for amplification from breast tumor cDNA

<400> 129
ccggaggagg aagctagagg aata 24

<210> 130
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 130
tttttttttt ttag 14

<210> 131
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Predicited Th Motifs (B-cell epitopes)

<400> 131
Ser Ser Gly Gly Arg Thr Phe Asp Asp Phe His Arg Tyr Leu Leu Val
1 5 10 15
Gly Ile

<210> 132
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Predicited Th Motifs (B-cell epitopes)

<221> VARIANT
<222> (1)...(22)
<223> Xaa = Any Amino Acid

<400> 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

<210> 133
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Predicited Th Motifs (B-cell epitopes)

<400> 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

<210> 134
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Predicited HLA A2.1 Motifs (T-cell epitopes)

<400> 134
Tyr Leu Leu Val Gly Ile Gln Gly Ala
1 5

<210> 135
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Predicited HLA A2.1 Motifs (T-cell epitopes)

<400> 135
Gly Ala Ala Gln Lys Pro Ile Asn Leu
1 5

<210> 136
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Predicited HLA A2.1 Motifs (T-cell epitopes)

<221> VARIANT
<222> (1)...(9)
<223> Xaa = Any Amino Acid

<400> 136
Asn Leu Ser Lys Xaa Ile Glu Val Val
1 5

<210> 137
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Predicited HLA A2.1 Motifs (T-cell epitopes)

<400> 137

Glu Val Val Gln Gly His Asp Glu Ser
1 5

<210> 138

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Predicited HLA A2.1 Motifs (T-cell epitopes)

<400> 138

His Leu Gln Glu Ala Tyr Arg Ile Tyr
1 5

<210> 139

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Predicited HLA A2.1 Motifs (T-cell epitopes)

<400> 139

Asn Leu Ala Phe Val Ala Gln Ala Ala
1 5

<210> 140

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Predicited HLA A2.1 Motifs (T-cell epitopes)

<400> 140

Phe Val Ala Gln Ala Ala Pro Asp Ser
1 5

<210> 141

<211> 9388

<212> DNA

<213> Homo sapien

<400> 141

gctcgcgggcc gcgagctcaa ttaaccctca ctaaagggag tcgactcgat cagactgtta	60
ctgtgtctat gtagaaagaa gtagacataa gagattccat tttgttctgt actaagaaaa	120
attcttctgc cttgagatgc tggttaatctg taaccctagc cccaaccctg tgctcacaga	180
gacatgtgct gtgttgactc aagggttcaat ggatttaggg ctatgctttg ttaaaaaagt	240
gcttgaagat aatatgcttg ttaaaagtca tcaccattct ctaatctcaa gtacccaggg	300
acacaataca ctgcggaagg ccgcagggac ctctgtctag gaaagccagg tattgtccaa	360
gatttctccc catgtgatag cctgagatat ggcctcatgg gaagggtaag acctgactgt	420
ccccagccc gacatcccc agcccgacat ccccccagccc gacacccgaa aagggctctgt	480
gctgaggagg attagtaaaa gaggaaggcc tctttgcagt tgaggtaaga ggaaggcatc	540
tgtctcctgc tcgtccctgg gcaatagaat gtcttggtgt aaaaccgat tgatatgttct	600

acttactgag	ataggagaaa	acatccttag	ggctggaggt	gagacacgct	ggcggcaata	660
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<210> 142

<211> 419

<212> DNA

<213> Homo sapien

<400> 142

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<210> 143

<211> 402

<212> DNA

<213> Homo sapien

<400> 143

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<211> 224

<212> DNA

<213> Homo sapien

<400> 144

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<210> 145

<211> 111

<212> DNA

<213> Homo sapien

<400> 145

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<210> 146

<211> 585

<212> DNA

<213> Homo sapien

<400> 146

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<210> 147

<211> 579

<212> DNA

<213> Homo sapien

<220>

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<223> n = A,T,C or G

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<210> 148

<211> 249

<212> DNA

<213> Homo sapien

<400> 148

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<210> 149

<211> 255

<212> DNA

<213> Homo sapien

<400> 149

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<210> 150

<211> 318

<212> DNA

<213> Homo sapien

<400> 150

ttacgctgca	acactgtgga	ggccaagctg	ggatcacttc	ttcattctaa	ctggagagga	60
gggaagtcca	agtccagcag	agggtgggtg	ggtagacagt	ggcactcaga	aatgtcagct	120
ggacccctgt	ccccgcatag	gcaggacagc	aaggctgtgg	ctctccaggg	ccagctgaag	180
aacaggacac	tgtctccgct	gccacaaagc	gtcagagact	cccatctttg	aagcacggcc	240
ttcttggtct	tcctgcactt	ccctgttctg	ttagagacct	ggttatagac	aaggcttctc	300
cacagtgttg	cagcgtaa					318

<210> 151

<211> 323

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(323)

<223> n = A,T,C or G

<400> 151tnacgcngcn acnntgtaga ganggnaagg cnttccccac attnccccctt
catnanagaa 60
ttattcnacc aagnntgacc natgcctttt atgacttaca tgcnnactnc ntaatctgtn 120
tcnngcctta aaagcnnntc cactacatgc ntcancactg tntgtgtnac ntcatnaact 180
gtcngnaata ggggncata actacagaaa tgcanttcac actgcttcca ntgccatcng 240
cgtgtggcct tncctactct tcttntattc caagtagcat ctctggantg cttccccact 300
ctccacattg ttgcagcnat aat 323

<210> 152

<211> 311

<212> DNA

<213> Homo sapien

<400> 152
tcaagattcc ataggctgac cagtccaagg agagttgaaa tcatgaagga gagtctatct 60
ggagagagct gtagttttga gggttgcaaa gacttaggat ggagttggtg ggtgtggtta 120
gtctctaagg ttgattttgt tcataaaatt catgccctga atgccttgct tgcctcaccc 180
tggtccaagc cttagtgaac acctaaaagt ctctgtcttc ttgctctcca aacttctcct 240
gaggatttcc tcagattgtc tacattcaga tcgaagccag ttggcaaaca agatgcagtc 300
cagaggggtca g 311

<210> 153

<211> 332

<212> DNA

<213> Homo sapien

<400> 153
caagattcca taggctgacc aggaggctat tcaagatctc tggcagttga ggaagtctct 60
ttaagaaaat agtttaaaca atttgttaaa atttttctgt cttacttcat ttctgtagca 120
gttgatatct ggctgtcctt tttataatgc agagtgggaa ctttccctac catgtttgat 180
aaatgttgct caggctccat tgccaataat gtgttggtcca aaatgcctgt ttagttttta 240
aagacggaac tccacccttt gcttggtctt aagtatgtat ggaatgttat gataggacat 300
agtagtagcg gtggtcagcc tatggaatct tg 332

<210> 154

<211> 345

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(345)

<223> n = A,T,C or G

<400> 154
tcaagattcc ataggctgac ctggacagag atctcctggg tctggcccag gacagcaggg 60
tcaagctcag tggagaaggc ttccatgacc ctcagattcc cccaaacctt ggattgggtg 120
acattgcatc tcctcagaga gggaggagat gtangtctgg gcttccacag ggacctggta 180

ttttaggatc agggtagcgc tggcctgagg cttggatcat tcanagcctg ggggtggaat	240
ggctggcagc ctgtggcccc attgaaatag gctctggggc actccctctg ttcctanttg	300
aacttgggta aggaacagga atgtgggtcan cctatggaat cttga	345

<210> 155
 <211> 295
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(295)
 <223> n = A,T,C or G

<400> 155	
gacgcttggc cacttgacac attaaacagt tttgcataat cactancatg tatttctagt	60
ttgctgtctg ctgtgatgcc ctgccctgat tctctggcgt taatgatggc aagcataatc	120
aaacgctgtt ctgttaattc caagttataa ctggcattga ttaaagcatt atctttcaca	180
actaaactgt tcttcatana acagcccata ttattatcaa attaagagac aatgtattcc	240
aatatccttt anggccaata tatttnatgt cccttaatta agagctactg tccgt	295

<210> 156
 <211> 406
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(406)
 <223> n = A,T,C or G

<400> 156	
gacgcttggc cacttgacac tgcagtggga aaaccagcat gagccgctgc cccaaggaa	60
cctcgaagcc caggcagagg accagccatc ccagcctgca ggtaaagtgt gtcacctgtc	120
aggtgggctt ggggtgagtg ggtgggggaa gtgtgtgtgc aaagggggtg tnaatgtnta	180
tgcgtgtgag catgagtgat ggctagtgtg actgcatgtc agggagtgtg aacaagcgtg	240
cgggggtgtg tgtgcaagtg cgtatgcata tgagaatatg tgtctgtgga tgagtgcatt	300
tgaaagtctg tgtgtgtgctg tgtggtcatg anggtaantt antgactgctg caggatgtgt	360
gagtgtgcat ggaacactca ntgtgtgtgt caagtggccn ancgtc	406

<210> 157
 <211> 208
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(208)
 <223> n = A,T,C or G

<400> 157	
tgacgcttgg ccacttgaca cactaaaggg tgttactcat cactttcttc tctcctcggt	60
ggcatgtgag tgcattctatt cacttggcac tcatttgttt ggcagtgact gtaanccana	120
tctgatgcat acaccagctt gtaaattgaa taaatgtctc taatactatg tgctcacaat	180
anggtanggg tgaggagaag gggagaga	208

<210> 158
 <211> 547
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(547)
 <223> n = A,T,C or G

<400> 158
 cttcaacctc cttcaacctc cttcaacctc ctggattcaa acaatcatcc cacctcagac 60
 tccttagtag ctgagactac agactcacgc cactacatct ggctaaattt ttgtagagat 120
 agggtttcat catgttgccc tggctggtct caaactcctg acctcaagca atgtgcccac 180
 ctcagcctcc caaagtgtct ggattacagg cataagccac catgcccagt ccatntttaa 240
 tctttcctac cacattctta ccacactttc ttttatgttt agatacataa atgcttacca 300
 ttatgataca attgcccaca gtattaagac agtaacatgc tgcacagggt tgtagcctag 360
 gaacagtagg caataccaca tagcttaggt gtgtggtaga ctataccatc taggtttgtg 420
 taagttagac tttatgtctgt ttacacaatg acaaaaccat ctaatgatgc atttctcaga 480
 atgtatcctt gtcagtaagc tatgatgtac aggggaacact gcccaaggac acagatattg 540
 tacctgt 547

<210> 159
 <211> 203
 <212> DNA
 <213> Homo sapien

<400> 159
 gctcctcttg ccttaccaac tcaccagta tgtcagcaat tttatcrgct ttacctacga 60
 aacagcctgt atccaaacac ttaacacact cacctgaaaa gttaggcaa caatgcgctt 120
 ctcaggggtc tctctgctcc agttctgaac ctttctcttt tcctagaaca tgcatttarg 180
 tcgatagaag ttcctctcag tgc 203

<210> 160
 <211> 402
 <212> DNA
 <213> Homo sapien

<400> 160
 tgtaagtcca gcagtgtgat ggggtggaaca ggggttgtaag cagtaattgc aaactgtatt 60
 taaacaataa taataatatt tagcatttat agagcacttt atatcttcaa agtacttgca 120
 aacattayct aattaaatac cctctctgat tataatctgg atacaaatgc acttaaaactc 180
 aggacagggt catgagaraa gtatgcattt gaaagttggt gctagctatg ctttaaaaac 240
 ctatacaatg atgggraagt tagagttcag attctgttgg actgtttttg tgcatttcag 300
 ttcagcctga tggcagaatt agatcatatc tgcactcgat gactytgctt gataacttat 360
 cactgaaatc tgagtgttga tcatcacact gctcgactta ca 402

<210> 161
 <211> 193
 <212> DNA
 <213> Homo sapien

<400> 161
 agcatgttga gccagacac tgaccaggag aaaaaccaac caatagaaac acgccagac 60

actgaccagg	agaaaaacca	accaataaaa	acaggcccgg	acataagaca	aataataaaa	120
ttagcggaca	aggacatgaa	aacagctatt	gtaagagcgg	atatagtggg	gtgtgtctgg	180
gctcaacatg	cta					193

<210> 162

<211> 147

<212> DNA

<213> Homo sapien

<400> 162

tgttgagccc	agacactgac	caggagaaaa	accaaccaat	aaaaacaggc	ccggacataa	60
gacaaataat	aaaattagcg	gacaaggaca	tgaaaacagc	tattgtaaga	gcggatatag	120
tggtgtgtgt	ctgggctcaa	catgcta				147

<210> 163

<211> 294

<212> DNA

<213> Homo sapien

<400> 163

tagcatgttg	agcccagaca	caaatctttc	cttaagcaat	aaatcatttc	tgcatatgtt	60
tttaaaacca	cagctaagcc	atgattattc	aaaaggacta	ttgtattggg	tattttgatt	120
tgggttctta	tctccctcac	attatcttca	tttctatcat	tgacctotta	tcccagagac	180
tctcaaactt	ttatgttata	caaatcacat	tctgtctcaa	aaaatatctc	accacttct	240
cttctgtttc	tgcggtgtgta	tgtgtgtgtg	tgtgtgtctg	ggctcaacat	gcta	294

<210> 164

<211> 412

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(412)

<223> n = A,T,C or G

<400> 164

cgggattggc	tttgagctgc	agatgctgcc	tgtgaccgca	cccggcgtgg	aacagaaagc	60
cacctggctg	caagtgcgcc	agagccgccc	tgactacgtg	ctgctgtggg	gctggggcgt	120
gatgaactcc	accgccctga	aggaagccca	ggccaccgga	tacccccgcg	acaagatgta	180
cggcgtgtgg	tgggcccgtg	cggagcccga	tgtgcgtgac	gtgggcgaag	gcgccaaggg	240
ctacaacgcg	ctggctctga	acggctacgg	cacgcagtcc	aaggtgatcc	angacatcct	300
gaaacacgtg	cacgacaagg	gccagggcac	ggggcccaaa	gacgaagtgg	gctcgggtgct	360
gtacacccgc	ggcgtgatca	tccagatgct	ggacaagggtg	tcaatcacta	at	412

<210> 165

<211> 361

<212> DNA

<213> Homo sapien

<400> 165

ttgacacctt	gtccagcatc	tgcatctgat	gagagcctca	gatggctacc	actaatggca	60
gaaggcaaag	gagaacaggc	attgtatggc	aagaaaggaa	gaaagagaga	ggggagaaag	120
gtgctaggtt	cttttcaaca	accagttctt	gatggaactg	agagtaagag	ctcaaggcca	180
ggtgtggtga	ctccaaccag	taatcccaac	attttaggag	gctgaggcag	gcagatgtct	240

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tgaccccatg agtttgtgac cagcctgaac aacatcatga gactccatct ctacaataat 300
tacaaaaatt aatcagggcat tgtggtatgc cctgtagtcc cagatgctgg acaaggtgtc 360
a 361

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<210> 166
<211> 427
<212> DNA
<213> Homo sapien

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<400> 166
twgactgact catgtcccct acacccaact atctttctcca ggtggccagg catgatagaa 60
tctgactcctg acttagggga atattttctt ttacttccc atcttgattc cctgccggtg 120
agtttctctgg ttcagggtaa gaaaggagct caggccaaag taatgaacaa atccatcctc 180
acagacgtac agaataagag aacwtggacw tagccagcag aacmcaaktg aaamcagaac 240
mcttamctag gatracaamc merraratar ktgcycmcmc wtataataga aaccaaactt 300
gtatctaatt aaatatattat ccacygtcag ggcattagtg gttttgataa atacgctttg 360
gctaggattc ctgagggttag aatggaaraa caattgcamc gagggtaggg gacatgagtc 420
aktctaa 427

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<210> 167
<211> 500
<212> DNA
<213> Homo sapien

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<220>
<221> misc_feature
<222> (1)...(500)
<223> n = A,T,C or G

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<400> 167
aacgtcgcac gctcccggcc gccatggccg cgggatagac tgactcatgt cccctaagat 60
agaggagaca cctgctaggt gtaaggagaa gatgggttagg tctacggagg ctccaggggtg 120
ggagtagttc cctgctaagg gagggtagac tgttcaacct gttcctgctc cggcctccac 180
tatagcagat gcgagcagga gtaggagaga gggaggtaag agtcagaagc ttatgttggtt 240
tatgcgggga aacgccttat cgggggcagc cragttatta ggggacantr tagwyartcw 300
agntagcatc caaagcgnng gagttntccc atatgggttg accctgcaggc ggccgcatta 360
gtgattagca tgtgagcccc agacacgcac agcaacaagg acctaaactc agatcctgtg 420
ctgattactt aacatgaatt attgtattta tttaacaact ttgagttatg aggcatatta 480
ttaggtccat attacctgga 500

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```

<210> 168
<211> 358
<212> DNA
<213> Homo sapien

```

```

<400> 168
ttcatcgctc ggtgactcaa gcctgtaatc ccagaacttt gggaggccga ggggagcaga 60
tcacctgagg ttgggagttt gagaccagcc tggccaacat ggtgacaacc cgtctctgct 120
aaaaatacaa aaattagcca agcatgggtg catgcacttg taatcccagc tactcggggag 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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```

<210> 169
<211> 1265

```

<212> DNA

<213> Homo sapien

<400> 169

ttctgtccac	accaatctta	gagctctgaa	agaatttgct	tttaaatact	ttttaatagt	60
aacatgtatt	ttatggacca	aattgacatt	ttcgactatt	ttttcccaa	aaaagtcagg	120
tgaatttcag	cacactgagt	tggaatttc	ttatcccaga	agwgcgcacg	agcaatttca	180
tatttattta	agattgattc	catactccgt	tttcaaggag	aatccctgca	gtctccttaa	240
aggtagaaca	aatactttct	atTTTTTTTT	caccattgtg	ggattggact	ttaagagggtg	300
actctaaaaa	aacagagAAC	aaatatgtct	cagttgtatt	aagcacggac	ccatattatc	360
atattcactt	aaaaaaatga	tttctgtgtc	accttttggc	aacttctctt	ttcaatgtag	420
ggaaaaactt	agtcaccctg	aaaaccacaca	aaataaataa	aacttgtaga	tgtgggcaga	480
argtttgggg	gtggacattg	tatgtgttta	aattaaaccc	tgtatcactg	agaagctggt	540
gtatgggtca	gagaaaatga	atgcttagaa	gctgttcaca	tcttcaagag	cagaagcaaa	600
ccacatgtct	cagctatatt	attattttatt	ttttatgcat	aaagtgaatc	atctctctctg	660
tattaatttc	caaagggttt	taccctctat	ttaaatgctt	tgaaaaacag	tgcattgaca	720
atgggttgat	atTTTTCTTT	aaaagaaaaa	tataattatg	aaagccaaga	taatctgaag	780
cctgttttat	tttaaaactt	tttatgttct	gtggttgatg	ttgtttgttt	gtttgtttct	840
atTTTgttgg	TTTTTtactt	tgtTTTTtgt	tttgtTTTTg	tttggTTTTd	catactacat	900
gcagtttctt	taaccaatgt	ctgtttggct	aatgtaatta	aagttgttaa	tttatatgag	960
tgcatttcaa	ctatgtcaat	ggtttcttaa	tatttattgt	gtagaagtac	tggttaatttt	1020
tttattttaca	atatgtttta	agagataaca	gtttgatatg	ttttcatgtg	tttatagcag	1080
aagttatttta	tttctatggc	attccagcgg	atattttggg	gtttgcgagg	catgcagtca	1140
atatttttgta	cagttagtgg	acagtattca	gcaacgcctg	atagcttctt	tggccttatg	1200
ttaaataaaa	agacctgttt	gggatgtaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1260
aaaaa						1265

<210> 170

<211> 383

<212> DNA

<213> Homo sapien

<400> 170

tgtaagtcca	gcagtgtgat	gacgatattc	ttcttattaa	tgtggtaatt	gaacaaatga	60
tctgtgatac	tgatcctgag	ctaggaggcg	ctgttcagtt	aatgggactt	cttcgtactc	120
taattgatcc	agagaacatg	ctggctacaa	ctaataaaac	cgaaaaaagt	gaattttctaa	180
atTTTTtcta	caaccattgt	atgcatgttc	tcacagcacc	acttttgacc	aatacttcag	240
aagacaaatg	tgaaaaggat	aatatagttg	gatcaaaca	aaacaacaca	atTTTgtccg	300
ataattatca	aacagcacag	ctacttgcct	taattttaga	gttactcaca	ttttgtgtgg	360
aacatcacac	tgctcgactt	aca				383

<210> 171

<211> 383

<212> DNA

<213> Homo sapien

<400> 171

tgggcacctt	caatatcgca	agttaaaaat	aatgttgagt	ttattatact	tttgacctgt	60
ttagctcaac	aggggtgaagg	catgtaaaga	atgtggactt	ctgaggaatt	ttctttttaa	120
agaacataa	tgaagtaaca	ttttaattac	tcaaggacta	cttttggttg	aagtttataa	180
tctagatacc	tctacttttt	gtttttgctg	ttcgacagtt	cacaaagacc	ttcagcaatt	240
tacagggtaa	aatcgttgaa	gtagtggagg	tgaaactgaa	atTTTaaatt	attctgtaaa	300
tactataggg	aaagaggctg	agcttagaat	cttttggttg	ttcatgtgtt	ctgtgctctt	360
atcatcacac	tgctcgactt	aca				383

<210> 172
 <211> 699
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(699)
 <223> n = A,T,C or G

<400> 172

tcgggtgatg	cctcctcagg	cttgctcgta	gtgtacacag	agctgctcat	gaagcgacag	60
cggctgcccc	tggcacttca	gaacctcttc	ctctacactt	ttggtgcgct	tctgaatcta	120
ggtctgcatg	ctggcgccgg	ctctggccca	ggcctcctgg	aaagtttctc	aggatgggca	180
gcactcgtgg	tgctgagcca	ggcactaaat	ggactgctca	tgtctgctgt	catggagcat	240
ggcagcagca	tcacacgcct	ctttgtggtg	tcctgctcgc	tggtggtcaa	cgccgtgctc	300
tcagcagtc	tgctacggct	gcagctcaca	gccgccttct	tcctggccac	attgctcatt	360
ggcctggcca	tgcgctgta	ctatggcagc	cgctagtc	tgacaacttc	cacctgatt	420
ccggaccctg	tagattgggc	gccaccacca	gatccccctc	ccaggccttc	ctccctctcc	480
catcagcggc	cctgtaacaa	gtgccttggtg	agaaaagctg	gagaagtgag	ggcagccagg	540
ttattctctg	gagggtggtg	gatgaagggg	tacccttagg	agatgtgaag	tgtgggtttg	600
gttaaggaaa	tgcttaccat	ccccacccc	caaccaagtt	nttcagact	aaagaattaa	660
ggtaacatca	atacctaggc	ctgaggaggc	atcacccga			699

<210> 173
 <211> 701
 <212> DNA
 <213> Homo sapien

<400> 173

tcgggtgatg	cctcctcagg	ccagatcaaa	cttgggggttg	aaaactgtgc	aaagaaatca	60
atgtcggaga	aagaattttg	caaaagaaaa	atgcctaata	agtactaatt	taatagggtca	120
cattagcagt	ggaagaagaa	atgttgatat	tttatgtcag	ctattttata	atcaccagag	180
tgcttagctt	catgtaagcc	atctcgtatt	cattagaaat	aagaacaatt	ttattcgtcg	240
gaaagaactt	ttcaatttat	agcatcttaa	ttgctcagga	ttttaaattt	tgataaagaa	300
agctccactt	ttggcaggag	tagggggcag	ggagagagga	ggctccatcc	acaaggacag	360
agacaccagg	gccagtaggg	tagctgggtg	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
catgcctctt	ccttttcattg	ggcagagcaa	gtcacttatg	gccagaagtc	acactgcagg	660
gcagtgccat	cctgctgtat	gcctgaggag	gcatacccca	a		701

<210> 174
 <211> 700
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(700)
 <223> n = A,T,C or G

<400> 174

tcgggtgatg	cctcctcagg	cccctaaatc	agagtccagg	gtcagagcca	caggagacag	60
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ggaaagacat agattttaac cggccccctt caggagattc tgaggctcag ttcactttgt 120
tgcagtttga acagaggcag caaggctagt ggtaggggc acggtctcta aagctgcact 180
gcctggatct gcctcccagc tctgccagga accagctgcg tggccttgag ctgctgacac 240
gcagaaagcc ccctgtggac ccagtctcct cgtctgtaag atgaggacag gactctagga 300
accctttccc ttggtttggc ctcactttca caggctccca tcttgaactc tatctactct 360
tttcctgaaa ccttgtaaaa gaaaaaagtg ctagcctggg caacatggca aaaccctgtc 420
tctacaaaaa atacaaaaat tagttgggtg tggtagcatg tgcctgtagt cccagccact 480
tgaggaggtg tgagggtggg ggatcacttg agcccgggag gtggaggttg cagtgaagca 540
agatcatgcc actgcactcc agcctgagta atagagtaag actctgtctc aaaaacaaca 600
acaacaacag tgagtgtgcc tctgtttccg ggttggatgg ggcaccacat ttatgcatct 660
ctcagatttg gacgctgcag cctgaggagg catcacccga 700

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<210> 175

<211> 484

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(484)

<223> n = A,T,C or G

<400> 175

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tatagggcga attgggcccg agttgcatgn tcccggccgc catggccgcg ggattcgggt 60
gatgcctcct caggcttgtc tgccacaagc tacttctctg agctcagaaa gtgccccttg 120
atgagggaaa atgtcctact gcactgcgaa tttctcagtt ccattttacc tcccagtcct 180
ccttctaaac cagttaataa attcattcca caagtattta ctgattacct gcttgtgcca 240
gggactatct tcaggctgaa gaagggtggg ggggagggcg gaacctgagg agccacctga 300
gccagcttta tatttcaacc atggctggcc catctgagag catctcccca ctctcgccaa 360
cctatcgggg catagcccag ggatgcccc aggcggccca ggttagatgc gtcccttttg 420
cttgtcagtg atgacataca ccttagctgc ttagctggtg ctggcctgag gaggcacac 480
ccga 484

```

<210> 176

<211> 432

<212> DNA

<213> Homo sapien

<400> 176

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gacaaatgcc aggtagcgga attggtactg gtccaggagt tatccaggat agattttcac 180
ccaccatggg acgtcatcgt tcaaataaac tcttcaatgg ccatggggga cacatcatgc 240
ctcccacaca atcgcatgtt ggagagatgg gaggcaagtt tatgaaaagc caggggctaa 300
gccagctcta ccataaccag agtcagggac tcttatccca gctgcaagga cagtcgaagg 360
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ggcatcaccc ga 432

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<210> 177

<211> 788

<212> DNA

<213> Homo sapien

<400> 177

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cccaactgac	aagcccttg	gcctgcctct	ccaggatgtc	tacaaaattg	gtggtattgg	240
tactgttct	gttggccgag	tggagactgg	tgctctcaaa	cccggtatgg	tggtcacctt	300
tgctccagtc	aacgtttacaa	cggaagtaaa	atctgtcgaa	atgcaccatg	aagctttgag	360
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tcgtcgtggc	aacgttgctg	gtgacagcaa	aaatgaccca	ccaatggaag	cagctggctt	480
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cattgttgat	atgggttctg	gcaagcccat	gtgtgttgag	agcttctcag	actatccacc	720
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acatgcta						788

<210> 178

<211> 786

<212> DNA

<213> Homo sapien

<400> 178

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attgttggtc	gtttcttttc	attaaagggt	taatcagaca	gatcagacag	cataattttg	180
tatttaataga	cagaaacgtt	ggtacatttc	ttcatgaatg	agcttgcat	ctgaagcaag	240
agcctacaaa	aggcacttgt	tataaatgaa	agttctggct	ctagaggcca	gtactctgga	300
gtttcagagc	agccagtgat	tggtccagtc	agtgatgcct	agttatatag	aggaggagta	360
cactgtgcac	tcttctaggt	gtaagggtat	gcaactttgg	atcttaaaat	tctgtacaca	420
tacacacttt	atatatatgt	atgtatgtat	gaaaacatga	aattagtttg	tcaaatatgt	480
gtgtgttttag	tatttttagct	tagtgcaact	atttccacat	tatttattaa	attgatctaa	540
gacactttct	tggtgacacc	ttgaatatta	atgttcaagg	gtgcaatgtg	tattccttta	600
gattgttaaaa	gcttaattac	tatgatttgt	agtaaattaa	cttttaaaat	gtatttgagc	660
ccttctgtag	tgctgtaggg	ctcttacagg	gtgggaaaga	ttttaatttt	ccagttgcta	720
attgaacagt	atggcctcat	tatatatttt	gatttatagg	agtttgtgtc	tgggctcaac	780
atgcta						786

<210> 179

<211> 796

<212> DNA

<213> Homo sapien

<400> 179

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acaccccat	ccgcccttg	tttggagtgc	agagtttggc	tttgggttct	tgccctgcct	180
ggagtatact	tctaattcct	gttgctctgc	acaagctgaa	taccgagcta	cccaccgcca	240
cccaggccag	gtttccactc	atttattact	ttatgtttct	gttccattgc	tggtccacag	300
aaataagttt	tcctttggag	gaatgtgatt	ataccctttt	aatttcctcc	ttttgctttt	360
ttttaatatc	attgggtatg	gtttggccca	gaggaaactg	aaattcacca	tcatcttgac	420
tggcaatccc	attaccatgc	tttttttaaa	aaacgtaatt	tttcttgctt	tacattggca	480
gagtagccct	tcctggctac	tggcttaatg	tagtcaactca	gtttctaggt	ggcattaggc	540
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aaagggtat	gtcaggtttc	aatgctatct	gcttctgttc	ctgctcactg	ttctggattt	660
tgctcttctt	catccctagc	accagaattt	cccagtctcc	ctccctacct	tccctgtttt	720
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tgggctcaac	atgcta					796

<210> 180
 <211> 488
 <212> DNA
 <213> Homo sapien

<400> 180
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 aaaacgacgg ccagtgaatt gtaatacgac tcactatagg gcgaattggg cccgacgtcg 120
 catgctcccg gccgccatgg ccgcgggata gcatgttgag cccagacacc tgcagggtcat 180
 ttggagagat ttttcacgtt accagcttga tggctttttt caggaggaga gacactgagc 240
 actcccaagg tgaggttgaa gatttcctct agatagccgg ataagaagac taggagggat 300
 gcctagaaaa tgattagcat gcaaatttct acctgccatt tcagaactgt gtgtcagccc 360
 acattcagct gcttcttgtg aactgaaaag agagaggat tgagactttt ctgatggccg 420
 ctctaacatt gtaacacagt aatctgtgtg tgtgtgggtg tgtgtgtgtg tctgggctca 480
 acatgcta 488

<210> 181
 <211> 317
 <212> DNA
 <213> Homo sapien

<400> 181
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 aaaggaggaa cgtcatcccc catgatattg gggaccaga tgatgaacca tggctccgcg 120
 tcaatgcata tttaatccat gatactgctg attggaagga cctgaacctg aagtttgtgc 180
 tgcagggttta tggggactat tacctcacgg gtgatcaaaa cttcctgaag gacatgtggc 240
 ctgtgtgtct agtaagggat gcacatgcag tggccagtgt gccaggggta tggttgggtg 300
 ctgggctcaa catgcta 317

<210> 182
 <211> 507
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(507)
 <223> n = A,T,C or G

<400> 182
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 agcagagagc accacataca ttagaatggg aaggactgcc acctccttca agaacaggag 180
 tgaggggtggg ggtgaatggg aatggaagcc tgcattccct gatgcatttg tgctctctca 240
 aatcctgtct tagtcttagg aaaggaagta aagtttcaag gacggttccg aactgctttt 300
 tgtgtctggg ctcaacatgc tatcccgagg ccatggcgcc cgggagcatg cgacgtcggg 360
 cccaattcgc cctatagtga gtcgtattac aattcactgg ccgtcgtttt acaacgtcgt 420
 gactgggaaa accctggcgt tacccaactt aatcgccctg cagcacatcc ccctttccca 480
 gctggcgtaa tancgaaaag gcccgca 507

<210> 183
 <211> 227
 <212> DNA
 <213> Homo sapien

<400> 183

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aatccccaaa	tggagcctgg	tatttcagcc	aggaatctga	gcagagcccc	ctctaattgt	120
agcaatgata	agttattctc	tttgttcttc	aaccttccaa	tagccttgag	cttccagggg	180
agtgtcgta	atcattacag	cctggtctcc	acagtgttgc	agcgtaa		227

<210> 184

<211> 225

<212> DNA

<213> Homo sapien

<400> 184

ttacgctgca	acactgtgga	gcagattaac	atcagacttt	tctatcaaca	tgactggggg	60
tactaaaaag	acaacaaatc	aatggcttca	aaagtctaag	gaataatttc	gatacttcaa	120
ctttataaaa	cctgacaaaa	ctatcaatca	agcataaaga	cagatgaaga	acatttccag	180
attttggcca	atcagatatt	ttacctccac	agtgttgcag	cgtaa		225

<210> 185

<211> 597

<212> DNA

<213> Homo sapien

<400> 185

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ctgggaccca	taggctagtc	agagtattta	gagttgagtt	cctttctgct	tcccagaatt	120
tgaaagaaaa	ggagtgaggt	gatagagctg	agagatcaga	tttgccctctg	aagcctgttc	180
aagatgtatg	tgctcagacc	ccaccactgg	ggcctgtggg	tgaggctcctg	ggcatctatt	240
tgaatgaatt	gctgaagggg	agcactatgc	caaggaaggg	gaacccatcc	tggcactggc	300
acaggggtca	ccttatccag	tgctcagtgc	ttctttgctg	ctacctgggt	ttctctcata	360
tgtgaggggc	aggtagaag	aagtgcccr	tggtgtgcga	gttttagaac	atctaccagt	420
aagtggggaa	gtttcacaaa	gcagcagctt	tgttttgtgt	attttcacct	tcagttagaa	480
gaggaaggct	gtgagatgaa	tgtagttga	gtggaaaaga	cgggtaagct	tagtgatag	540
agaccctaac	gaatcactag	tgcggccgcc	ttgcaggctc	accatatggg	agagctc	597

<210> 186

<211> 597

<212> DNA

<213> Homo sapien

<400> 186

ggcccgaaagt	tgcatgttcc	cggccgccat	ggccgcggga	ttcgttaggg	tctctatcca	60
ctacctaaaa	aatcccaaac	atataactga	actcctcaca	cccaattgga	ccaatccatc	120
acccagagag	cctacagatc	ctcctttgat	acataagaaa	atttcccca	actacctaac	180
tatatcattt	tgcaagattt	gttttaccaa	attttgatgg	cctttctgag	cttgtcagtg	240
tgaaccacta	ttacgaacga	tcggatatta	actgcccctc	accgtccagg	tgtagctggc	300
aacatcaagt	gcagtaaata	ttcattaagt	tttcacctac	taagggtgctt	aaacacccta	360
gggtgccatg	tcggtagcag	atcctttgat	ttgtttttat	ttcccataag	ggtcctgttc	420
aaggtcaatc	atacatgtag	tgtgagcagc	tagtcactat	cgcagtactt	ggaggggtgat	480
aatagaggcc	tcctttgctg	ttaaagaact	cttgtcccag	cctgtcaaag	tggatagaga	540
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<210> 187

<211> 324

<212> DNA

<213> Homo sapien

<400> 187

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ccatatgtag tgggtcaaga gactgcagtt ccagaaagac tagccgagcc catccatgtc	120
ttccacttaa ccctgctttg gggtacacat cttaactttt ctgttcaagt ttctctgtgt	180
agtttatagc atgagtattg ggawaatgcc ctgaaacctg acatgagatc tgggaaacac	240
aaacttactc aataagaatt tctcccatat ttttatgatg gaaaaatttc acatgcacag	300
aggagtggat agagacccta acga	324

<210> 188

<211> 178

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(178)

<223> n = A,T,C or G

<400> 188

gcgcgggggat tcgggggtgat acctcctcat gccaaaatac aacgtntaat ttcacaactt	60
gccttccaat ttacgcattt tcaatttgct ctccccattt gttgagtcac aacaaacacc	120
attgcccgaga aacatgtatt acctaacatg cacatactct taaaactact catccctt	178

<210> 189

<211> 367

<212> DNA

<213> Homo sapien

<400> 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
aaaaaagctc aacatcactg atcattagaa aacttccatt caaaccacca atgagatacc	300
atctcatacc agtcagaatg gctattatta aaaagtcaaa aaataacaga tgctggacaa	360
ggtgtca	367

<210> 190

<211> 369

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(369)

<223> n = A,T,C or G

<400> 190

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agtttttact ctggctaggc agatgggtggc taaaacattc atttaccat ttattcattt	120
aattgttcct gcaaggccta tggatagagt attgtccagc actgctctgg aagctaggag	180
catggggatg aacaagatag gctacatcct gttccacacag aacttccact ttagtctggg	240
aaacagatga tatatacaaa tatataaatg aattcaggta gttttaagta cgaaaagaat	300

aagaaagcag agtcatgatt tanaatgctg gaaacagggg ctattgcttg agatattgaa 360
 ggtgcccaa 369

<210> 191
 <211> 369
 <212> DNA
 <213> Homo sapien

<400> 191
 tgacaccttg tccagcatct gcacagggaa aagaaactat tatcagagtg aacaggcaac 60
 ctacagaatg ggagaaaatt ttgcaatct atccatctga caaagggcta atatccagaa 120
 tctacaaaga acttatacaa atttacaaga aacaaacaaa caaacaactc ctcaaaaagt 180
 ggggtgaagga tgtgaacaga cacttctcaa aagaagacat ttatggggcc aacaaacata 240
 tgaaaaaaag ctcacatca ctggtcacta gataaatgca aatcaaaacc acaatgagat 300
 accatctcat tccagttaga atggcaatca ttaaaaagtc aggaaacaac agatgctgga 360
 caaggtgctc 369

<210> 192
 <211> 449
 <212> DNA
 <213> Homo sapien

<400> 192
 tgacgcttg ccacttgaca cttcatcttt gcacagaaaa acttctttac agatttaatt 60
 caagactggc ctagtgacag tcctccagac attttttcat ttgttccata tacgtggaat 120
 tttaaaatca tgtttcatca gtttgaaatg atttgggctg ctaatcaaca caattggatc 180
 gactgttcta ctaaacaaca ggaaaatgtg tatctggcag cctgtggaga aacactaaac 240
 attgattttt ctttgccttt tacggacttt gttccagcta catgtaatac caagttctct 300
 ttaagaggag aagatgttga tcttcatttg tttctaccag actgccaccc tagtaaatat 360
 tctttattta tgctggtaaa aaattgccat ccaaataaga tgattcatga tactggtatt 420
 cctgctgagt gtcaagtggc caagcgtca 449

<210> 193
 <211> 372
 <212> DNA
 <213> Homo sapien

<400> 193
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 tattggcaat ttcccatcaa acattctaga aagagacaac caggattgct aggccataaa 120
 agctgcaata aataactggc aattgcagta atcatttcag gccattcaa tccagtttgg 180
 ctcagaggtg cctttggctg agagaagagg tgagatataa tgtgttttct tgcaacttct 240
 tggaagaata actccacaat agtctgagga ctagatacaa acctatttgc cattaaagca 300
 ccagagtctg ttaattccag tactgataag tgttgagat tagactccag tgtgtcaagt 360
 ggccaagcgt ca 372

<210> 194
 <211> 309
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)... (309)
 <223> n = A,T,C or G

<400> 194
 tgacgcttg ccacttgaca cttatgtaga atccatcgtg ggctgatgca agccctttat 60
 ttaggcttag tgttgtgggc accttcaata tcacactaga gacaaacgcc acaagatctg 120
 cagaaacatt cagttctgan cactcgaatg gcaggataac tttttgtgtt gtaatccttc 180
 acatatacaa aaacaaactc tgcantctca cgttacaaaa aaacgtactg ctgtaaaata 240
 ttaagaagg gtaaaggata ccatctataa caaagtaact tacaactagt gtcaagtggc 300
 caagcgtca 309

<210> 195
 <211> 312
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(312)
 <223> n = A,T,C or G

<400> 195
 tgacgcttg ccacttgaca cccaatctcg cacttcatcc tcccagcacc tgatgaagta 60
 ggactgcaac tatccccact tcccagatga ggggaccaan gtacacatta ggaccggat 120
 gggagcacag atttgtccga tcccagactc caagcactca gcgtcactcc aggacagcgg 180
 ctttcagata aggtcacaaa catgaatggc tccgacaacc ggagtcagtc cgtgctgagt 240
 taaggcaatg gtgacacgga tgcacgtgtn acctgtaatg gttcatcgta agtgtcaagt 300
 ggccaagcgt ca 312

<210> 196
 <211> 288
 <212> DNA
 <213> Homo sapien

<400> 196
 tgtatcgacg tagtgggtctc ctcagccatg cagaactgtg actcaattaa acctctttcc 60
 tttatgaatt acccaatctc gggtagtgtc tttatagtag tgtgagaatg gactaataca 120
 agtacatttt acttagtaat aataataaac aaatatatta catttttgtg tattttactac 180
 accatatttt ttattgttat tgtagtgtag accttctact tattaaaaga aataggcccg 240
 aggcgggcag atcacgaggt caggagatgg agaccactac gtcgatac 288

<210> 197
 <211> 289
 <212> DNA
 <213> Homo sapien

<400> 197
 ttgggcacct tcaatatcat gacaggatgat gtgataacca agaaggctac taagtgatta 60
 atgggtgggt aatgtatata gagtaggtac actggacaga ggggtaattc atagccaagg 120
 caggagaagc agaatggcaa aacatttcat cacactactc aggatagcat gcagtttaaa 180
 acctataagt agtttatttt tggaattttc cacttaatat tttcagactg caggtaacta 240
 aactgtggaa cacaagaaca tagataaggg gagaccacta cgtcgatac 289

<210> 198
 <211> 288
 <212> DNA
 <213> Homo sapien

<400> 198
 gtatcgacgt agtgggtctcc caagcagtgg gaagaaaacg tgaaccaatt aaaatgtatc 60
 agatacccca aagaaaggcg cttgagtaaa gattccaagt gggtcacaaat ctcagatctt 120
 aaaattcagg ctgtcaaaga gatttgctat gaggttgctc tcaatgactt caggcacagt 180
 cggcaggaga ttgaagccct ggccattgtc aagatgaagg agctttgtgc catgtatggc 240
 aagaaagacc ccaatgagcg ggactcctgg agaccactac gtcgatac 288

<210> 199
 <211> 1027
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(1027)
 <223> n = A,T,C or G

<400> 199
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 aancccaggg tttccccatt cagggagggtg taaaaagncg gccaggggat tgtaanagga 120
 ttcaataata gggggaatgg gccngaagt tgcaagggtc cngcccgccca tgnccgcggg 180
 atttagtgac attacgacgs tggtaataaa gtgggsgcaa waaatatttg tgatgtgatt 240
 tttsgaccag tgaaccatt gwacaggacc tcatttccty tgagatgrta gccataatca 300
 gataaaaagrt tagaagtytt tctgcacgtt aacagcatca ttaaattggag tggcatcacc 360
 aatttcaccc tttgttagcc gataccttcc ccttgaaggc attcaattaa gtgaccaatc 420
 gtcatacgag aggggatggc atggggattg atgatgatat caggggtgat accttcacag 480
 gtgaaaggca tatcctcttg tctatactga ataccacaag tacccttttg accatgtcga 540
 ctagcaaatt tgtctccaat ctgtgtwac cctaacagag cgtaccctta ttttacaaaa 600
 tttatatacct tcctgattga gagttaccat aacctgatcc acaatgcccg tctcgctwgt 660
 tctgagaaaa gtgctacagt ctctcttggt atagcgtcta ttggtgctct ccaattcatc 720
 ttcatttttc aggcaagggtg aactgttttg cctataataa cmtcatctcc tgatacmcga 780
 aacccckgga rctatcaaac catcatcatc cagcgttckt watgtymcta aatccctatt 840
 gcgccgcgct gcagggtcaac atatnggaaa acccccacc ccttnggagc ntaccttgaa 900
 ttttccatag gtcccntaaa ttanctngnc ttancttggc cntaacctnt tccggtttta 960
 attgtttccg ccccnttcc cccncttnna accggaaacc ttaatttttna accnggggtt 1020
 cctatcc 1027

<210> 200
 <211> 207
 <212> DNA
 <213> Homo sapien

<400> 200
 agtgacatta cgacgctggc catcttgaat cctagggcat gaagttgccc caaagttcag 60
 cacttggtta agcctgatcc ctctggttta tcacaaagaa taggatggga taaagaaagt 120
 ggacacttaa ataagctata aattatatgg tccttgctta gcaggagaca actgcacagg 180
 tatactacca gcgtcgtaat gtcacta 207

<210> 201
 <211> 209
 <212> DNA
 <213> Homo sapien

<400> 201

tgggcacctt caatatctat taaaagcaca aatactgaag aacacaccaa gactatcaat	60
gaggttacat ctggagtcct cgatatatca ggaaaaaatg aagtgaacat tcacagagtt	120
ttacttcttt gggaactcaa atgctagaaa agaaaagggt gccctctttc tctggcttcc	180
tggtcctatc cagcgtcgta atgtcacta	209

<210> 202
 <211> 349
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(349)
 <223> n = A,T,C or G

<400> 202	
ntacgctgca acactgtgga gccactgggt tttattcccg gcaggttatc cagcaaacag	60
tactgaaca caccgaagac cgtgggtatgg taaccgttca cagtaatcgt tccagtcgtc	120
tgccgggaccc cgacgagcgt cactgggtac agaccagatt cagccggaag agaaagcgcc	180
gcaggagag actcgaactc cactccgctg gtgagcagcc ccatgttttc aactcgaagt	240
tcaaacggca ttgggttata taccatcagc tgaacttcac acacatctcc ttgaaccac	300
tggaatcta ttttcttgtt ccgctcttct ccacagtgtt gcagcgtaa	349

<210> 203
 <211> 241
 <212> DNA
 <213> Homo sapien

<400> 203	
tgctcctctt gccttaccaa cccaaagccc actgtgaaat atgaagtga tgacaaaatt	60
cagttttcaa cgcaatatag tatagtttat ctgattcttt tgatctccag gacacttta	120
acaactgcta ccaccaccac caacctaggg atttaggatt ctccacagac cagaaattat	180
ttctcctttg agtttcaggc tctctggga ctctgttca tcaatgggtg gtaaatggct	240
a	241

<210> 204
 <211> 248
 <212> DNA
 <213> Homo sapien

<400> 204	
tagccattta ccaccatct gcaaaccswg acmwwcargr cywgwackya ggcgatttga	60
agtactggta atgctctgat catgttagtt acataagtgt ggtcagttta caaaaattca	120
cagaactaaa tactcaatgc tatgtgttca tgtctgtgtt tatgtgtgtg taatgtttca	180
attaagtttt tttaaaaaaa agagatgatt tccaaataag aaagccgtgt tggttaaggca	240
agaggagc	248

<210> 205
 <211> 505
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(505)

<223> n = A,T,C or G

<400> 205

tacgctgcaa cactgtggag ccattcatac aggtccctaa ttaaggaaca agtgattatg	60
ctacctttgc acggttaggg taccgcggcc gttaaacaatg tgtcactggg caggcgggtgc	120
ctctaataact ggtgatgcta gaggtgatgt ttttggtaaa caggcggggg aagatttgcc	180
gagttccttt tacttttttt aacctttcct tatgagcatg cctgtgttggt gttgacagtg	240
ggggtataaa tgacttggtg gttgattgta gatattgggc tgttaattgt cagttcagtg	300
ttttaatctg acgcaggcct atgcggagga gaatgttttc atgttactta tactaacatt	360
agttcttcta taggggtgata gattgggtcca attgggtgtg aggagttcag ttatatgttt	420
gggatttttt aggtagtggg tgttgancct gaacgccttc ttaattgggt gctgctttta	480
rgcctactat ggggtggtaaa tggct	505

<210> 206

<211> 179

<212> DNA

<213> Homo sapien

<400> 206

tagactgact catgtcccct accaaagccc atgtaaggag ctgagttcct aaagactgaa	60
gacagactat tctctggaga aaaataaaat ggaaattgta ctttaaaaaa aaaaaaatc	120
ggccgggcat ggtagcacac acctgtaatc ccagctacta ggggacatga gtcagtcta	179

<210> 207

<211> 176

<212> DNA

<213> Homo sapien

<400> 207

agactgactc atgtccccta cccacacctc tgctgtgctg ccgtgttcct aacagggtcac	60
agactggtac tggtcagtgg cctgggggtt ggggacctct attatatggg atacaaatct	120
aggagttgga attgacacga tttagtact gatgggatat ggggtggtaaa tggcta	176

<210> 208

<211> 196

<212> DNA

<213> Homo sapien

<400> 208

agactgactc atgtccccta tttaacaggg tctctagtgc tgtgaaaaaa aaaaatgctg	60
aacattgcat ataacttata ttgtaagaaa tactgtacaa tgactttatt gcatctgggt	120
agctgtaagg catgaaggat gccagaagt ttaaggaata tgggtggtaa atggctaggg	180
gacatgagtc agtcta	196

<210> 209

<211> 345

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(345)

<223> n = A,T,C or G

<400> 209

gacgcttggc	cacttgacac	cttttat	tttaaggattc	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
gtgccaahta	tctaggaagt	acttgggcat	gggtggtaaa	tggct		345

<210> 210

<211> 178

<212> DNA

<213> Homo sapien

<400> 210

gacgcttggc	cacttgacac	tagagtaggg	tttggccaac	tttttctata	aaggaccaga	60
gagtaaata	ttcaggcttt	gtgggttggtg	cagtctctct	tgcaactact	cagctctgcc	120
attgtagcat	agaaatcagc	catagacagg	acagaaatga	atgggtggta	aatggcta	178

<210> 211

<211> 454

<212> DNA

<213> Homo sapien

<400> 211

tgggcacctt	caatatctat	ccagcgcac	taaattcgt	tttttcttga	ttaaaaattt	60
caccacttgc	tgtttttgct	catgtatacc	aagtagcagt	ggtgtgaggc	catgcttggt	120
ttttgattcg	atatcagcac	cgtataagag	cagtgccttg	gccattaatt	tatcttcatt	180
gtagacagca	tagtgtagag	tggatctctc	atactcatct	ggaatatttg	gatcagtgcc	240
atgttccagc	aacattaacg	cacattcatc	ttcctggcat	tgtacggcct	ttgtcagagc	300
tgtcctcttt	ttgttgtcaa	ggacattaag	ttgacatcgt	ctgtccagca	cgagttttac	360
tactttctgaa	ttcccattgg	cagaggccag	atgtagagca	gtcctctttt	gcttgtccct	420
cttgttcaca	tcagtgtccc	tgagcataac	ggaa			454

<210> 212

<211> 337

<212> DNA

<213> Homo sapien

<400> 212

tccgttatgc	caccagaaa	acctactgga	gttacttatt	aacatcaagg	ctggaacctta	60
tttgccctcag	tcctatctga	ttcatgagca	catgggttatt	actgatcgca	ttgaaaacat	120
tgatcacctg	ggtttcttta	tttatcgact	gtgtcatgac	aaggaaactt	acaaaactgca	180
acgcagagaa	actattaaag	gtattcagaa	acgtgaagcc	agcaattggt	tcgcaattcg	240
gcatttttgaa	aacaaatttg	ccgtggaaac	tttaatttgt	tcttgaacag	tcaagaaaaa	300
cattattgag	gaaaattaat	atcacagcat	aacggaa			337

<210> 213

<211> 715

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(715)

<223> n = A,T,C or G

<400> 213

tcgggtgatg cctcctcagg catcttccat ccatctcttc aagattagct gtcccaaagt	60
tttttccttc tcttctttac tgataaattt ggactccttc ttgacactga tgacagcttt	120
agtatccttc ttgtcacctt gcagacttta aacataaaaa tactcattgg ttttaaaagg	180
aaaaaagtat acattagcac tattaagctt ggccttgaaa ctttttctat cttttattaa	240
atgtcggtta gctgaacaga attcatttta caatgcagag tgagaaaaga agggagctat	300
atgcatttga gaatgcaagc attgtcaaata aaacatttta aatgctttct taaagtgagc	360
acatacagaa atacattaag atattagaaa gtgtttttgc ttgtgtacta ctaattaggg	420
aagcaccttg tatagttcct cttctaaaat tgaagtagat tttaaaaacc catgtaattt	480
aattgagctc tcagttcaga ttttaggaga attttaacag ggatttggtt ttgtctaaat	540
tttgtcaatt tntttagtta atctgtataa ttttataaat gtcaaactgt atttagtccg	600
ttttcatgct gctatgaaag aaatacccan gacagggtta tttataaang gaaagangtt	660
aatttgactc ccagttcaca ggcctgagga ngnatcnccc gaaatcctta ttgog	715

<210> 214

<211> 345

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(345)

<223> n = A,T,C or G

<400> 214

ggtaangngc atacntcggg gctccggccg ccggagtcgg gggattcggg tgatgcctcc	60
tcaggcccac ttgggcctgc ttttcccaa tggcagctcc tctggacatg ccattccttc	120
tcccacctgc ctgattcttc atatgttggg tgtccctggt tttctgggtc tatttcctga	180
ctgctgttca gctgccactg tcctgcaaag cctgcctttt taaatgcctc accattcctt	240
catttggttc ttaaataatg gaagtgaag tgccacctga ggccggggcac agtgggtcac	300
gcctgtaatc ccagcacttt gggagcctga ggaggcatca cccga	345

<210> 215

<211> 429

<212> DNA

<213> Homo sapien

<400> 215

ggtgatgcct cctcaggcga agctcaggga ggacagaaac ctcccgtgga gcagaagggc	60
aaaagctcgc ttgatcttga ttttcagtac gaatacagac cgtgaaagcg gggcctcacg	120
atccttctga ctttttgggt ttttaagcagg aggtgtcaga aaagttacca cagggataac	180
tggcttgtgg cggccaagcg ttcatagcga cgtcgctttt tgatccttcg atgtcggctc	240
ttcctatcat tgtgaagcag aattcaccaa gcgttggtt gttcaccacac taatagggaa	300
cgtgagctgg gtttagaccg tcgtgagaca ggtagtgggt accctactga tgatgtgtkg	360
ttgccatggg aatcctgctc agtacgagag gaaccgcagg ttcasacatt tgggtgtatgt	420
gcttgctt	429

<210> 216

<211> 593

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(593)

<223> n = A,T,C or G

<400> 216

tgacacctat	gtccngcatc	tgttcacagt	ttccacaaat	agccagcctt	tggccacctc	60
tctgtcctga	ggtatacaag	tatatcagga	ggtgtatacc	ttctcttctc	ttccccacca	120
aagagaacat	gcaggctctg	gaagctgtct	taggagcctt	tgggctcaga	atttcagagt	180
cttgggtacc	ttggatgtgg	tctggaagga	gaaacattgg	ctctggataa	ggagtacagc	240
cggaggaggg	tcacagagcc	ctcagctcaa	gcccctgtgc	cttagtctaa	aagcagcttt	300
ggatgaggaa	gcaggttaag	taacatacgt	aagcgtacac	aggtagaaaag	tgctggggagt	360
cagaattgca	cagtgtgtag	gagtagtacc	tcaatcaatg	agggcaaata	aactgaaaga	420
agaagaccna	ttaatgaatt	gcttangggg	aaggatcaag	gctatcatgg	agatctttct	480
aggaagatta	ttgtttanaa	ttatgaaagg	antagggcag	ggacagggcc	agaagtanaa	540
ganaacattg	cctatanccc	ttgtcttgca	cccagatgct	ggacaagggtg	tca	593

<210> 217

<211> 335

<212> DNA

<213> Homo sapien

<400> 217

tgacaccttg	tccagcatct	gacgtgaaga	tgagcagctc	agaggaggtg	tcttggattt	60
cctgggttctg	tgggctccgt	ggcaatgaat	tcttctgtga	agtggatgaa	gactacatcc	120
aggacaaaatt	taatcttact	ggactcaatg	agcagggtccc	tcactatcga	caagctctag	180
acatgatctt	ggacctggag	cctgatgaag	aactggaaga	caaccccaac	cagagtgacc	240
tgattgagca	ggcagccgag	atgctttatg	gattgatcca	cgcccgtctac	atccttacca	300
accgtggcat	cgcccagatg	ctggacaagg	tgtca			335

<210> 218

<211> 248

<212> DNA

<213> Homo sapien

<400> 218

tacgtactgg	tcttgaaggt	cttaggtaga	gaaaaaatgt	gaatatttaa	tcaaagacta	60
tgtatgaaat	gggactgtaa	gtacagaggg	aagggtggcc	cttatcgcca	gaagttggta	120
gatgcgtccc	cgtcatgaaa	tgttgtgtca	ctgcccagaca	tttgccgaat	tactgaaatt	180
ccgtagaatt	agtgc aaatt	ctaacgttgt	tcatctaaga	ttatgggtcc	atgtttctag	240
tactttta						248

<210> 219

<211> 530

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(530)

<223> n = A,T,C or G

<400> 219

tgacgcttgg	ccacttgaca	caagtagggg	ataaggacaa	agacccatna	ggtggcctgt	60
cagccttttg	ttactgttgc	ttccctgtca	ccacggcccc	ctctgtaggg	gtgtgctgtg	120
ctctgtggac	attgggtgcat	tttcacacat	accattctct	ttctgcttca	cagcagtcct	180
gaggcgggag	cacacaggac	taccttgtca	gatgangata	atgatgtctg	gccaaactcac	240
cccccaacct	tctcactagt	tatangaaga	gccangccta	naaccttcta	tctgncccc	300

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ttgccctatg acctcatccc tgttccatgc cctattctga tttctggtga actttggagc 360
agcctggttt ntccctctca ctccagcctc tctccatacc atggtanggg ggtgctgttc 420
cacncaaang gtcaggtgtg tctggggaat cctnananct gccnggagtt tccnangcat 480
tcttaaaaac cttcttgctt aatcanatng tgtccagtgg ccaaccntcn 530

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<210> 220

<211> 531

<212> DNA

<213> Homo sapien

<400> 220

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tgacgcttgg ccacttgaca ctaaatagca tcttctaaag gcctgattca gagttgtgga 60
aaattctccc agtgtcaggg attgtcagga acagggctgc tcctgtgctc actttacctg 120
ctgtgtttct gctggaaaag gagggagag gaatggctga tttttaccta atgtctccca 180
gtttttcata ttcttcttgg atcctcttct ctgacaactg ttcccttttg gtcttcttct 240
tcttgctcag agagcaggtc tctttaaacc tgagaaggga gaatgagcaa atgattaaag 300
aaaacacact tctgaggccc agagatcaaa tattaggtaa atactaaacc gcttgcttgc 360
tgtggtcact tttctctctt ttcacatgct ctatccctct atccccacc tattcatatg 420
gcttttatct gccaaagttat ccggcctctc atcaaccttc tcccctagcc tactggggga 480
tatccatctg ggtctgtctc tgggtgtattg gtgtcaagtg gccaaagcgtc a 531

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<210> 221

<211> 530

<212> DNA

<213> Homo sapien

<400> 221

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attgacgctt ggccacttga caccgccttg cctgcaatac tggggcaagg gccttcactg 60
ctttctctgcc accagctgcc actgcacaca gagatcagaa atgctaccaa ccaagactgt 120
tggtctctcag cctctctgag gagaaagagc agaagcctgg aagtcagaag agaagctaga 180
tcggctacgg ccttggcagc cagcttcccc acctgtggca ataaagtcgt gcatggctta 240
acaatggggg cacctcctga gaaacacatt gtaggcaat tcggcgtgtg ttcacagag 300
catatttaca caaacctcga tagtgagcc tactatccac tattgctcct acgctgcaaa 360
cctgaacagc atgggactgt actgaatact ggaagcagct ggtgatggta cttatttgtg 420
tatctaaaca cagagaaggt acagtaagaa tatggtatca taaacttaca gggaccgcca 480
tcctatatgc agtctgttgt gaccaaagtg tgtcaagtgg ccaagcgtca 530

```

<210> 222

<211> 578

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(578)

<223> n = A,T,C or G

<400> 222

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tgtatcgacg tagtgggtctc cgggctacta ggccgttgtg tgctggtagt acctggttca 60
ctgaaaggcg catctccctc cccgcgtcgc cctgaagcag ggggaggact tcgcccagcc 120
aaggcagttg tatgagtttt agctgcggca ctctgagacc tctgagccca cctccttcag 180
gagccttccc cgattaagga agccagggtg aggattcctt cctccccccag acaccacgaa 240
caaaccacca cccccctat tctggcagcc catatacatc agaacgaaac aaaaataaca 300
aataaacnaa aaccaaataa aaaagagaag gggaaatgta tatgtctgtc catcctgttg 360
ctttagcctg tcagctccta nagggcaggg accgtgtctt ccgaatgggtc tgtgcagcgc 420

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cgactgcggg	aagtatcgga	ggaggaagca	gagtcagcag	aagttgaacg	gtgggcccgg	480
cggtctcttg	gggctgggtg	tgtacttcga	gaccgctttc	gctttttgtc	ttagatttac	540
gtttgctctt	tggagtggga	naccactacn	tcnatata			578

<210> 223
 <211> 578
 <212> DNA
 <213> Homo sapien

<400> 223						
tgtatcgacg	tagtgggtctc	ctcttgcaaa	ggactggctg	gtgaatgggt	tccctgaatt	60
atggacttac	cctaaacata	tcttatcatc	attaccagtt	gcaaaatatt	agaatgtggt	120
gtcactgttt	catttgattc	ctagaagggt	agtcttagat	atgttacttt	aacctgtatg	180
ctgtagtgct	ttgaatgcat	tttttgtttg	catttttggt	tgcccaacct	gtcaattata	240
gctgcttagg	tctggactgt	cctggataaa	gctgttaaaa	tattcaccag	tccagccatc	300
ttacaagcta	attaagtcaa	ctaaatgctt	ccttgttttg	ccagacttgt	tatgtcaatc	360
ctcaatttct	gggttcattt	tgggtgccct	aaatcttagg	gtgtgacttt	cttagcatcc	420
tgtaacatcc	attcccaagc	aagcacaact	tcacataata	ctttccagaa	gttcattgct	480
gaagcctttc	cttcacccag	cggagcaact	tgattttcta	caacttcctc	catcagagcc	540
acaagagtat	gggatatgga	gaccactacg	tcgatata			578

<210> 224
 <211> 345
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(345)
 <223> n = A,T,C or G

<400> 224						
tgtatcgacg	tantgggtctc	ccaagggtgct	gggattgcag	gcatgagcca	ccactcccag	60
gtggatcttt	ttcttttatac	ttacttcatt	aggtttctgt	tattcaagaa	gtgtagtggt	120
aaaagtcttt	tcaatctaca	tggttaaata	atgatagcct	gggaaataaa	tagaaatttt	180
ttctttcatc	tttaggttga	ataaagaaac	agaaaaata	gaacatactg	aaaataatct	240
aagttccaac	catagaagaa	ctgcagaaga	aatgaagaaa	gtgatgatga	tttagatttt	300
gatattgatt	tagaagacac	aggaggagac	cactacgtcg	atata		345

<210> 225
 <211> 347
 <212> DNA
 <213> Homo sapien

<400> 225						
tgtatcgacg	tagtgggtctc	caaactgagg	tatgtgtgcc	actagcacac	aaagccttcc	60
aacagggacg	caggcacagg	cagtttaaag	ggaatctggt	tctaaattaa	tttccacctt	120
ctctaagtat	tctttcctaa	aactgatcaa	ggtgtgaagc	ctgtgctctt	tcccaactcc	180
cctttgacaa	cagccttcaa	ctaacacaag	aaaaggcatg	tctgacactc	ttcctgagtc	240
tgactctgat	acgttggtct	gatgtctaaa	gagctccaga	acaccaaagg	gacaattcag	300
aatgctgggtg	tataacagac	tccaatggag	accactacgt	cgatata		347

<210> 226
 <211> 281
 <212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(281)

<223> n = A,T,C or G

<400> 226

aggngngggga	ntgtatcgac	gtagtgggtct	cccaacagtc	tgtcattcag	tctgcagggtg	60
tcagtgtttt	ggacaatgag	gcaccattgt	cacttattga	ctcctcagct	ctaaatgctg	120
aaattaaatc	ttgtcatgac	aagtctggaa	ttcctgatga	ggttttacaa	agtattttgg	180
atcaatactc	caacaaatca	gaaagccaga	aagaggatcc	tttcaatatt	gcagaaccac	240
gagtggattt	acacacctca	ggagaccact	acgtcgatac	a		281

<210> 227

<211> 3646

<212> DNA

<213> Homo sapien

<400> 227

gggaaacact	tcctcccagc	cttgtaaggg	ttggagccct	ctccagtata	tgctgcagaa	60
tttttctctc	ggtttctcag	aggattatgg	agtcgcgctt	aaaaaaggca	agctctggac	120
actctgcaaa	gtagaatggc	caaagtttgg	agttgagtg	ccccttgaag	ggctactgaa	180
cctcacaatt	gttcaagctg	tgtggcgggt	tgttactgaa	actcccggcc	tccctgatca	240
gtttccctac	attgatcaat	ggctgagttt	ggtcaggagc	accccttccg	tggctccact	300
catgcaccat	tcataatttt	acctccaagg	tcctcctgag	ccagaccgtg	ttttcgcttc	360
gaccctcagc	cggttcggct	cgccctgtac	tgccctctctc	tgaagaagag	gagagtctcc	420
ctcaccacgt	cccaccgcct	taaaaccagc	ctactccctt	agggtcaccc	catgtctcct	480
cggctatgtc	ccctgtaggc	tcatacacca	ttgcctcttg	gttgcaaccg	tgggtgggagg	540
aagtagcccc	tctactacca	ctgagagagg	cacaagtccc	tctgggtgat	gagtgtcca	600
cccccttctc	ggtttatgtc	ccttctttct	acttctgact	tgtataattg	gaaaaacccat	660
aatcctccct	tctctgaaaa	gccccaggct	ttgacctcac	tgatggagtc	tgtactctgg	720
acacattggc	ccacctggga	tgactgtcaa	cagctccttt	tgaccctttt	cacctctgaa	780
gagagggaaa	gtatccaaag	agaggccaaa	aagtacaacc	tcacatcaac	caataggccg	840
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tgagtaccca	ggagtgtttt	tagagcacct	ccaggaggct	tatcagattt	acaccccttt	1080
tgacctggca	gcccccgaaa	atagccatgc	tcttaatttg	gcatttgtgg	ctcaggcagc	1140
cccagatagt	aaaaggaaac	tccaaaaact	agagggattt	tgctggaatg	aataccagtc	1200
agctttttaga	gatagcctaa	aaggtttttg	acagtcaaga	ggttgaaaaa	caaaaaacaag	1260
cagctcaggc	agctgaaaaa	agccactgat	aaagcatect	ggagtatcag	agtttactgt	1320
tagatcagcc	tcatttgact	tcccctccca	catggtgttt	aaatccagct	acactacttc	1380
ctgactcaaa	ctccactatt	cctgttcatg	actgtcagga	actgttggaa	actactgaaa	1440
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ggtaaccaga	aagctgattc	agcagctcaa	gatgcagtgt	gactttcagt	cacgcctcta	1860
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acagaagaag	aaaactggcc	tcagaactca	gagccaataa	aaatcaggaa	ggttgggtgga	1980
ttcttctctga	ctctagaatc	ttcatacccc	gaactcttgg	gaaaacttta	atcagtcacc	2040
tacagtctac	caccatttta	ggaggagcaa	agctacctca	gctcctccgg	agccgttttta	2100

```

agatccccc  tcttcaaagc  ctaacagatc  aagcagctct  ccggtgcaca  acctgcgccc  2160
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ggccctccac  cagcaaaaag  attctgactc  actgaagact  tggatgatca  ttagtatttt  3600
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```

<210> 228

<211> 419

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(419)

<223> n = A,T,C or G

<400> 228

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taagagggta  caagatctaa  gcacagccgt  caatgcagaa  cacagaacgt  agcctggtaa  60
gtgtgttaag  agtgggaatt  tttggagtac  agagtaaggc  acctaaccct  agctgggggt  120
tggtgacggg  cccagatggc  ttacagaaga  aagtgtcctg  agatgagttt  ttaagaatga  180
ataaggatag  acacaagtga  ggactgactt  ggcagtgggt  aatgggtggg  ggcaaaaaac  240
ttcgcagtga  tggaaactgc  acgtacagga  atgaagaatg  agactgtgtg  gtgtttaatg  300
agctgcaaat  actaatttta  tcctgaaagt  tttgaagagt  taactaaaaa  gtatttttta  360
gtaaggaaat  aaccctacat  ttcagggtta  ttgtttgttt  anatattgaa  ggtgcccaa  419

```

<210> 229

<211> 148

<212> DNA

<213> Homo sapien

<400> 229

```

aagagggtag  ctgtatgtag  ccatgggtgg  aatgagagac  tgattactac  ctgctggaga  60
ttgtttaagt  gagttaatat  attaaggata  aaggagacca  ggttttttga  ctgttggaga  120
aggaaattac  agatattgaa  ggtcccaa  148

```

<210> 230
 <211> 257
 <212> DNA
 <213> Homo sapien

<400> 230
 taagaggggta cmaaaaaaaaa aaaatagaac gaatgagtaa gacctactat ttgatagtac 60
 aacaggggtga ctatagtcaa tgataactta attatacatt taacatagag tgtaattgga 120
 ttgtttgttaa ctcgaaggat aaatgcttga gaggatggat accccattct ccatgatgta 180
 cttatttcac attacatgcc tgtatcaaag catctcatat accctataaa tatgtacacc 240
 tactatgtac cctctta 257

<210> 231
 <211> 260
 <212> DNA
 <213> Homo sapien

<400> 231
 taagaggggta cgggtatttg ctgatgggat ttttttttct ttctttttct ttggaaaaca 60
 aaatgaaagc cagaacaaaa ttattgaaca aaagacaggg actaaatctg gagaaatgaa 120
 gtcccctcac ctgactgcc tttcattcta tctgaccttc cagtctaggt taggagaata 180
 ggggggtggag gggattaatc tgatacaggt atattttaag caactctgca tgtgtgccag 240
 aagtccatgg taccctctta 260

<210> 232
 <211> 596
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(596)
 <223> n = A,T,C or G

<400> 232
 tgctcctctt gccttaccaa ccacaaatta gaaccataat gagatgtcac ctcatacctg 60
 gtgggattaa cattatttaa aaaatcagaa gtattgacaa ggatgtgaag aaattagaac 120
 atctgtgcac tgttggtggg aatgtaaaaa aggtgtggcc actatgggta acagcatgaa 180
 ggttcctcaa aaaaaatttt ttttaatcta ctctatgatc gatcttgagg ttgtttatgc 240
 aaaagaactg aaatcaggat tttgaggaaa tattcacatt cccacatcca tttctgcttt 300
 attcataata ctcaagagat ggaaacaacc taaatgtcca tcccgggatg aatggataaa 360
 cacagtgtgg tatatgcata caatggaata ttatttagtc tttaaaaaga aaaattctat 420
 catatactac aacttanatn aaccttgagg acacaatgct nagtgaaata agccacggaa 480
 ggacgaatac tgcattattc ccttatatga agtatctaaa gtgggtcaaac tcttanagca 540
 naaagtaaaa atgggtgggt gccanacagt tgggttaggcn agaaganaan cctant 596

<210> 233
 <211> 96
 <212> DNA
 <213> Homo sapien

<400> 233
 tcttctgaag acctttcgcg actcttaagc tcgtggttgg taaggcaaga ggagcgttgg 60
 taaggcaaga ggagcgttgg taaggcaaga ggagca 96

<210> 234
 <211> 313
 <212> DNA
 <213> Homo sapien

<400> 234
 tgtaagtcca gcagtgtgat gataaaactt gaatggatca atagttgctt cttatggatg 60
 agcaaagaaa gtagtttctt gtgatggaat ctgctcctgg caaaaatgct gtgaacgttg 120
 ttgaaaagac aacaaagagt ttagagtagt acataaattt agaatagtac ataaacttag 180
 aatagtacat aaacttagta cataaataat gcacgaagca ggggcagggc ttgagagaat 240
 tgacttcaat ttggaaagag tatctactgt aggttagatg ctctcaaaca gcatcacact 300
 gctcgactta caa 313

<210> 235
 <211> 550
 <212> DNA
 <213> Homo sapien

<400> 235
 aacgaggaca gatccttaaa aagaatgttg agtgaaaaaa 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 tattttgtacc wgaagtccag aaagagtgga 300
 ggcagaaggg ggagaagagg gcgaagaaac gtttttggga gaggggtccc asaagagaga 360
 ttttcgcgat gtggcgctac atacgttttt ccaggatgcc ttaagctctg caccctatatt 420
 ttctcatcac taatattaga ttaaaccctt tgaagacagc gtctgtgggt tctctacttc 480
 agctttccct ccgtgtcttg cacacagtag ctgttttaca agggttgaac tgactgaagt 540
 gagattattc 550

<210> 236
 <211> 325
 <212> DNA
 <213> Homo sapien

<400> 236
 tagactgact catgtcccct accagagtag ctagaattaa tagcacaagc ctctacaccc 60
 aggaactcac tattgaatac ataaatggaa tttattcagc cttaaaaagt ttggaaggaa 120
 attctgacat atgctaaaac atggatgaac cttgaagact ttatgataag taaaagaagc 180
 cagtcataaa aggaaaaata ttgcatgatt ccacttatat gaggtaccta gagtagtcaa 240
 tttcatagaa acacaaaata gaatggtgtt tgccagggtc tttgaggaaa aggggaatgac 300
 aagttagggg acatgagtca gtcta 325

<210> 237
 <211> 373
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)... (373)
 <223> n = A,T,C or G

<400> 237

```

tagactgact catgtcccct atctactcaa catttccact tgaagtctga taggcatctc      60
agacttatct tgtcccaaag caaactcttt atttcttttc atcctagtct ttatttcttg      120
tgctgtctta cccatctcaa aagagtgccaa aaatccacca agttgctgaa acagaaatct      180
aagaaatata cttgattctt ctttttccca tctacttcac ttctaattca ttagtaaata      240
atctgtttca gaaaaccaa cacctcatgt tctcactcat aagggggagt tgaacaatga      300
gaacacacag acacagggag gggaacatca cacaccacgg cccgtcaggg agtangggac      360
atgagtcagt cta                                     373

```

```

<210> 238
<211> 492
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(492)
<223> n = A,T,C or G

```

```

<400> 238
tagactgact catgtcccct ataatgctcc caggcatcag aaagcatctc aaactggagc      60
tgacaccatg gcagagggttt caggtaagtc acaaaagggg tcctaaagaa tttgccctca      120
atatcagagt gattagaaga agtggacaga gctacccaag ttaaaccatat gcgagataaa      180
aaaaatatgg cacttgtgaa cacacactac aggaggaaaa taaggaacat aatagcatat      240
tgtgctatta tgatgatgaa gaacctctct anaagaaaac ataaccaaaag aaacaaagaa      300
aattcctgcn aatgtttaat gctatagaag aaattaacaa aaacatatat tcaatgaatt      360
cagaaaagtt agcagggtcan aagaaaacaa atcaaagacc agaataatcc catttttagat      420
tgtcgagtaa actanaacag aaagaatacc actggaaatt gaattcctac gtangggaca      480
tgantcantc ta                                     492

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```

<210> 239
<211> 482
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(482)
<223> n = A,T,C or G

```

```

<400> 239
tggaaagtat ttaatgatgg gcaacttgct gtttacttcc tacatatccc atcatcttct      60
gtattttttt aaataacttt tttttggatt tttaaagtaa ccttattctg agaggtaaca      120
tggattacat acttctaagc cattaggaga ctctatgtta aacccaaaagg aaatgttact      180
agatcttcat ttgatcaata ggatgtgata atcatcatct ttctgctcta atggaaaagt      240
actanaaaca tggaaccata atcttagatg aacaacgtta gaatttgcac taattctacg      300
gaatttcagt aattcggcaa atgtcgggca gtgacacaac atttcatgac ggggacgcat      360
ctaccaactt ctggcgataa gggccaccct tccctctgta cttacagtcc catttcatac      420
acagtctttg attaaatatt cacatttttt ctctacctaa agaccttcaa gaccagtacg      480
ta                                     482

```

```

<210> 240
<211> 519
<212> DNA
<213> Homo sapien

```

<220>

<221> misc_feature

<222> (1)...(519)

<223> n = A,T,C or G

<400> 240

tgtatcgacg	tagtgggtctc	cccatgtgat	agtctgaaat	atagcctcat	gggatgagag	60
gctgtgcccc	agcccgacac	cogtaaaggg	tctgtgctga	ggtggattag	taaaagagga	120
aagccttgca	gttgagatag	aggaagggca	ctgtctcctg	cctgccccctg	ggaactgaat	180
gtctcgggat	aaaacccgat	tgtacatttg	ttcaattctg	agataggaga	aaaaccaccc	240
tatggcggga	ggcgagacat	gttggcagca	atgctgcctt	gttatgcttt	actccacaga	300
tgtttgggcg	gagggaaaca	taaatctggc	ctacgtgcac	atccaggcat	agtacctccc	360
tttgaactta	attatgacac	agattccttt	gctcacatgt	ttttttgctg	accttctcct	420
tattatcacc	ctgctctcct	accgcattcc	ttgtgctgag	ataatgaaaa	taatatcaat	480
aaaaacttga	nggaactcgg	agaccactac	gtcgataca			519

<210> 241

<211> 771

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(771)

<223> n = A,T,C or G

<400> 241

tgtatcgacg	tagtgggtctc	cactcccgcc	ttgacggggc	tgctatctgc	cttccaggcc	60
actgtcacgg	ctcccggtga	gaagtcactt	atgagacaca	ccagtgtggc	cttggttggct	120
tgaagctcct	cagaggaggg	tggaacaga	gtgaccgagg	gggcagcctt	gggctgacct	180
aggacggtca	gcttgggtccc	tccgccaaac	acgagagtgc	tgctgcttgt	atatgagctg	240
cagtaataat	cagcctcgte	ctcagcctgg	agcccagaga	tggtcaggga	ggcctgtgtg	300
ccanacttgg	agccagagaa	gcgattagaa	acccctgagg	gccgattacc	gacctcataa	360
atcatgaatt	tgggggcttt	gcctgggtgc	tggttggtacc	angagacatt	attataacca	420
ccaacgtcac	tgctgggtcc	antgcaggga	aaatggttga	tcnaactgtc	caagaaaacc	480
actacgtcca	taccaatcca	ctaattgcn	gccgcctgca	ggttcaacca	tattggggaa	540
naactcccn	ccgcggtttg	ggattgncat	naacctttga	aattttttcc	tattanttgt	600
ccccctaaaa	taaacnnttg	ggcnnttaate	cattgggtcc	atancttntt	tnccegggtt	660
ttaaaanttg	tttatcccg	cncnntttt	cccccccaac	tttccaaaac	ccgaaacct	720
tnaaatttnt	tnaaacctg	gggggttccc	nnaattnnan	ttnaanctnc	c	771

<210> 242

<211> 167

<212> DNA

<213> Homo sapien

<400> 242

tgggcacctt	caatatcggg	ctcatcgata	acatcacgct	gctgatgctg	ctggttctgg	60
tcctctctag	gaacctctgg	attttcaa	tctttgagga	attcatccaa	attatctgcc	120
tctcctcctt	tcctcctttt	tctaaggtct	tctggtacaa	gcggtca		167

<210> 243

<211> 338

<212> DNA

<213> Homo sapien

<400> 243

ttggggcacct tcaatatcta ctgatctaaa tagtgtgggt tgaggcctct tgttcctggc	60
taaaaatcct tggcaagagt caatctccac tttacaatag aggtaaaaat cttacaatgg	120
atattcttga caaagctagc atagagacag caattttaca caaggatatt ttcacctgtt	180
taataacagt ggttttcccta caccatagg gtgccaccaa gggaggagtg cacagttgca	240
gaaacaaatt aagatactga agacaacact acttaccatt tcccgtatag ctaaccacca	300
gttcaactgt acatgtatgt tcttatgggc aatcaaga	338

<210> 244

<211> 346

<212> DNA

<213> Homo sapien

<400> 244

tttttggctc ccatacagca cactctcatg ggaaatgtct gttctaagggt caaccataa	60
tgcaaaaatc atcaatatac ttgaagatcc ccgtgtaagg tacaatgtat ttaatatatt	120
cactgatatac attgatccaa taccagtttt agtctggcat tgaatcaaat cactgttttt	180
gttgtataaa aagagaaata tttagcttat atttaagtac catattgtaa gaaaaaagat	240
gcttatcttt acatgctaaa atcatgatct gtacattgggt gcagtgaata ttactgtaaa	300
aggggaagaag gaatgaagac gagctaagga tattgaagggt gcccaa	346

<210> 245

<211> 521

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(521)

<223> n = A,T,C or G

<400> 245

accaatccca cacggatact gagggacaag tatatcatcc catttcatcc ctacagcagc	60
aacttcatga ggcaggagtt attagtccca ttttacagaa gaggaaactg agacttaggg	120
agatcaagta atttgccag gtgcacaaat tagtgataga gccagggtt gaagcgacgt	180
ctgtcttaag ccaatgaccc ctgcagatta ttagagcaac tgttctccac aacagtgtaa	240
gcctcttgct anaagctcag gtccacaagg gcagagattt ttgtctgttt tgctcattgc	300
tccttcccca ttgcttagag cagggctctgc cacgaancag gttctcaatg catagttatt	360
aaatgtatat aagagcaaac atatgttaca gagaactttc tgtatgcttg tcaattacat	420
gaatcacctg tganatgggt atgcttgctc cccantgttg cagatnaaga tattgaangt	480
gcccaaatca ctanttgagg gcgcctgcan gtccancata t	521

<210> 246

<211> 482

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(482)

<223> n = A,T,C or G

<400> 246

tggaaccaat ccaaataccc atcaatgata gactggataa agaaaatttg gcacatgttc	60
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```

accatgaaat actatgcagc cataaaaaaag gatgagttca tatcctttgc agggacatgg      120
atgaagctgg agaccatcat tctcagcaaa ctaacaaggg aacagaaaac caaactctgc      180
atgttctcac tcttaagtgg gagctgaaca atgagaacac atggacacag ggaggggaac      240
atcacacagt ggggcctgct ggtgggtagg ggtctagggg agggatagca ttaggagaaa      300
tacctaattg agatgacggg ttgatgggtg cagcaaacca ccatgacacg tgtataccta      360
tgtaacaaac ctgcatgttc tgcacatgta ccccgaaact taaagtgtta ataaaaaat      420
taagaaaaaa gttaagtatg tcatagatac ataaaatatt gtanatattg aagggtgccca      480
aa

```

```

<210> 247
<211> 474
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(474)
<223> n = A,T,C or G

```

```

<400> 247
ttcgatacag gcacagagta agcagaaaaa tggctgtggt ttaaccaagt gagtacagtt      60
aagtgagaga ggggcagaga agacaagggc atatgcaggg ggtgattata acaggtgggt      120
gtgctgggaa gtgagggtac tccgggatga ggaacagtga aaaagtggca aaaagtggta      180
agatcagtga attgtacttc tccagaattt gatttctggn ggagtcaaat aactatccag      240
tttggggtat catanggcaa cagttgaggt ataggaggta gaagtcncag tgggataatt      300
gaggttatga anggtttggt actgactggg actgacaang tctgggttat gaccatggga      360
atgaatgact gtanaagcgt anaggatgaa actattccac ganaaagggg tccnaaaact      420
aaaaannnaa gnnnnngggg aatattattt atgtggatat tgaangtgcc caaa          474

```

```

<210> 248
<211> 355
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(355)
<223> n = A,T,C or G

```

```

<400> 248
ttcgatacag gcaaacatga actgcaggag ggtggtgacg atcatgatgt tgccgatggg      60
ccggatggnc acgaagacgc actggancac gtgcttacgt ccttttgctc tgttgatggc      120
cctgagggga cgcaggaccc ttatgaccct cagaatcttc acaacgggag atggcactgg      180
attgantccc antgacacca gagacacccc aaccaccagn atatcantat attgatgtag      240
ttcctgtaga nggccccctt gtggaggaaa gctccatnag ttggtcatct tcaacaggat      300
ctcaacagtt tccgatgggt gtgatgggca tagtcatant taacntgtn tcgaa          355

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```

<210> 249
<211> 434
<212> DNA
<213> Homo sapien

```

```

<400> 249
ttggattggg cctccaggag aacaagggga aaaaggtgac cgagggctcc ctggaactca      60
aggatctcca ggagcaaaaag gggatggggg aattcctggg cctgctgggc ccttaggtcc      120

```

acctggtcct	ccaggccttac	caggtcctca	aggcccaaaag	ggtaacaaaag	gctctactgg	180
acccgctggc	cagaaagggtg	acagtgggtct	tccagggcct	cctggggcctc	caggctccacc	240
tggtgaagtc	attcagcctt	taccaatctt	gtcctccaaa	aaaacgagaa	gacatactga	300
aggcatgcaa	gcagatgcag	atgataatat	tcttgattac	tcggatggaa	tggaagaaat	360
atttggttcc	ctcaattccc	tgaacaaga	catcgagcat	atgaaatttc	caatgggtac	420
tcagaccaat	ccaa					434

<210> 250

<211> 430

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(430)

<223> n = A,T,C or G

<400> 250

tggtattggc	acatggcaga	gacaggatcc	caaggcagtg	agaggaggat	acaatgcttc	60
tactagtta	ttattattta	ttttattttt	gagatgaagt	ctcgctttgt	ctcccaggct	120
ggagagcgg	ggtgcgatct	tggtctctctg	caacccccgc	ctcaagcaat	tctcctgtct	180
tagcctcgcg	ggtagatgga	attacaggcg	cccaccgcca	tgcccaacta	atTTTTTTgt	240
gtcttcagta	gagacagggt	ttcgccatgt	tgggcaggct	ggtcttgaac	tctgacctc	300
nagtgatctg	ccctcctcgg	cctcacaaaag	tgtctggaatt	acaggcatgg	gctgctgcac	360
ccagtcaact	tctcactagt	tatggcctta	tcatttttcac	cacattctat	tggcccaaaa	420
aaaaaaaaan						430

<210> 251

<211> 329

<212> DNA

<213> Homo sapien

<400> 251

tggtactcca	ccatyatggg	gtcaaccgcc	atcctcgccc	tctcctggc	tggtctccaa	60
ggagtctgtg	ccgagggtgca	gctgrtgag	tctggagcag	aggtgaaaaa	gtccggggag	120
tctctgaaga	tctcctgtaa	gggttctgga	tacaccttta	agatctactg	gatcgcttgg	180
gtgcgccagt	tgccccggaa	aggcctggag	tggatggggc	tcattcttcc	tgatgactct	240
gataccagat	acagcccgtc	cttccaaggc	caggtcacca	tctcagtcga	taagtccatc	300
agcaccgcct	atctgcagtg	gagtaccaa				329

<210> 252

<211> 536

<212> DNA

<213> Homo sapien

<400> 252

tggtactcca	ctcagcccaa	ccttaattaa	gaattaagag	ggaacctatt	actattctcc	60
caggctcctc	tgtcttaacc	aggtctcttg	gacagtatta	gaaaaggatg	tctcaacaag	120
tatgtagatc	ctgtactggc	ctaagaagtt	aaactgagaa	tagcataaat	cagaccaaac	180
ttaatggctg	ttgagacttg	tgtcctggag	cagctgggat	aggaaaaactt	ttggggcagca	240
agaggaagaa	ctgcctggaa	gggggcatca	tgtaaaaaat	tacaagggga	acccacacca	300
ggcccccttc	ccagctctca	gcctagagta	ttagcatttc	tcagctagag	actcacaact	360
tccttgctta	gaatgtgcc	ccggggggag	tcctgtggg	tgatgaggct	ctcaagagtg	420
agagtggcat	cctatcttct	gtgtgccac	aggagcctgg	cccagagactt	agcaggtgaa	480
gtttctggtc	caggctttgc	ccttgactca	ctatgtgacc	tctgggtggag	taccaa	536

<210> 253
 <211> 507
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(507)
 <223> n = A,T,C or G

<400> 253
 ntgttgcgat cccagtaact cggaagctg aggcgggagg atcacctgag ctcaggaggt 60
 tgaggccgca gtgagccggg accacgccac tacactccag 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 attcctgctc tcacttaatt ctcaccactc 420
 tgatataaat acaattgctg ccgggtgtgg tggctcatgc ctgtaatccc ggcactttgg 480
 gagaccgagg tgggcggats gcaacaa 507

<210> 254
 <211> 222
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(222)
 <223> n = A,T,C or G

<400> 254
 ttggattggt cactgtgagg aagccaaatc ggatccgaga gtctttttct aaaggccagt 60
 actggccaca ctttctcctg ccgccttcct caaagctgaa gacacacaga gcaaggcgct 120
 tctgttttac tcccgaatgg taactccaaa ccatagatgg ttagctnccc tgctcatctt 180
 tccacatccc tgctattcag tatagtcctg ggaccaatcc aa 222

<210> 255
 <211> 463
 <212> DNA
 <213> Homo sapien

<400> 255
 tgttgcgatc cataaatgct gaaatggaaa taaacaacat gatgaggagg gattaagttg 60
 gggagggagc acattaaggt ggccatgaag tttgttggaa gaagtgactt ttgaacaagg 120
 ccttggtgtt aagagctgat gagagtgtcc cagacagagg ggccactggg acaatagacg 180
 agatgggaga gggcttggaa ggtgtgcaa ataggaagga gtttgttctg gtatgagtct 240
 agtgaacaca gaggcgagag gccctggtgg gtgcagctgg agagttagtc agaataacat 300
 taggccctgt gggggactgt agactgtcag caataatcca cagtttggat tttattctaa 360
 gagtgatggg aagccgtgga aaggggggta agcaaggagt gaaattatca gatttacagt 420
 gataaaaaata aattggtctg gctactgggg aaaaaaaaaa aaa 463

<210> 256
 <211> 262

<212> DNA

<213> Homo sapien

<400> 256

ttggattggt caacctgctc aactctacyt ttctctcttc ttcttaaaaa attaatgaat	60
ccaatacatt aatgccaaaa cccttggtgt ttatcaatat ttctgttaaa aagtattatc	120
cagaactgga cataatacta cataataata cataacaacc ccttcatctg gatgcaaaaca	180
tctattaata tagcttaaga tcactttcac ttacagaag caacatctctg ttgatgttat	240
tttgatgttt ggaccaatcc aa	262

<210> 257

<211> 461

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(461)

<223> n = A,T,C or G

<400> 257

gnngnnnnnnn nnncaattcg actcngttcc cntggtancc ggctcgacatg gccgcgggat	60
taccgcttgt nnctgggggt gtatggggga ctatgaccgc ttgtagctgg ggggtgatgg	120
gggactatga ccgctttag mtggkgtgt atgggggact atgaccgctt gtcgggtggt	180
cggataaacc gacgcaagg acgtgatcga agctgcgttc ccgctctttc gcatcggtag	240
ggatcatgga cagcaatc cgcattcgyt tgaaggcggt cgaccatcgc gtgctcgatc	300
aggcgaccgg cgacatcgcc gacaccgcac gccgtaccgg cgcgctcatc cgcgggtccga	360
tcccgttcc cagcgcgcatc gagaagttca cgggtcaaccg tggcccgcac gtcgacaaga	420
agtcgcgcga gcagttcgag gtgcgtacct acaagcgggtc a	461

<210> 258

<211> 332

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(332)

<223> n = A,T,C or G

<400> 258

tgaccgcttg tagctggggg tgtatggggg actacgaccg cttgtagctg ggggtgtatg	60
ggggactatg accgcttgta gctgggggtg tatgggggac tatgaccgct ttagctggg	120
ggtgtatggg ggactaggac cgctttagtc tgggggtgta tgggggacta tgaccgcttg	180
tagctggggg tgtatggggg actacgaccg cttgtagctg ggggtgtatg ggggactatg	240
accgcttgta nctgggggtg tatgggggac tatgaccgct tggctgcct gggggatggg	300
aggagagttg tgggtgggga aaaaaaaaaa aa	332

<210> 259

<211> 291

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (291)

<223> n = A,T,C or G

<400> 259

taccgcttgt gaccgcttgt gaccgcttgt gaccgcttgt gaccgcttgt gaccgcttgt	60
gaccgcttgt gaccgcttgt gaccgcttgt gaccgcttgt gaccgcttgt gaccgcttgt	120
gaccgcttgt gaccgcttgt nacnggggggt gtctggggga ctatgannga ntgtactgg	180
gggtgtctgg ggggctatga nngantgtna cnggggggtgt ctgggggact atganngact	240
gtgcnnctg ggggacnnga ggagantngn ggntagngat ggttngggan a	291

<210> 260

<211> 238

<212> DNA

<213> Homo sapien

<400> 260

taagagggta ctgggttaaaa tacaggaaat ctggggtaat gaggcagaga accaggatac	60
tttgaggtca gggatgaaaa ctagaatttt tttctttttt tttgcctgag aaacttgctg	120
ctctgaagag gcccatgtat taattgcttt gatcttcctt ttcttacagc cctttcaagg	180
gcagagccct ccttatcctg aaggaatctt atccttagct atagtatgta ccctctta	238

<210> 261

<211> 746

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (746)

<223> n = A,T,C or G

<400> 261

ttgggacact tcaatatcaa tagctaakat ttattgagtgt tttatcgtat cataaaacac	60
tggttctaagc ctttaaacgt actaattcat ttaatgctca taatcacttt agaagggtggg	120
tactagtatt agtctcattt acagatgcaa catgcaggca cagagagggt aattaacttg	180
cccaaggtaa cacagctaag aatagaaaa aatattgaat ctggaaagtt gggcttctgg	240
gtaaccacaca gagtcttcaa tgagcctggg gcctcactca gtttgccttt acaaagcgaa	300
tgagtaacat cacttaattc agtgagtagg ccaaattggag gtcagctacg agtttctgct	360
gttcttgcag tggactgaca gatgtttaca acgtctggcc atcagtwaat ggactgatta	420
tcattgggaw gtgggtgggc tgaatgttgg ccagtgaagt ttattcawgc catattttta	480
tgtttaggat gacttttggc tggctcctagg gcaagctctg tctgscacgg aacacagaat	540
wacacagggg cccctcaat ttctggtgtg gctagaacca tgaaccactg gttgggggaa	600
caagcgggtca aaacctaagt gcggccggct ggcagggtcc acccatatgg ggaaaactcc	660
cnacgcgttt ggaatgcctn agctngaatt attctaanag ttgtccnctt aaaattagcc	720
tgggcgttaa tcangggctn naagcc	746

<210> 262

<211> 588

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (588)

<223> n = A,T,C or G

<400> 262

tgaccgcttg	tcattctcaca	tggggtcctg	cacgcttttg	cctttgtagg	aaacctgaca	60
tttgtctgtt	tcttctttct	cttttcttct	ccatatactc	ctaatttacg	tttgacttgt	120
ttgctgagga	ggcaggagct	agagactgct	gtgagctcat	aggggtggga	agtttatcct	180
tcaagtcccg	cccactcatc	actgcttctc	accttccctc	gaccaggctt	acaagtgggt	240
tcttgccctg	tttccctttg	gacccaacaa	gcccctgtaa	tgagtgtgca	tgactctgac	300
agctgtggac	tcagggtcct	tggctacagc	tgccatgtaa	aatatctcat	ccagttctcg	360
caaattgtta	aaataaccac	atttcttaga	ttccagtacc	caaatacatgt	ctttacgaac	420
tgctcctcac	acccagaagt	ggcacaataa	ttcttgggga	attattactt	ttttttttct	480
ctctnttnnc	gnnnngnnng	gnnnngnccag	gaattaccac	nttggaagac	ctggccngaa	540
tttattatan	agggggagccg	attntttttc	ctaacacaaa	gcgggtca		588

<210> 263

<211> 730

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (730)

<223> n = A,T,C or G

<400> 263

tttttttttt	tttggcctga	gcaactgaaa	ttatgaaatt	tccatatact	caaaagagta	60
agactgcaaa	aagattaaat	gtaaaagttg	tcttgtatac	agtaatgttt	aagataccta	120
ttanatttat	aaatggaaaa	ttagggcatt	tggatataca	agttgaaaat	tcaggagtga	180
ggttgggctg	gctgggtata	tactgaaaac	tgtcagtaca	cagatgacat	ctaaaaccac	240
aaatctgggt	ttatttttagc	agtgatatgt	gtcactccca	caaaagcctt	cccaattggc	300
ctcagcatac	acaacaagtc	acctccccac	agccctctac	acataaacia	attccttagt	360
ttagttcagg	aggaaaatgcg	cccttttctc	tccgctctag	gtgaccgcaa	ggcccagttc	420
tcgtcaccaa	gatgttaagg	gaagtctgcc	aaagaggcat	ctgaaaggaa	ataaggggaa	480
tgggagtgc	cacaaaggaa	agccaaggan	aaactttgga	gaccgtttct	aganccctgg	540
catttcacaa	caaaaactcng	gaacaaacct	tgtctcatca	atcatttaag	cccttcgttt	600
ggannagact	ttctgaactg	ggcgctgaac	ataancctca	ttgaatgtct	tcacagtctc	660
ccagctgaag	gcacaccttg	ggccagaagg	ggaatcttcc	aggtcctcaa	nacagggtctc	720
gccctttgnc						730

<210> 264

<211> 715

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (715)

<223> n = A,T,C or G

<400> 264

tttttttttt	tttggccagt	atgatagtct	ctaccactat	attgaagctc	ttaggtcatt	60
tacacttaat	gtggttatag	atgctgttga	gcttacttct	accaccttgc	tattttctccc	120
gtctcttttt	tgttcttttt	ctcttctttt	cctcccttat	tttataattg	aatttttttag	180
gattctatatt	tatatagatt	tatcagctat	aacactttgt	attctttttgt	tttgtgggtc	240
ttctgtcatt	tcaatgtgca	tcttaaactc	atcacaaatc	attttcaaat	aatatcatat	300
aaccttacat	ataatgtaag	aatctaccac	catatatattc	cattttctccc	ttccatccta	360

tgtntgtcat	atTTTTTtct	ttatatatgt	tttaaagaca	taatagtata	tgggaggttt	420
ttgcttaaaa	tgtgatcaat	attccttcaa	ngaaaacgtaa	aaattcaaaa	taaatntctg	480
tttattctca	aatnnaccta	atatttcccta	ccatntctna	tacntttcaa	gaatctgaag	540
gcattgggtt	tttccggctt	aagaacctcc	tctaaagcac	tctaagcaga	attaagtctt	600
ctgggagagg	aattctccca	agcttggggc	ttnanntgta	ctccntnang	gttaaanttt	660
ggccgggaaa	tagaaattcc	aagttaacag	gntanttttt	ntttttnttn	tcncc	715

<210> 265
 <211> 152
 <212> DNA
 <213> Homo sapien

<400> 265						
tttttttttt	tttcccaaca	caaagcacca	ttatctttcc	tcacaatttt	caacatagtt	60
tgattcccat	gaagagggtta	tgattttctaa	agaaaacatg	gctactatac	tatcaatcag	120
ggttaaactct	tttttttttg	agacggagtt	ta			152

<210> 266
 <211> 193
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (193)
 <223> n = A,T,C or G

<400> 266						
taaactccgt	ccccttctta	atcaatatgg	aggctaccca	ctccacatta	ccttcttttc	60
aagggactgt	ttccgtaact	gttgtgggta	ttcacgacca	ggcttctaaa	cctcttaaaa	120
ctccccaatt	ctggtgccaa	cttggacaac	atgctttttt	tttttttttt	tttttttttn	180
gagacggagt	tta					193

<210> 267
 <211> 460
 <212> DNA
 <213> Homo sapien

<400> 267						
tgttgcgatc	ccttaagcat	gggtgctatt	aaaaaaatgg	tggagaagaa	aatacctgga	60
atttacgtct	tatcttttaga	gattgggaag	accctgatgg	aggacgtgga	gaacagcttc	120
ttcttgaatg	tcaattccca	agtaacaaca	gtgtgtcagg	cacttgctaa	ggatcctaaa	180
ttgcagcaag	gctacaatgc	tatgggattc	tcccagggag	gccaatctct	gagggcagtg	240
gctcagagat	gcccttcacc	tcccatgata	aatctgatct	cggttggggg	acaacatcaa	300
ggtgtttttg	gactccctcg	atgcccagga	gagagctctc	acatctgtga	cttcatccga	360
aaaacactga	atgctggggc	gtactccaaa	gttgttcagg	aacgcctcgt	gcaagccgaa	420
tactggcatg	acccataaaa	ggaggatgtg	gatcgcaaca			460

<210> 268
 <211> 533
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature

<222> (1) ... (533)

<223> n = A,T,C or G

<400> 268

tggttgcatc	cgttgataga	atagcgacgt	ggtaatgagt	gcatggcacg	cctccgactt	60
accttcgccc	gtggggaccc	cgagtacgtc	tacggcgctc	tcacttagag	taccctctgg	120
acgcccgggc	gcgttcgatt	taccggaagc	gcgagctgca	gtgggcttgc	gccccgggcc	180
aaattctttg	gggggtttta	ggccgcgggg	aatttgaggt	atctctatca	gtatgtagcc	240
aagttggaac	agtcgccatt	cccgaaatcg	ctttctttga	atccgcaccg	cctccagcat	300
tgcctcattc	atcaacctga	aggcacgcat	aagtgcggt	tgtgtcttca	gcagctccac	360
tccataacta	gcgcgctcga	cctcgtcttc	gtacgcgcca	ggcccgctgc	tgcaattcc	420
caactccggt	gagttgcgca	tttcaagttt	cgaaactgtt	cgctccacn	atttggcatg	480
ttcacgcatg	acacggaata	aactcgtcca	gtaccgggaa	tgggatcgca	aca	533

<210> 269

<211> 50

<212> DNA

<213> Homo sapien

<400> 269

tttttttttt	ttcgctgaa	ttagctacag	atcctcctca	caagcgtca	50
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<210> 270

<211> 519

<212> DNA

<213> Homo sapien

<400> 270

tggttgcatc	caaataaccc	accagcttct	tgcacacttc	gcagaagcca	ccgtcctttg	60
gctgagtcac	gtgaacggtc	agtgcgaagc	gccgcgtgcc	agagcagagg	tgcagcatgc	120
tgcacaccag	ctcagggctg	acctcctcca	gcaggatgga	caggatggag	ctgccgtacg	180
tgtccaccac	ctcctggcac	tcttcgcaca	gggacttcgg	cagcttcgag	cacattttgt	240
caaaagcgtc	gagtatttct	ttctcagtct	tgttggtgtc	aatcagcttg	gtcacctcct	300
tcaccaggaa	ttcacacacc	tcacagtaaa	catcagactt	tgctgggacc	tcgtgcttct	360
taatgggctc	caccagttcc	agggcaggga	tgacattctt	ggaggccact	ttggcgggga	420
ccagagtctg	catgggcatc	tctttcacct	catcacagaa	ccaaccagc	gcacagatct	480
ccttgggttg	catgtgcatc	atcatctggg	atcgcaaca			519

<210> 271

<211> 457

<212> DNA

<213> Homo sapien

<400> 271

tttttttttt	ttcgggcggc	gaccggacgt	gcactcctcc	agtagcggct	gcacgtcgtg	60
ccaatggccc	gctatgagga	ggtgagcgtg	tccggcttcg	aggagttcca	ccgggcccgtg	120
gaacagcaca	atggcaagac	cattttcgcc	tactttacgg	gttctaagga	cgccgggggg	180
aaaagctggt	gccccgactg	cgtgcaggct	gaaccagtcg	tacgagaggg	gctgaagcac	240
attagtgaag	gatgtgtgtt	catctactgc	caagtaggag	aagagcctta	ttggaaagat	300
ccaaataatg	acttcagaaa	aaacttgaaa	gtaacagcag	tgctacact	acttaagtat	360
ggaacacctc	aaaaactggt	agaatctgag	tgtcttcagg	ccaacctggt	ggaaatgttg	420
ttctctgaag	attaagattt	taggatggca	atcaaga			457

<210> 272

<211> 102

<212> DNA

<213> Homo sapien

<400> 272

tttttttttt	ttgggcaaca	acctgaatac	cttttcaagg	ctctggcttg	ggctcaagcc	60
cgcaggggaa	atgcaactgg	ccaggtcaca	gggcaatcaa	ga		102

<210> 273

<211> 455

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(455)

<223> n = A,T,C or G

<400> 273

tttttttttt	ttggcaatca	acaggtttaa	gtcttcggcc	gaagttaatc	tcgtgttttt	60
ggcaatcaac	aggtttaagt	cttcggccga	agttaatctc	gtgttttttg	caatcaacag	120
gtttaagtct	tcggccgaag	ttaatctcgt	gtttttggca	atcaacaggt	ttaagtcttc	180
ggccgaagtt	aatctcgtgt	ttttggcaat	caacaggttt	aagtcttcgg	ccgaagttaa	240
tctcgtgttt	ttggcaatca	acaggtttaa	gtcttcggcc	gaagttaatc	tcgtgttttt	300
ggcaatcaag	aggtttaagt	cttcggccga	agttaatctc	gtgttttttg	caatcaacag	360
gtttaagtct	tcggccgaan	ttaatctcgt	gtttttggca	atcaacaggt	ttaantcttc	420
ggccgaagtt	aatctcgtgt	ttttggcaat	caana			455

<210> 274

<211> 461

<212> DNA

<213> Homo sapien

<400> 274

tttttttttt	ttggccaata	cccttgatga	acatcaatgt	gaaaatcctc	ggtaaaatac	60
tggaacaaca	aatccagcag	cacatcaaaa	agcttatcca	ccatgatcaa	gtgggcttca	120
tccctgggat	gcaaggctgg	ttcaacataa	gaaaatcaat	aaatgtaatc	catcacataa	180
acagaaccaaa	agacaaaaac	cacatgatta	tctcaataga	tgcagaaaag	gccttggaca	240
aattcaacag	cccttcatgc	taaacactct	taataaacta	gatattgatg	gaatgtatct	300
caaaataata	agagctatct	atgacaaacc	cacagccaat	atcatactga	atgggcaaa	360
actggaagca	ttccctttga	aaactggcac	aagacaagga	tgccctctct	caccgctcct	420
attcaacata	gtattggaag	ttctggccag	ggcaatcaag	a		461

<210> 275

<211> 729

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(729)

<223> n = A,T,C or G

<400> 275

tttttttttt	ttggccaaca	ccaagtcttc	cacgtgggag	gttttattat	gttttacaac	60
catgaaaaca	taggaaggtg	gctgttacag	caaacatttc	agatagacga	atcggccaag	120

ctccccaaac	cccaccttca	cagcctcttc	cacacgtctc	ccanagattg	ttgtccttca	180
cttgcaaatt	canggatggt	ggaagtngac	attnnagtn	gcnggaaccc	catcagtga	240
ncantaagca	gaantacgat	gactttgana	nacanctgat	gaagaacacn	ctacnganaa	300
ccctttctnt	cgtgttanga	tctcnngtcc	ntcactaatg	cggccccctg	cnggtccacc	360
atttgaggaga	actccccccn	cggttgatcc	ccccttgagt	ntcccattct	ngtcccccan	420
accngncttg	ngngncantn	cnnccctnca	ccntgtttcc	ctgnngtnaa	aatnngtttt	480
nccgcncccc	naattcccac	ccnaatcaca	gcgaanccng	aaggcccttcn	naagtgttta	540
angcccngng	gtttcctcnt	ntanttgag	cctaccctcc	cncttnnnnt	tnccngttgg	600
tcgcgccttg	gncncgcctn	gttcctcttt	nnggnnacia	cctngntcnn	nggcncntcn	660
nnctntttcc	tnnnactagc	tngcctntcc	ncnccngngn	ncanngcaca	ttncncnnac	720
tntgtnncc						729

<210> 276

<211> 339

<212> DNA

<213> Homo sapien

<400> 276

tgacctgaca	tgtagtagat	acttaataaa	tatttgtgga	atgaatggat	gaagtggagt	60
tacagagaaa	aatagaaaag	tacaaattgt	tgtagtggt	ttgaaggaaa	attatgatct	120
ttcccaaagt	tctgacttca	ttctaagaca	gggttagtat	ctccatacat	aattttactt	180
gcttttgaaa	atcaaagtga	ataatctatt	tagattgata	attttatttag	actggctata	240
aactattaag	tgctagcaaa	tatacatctt	aatctcattt	tccacctctt	gtgatatagc	300
tatgtagggt	ttgactttta	tggatgtcag	gtcaatccc			339

<210> 277

<211> 664

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (664)

<223> n = A,T,C or G

<400> 277

tgacctgaca	tccataacaa	aatctttctc	catttatattc	ttctagggga	atttcttgaa	60
aagcatccaa	aggaaacaaa	tgatggtaag	accgtgccaa	gtggggagca	gacaccaaag	120
taagaccaca	gattttacat	tcaacaggta	gtcacagta	ctttgcccga	cactgtgggc	180
agaaatagcc	tcctaagtga	agccctggct	cagtattgcc	atccaaatgc	gccatgctga	240
aagaggggtt	tgcacccctg	tcagatnaag	aagcaatggg	gtgctgagga	aatcccatat	300
gaataagtga	gcattcagaa	cttgagctag	caggaggagg	actaagatga	tgtgtgagca	360
actcttttgta	atggctttca	tctaaaataa	catggtacgt	gccaccagtt	tcacgagcaa	420
gtacagtgc	aacgcgaact	tctgcagaca	atccaataac	agatactcta	atttttagctg	480
ccttttaggg	cttgattaaa	tcataaatat	tagatggatc	gcaagttgta	aggntgctaa	540
aagatgatta	gtacttctcg	acttgatgtg	ccaggcatgt	tgttttaaan	tctgccttag	600
nccctgctta	ggggaatttt	taaagaagat	ggctctccat	gttcanggtc	aatcacnaat	660
tgcc						664

<210> 278

<211> 452

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(452)
 <223> n = A,T,C or G

<400> 278
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 gacacagagt gggcctctga taattcatga aaagcattct gaagtcaccc agaattggagg 120
 ctgcaatctg ctgtgctttg ggggttgccct cactgtgctc ctggatatca cacaaaagct 180
 gcaatccttc ttcttcaact aacattttgc agtatttgct gggattttta ctgcagacat 240
 gatacatagc ccatagtgcc cagagctgaa cctctgggtg agagaagttg ccaaggagcg 300
 ggaaaaatgt cttgaaagat ctataggtca ccaatgctgt catcttaciaa cttgaacttg 360
 gccaaattctg tatggttgca tgcagatctt ggagaagagt acgcctctgg aagtcacggg 420
 atatccaaan ctgtctgtca gatgtcaggt ca 452

<210> 279
 <211> 274
 <212> DNA
 <213> Homo sapien

<400> 279
 tttttttttt ttcggcaagg caaatttact tctgcaaaag ggtgctgctt gcacttttgg 60
 ccactgagag agcacaccaa acaaagtagg gaaggggttt ttatccctaa cgcgggttatt 120
 ccctggttct gtgtcgtgtc ccattgggtt ggagtcagac tgcacaatct acactgaccc 180
 aactggctac tgttttaaat tgaatatgaa taattaggtg ggaaggggga ggctgtttgt 240
 tacggtacaa gacgtgtttg ggcatgtcag gtca 274

<210> 280
 <211> 272
 <212> DNA
 <213> Homo sapien

<400> 280
 tacctgacat ggagaaataa cttgtagtat tttgcgtgca atggaatact atatgagggt 60
 gaaaatgaat gaactagcaa tgcgtgtatc aacatgaata aatccccaaa acataataat 120
 gttgaatgga aaaggtgagt ttcagaagga tatatatgcc ctctaaatcc atttatgtaa 180
 acctttaaaa aactacatta tttatgggtc taagtccatc cagaaaatat ttaaaaacct 240
 acatgggatt gataactact gatgtcaggt ca 272

<210> 281
 <211> 431
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(431)
 <223> n = A,T,C or G

<400> 281
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 aatttttatg ttctcttgaa taatcaaaag agtaggcaac attggttcct cattcttgaa 120
 tagcattaat cagaaaatat tgcatagcct ctagcctcct tagagtaggt gtgctctctc 180
 aaatatatca tagtcccaca gtttatttca tgtatatatt ctgcctgaat cacatagaca 240
 tttgaatttg caacgcctga tgtaaatata taaattctta ccaatcagaa acatagcaag 300
 aaattcaggg acttggtcat yatcagggtg tgacagcana tccctgtara aacactgata 360

cacactcaca cacgtatgca acgtggagat gtcgcyttww kkktywycwm rmrycrwcgn 420
aatcacttan n 431

<210> 282
<211> 98
<212> DNA
<213> Homo sapien

<400> 282
attcgattcg atgcttgagc ccaggagttc aagactgcag tgagccactg cacttcaggc 60
tggacaacag agcgagtcctc tgtgccaata aaaaaaaa 98

<210> 283
<211> 764
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(764)
<223> n = A,T,C or G

<400> 283
tttttttttt ttcgcaagca cgtgcacttt attgaatgac actgtagaca ggtgtgtggg 60
tataaaactgc tgtatctagg ggcaggacca aggggggcagg ggcaacagcc ccagcgtgca 120
gggccascac tgcacagtgg astgcaaagg ttgcaggcta tgggcggcta ctavtaaccc 180
cgtttttctc gtattatctg taacataata tggtagactg tcacagagcc gaatwccart 240
hacagatga atccaawggc caygaggatg ccacasaatca gggcccasat sttcaggcac 300
ttggcgggtg gggcatasgc ctgkgccccg gtcacgtcsc caaccwtcty cctgtcccta 360
cmcttgawtc cncnecctnn nntnccntna tntgcccgc cncctcctng ngtaaccng 420
natctgcact anctccctcn ccccttntgg antctctncc ttcaantaan nttatccttn 480
acnccccct cncctttccc ctncncccn tnatcccnng nccnctatca ntentnccct 540
cncntnctn cnnatcgctc cncctnntaa ctacnctttn nacnanncc cactnatncc 600
ngnnantctt ttccttccct ccnaccgenn tgcgtgcgcc cgtctngcct nnnctnccna 660
ccnnaacttt atttaccttt ncaccctagc nctctacttn acccancnc tectacctcc 720
ngnccaccc nncctnctc nctnctctn tcnctctnt cccc 764

<210> 284
<211> 157
<212> DNA
<213> Homo sapien

<400> 284
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atttctcccc ttccaggaac gtcttgcatt gatgatcaaa gatcagctcc tggtaacat 120
aaataagcta gtttaagata cgttccccct cacttga 157

<210> 285
<211> 150
<212> DNA
<213> Homo sapien

<400> 285
attcgattgt actcagacaa caatatgcta agtgggaagaa gtcagtcaca aaagaccaca 60
tactgtatga cttcatctac attaatgtgc cagaataggc aaatccgtag agacagaaag 120

tagatgagca gctgcctagg tctgagtaca

150

<210> 286

<211> 219

<212> DNA

<213> Homo sapien

<400> 286

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ataaatgcaa gtctcaccac cagatgtgaa attacagtaa actttgaagg aatctcctga	120
gcaaccttgg ttaggatcaa tccaatattc accatctggg aagtcaggat ggctgagttg	180
caggtcttta caagttcggg ctggattggt ctgagtaca	219

<210> 287

<211> 196

<212> DNA

<213> Homo sapien

<400> 287

attcgattct tgaggctacc aggagctagg agaagaggca tggaacaaat tttccctcat	60
atccatactc agaaggaacc aaccctgctg acaccttaat ttcagcttct ggcctctaga	120
actgtgagag agtacatttc tcttggttta agccaagaga atctgtcttt tgggtacttta	180
tatcatagcc tcaaga	196

<210> 288

<211> 199

<212> DNA

<213> Homo sapien

<400> 288

attcgatttc agtccagtcc cagaaccac attgtcaatt actactctgt araagattca	60
tttggtgaaa ttcattgagt aaaacattta tgatccctta atatatgcc attaccatgc	120
taggtactga agattcaagt gaccgagatg ctagcccttg ggttcaagt atccctctcc	180
cagagtgcac tggactgaa	199

<210> 289

<211> 182

<212> DNA

<213> Homo sapien

<400> 289

attcgattct tgaggctaca aacctgtaca gtatgttact ctactgaata ctgtaggcaa	60
tagtaataca gaagcaagta tctgtatatg taaacattaa aaaggtagag tgaaaacttca	120
gtattataat cttagggacc accattatat atgtggtcca tcattggcca aaaaaaaaaa	180
aa	182

<210> 290

<211> 1646

<212> DNA

<213> Homo sapien

<400> 290

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tattgagtga ttgggttatc aaacaccac aaactttaat tttgttaaatt ttatatggct	120
ttgaaataga agtataagtt gctaccattt tttgataaca ttgaaagata gtattttacc	180

atctttaatc	atcttgga	atacaagtcc	tgtgaacaac	cactctttca	cctagcagca	240
tgaggccaaa	agtaaaggct	ttaaattata	acatatggga	ttcttagtag	tatgtttttt	300
tcttgaaact	cagtggctct	atctaaccct	actatctcct	cactctttct	ctaagactaa	360
actctaggct	cttaaaaaatc	tgcccacacc	aatcttagaa	gctctgaaaa	gaatttgtct	420
ttaaataatct	tttaatatga	acatgtatct	tatggaccaa	attgacattt	tcgactatct	480
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gcagtctcct	taaaggtaga	acaaataactt	tctatctttt	tttcaccatt	gtgggattgg	660
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atcatttctt	ctgtattaat	ttccaaaggg	ttttaccctc	tatttaaattg	ctttgaaaaa	1080
cagtgcattg	acaatgggtt	gataatcttc	tttaaaagaa	aatataaatt	atgaaagcca	1140
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ctggtaattt	ttttattttac	aatatgttta	aagagataac	agtttgatat	gttttcatgt	1440
gtttatagca	gaagttatct	atttctatgg	cattccagcg	gatattttgg	tgtttgcgag	1500
gcattgcagtc	aatattttgt	acagtttagtg	gacagtattc	agcaacgcct	gatagcttct	1560
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aaaaaaaaaa	aaaaaaaaaa	aaaaaa				1646

<210> 291

<211> 1851

<212> DNA

<213> Homo sapien

<400> 291

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cttccgtgtt	cttcattctt	cttcaatagc	cataaatctt	ctagctctgg	ctggctgttt	120
tcacttcctt	taagcctttg	tgactcttcc	tctgatgtca	gctttaagtc	ttgttctgga	180
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ggccatgctt	gttttttgat	tcgatatcag	caccgtataa	gagcagtgtc	ttggccatta	540
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acagaggatg	agatccagaa	accacaatat	ccattcacia	acaaacactt	ttcagccaga	1260
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cttttcccca	tttagtatta	tgttggctgt	gggcttgtca	taggtgggtt	ttattacttt	1800
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<210> 292

<211> 1851

<212> DNA

<213> Homo sapien

<400> 292

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cttccgtggt	cttcattctt	cttcaatagc	cataaatctt	ctagctctgg	ctggctgttt	120
tcacttcctt	taagcctttg	tgactcttcc	tctgatgtca	gctttaagtc	ttgttctgga	180
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caaattacat	gatgatgact	agaaacagca	tactctctgg	cgtcttttcc	agatcttgag	300
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cagcaagtat	gagagcagtt	cttccatatc	tatccagcgc	atttaaattc	gcttttttct	420
tgattaaaaa	tttcaccact	tgctgttttt	gctcatgtat	accaagtagc	agtgggtgtga	480
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<210> 293

<211> 668

<212> DNA

<213> Homo sapien

<400> 293

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accrtataag	agcagtgctt	tggccattaa	tttatctttc	atrttagaca	gcrtagtgya	180
gagtgggtatt	tccatactca	tctggaatat	ttggatcagt	gccatgttcc	agcaacatta	240
acgcacattc	atcttcctgg	cattgtacgg	cctgtcagta	ttagacccaa	aaacaaatta	300
catatcttag	gaattcaaaa	taacattcca	cagctttcac	caactagtta	tatttaaagg	360
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gcagtcctat	gagagtgaga	agacttttta	ggaaattgta	gtgcactagc	tacagccata	600
gcaatgattc	atgtaactgc	aaacactgaa	tagcctgcta	ttactctgcc	ttcaaaaaaa	660
aaaaaaaa						668

<210> 294

<211> 1512

<212> DNA

<213> Homo sapien

<400> 294

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tccatgccgg	ctgcttcttc	tgtgaagaag	ccatttggtc	tcaggagcaa	gatgggcaag	300
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<210> 295

<211> 1853

<212> DNA

<213> Homo sapien

<400> 295

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cactgccttc	cctgctgcag	ggggagtggc	aagagcaacg	tgggcgcttc	tggagaccac	480
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<210> 296

<211> 2184

<212> DNA

<213> Homo sapien

<400> 296

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ttattgactt	gcctgtgtta	gaccggaaga	gctgggggtg	ttctcaggag	ccaccgtgtg	300
ctgcggcagc	ttcgggataa	cttgaggctg	catcactggg	gaagaaacac	aytccgtgcc	360
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ggagtctctc	cttcatagtt	catccatatg	gtccagagg	aaaattatat	tattttgtta	480
tggatgaaga	gtattacgtt	gtgcagatat	actgcagtgt	cttcatctct	tgatgtgtga	540
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gctttctcca	ccttgctgga	agtgaacctgc	tgtccagaag	tttgatggct	gaggagtata	720
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<210> 297

<211> 1855

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(1855)

<223> n = A,T,C or G

<400> 297

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tcgcgttctc	ttgctggact	tgacctttty	tctgctgggt	ttggcattcc	tttgggggtg	420
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acatgtttca gtgaatagag atcctgctcc tttggcaagt tcctaaaaaa cagtaataga 1800
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<210> 298
<211> 1059
<212> DNA
<213> Homo sapien

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<400> 298
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gcgcttgrgg agactmcgat gacagygcct tcatggagcc caggtagcac gtccgtggag 180
aagatctgga caagctccac agagctgccc tgggtggggt aagtccccag aaaggatctc 240
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<210> 299
<211> 329
<212> PRT
<213> Homo sapien

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<400> 299
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Leu His Leu Ala Gly Ser Asp Leu Leu Ser Arg Ser Leu Met Ala Glu
20 25 30
Glu Tyr Thr Ile Val His Ala Ser Phe Ile Ser Cys Ile Ser Ser Ser
35 40 45
Leu Asp Gly Gln Gly Glu Arg Gln Glu Gln Arg Gly His Phe Trp Arg
50 55 60
Pro Gln Arg Leu Leu Cys Glu Asp Ala Trp Glu Gln Glu Val Gln Val
65 70 75 80
Val Leu Pro Leu Leu Pro Leu Leu Gln Gly Ser Gly Lys Ser Asn Val
85 90 95
Val Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr
100 105 110
His Val His Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp
115 120 125
Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp
130 135 140
Val Asn Lys Arg Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser

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145          150          155          160
Ala Asn Gly Asn Ser Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys
          165          170          175
Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala
          180          185          190
Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly
          195          200          205
Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr
          210          215          220
Ala Val Tyr Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr
225          230          235          240
Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu
          245          250          255
Leu Gly Ile His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys
          260          265          270
Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu
          275          280          285
Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu
          290          295          300
Glu Gln Asn Val Asp Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu
305          310          315          320
Ser Met Leu Phe Leu Val Ile Ile Met
          325

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<210> 300
<211> 148
<212> PRT
<213> Homo sapien

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<220>
<221> VARIANT
<222> (1)...(148)
<223> Xaa = Any Amino Acid

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<400> 300
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Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Xaa Asp Lys
          35          40          45
Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu
          50          55          60
Val Val Lys Leu Xaa Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp
65          70          75          80
Asn Lys Lys Arg Thr Ala Leu Xaa Lys Ala Val Gln Cys Gln Glu Asp
          85          90          95
Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro
          100          105          110
Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Xaa Tyr Asn Glu Asp
          115          120          125
Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser
          130          135          140
Lys Asn Lys Val
145

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<210> 301
 <211> 1155
 <212> DNA
 <213> Homo sapien

<400> 301

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ggcgcttctg	gagaccacga	cgactctgct	atgaagacac	tcaggaacaa	gatgggcaag	300
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gccagagagt	atgctgtttc	tagtcatcat	catgtaattt	gccagttact	ttctgactac	1080
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accagaaata	aataa					1155

<210> 302
 <211> 2000
 <212> DNA
 <213> Homo sapien

<400> 302

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<210> 303

<211> 2040

<212> DNA

<213> Homo sapien

<400> 303

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gacaagctcc	acagagctgc	ctggtggggg	aaagtcccca	gaaaggatct	catcgatcat	480
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gaaaagcaga	tagaagtggg	tgaaaaaatg	aattctgagc	tttctcttag	ttgtaagaaa	1920
gaaaaagaca	tcttgcatga	aaatagtacg	ttgcgggaag	aaattgccat	gctaagactg	1980
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<210> 304
 <211> 384
 <212> PRT
 <213> Homo sapien

<400> 304
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 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
 20 25 30
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355 360 365
 Ser Ser Glu Asn Ser Asn Pro Glu Asn Val Ser Arg Thr Arg Asn Lys
 370 375 380

<210> 305
 <211> 656
 <212> PRT
 <213> Homo sapien

<400> 305
 Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
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 20 25 30
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355 360 365
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu
 370 375 380
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys

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385          390          395          400
Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu
          405          410          415
Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn
          420          425          430
Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro
          435          440          445
Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu
          450          455          460
Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu
465          470          475          480
Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp
          485          490          495
Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu
          500          505          510
Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys
          515          520          525
Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly
          530          535          540
Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser
545          550          555          560
Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr
          565          570          575
His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln
          580          585          590
Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln
          595          600          605
Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys
          610          615          620
Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile
625          630          635          640
Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu
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<210> 306
<211> 671
<212> PRT
<213> Homo sapien

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<400> 306
Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
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Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
          20          25          30
Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
          35          40          45
His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
          50          55          60
Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
65          70          75          80
Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
          85          90          95
Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
          100          105          110
Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe

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		115					120					125						
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	130					135					140							
Arg	Ala	Ala	Trp	Trp	Gly	Lys	Val	Pro	Arg	Lys	Asp	Leu	Ile	Val	Met			
145					150					155					160			
Leu	Arg	Asp	Thr	Asp	Val	Asn	Lys	Lys	Asp	Lys	Gln	Lys	Arg	Thr	Ala			
				165					170					175				
Leu	His	Leu	Ala	Ser	Ala	Asn	Gly	Asn	Ser	Glu	Val	Val	Lys	Leu	Leu			
			180					185					190					
Leu	Asp	Arg	Arg	Cys	Gln	Leu	Asn	Val	Leu	Asp	Asn	Lys	Lys	Arg	Thr			
		195					200					205						
Ala	Leu	Ile	Lys	Ala	Val	Gln	Cys	Gln	Glu	Asp	Glu	Cys	Ala	Leu	Met			
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Leu	Leu	Glu	His	Gly	Thr	Asp	Pro	Asn	Ile	Pro	Asp	Glu	Tyr	Gly	Asn			
225					230					235					240			
Thr	Thr	Leu	His	Tyr	Ala	Ile	Tyr	Asn	Glu	Asp	Lys	Leu	Met	Ala	Lys			
				245					250					255				
Ala	Leu	Leu	Leu	Tyr	Gly	Ala	Asp	Ile	Glu	Ser	Lys	Asn	Lys	His	Gly			
			260					265					270					
Leu	Thr	Pro	Leu	Leu	Leu	Gly	Val	His	Glu	Gln	Lys	Gln	Gln	Val	Val			
		275				280						285						
Lys	Phe	Leu	Ile	Lys	Lys	Lys	Ala	Asn	Leu	Asn	Ala	Leu	Asp	Arg	Tyr			
	290					295					300							
Gly	Arg	Thr	Ala	Leu	Ile	Leu	Ala	Val	Cys	Cys	Gly	Ser	Ala	Ser	Ile			
305					310					315					320			
Val	Ser	Leu	Leu	Leu	Glu	Gln	Asn	Ile	Asp	Val	Ser	Ser	Gln	Asp	Leu			
				325					330					335				
Ser	Gly	Gln	Thr	Ala	Arg	Glu	Tyr	Ala	Val	Ser	Ser	His	His	His	Val			
			340					345					350					
Ile	Cys	Gln	Leu	Leu	Ser	Asp	Tyr	Lys	Glu	Lys	Gln	Met	Leu	Lys	Ile			
		355				360						365						
Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Gln	Asp	Leu	Lys	Leu	Thr	Ser	Glu			
	370					375					380							
Glu	Glu	Ser	Gln	Arg	Phe	Lys	Gly	Ser	Glu	Asn	Ser	Gln	Pro	Glu	Lys			
385					390					395					400			
Met	Ser	Gln	Glu	Pro	Glu	Ile	Asn	Lys	Asp	Gly	Asp	Arg	Glu	Val	Glu			
				405					410					415				
Glu	Glu	Met	Lys	Lys	His	Glu	Ser	Asn	Asn	Val	Gly	Leu	Leu	Glu	Asn			
			420					425					430					
Leu	Thr	Asn	Gly	Val	Thr	Ala	Gly	Asn	Gly	Asp	Asn	Gly	Leu	Ile	Pro			
		435					440					445				</		

Asp	Tyr	Asn	Thr	Ile	Leu	Gln	Leu	Asp	Leu	Phe	Cys	Lys	Arg	Glu	Gly
65					70					75					80
Lys	Trp	Ser	Glu	Ile	Pro	Tyr	Val	Gln	Ala	Phe	Phe	Ser	Leu	Lys	Glu
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Asn	Thr	Leu	Cys	Lys	Ala										
			100												

<210> 309
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in the lab

<400> 309
 Leu Met Ala Glu Glu Tyr Thr Ile Val
 1 5

<210> 310
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in the lab

<400> 310
 Lys Leu Met Ala Lys Ala Leu Leu Leu
 1 5

<210> 311
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in the lab

<400> 311
 Gly Leu Thr Pro Leu Leu Leu Gly Ile
 1 5

<210> 312
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in the lab

<400> 312
 Lys Leu Val Leu Asp Arg Arg Cys Gln Leu
 1 5 10

<210> 313
 <211> 1852
 <212> DNA
 <213> Homo sapiens

<400> 313
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 tgtgtctgtt gagatgctta tgtgactttg cttttaattc tgtttatgtg attatcacat 240
 ttattgactt gcctgtgtta gaccggaaga gctgggggtg ttctcaggag ccaccgtgtg 300
 ctggcgcagc ttccgggataa cttgaggctg catcactggg gaagaaacac aytccctgtcc 360
 gtggcgctga tggctgagga cagagcttca gtgtggcttc tctgcgactg gcttcttcgg 420
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 aacgtggctg cttggggaga ctacgatgac agcgccttca tggatcccag gtaccacgtc 960
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 agccagagct agaagattta tggctattga agaagaatga agaacacgga agtactcatg 1800
 tgggattccc agaaaacctg actaacgggt ccgctgctgg caatgggtgat ga 1852

<210> 314
 <211> 879
 <212> DNA
 <213> Homo sapiens

<400> 314
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 tgcaagtggg gctgccactg ctccccctgc tgcaggggga gcggcaagag caacgtgggc 180
 gcttggggag actacgatga cagcgccttc atggatccca ggtaccacgt ccatggagaa 240
 gatctggaca agctccacag agctgcctgg tggggtaaaag tccccagaaa ggatctcatc 300
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 cttaatgtcc ttgacaacaa aaagaggaca gctctgacaa aggcggtaca atgccaggaa 480
 gatgaatgtg cgttaatgtt gctggaacat ggcactgatc caaatatttc agatgagtat 540
 ggaaatacca ctctacacta tgctgtctac aatgaagata aattaatggc caaagcactg 600
 ctcttatacg gtgctgatat cgaatcaaaa aacaagcatg gcctcacacc actgctactt 660

ggtatacatg agcaaaaaaca gcaagtgggtg aaatttttta tcaagaaaaa agcgaattta 720
aatgcgctgg atagatatgg aagaactgct ctcatacttg ctgtatgttg tggatcagca 780
agtatagtca gccctctact tgagcaaaat gttgatgtat cttctcaaga tctggaaaga 840
cggccagaga gtatgctgtt tctagtcatt atcatgtaa 879

<210> 315

<211> 293

<212> PRT

<213> Homo sapiens

<400> 315

Met His Leu Ser Phe Pro Ala Phe Leu Pro Pro Trp Met Asp Arg Gly
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Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp His Asn Asp Ser Ser
20 25 30

Val Lys Thr Leu Gly Ser Lys Arg Cys Lys Trp Cys Cys His Cys Phe
35 40 45

Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val Val Ala Trp Gly Asp
50 55 60

Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr His Val His Gly Glu
65 70 75 80

Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg
85 90 95

Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Arg Asp
100 105 110

Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser
115 120 125

Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys Gln Leu Asn Val Leu
130 135 140

Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala Val Gln Cys Gln Glu
145 150 155 160

Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile
165 170 175

Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Val Tyr Asn Glu
180 185 190

Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu
195 200 205

Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Ile His Glu
210 215 220

Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu
225 230 235 240

Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys
 245 250 255

Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu Glu Gln Asn Val Asp
 260 265 270

Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu Ser Met Leu Phe Leu
 275 280 285

Val Ile Ile Met
 290

<210> 316

<211> 584

<212> DNA

<213> Homo sapiens

<400> 316

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gaggcttata actaatagga aggggagcta tagggaggct aggatatggg ggtaagctga 180
gaggtcctcc tgtgggatgt aaatttcaag ctttgcatag tgtattctcc ttcaatgaaa 240
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<212> DNA

<213> Homo sapiens

<400> 317

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专利名称(译)	用于治疗 and 诊断乳腺癌的组合物和方法		
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申请(专利权)人(译)	Corixa公司CORPORATION		
当前申请(专利权)人(译)	Corixa公司CORPORATION		
[标]发明人	FRUDAKIS TONY N SMITH JOHN M REED STEVEN G MISHER LYNDA E RETTTER MARC W DILLON DAVIN C		
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IPC分类号	G01N33/53 A61K31/711 A61K35/12 A61K35/26 A61K35/76 A61K38/00 A61K39/00 A61K39/395 A61K48/00 A61P35/00 C07K14/47 C07K14/82 C07K16/32 C07K19/00 C12N1/15 C12N1/19 C12N1/21 C12N5/06 C12N5/10 C12N15/09 C12N15/12 C12P21/02 C12Q1/68 G01N33/566 G01N33/574 C12N15 /63 C07K16/18 C12N15/62 A61K38/17 G01N33/68		
CPC分类号	C07K14/47 A61K35/12 A61K38/00 A61K39/00 A61K48/00 A61K2039/505 A61K2039/5154 A61K2039 /53 A61K2039/57 C07K2319/00		
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摘要(译)

公开了用于检测和诊断乳腺癌的组合物和方法。所提供的化合物包括首先在乳腺肿瘤组织中表达的核苷酸序列，以及由这些核苷酸序列编码的多肽。还提供了疫苗和包含这些化合物的药物组合物，并且可以用于例如预防和治疗乳腺癌。多肽还可以用于产生抗体，其可用于诊断和监测患者中乳腺癌的进展。