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(54) **MARKER AND REAGENT FOR DETECTION OF HUMAN IL-17-PRODUCING HELPER T CELLS, AND METHOD FOR DETECTION OF HUMAN IL-17-PRODUCING HELPER T CELLS**

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Jul. 29, 2009 (JP) 2009-176755

(51) **Int. Cl.**

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C12Q 1/68	(2006.01)
C07K 14/54	(2006.01)
G01N 33/50	(2006.01)
G01N 33/68	(2006.01)

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

CPC ***C12Q 1/6888*** (2013.01); ***C07K 14/54*** (2013.01); ***C12Q 1/6881*** (2013.01); ***G01N 33/505*** (2013.01); ***G01N 33/68*** (2013.01); *C12Q 2600/158* (2013.01); *G01N 2333/54* (2013.01)

(58) **Field of Classification Search**

None

See application file for complete search history.

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(57) **ABSTRACT**

The present invention relates to a marker allowing specific detection of human IL-17-producing helper T-cells (human Th17 cells), a method for specifically detecting human Th17 cells and a reagent for detecting human Th17 cells.

6 Claims, 3 Drawing Sheets

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FIG. 1

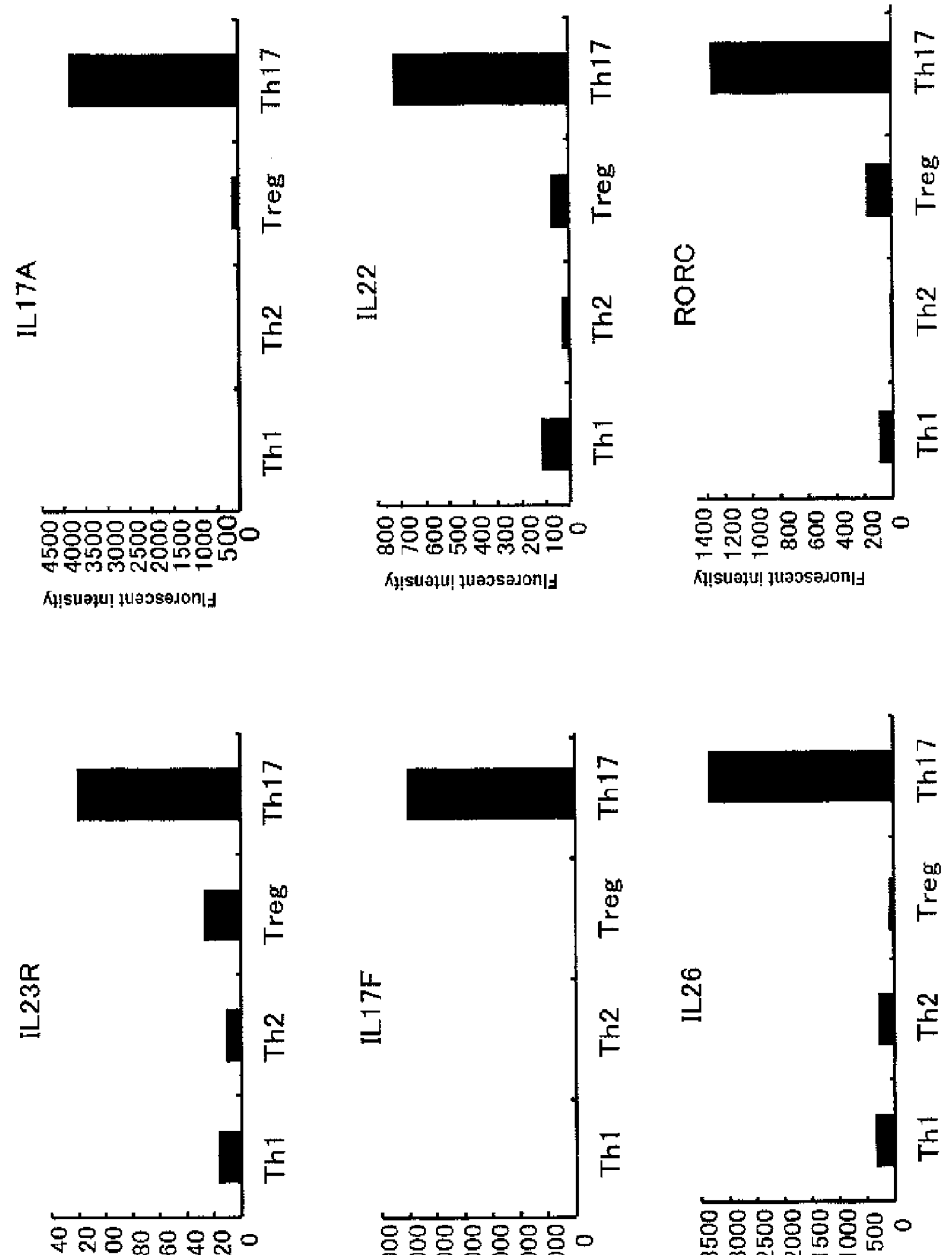

IL23R
Fluorescent intensity
140
120
100
80
60
40
20
0
Th1
Th2
Treg
Th17
IL17A
Fluorescent intensity
4500
4000
3500
3000
2500
2000
1500
1000
500
0
Th1
Th2
Treg
Th17
IL17F
Fluorescent intensity
7000
6000
5000
4000
3000
2000
1000
0
Th1
Th2
Treg
Th17
IL22
Fluorescent intensity
800
700
600
500
400
300
200
100
0
Th1
Th2
Treg
Th17
IL26
Fluorescent intensity
3500
3000
2500
2000
1500
1000
500
0
Th1
Th2
Treg
Th17
RORC
Fluorescent intensity
1400
1200
1000
800
600
400
200
0
Th1
Th2
Treg
Th17

FIG. 2

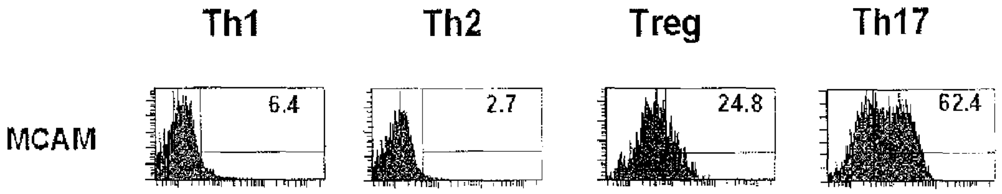


FIG. 3

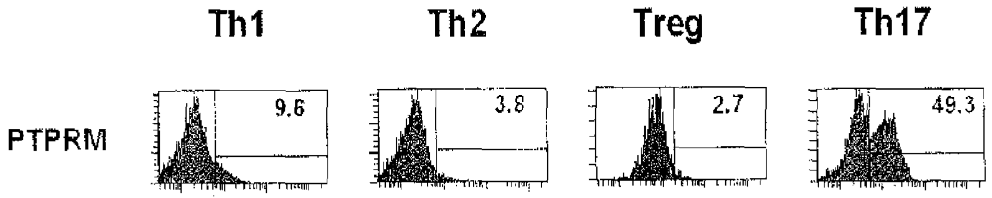


FIG. 4

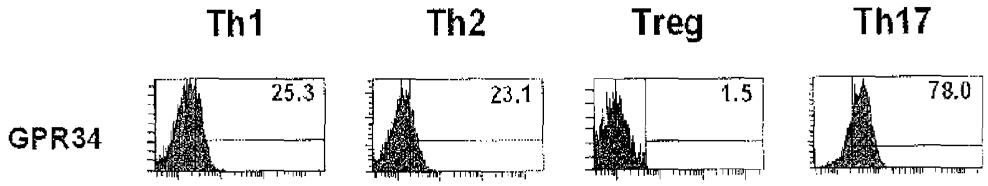


FIG. 5

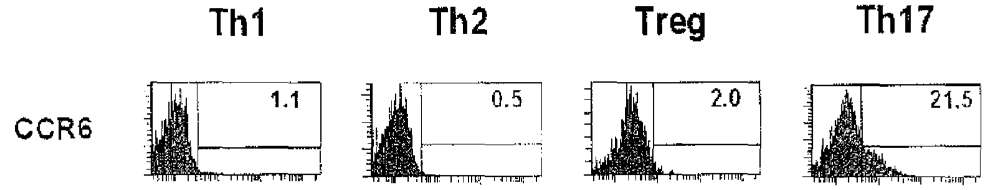


FIG. 6

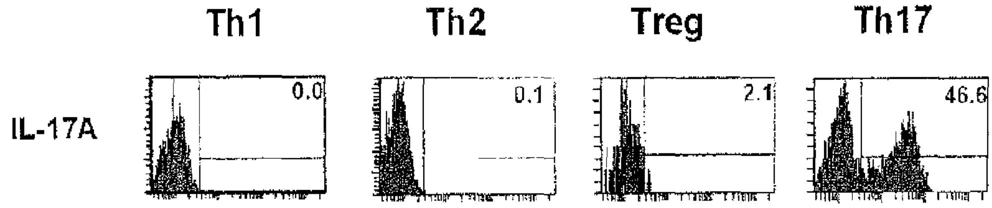


FIG. 7

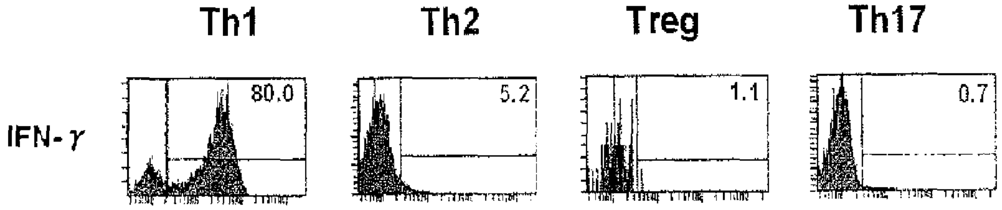


FIG. 8

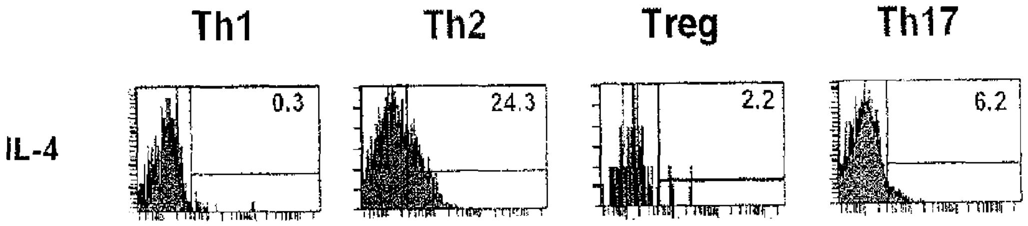
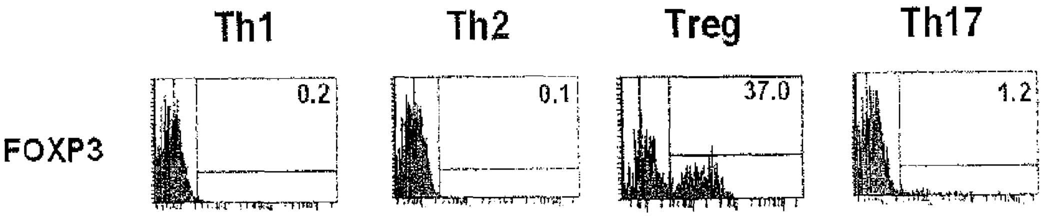

Th1
Th2
Treg
Th17
IL-4
0.3
24.3
2.2
6.2

FIG. 9


Th1
Th2
Treg
Th17
FOXP3
0.2
0.1
37.0
1.2

MARKER AND REAGENT FOR DETECTION OF HUMAN IL-17-PRODUCING HELPER T CELLS, AND METHOD FOR DETECTION OF HUMAN IL-17-PRODUCING HELPER T CELLS

CROSS REFERENCE TO RELATED APPLICATIONS

This is a divisional of U.S. patent application Ser. No. 13/360,324, filed Jan. 27, 2012, which is a continuation of International Application PCT/JP2010/062807 filed Jul. 29, 2010, which claims benefit of JP 2009-176755, filed Jul. 29, 2009, all of which are incorporated herein by reference in their entirety.

BACKGROUND OF THE INVENTION

1. Field of the Invention

The present invention relates to a marker and reagent for detecting human IL-17-producing helper T-cells (hereinafter also referred to as "Th17 cells") and a method for detecting human Th17 cells.

2. Description of the Related Art

Rheumatoid arthritis (hereinafter referred to as "RA") is the systemic inflammatory autoimmune disease whose main clinical symptom is arthritis. The state of RA is diagnosed by rational symptoms such as joint pain or by visual procedures such as the observations on the extent of swelling or bone X-ray. However, no quantitative index has been established. Thus, no quantitative method for continuously monitoring the treatment effects has been established under the current state of the art.

The pathogenesis of RA has not been elucidated. It is considered that bacterial infections and the like trigger an inflammation in joint tissues via complicated networks of immunocytes and cytokines.

Helper T-cells play a central role in immune reactions. Immature helper T-cells (naïve T-cells) are differentiated into helper T-cells when an antigen is presented by antigen-presenting cells. When specific cytokines are present at this time, naïve T-cells are differentiated into four types of the cells, which are helper T-cells producing interferon (IFN)-γ (Th1 cells), helper T-cells producing interleukin (IL)-4 (Th2 cells), helper T-cells producing IL-17 (Th17 cells) and regulatory T-cells having immunosuppressive effects (Treg cells).

It has been shown that among these helper T-cells, Th17 cells can be involved in the onset of RA.

It has been suggested that IL-17 is deeply involved in the formation of pathological conditions and in particular joint and bone deformities because the level of IL-17 is significantly higher in synovial fluid of RA patients than in that of the patients of osteoarthritis and T-cells in synovial tissue from RA patients include IL-17 positive cells (see Japanese Unexamined Patent Publication No. 2000-186046). Japanese Unexamined Patent Publication No. 2000-186046 also discloses that IL-17 can be used as a diagnostic marker of RA.

Japanese Unexamined Patent Publication No. 2007-506100 discloses that the analysis of cytokines in peripheral blood serum of RA patients revealed that the levels of IFN-γ, IL-1β, TNF-α, G-CSF, GM-CSF, IL-6, IL-4, IL-10, IL-13, IL-5 and IL-7 were significantly high and the levels of IL-2, CXCL8/IL-8, IL-12 and CCL2/MCP-1 were not high in RA patients.

According to the studies by Ivanov et al. ("The Orphan Nuclear Receptor RORγt Directs the Differentiation Program of Proinflammatory IL-17+ T Helper Cells", Cell, 2006, 126, p. 1121-1133), Stumhofer et al. ("Interleukin 27 negatively regulates the development of interleukin 17-producing T helper cells during chronic inflammation of the central nervous system", Nature Immunology, 2006, vol. 7, p. 937-945), and Wilson et al. ("Development, cytokine profile and function of human interleukin 17-producing helper T cells", Nature Immunology, 2007, vol. 8, p. 950-95'7), the following facts have been shown about Th17 cells:

- a nuclear receptor called RORγt has an important role in the differentiation of Th17 cells;
- IL-6, IL-23 and TGF-β induce the differentiation of immature helper T-cells (naïve T-cells) to Th17 cells;
- they express IL-17A, IL-17F, IL-6, IL-22, IL-26, TNF, IFN-γ and CCL20; and
- IL-23 receptor and IL-12 receptor β are located on the surface of Th17 cells.

SUMMARY OF THE INVENTION

In the above documents by Ivanov et al., Stumhofer et al. and Wilson et al., the amount of IL-17 is measured by enzyme linked immunosorbent assay (ELISA) using antibodies specific to IL-17.

The relations between Th17 cells and autoimmune diseases, preferably RA may be more deeply understood by establishing a method which allows not only measurement of the amount of IL-17 but also detection of Th17 cells per se.

The present inventors aimed to find molecular markers that allows specific detection of human Th17 cells.

The present inventors isolated Th17 cells from peripheral blood of a healthy adult and identified the genes which are specifically expressed in the obtained Th17 cells, thereby completing the present invention.

Thus, the present invention provides a polynucleotide marker for detecting human Th17 cells which is a polynucleotide having a nucleic acid sequence of at least one gene selected from the group consisting of:

- genes encoding membrane proteins consisting of: ADAM12 (ADAM metallopeptidase domain 12), ANKS1B (ankyrin repeat and sterile alpha motif domain containing 1B), ATP6V0A4 (ATPase, H+ transporting, lysosomal V0 subunit a4), ATP9A (ATPase, class II, type 9A), BVES (blood vessel epicardial substance), C5orf40 (chromosome 5 open reading frame 40), CDH4 (cadherin 4, type 1, R-cadherin (retinal)), DIO2 (deiodinase, iodothyronine, type II), DMD (dystrophin), GPR34 (G protein-coupled receptor 34), IRS2 (insulin receptor substrate 2), KCNE3 (potassium voltage-gated channel, Isk-related family, member 3), L1CAM (L1 cell adhesion molecule), MCAM (melanoma cell adhesion molecule), MFAP3L (microfibrillar-associated protein 3-like), MYO7A (myosin VIIA), PTPRM (protein tyrosine phosphatase, receptor type, M), SHROOM2 (shroom family member 2), SLC16A4 (solute carrier family 16, member 4 (monocarboxylic acid transporter 5)), SLCO2B1 (solute carrier organic anion transporter family, member 2B1), TANC2 (tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2), TJP1 (tight junction protein 1 (zona occludens 1)), TMEM163 (transmembrane protein 163), TNS3 (tensin 3), UPK1B (uroplakin 1B), WDFY3 (WD repeat and FYVE domain containing 3), DRD2 (dopamine receptor D2), GJC1 (gap junction protein, gamma 1, 45 kDa), PGBD5 (LOC100134440) (piggyBac transposable element derived 5 (similar to PGBD5 protein)), MS4A 7 (membrane-spanning 4-domains, subfamily A, member 7), ODZ4 (odz, odd Oz/ten-m homolog 4), PHKA1 (phosphorylase kinase, alpha 1), RGS1 (regulator of G-protein signaling 1), SHB (Src homology 2 domain containing adaptor protein B), SLC44A3 (solute carrier family 44, member 3), SLC6A15 (solute carrier family 6 (neutral amino acid transporter), member 15), SYNGR3 (synaptogyrin 3), AKAP12 (A kinase (PRKA) anchor protein 12), C9orf125 (chromosome 9 open reading frame 125), DPY19L2 (dpy-19-like 2), HRH4 (histamine receptor H4), MUC20 (mucin 20, cell surface associated), POPDC3 (popeye domain containing 3), SORBS1 (sorbin and SH3 domain containing 1), TANC1 (tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1), TMEM44 (transmembrane protein 44) and UNC13C (unc-13 homolog C);

genes encoding secretory proteins consisting of: CXCL13 (chemokine (C—X—C motif) ligand 13), PCOLCE2 (procollagen C-endopeptidase enhancer 2), PNOC (prepronociceptin), SMPDL3A (sphingomyelin phosphodiesterase, acid-like 3A), TGFBI (transforming growth factor, beta-induced), C17orf99 (chromosome 17 open reading frame 99), EBI3 (Epstein-Barr virus induced 3), IL1A (interleukin 1, alpha) and WNT3 (wingless-type MMTV integration site family, member 3);

genes encoding intracellular proteins consisting of: BCAT1 (branched chain aminotransferase 1, cytosolic), BHLHE22 (basic helix-loop-helix family, member e22), C13orf18 (LOC728970) (chromosome 13 open reading frame 18 (hypothetical LOC728970)), CA2 (carbonic anhydrase II), CCDC3 (coiled-coil domain containing 3), CDS1 (CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1), CHN1 (chimerin (chimaerin) 1), CLIC5 (LOC100131610) (chloride intracellular channel 5 (similar to chloride intracellular channel 5)), CTSH (cathepsin H), CYP7B1 (cytochrome P450, family 7, subfamily B, polypeptide 1), DAPK2 (death-associated protein kinase 2), DMRT1 (doublesex and mab-3 related transcription factor 1), DSE (dermatan sulfate epimerase), FBXL17 (F-box and leucine-rich repeat protein 17), FBXL21 (F-box and leucine-rich repeat protein 21), FHOD3 (formin homology 2 domain containing 3), H2AFY2 (H2A histone family, member Y2), HLX (H2.0-like homeobox), IRAK3 (interleukin-1 receptor-associated kinase 3), MACC1 (metastasis associated in colon cancer 1), MAML3 (mastermind-like 3), MYO10 (myosin X), OTUB2 (OTU domain, ubiquitin aldehyde binding 2), PAPSS2 (3'-phosphoadenosine 5'-phosphosulfate synthase 2), PCBP3 (Poly (rC) binding protein 3 (PCBP3), transcript variant 2), PDE4DIP (phosphodiesterase 4D interacting protein), PLD1 (phospholipase D1, phosphatidylcholine-specific), PPARG (peroxisome proliferator-activated receptor gamma), PTPN13 (Protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)), RGS18 (regulator of G-protein signaling 18), SIM1 (single-minded homolog 1), SNAI2 (snail homolog 2), SOX2 (SRY (sex determining region Y)-box 2), SPIRE1 (spire homolog 1), TBC1D12 (TBC1 domain family, member 12), TGM5 (transglutaminase 5), TMOD1 (tropomodulin 1), TUBB6 (tubulin, beta 6), DDIT4L (DNA-damage-inducible transcript 4-like), DHRS9 (dehydrogenase/reductase (SDR family) member 9), ERC2 (ELKS/RAB6-interacting/CAST family member 2), FERMT2 (fermitin family homolog 2), HHEX (hematopoietically expressed homeobox), HS3ST1 (heparan sulfate (glucosamine) 3-O-sulfotransferase 1), NR5A2 (nuclear receptor subfamily 5, group A, member 2), PHLDA1 (pleckstrin homology-like domain, family A, member 1), RBM20 (RNA binding motif protein 20), NINL (ninein-like), RTN2 (reticulon 2), SH3RF2 (SH3 domain containing ring finger 2), TSHZ2 (teashirt zinc finger homeobox 2), EML1 (echinoderm microtubule associated protein like 1), HIST1H2BC (histone cluster 1, H2bc), MAP3K4 (mitogen-activated protein kinase kinase kinase 4), PDK4 (pyruvate dehydrogenase kinase, isozyme 4), RGS2 (regulator of G-protein signaling 2) and RGS20 (regulator of G-protein signaling 20);

genes consisting of: C1orf106 (chromosome 1 open reading frame 106), C6orf145 (chromosome 6 open reading frame 145), LOC401097 (Similar to LOC166075), MAMLD1 (mastermind-like domain containing 1), ZC3H12C (zinc finger CCCH-type containing 12C), C12orf64 (chromosome 12 open reading frame 64), C6orf168 (chromosome 6 open reading frame 168), CAMSAP1L1 (calmodulin regulated spectrin-associated protein 1-like 1) and MAGED4 (MAGED4B) (melanoma antigen family D, 4, (melanoma antigen family D, 4B)); and

genes comprising at least one nucleic acid sequence selected from SEQ ID NOs:147 to 151, 157 to 162 and 167 to 174;

or a variant and fragment thereof.

The present invention also provides a protein marker for detecting human Th17 cells which is a protein encoded by at least one of the above genes or a functionally equivalent variant and fragment thereof.

The present invention further provides a method for detecting human Th17 cells comprising detecting the presence of at least one polynucleotide marker for detecting human Th17 cells or at least one protein marker for detecting human Th17 cells in a sample containing cells derived from human.

In addition, the present invention provides a reagent for detecting human Th17 cells comprising at least one substance selected from a nucleic acid probe which specifically hybridizes to the above polynucleotide marker; and a nucleic acid aptamer, antibody, ligand or receptor which specifically binds to the above protein marker.

Human Th17 cells can be specifically detected by detecting at least one polynucleotide marker or protein marker for detecting human Th17 cells of the present invention. It may also allow detection of the possibility that a patient has a disease in which Th17 cells may be involved such as autoimmune diseases, e.g. RA.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. **1** shows graphs of the expression levels of the genes which are known to be specifically expressed in Th17 cells (IL23R, IL17A, IL17F, IL22, IL26 and RORC) in Th1, Th2, Treg and Th17 cells;

FIG. **2** shows histograms of fluorescent intensity obtained by the analysis of MCAM measurement samples;

FIG. **3** shows histograms of fluorescent intensity obtained by the analysis of PTPRM measurement samples;

FIG. **4** shows histograms of fluorescent intensity obtained by the analysis of GPR34 measurement samples;

FIG. **5** shows histograms of fluorescent intensity obtained by the analysis of CCR6 measurement samples;

FIG. **6** shows histograms of fluorescent intensity obtained by the analysis of IL-17A measurement samples;

FIG. **7** shows histograms of fluorescent intensity obtained by the analysis of IFN-γ measurement samples;

FIG. **8** shows histograms of fluorescent intensity obtained by the analysis of IL-4 measurement samples; and

FIG. **9** shows histograms of fluorescent intensity obtained by the analysis of FOXP3 measurement samples.

DETAILED DESCRIPTION OF THE EMBODIMENTS

The polynucleotide marker for detecting human Th17 cells of the present invention is the polynucleotide having a nucleic acid sequence of at least one gene selected from the group consisting of the above genes, or a variant and fragment thereof.

Preferably, the polynucleotide has a nucleic acid sequence of at least one gene selected from the group consisting of:

genes encoding membrane proteins consisting of: ADAM12, ATP6V0A4, ATP9A, BVES, C5orf40, CDH4, DIO2, GPR34, L1CAM, MCAM, PTPRM, SHROOM2, TMEM163, UPK1B, DRD2, PGBD5 (LOC100134440), ODZ4, SLC6A15, AKAP12, C9orf125, POPDC3 and UNC13C;

genes encoding secretory proteins consisting of: PCOLCE2, PNOC, TGFBI and IL1A; and

genes encoding intracellular proteins consisting of: BHLHE22, PPARG, SIM1 and SNAI2.

The present polynucleotide marker for detecting human Th17 cells is the polynucleotide, variant or fragment thereof which has been found to be specifically present in Th17 cells rather than in other helper T-cells derived from human peripheral blood (Th1, Th2 and Treg cells).

Therefore, by detecting at least one of the above polynucleotide markers, Th17 cells can be distinguished from Th1, Th2 and Treg cells and specifically identified, and an index for activity of diseases in vivo can be studied in which Th17 cells may be involved.

As used herein, the term "gene" has the same meaning as that is commonly recognized in the art, and refers to a part of a genome which is transcribed into mRNA and translated into a protein.

In the present specification, genes containing at least one nucleic acid sequence selected from SEQ ID NOs: 147 to 151, 157 to 162 and 167 to 174 are the genes to be transcribed into mRNAs containing at least one of these nucleic acid sequences or a complementary sequence thereof. Thus, genes containing at least one nucleic acid sequence selected from SEQ ID NOs: 147 to 151, 157 to 162 and 167 to 174 comprise genes containing a nucleic acid sequence complementary to at least one nucleic acid sequence selected from SEQ ID NOs: 147 to 151, 157 to 162 and 167 to 174.

As used herein, a membrane protein means a protein existing in a cell membrane and being contained in a membrane fraction of cells. A secretory protein means a protein synthesized in cells and secreted to the outside of the cell membrane. An intracellular protein means a protein which is mainly present in cells.

As used herein, the phrase that a polynucleotide is "specifically expressed" in Th17 cells means that the expression level of the polynucleotide in Th17 cells is significantly higher than the expression level of the polynucleotide in cells other than Th17 cells.

Specifically, it means that the expression level of the polynucleotide in Th17 cells is about two times or more of the expression level of the polynucleotide in cells other than Th17 cells. Preferably, the expression level of the polynucleotide in Th17 cells is about two times or more of the expression level of the polynucleotide in helper T-cells other than Th17 cells (Th1, Th2 and Treg cells).

The nucleotide sequences of the present polynucleotide markers are already known. They can be obtained from, for example, Unigene (a database provided by National Center for Biotechnology Information (NCBI) of National Library of Medicine). Unigene codes for the nucleic acid sequences of the present polynucleotide markers are specified in Table 9.

As used herein, "variant" of a polynucleotide means a polynucleotide into which a mutation has been introduced that does not alter the nature of the protein encoded by the above gene. Such mutation includes a deletion, substitution or addition of one or more nucleotides to the nucleic acid sequence of the above gene.

As used herein, "fragment" of a polynucleotide means a polynucleotide having a contiguous part of the nucleic acid sequence of the above gene and having a length which allows its specific hybridization with a nucleic acid probe for detecting human Th17 cells described hereinafter.

The variant of the polynucleotide as the present polynucleotide marker for detecting human Th17 cells has generally at least 80%, more preferably at least 85%, further preferably at least 90% and particularly preferably at least 95% homology with the nucleic acid sequence of the above gene.

As used herein, the homology of nucleic acid and amino acid sequences is calculated in BLASTN, BLASTP, BLASTX or TBLASTN (e.g. available from http://www.ncbi.nlm.nih.gov) with default settings.

The polynucleotide marker may be any of DNA or RNA, and may be the gene per se (DNA), mRNA, cDNA or cRNA.

Human Th17 cells can also be detected by detecting at least one protein encoded by the above gene. Thus, the present invention also provides the protein marker for detecting human Th17 cells consisting of the protein encoded by at least one of the above genes or a functionally equivalent variant and fragment thereof.

Preferably, the above protein is encoded by at least one gene selected from the group consisting of:

genes encoding membrane proteins consisting of: ADAM12, ATP6V0A4, ATP9A, BVES, C5orf40, CDH4, DIO2, GPR34, L1CAM, MCAM, PTPRM, SHROOM2, TMEM163, UPK1B, DRD2, PGBD5 (LOC100134440), ODZ4, SLC6A15, AKAP12, C9orf125, POPDC3 and UNC13C;

genes encoding secretory proteins consisting of: PCOLCE2, PNOC, TGFBI and IL1A; and

genes encoding intracellular proteins consisting of: BHLHE22, PPARG, SIM1 and SNAI2.

More preferably, the above protein is a membrane protein encoded by at least one gene selected from the group consisting of GPR34, MCAM and PTPRM.

The amino acid sequence of such protein marker can be obtained based on the nucleic acid sequence of the polynucleotide marker obtained from Unigene and the like. It can also be obtained from databases provided by NCBI and the like. NCBI code numbers for the amino acid sequences of the present protein markers for detecting human Th17 cells are specified in Table 9.

The protein marker for detecting human Th17 cells is the protein encoded by the above gene, a functionally equivalent variant or fragment thereof.

As used herein, "functionally equivalent variant" of a protein means a protein into which a mutation has been introduced that does not alter functions of the protein. Such mutation includes a deletion, substitution or addition of one or more amino acids to the known amino acid sequence of the protein.

As used herein, "fragment" of a protein means a protein having a contiguous amino acid sequence of the protein encoded by the above gene or a functionally equivalent variant thereof and being able to specifically bind to a nucleic acid aptamer, antibody, ligand or receptor for detecting human Th17 cells described hereinafter.

The functionally equivalent variant of the protein corresponding to the present protein marker for detecting human Th17 cells has generally at least 80%, preferably at least 85%, more preferably at least about 90% and particularly preferably at least 95% homology with the known amino acid sequence of the protein encoded by the above gene.

A molecule that can specifically hybridize to the present polynucleotide marker can be used for detection of the marker, making it useful as a probe for detecting human Th17 cells. The probe may be a nucleic acid probe such as DNA or RNA, or a peptide probe that can specifically hybridize to the polynucleotide marker. The probe for detecting human Th17 cells is preferably a nucleic acid probe, particularly a DNA probe for detecting the polynucleotide marker.

As used herein, the phrase "can specifically hybridize" means that it can hybridize to a target nucleic acid molecule (the polynucleotide marker) under a stringent condition.

As used herein, "stringent condition" means a condition under which the probe for detecting human Th17 cells can hybridize to the target polynucleotide marker with a detectably higher extent than it does to a polynucleotide other than the target polynucleotide marker (e.g. more than at least two times of the background).

The stringent condition generally depends on the sequences and varies depending on various circumstances. Generally, the stringent condition is selected so that it is about 5° C. lower than a thermal melting point of the specific sequence under a certain ionic strength and pH. This Tm is a temperature at which 50% of the complementary probe hybridizes to the target sequence in equilibrium (under a certain ionic strength, pH and nucleic acid composition).

Such condition may be those which are used in conventional hybridization techniques between polynucleotides such as PCR, microarray or Southern blotting.

Specifically, it may be a condition of pH 7.0 to 9.0, a salt concentration of lower than about 1.5M Na-ion, more specifically about 0.01 to 1.0 M Na-ion concentration (or other salt) and a temperature of at least about 30° C. More specifically, the stringent condition in microarray technique includes the hybridization at 37° C. in 50% formamide, 1M NaCl and 1% SDS and washing at 60 to 65° C. in 0.1×SSC.

The stringent condition in PCR technique includes a condition of pH 7 to 9, 0.01 to 0.1 M Tris-HCl, 0.05 to 0.15 M potassium ion concentration (or other salt) and at least about 55° C.

The sequence of the nucleic acid probe for detecting human Th17 cells can be appropriately selected by a person skilled in the art based on the common technical knowledge in the art and the sequence of the polynucleotide marker so that it can specifically hybridize to the polynucleotide marker.

The nucleic acid probe for detecting human Th17 cells can be designed by using, for example, a commonly available primer designing software (e.g. Primer3 (available from frodo.wi.mit.edu/cgi-bin/primer3/primer3.cgi) or DNASIS Pro (Hitachi Software Engineering Co., Ltd.)).

The nucleic acid probe for detecting human Th17 cells can be prepared according to polynucleotide synthesis methods which are well-known in the art.

The nucleic acid probe for detecting human Th17 cells may be labeled with a labeling substance normally used in the art. The labeled nucleic acid probe allows an easy detection of the polynucleotide marker for detecting human Th17 cells, namely of human Th17 cells.

The labeling substance may be a labeling substance generally used in the art including radioisotopes such as ^{32}P, fluorescent substances such as fluorescein, enzymes such as alkaline phosphatase and horseradish peroxidase, and biotin.

Human Th17 cells can be specifically detected by using one or more nucleic acid probes for detecting human Th17 cells. For example, a DNA chip or microarray for detecting the polynucleotide marker for detecting human Th17 cells can be obtained by immobilizing one or more probes on a substrate according to a method well-known in the art.

The nucleic acid probe for detecting human Th17 cells may include a set of two or more primers for amplifying the polynucleotide marker by nucleic acid amplification methods such as PCR technique, for example.

A molecule that can specifically bind to the present protein marker can be used for the detection of the marker, making it useful in the detection of human Th17 cells. Such molecule may be a nucleic acid aptamer such as DNA or RNA, an antibody, a ligand or a receptor that can specifically bind to the present protein marker, and preferably an antibody.

When the protein marker for detecting human Th17 cells is an enzyme, it can be detected by applying a substrate for the enzyme to develop color or emit light or fluorescent.

The antibody for detecting human Th17 cells can be prepared by the following well-known procedure, for example. A DNA molecule encoding a protein having an amino acid sequence of the present protein marker is prepared based on the nucleic acid sequence of the present polynucleotide marker or the amino acid sequence of the present protein marker, and is introduced into an appropriate expression vector. The obtained expression vector is introduced into an appropriate host cells, and the obtained transformed cells are cultured to obtain a desired protein. The obtained protein is purified and used as an immunogen optionally with an adjuvant to immunize an appropriate mammal such as rat or mouse. Spleen cells of the immunized animals are screened for antibody producing cells that produce an antibody directed to the target immunogen. The selected antibody producing cells are fused with myeloma cells to obtain hybridomas. These hybridomas are screened for antibody producing hybridomas that produce an antibody having specific binding property to the protein encoded by the gene. The desired antibody can be obtained by culturing the obtained antibody producing hybridomas.

The nucleic acid aptamer that can be used for detecting human Th17 cells can be prepared by the following well-known procedure, for example. A nucleic acid library including random nucleic acid sequences is prepared according to the known technique, and an aptamer that specifically binds to the target protein (the protein marker) can be selected by the systematic evolution of ligands by exponential enrichment method (SELEX method) or the like.

The molecule which can specifically bind to the protein marker for detecting human Th17 cells may be labeled with a labeling substance normally used in the art. The labeled antibody for detecting human Th17 cells allows an easy detection of the protein marker for detecting human Th17 cells, namely of human Th17 cells.

The labeling substance may be a labeling substance generally used in the art including radioisotopes such as ^{32}P, fluorescent substances such as fluorescein, enzymes such as alkaline phosphatase and horseradish peroxidase, and biotin.

A method for detecting human Th17 cells by detecting the presence of at least one polynucleotide or protein marker for detecting human Th17 cells in a sample containing cells derived from human is also within the scope of the present invention.

In the method, it is preferred that two or more polynucleotide markers or protein markers for detecting human Th17 cells are detected in order to improve the detection sensitivity.

In the present method, the sample containing cells derived from human includes a biological sample obtained from human or a sample containing cultured human cells. The biological sample includes blood, tissue, synovial fluid, cerebrospinal fluid, pleural fluid, ascitic fluid and the like.

An embodiment of the method for detecting the presence of the polynucleotide marker for detecting human Th17 cells is described.

Nucleic acid (DNA or RNA) is extracted from a sample containing cells derived from human by a well-known method in the art such as the one using a phenolic extraction and ethanol precipitation or a commercial DNA extraction kit.

Then, the presence of the polynucleotide marker in the obtained nucleic acid sample is detected, preferably using the nucleic acid probe for detecting human Th17 cells. When the presence of the polynucleotide marker is detected by nucleic acid amplification method such as PCR, RT-PCR, real-time PCR, LAMP (Loop-mediated isothermal amplification) and the like, the nucleic acid probe for detecting human Th17 cells is preferably a primer set for amplifying the polynucleotide marker by a nucleic acid amplification method.

The presence of the polynucleotide marker for detecting human Th17 cells may also be detected by well-known methods in the art, for example hybridization methods such as Southern hybridization, Northern hybridization, fluorescence in situ hybridization (FISH), or DNA chip or microarray. Such methods are carried out under the stringent condition, and the hybridization of the nucleic acid probe for detecting human Th17 cells is detected by detecting the labeling substance and the like to detect the presence of the polynucleotide marker.

An embodiment of the method for detecting the presence of the protein marker for detecting human Th17 cells is described.

When the target protein marker is an intracellular protein, proteins are extracted from a sample containing cells derived from human by using well-known methods in the art. The extraction of proteins from a sample can be accomplished by known methods such as disruption of the cells by ultrasonic, lysis of the cells with a cell lysis solution. The protein marker in the obtained protein extract can be detected by using the molecule which specifically binds to the protein marker. Specifically, the protein marker for detecting human Th17 cells can be detected by well-known methods in the art such as ELISA or Western blotting. The molecule which specifically binds to the protein marker in the detection is preferably the above nucleic acid aptamer, antibody, ligand or receptor, and more preferably the antibody for detecting human Th17 cells.

When the target protein marker is a secretory protein, the protein marker secreted in the sample containing the cells can be detected by using the molecule which specifically binds to the protein marker.

Alternatively, the cells (lymphocytes) are recovered from the sample containing the cells from human and the obtained cells are stimulated with anti-CD3 antibody, anti-CD28 antibody, concanavalin A, phytohemagglutinin (PHA), phorbol myristate acetate (PMA), ionomycin or the like. Then, the secreted protein marker can be detected by using the molecule which specifically binds to the protein marker.

Specifically, the protein marker can be detected by well-known methods in the art such as ELISA or Western blotting. The molecule which specifically binds to the protein marker in the detection is preferably the above nucleic acid aptamer, antibody, ligand or receptor, and more preferably the antibody for detecting human Th17 cells.

When the target protein marker is a protein located on the cell surface, the protein marker located on the cell surface in the sample containing the cells derived from human can be detected by using the molecule which specifically binds to the protein marker.

Alternatively, a membrane fraction of the cells is obtained from the sample containing the cells derived from human and the protein marker in the membrane fraction can be detected by using the molecule which specifically binds to the protein marker. Specifically, the protein marker can be detected by well-known methods in the art such as ELISA, Western blotting or a method based on flow cytometry (FCM). The molecule which specifically binds to the protein marker in the detection is preferably the above nucleic acid aptamer, antibody, ligand or receptor, and more preferably the antibody for detecting human Th17 cells.

For example, the protein marker for detecting human Th17 cells can be detected by FCM as follows.

First, the sample containing the cells derived from human is brought into contact with the antibody for detecting human Th17 cells labeled with an appropriate labeling substance. Human Th17 cells, when exist, bind to the labeled antibody on their surfaces. Then, the sample containing the cells bound to the labeling substance can be applied to a flow cytometer to detect human Th17 cells. Human Th17 cells that have bound to the labeling substance can optionally be classified and fractionated by using a cell sorter.

Such method of FCM is well-known to a person skilled in the art and he can appropriately select the reaction conditions.

The present invention also provides a reagent for detecting human Th17 cells which can be used in the present method for detecting human Th17 cells

The reagent comprises at least one substance selected from a nucleic acid probe which specifically hybridizes to the polynucleotide marker for detecting human Th17 cells, and a nucleic acid aptamer, antibody, ligand and receptor which specifically binds to the protein marker for detecting human Th17 cells.

The present invention is now described in detail by way of Examples, which do not limit the present invention.

EXAMPLE 1

Analysis of Highly Expressed Genes in Cultured Th17 Cells Derived from Human Peripheral Blood

1. Isolation of Th1, Th2, Treg and Th17 Cells from Human Peripheral Blood

(1) Isolation of Th1, Th2 and Th17 Cells from Human Peripheral Blood

Buffy coat obtained from peripheral blood of a healthy adult was overlaid on Ficoll-paque plus solution (GE Healthcare Bioscience) and centrifuged to obtain a monocyte fraction. Crude CD4 positive cells were purified from the fraction by using magnetic beads bound to anti-CD4 antibody (Miltenyi Biotec).

The obtained CD4 positive cells were stained with the fluorescence labeled antibodies shown in Table 1 and then Th1, Th2 and Th17 cells were separated by a cell sorter (FACS Aria: Becton Dickinson). The separation was carried out with the gating shown in Table 2.

TABLE 1

Antigen	Fluorescence labeling substance	Clone	Manufacturer
CD4	APC-Cy7	RPA-T4	BD Biosciences
CD25	PE-Cy7	BC96	eBioscience
CXCR3	Alexa Fluor ™ 488	1C6/CXCR3	BD Biosciences
CCR4	APC	FAB1567A	R&D systems
CCR6	PE	11A9	BD Biosciences

TABLE 2

Cell	Gating
Th1	$CD4^{high}$ $CD25^{low\text{-}negative}$ $CXCR3^{+}$ $CCR6^{-}$ $CCR4^{-}$
Th2	$CD4^{high}$ $CD25^{low\text{-}negative}$ $CXCR3^{-}$ $CCR6^{-}$ $CCR4^{+}$
Th17	$CD4^{high}$ $CD25^{low\text{-}negative}$ $CXCR3^{-}$ $CCR6^{+}$ $CCR4^{+}$

The above gating is described in detail in the reference by Acosta-Rodriguez E V et al. (Surface phenotype and antigenic specificity of human interleukin 17-producing T helper memory cells, Nat Immunol., 2007, vol. 8, p. 639-646).

(2) Isolation of Treg Cells from Human Peripheral Blood

CD4 positive cells obtained in the same manner as the above (1) were stained with the fluorescence labeled antibodies shown in Table 3, and CD4high CD25high CD127internal-negative cells were purified as Treg cells by using the above cell sorter.

TABLE 3

Antigen	Fluorescence Labeling substance	Clone	Manufacturer
CD4	FITC	OKT4	eBioscience
CD25	PE-Cy7	BC96	eBioscience
GD45RO	PE	UCHL1	BioLegend
CD127	Alexa Fluor ™ 647	HIL-7R-M21	BD Biosciences

The above gating is described in detail in the reference by Weihong Liu et al. (CD 127 expression inversely correlates with FoxP3 and suppressive function of human CD4+ T reg cells, J Exp Med. 2006, vol. 203, p. 1701-1711).

2. Cell Culture

(1) Th1, Th2 and Th17 Cell Cultures

Th1, Th2 and Th17 cells derived from adult peripheral blood obtained in the above step 1. (1) were respectively plated in a 96-well plate at the density of 1.5×10^5 cells/0.3 ml/well. The medium used was Yssel medium (IMDM, 1% human serum of AB-type, 0.25% BSA, 1.8 mg/l 2-aminomethanol, 40 mg/l transferrin, 5 mg/l insulin, 2 mg/l linoleic acid, 2 mg/l oleic acid, 2 mg/l palmitic acid, 1% penicillin/streptomycin).

For activation and proliferation of the above cells, magnetic beads coated with anti-CD2/3/28 antibody (Miltenyi Biotec) (hereinafter also referred to as "antibody beads") were added at 0.75×10^5 per well. After addition of cytokines and neutralizing antibody(s) suitable for differentiation culture of respective Th1, Th2 and Th17 cells, cells were incubated in an incubator at 37° C. with 5% CO_2. Cytokines and neutralizing antibodies used are shown in Table 4.

TABLE 4

Cell	Cytokine	Neutralizing antibody (Clone)
Th1	IL-12, IL-2	Anti-IL-4 antibody (MP4-25D2)
Th2	IL-4, IL-2	Anti-IFN-γ antibody (R4-6A2)
Th17	TGF-β1, IL-6, IL-23, IL-21, IL-1β, TNFα, IL-2	Anti-IL-4 antlbody (MP4-25D2), Anti-IFN-γ antibody (R4-6A2)

The concentrations of the above cytokines were 50 ng/ml for IL-6 and 10 ng/ml for other than IL-6.

The concentrations of antibodies were 10 μg/ml for anti-IFN-γ antibody and 2.5 μg/ml for anti-IL-4 antibody. The cytokines and neutralizing antibodies were obtained from R&D systems and eBioscience, respectively.

After three days from the start of culture, cells were diluted three-fold with the medium containing the above cytokines and antibody(s) and cultured for further seven days (10 days in total).

After ten days from the start of culture, the obtained Th1, Th2 and Th17 cells were respectively divided into two equal parts, and one was washed with Yssel medium and PBS before centrifugation to collect cells, which were stored at −80° C. until the subsequent RNA extraction step. These cells were designated as Th1, Th2 and Th17 cells "without activation stimulation". The other half was added with the antibody beads and cultured for three more hours to re-activate the cells. The cells were collected by centrifugation and similarly stored at −80° C. These cells were designated as Th1, Th2 and Th17 cells "with activation stimulation".

(2) Treg Cell Culture

Treg cells obtained in the above step 1. (2) were cultured in the same manner in Yssel medium as the above step 2. (1) and activated with the antibody beads. To the medium were added cytokines IL-2 and TGF-β1 (R&D systems), and neutralizing antibodies anti-IFN-γ antibody, anti-IL-4 antibody (eBioscience) and anti-IL-6 antibody (BD Bioscience).

These cytokines and neutralizing antibodies were used at the concentrations of 10 ng/ml and 5 μg/ml, respectively.

After three days from the start of culture, cells were added with the cytokines and neutralizing antibodies at the same amounts as those at the start of the culture. After culturing for three more days, cells were divided into two equal parts, one half was not added with the antibody beads used for activation and the other half was added with the antibody beads before culturing further three hours, thereby obtaining Treg cells "without activation stimulation" and Treg cells "with activation stimulation", respectively. The cells were then collected by centrifugation and stored at −80° C. until the subsequent RNA extraction step.

3. Extraction of Total RNA

The cells obtained as the above step 2. were subjected to extraction of total RNAs using RNeasy Plus Mini kit and RNeasy micro kit (QIAGEN).

The specific procedures were according to the attached instructions of the kits.

4. Expression Analysis by Microarray

Total RNAs (10 to 100 ng) extracted from the cells as the above step 3. were reverse-transcribed to cDNAs with Two-Cycle Target Labeling and Control Reagents (Affymetrix), and further transcribed to biotinylated-cRNAs. The amplified biotinylated-cRNAs (20 μg) were fragmented. The specific procedures were according to the attached instruction of the kit.

The biotinylated-cRNAs derived from the cells as obtained above (15 μg) were applied to GeneChip Human Genome U-133 Plus 2.0 Array (Affymetrix) as samples, transferred to GeneChip Hybridization Oven 640 (Affymetrix) and hybridized under the conditions of 45° C. and 60 rpm for 16 hours.

After completion of the hybridization, the microarray was washed and fluorescence-labeled in GeneChip Fluidic Station 450 (Affymetrix), and scanned in GeneChip Scanner 3000 7G (Affymetrix) to obtain fluorescent intensity data.

5. Selection of Genes Specifically Expressed in Human Th17 Cells

The fluorescent data obtained in the above step 4. was standardized with the expression analysis software GeneSpring Ver. 10 (Agilent Technologies) based on MAS5 algorithm. Relative fluorescent intensities of the genes from Th17 cells were compared with those from Th1, Th2 and Treg cells.

The genes whose relative fluorescent intensities in Th17 cells were three or more times higher than any of those of Th1, Th2 and Treg cells and which were significantly expressed (which showed "p value <0.05" after ANOVA test between four groups of relative fluorescent intensities in Th1, Th2, Treg and Th17 cells) were identified as the genes which were specifically expressed in Th17 cells.

The number of samples used in the above selection step is shown in Table 5.

TABLE 5

	Th1	Th2	Th17	Treg
w/ activation stimulation	5	5	5	4
w/o activation stimulation	5	5	5	3

The genes specifically expressed in Th17 cells "without activation stimulation" and "with activation stimulation" are shown in Tables 6 and 7, respectively.

TABLE 6

Without activation stimulation

							Expression ratio		
Location of encoded protein	Gene symbol	Entrez Gene ID	Protein ID	Transcript ID	UniGene ID	Probe Set ID	Th17/ Th1	Th17/Th2	Th17/Treg
Membrane	ADAM12	8038	NP_003465, NP_067673	NM_003474, NM_021641	Hs.594537	202952_s_at	21.8	80.1	3.2
	ANKS1B	56899	NP_064525, NP_690001, NP_858056	NM_020140, NM_152788, NM_181670	Hs.506458	227439_at 240292_x_at	6.9 7.8	11.7 10.3	4.3 4.6
	ATP6V0A4	50617	NP_065683, NP_570855, NP_570856	NM_020632, NM_130840, NM_130841	Hs.98967	220197_at	22.8	244.1	153.8
	ATP9A	10079	NP_006036	NM_006045	Hs.714307	212062_at	5.7	53.5	44.3
	BVES	11149	NP_009004, NP_671488	NM_007073, NM_147147	Hs.221660	228783_at	3.0	6.5	16.2
	C5orf40	408263	NP_001001343	NM_001001343	Hs.437066	1554801_at	9.4	12.8	3.1
	CDH4	1002	NP_001785	NM_001794	Hs.473231	206866_at	19.2	16.0	7.6
	DIO2	1734	NP_000784, NP_001007024, NP_054644	NM_000793, NM_001007023, NM_013989	Hs.202354	203700_s_at	9.2	3.4	17.1
	DMD	1756	NP_000100, NP_003997, NP_003998, NP_004000, NP_004001, NP_004002, NP_004003, NP_004004, NP_004005, NP_004006, NP_004007, NP_004008, NP_004009, NP_004010, NP_004011, NP_004012, NP_004013, NP_004014	NM_000109, NM_004006, NM_004007, NM_004009, NM_004010, NM_004011, NM_004012, NM_004013, NM_004014, NM_004015, NM_004016, NM_004017, NM_004018, NM_004019, NM_004020, NM_004021, NM_004022, NM_004023	Hs.495912	203881_s_at	10.3	3.2	10.0
	DRD2	1813	NP_000786, NP_057658	NM_000795, NM_016574	Hs.73893	216938_x_at	5.3	5.6	5.4
	GJC1	10052	NP_001073852, NP_005488	NM_001080383, NM_005497	Hs.532593	228776_at 243502_at	7.0 3.8	10.7 10.5	4.9 8.3
	GPR34	2857	NP_001091048, NP_005291	NM_001097579, NM_005300	Hs.495989	223620_at	4.2	7.9	7.0
	IL23R	149233	NP_653302	NM_144701	Hs.677426	1552912_a_at	8.2	15.3	4.1
	IRS2	8660	NP_003740	NM_003749	Hs.442344	209184_s_at 209185_s_at	3.5 6.0	4.0 5.9	3.3 4.3
	KCNE3	10008	NP_005463	NM_005472	Hs.523899	227647_at	9.8	8.3	5.9
	L1CAM	3897	NP_000416, NP_076493	NM_000425, NM_024003	Hs.522818	204584_at	8.5	9.4	5.1
	PGBD5, LOC100134440	79605, 100134440	NP_078830, XP_001716155	NM_024554, XM_001716103	Hs.520463	219225_at	9.9	17.3	11.3
	MCAM	4162	NP_006491	NM_006500	Hs.599039	210869_s_at	9.5	18.0	5.6
	MFAP3L	9848	NP_001009554, NP_067679	NM_001009554, NM_021647	Hs.593942	205442_at	11.5	29.9	7.1
	MS4A7	58475	NP_067024, NP_996821, NP_996822, NP_996823	NM_021201, NM_206938, NM_206939, NM_206940	Hs.530735	223343_at	16.6	11.7	3.2
	MYO7A	4647	NP_000251, NP_001120651, NP_001120652	NM_000260, NM_001127179, NM_001127180	Hs.370421	208189_s_at	19.4	22.9	6.5
	ODZ4	26011	NP_001092286	NM_001098816	Hs.213087	213273_at	9.8	13.1	7.0
	PHKA1	5255	NP_001116142, NP_002628	NM_001122670, NM_002637	Hs.201379	229876_at	4.2	3.7	15.8
	PTPRM	5797	NP_001098714, NP_002836	NM_001105244, NM_002845	Hs.49774	1555579_s_at	3.6	76.0	3.7
	RGS1	5996	NP_002913	NM_002922	Hs.75256	202988_s_at	3.3	3.6	3.9
	SHB	6461	NP_003019	NM_003028	Hs.521482	1557458_s_at	14.9	27.8	7.4
	SHROOM2	357	NP_001640	NM_001649	Hs.567236	204967_at	3.4	3.4	3.4
	SLC16A4	9122	NP_004687	NM_004696	Hs.351306	205234_at	66.3	20.4	3.4
	SLC44A3	126969	NP_001107578, NP_689582	NM_001114106, NM_152369	Hs.483423	228221_at	3.1	9.3	3.5
	SLC6A15	55117	NP_060527, NP_877499	NM_018057, NM_182767	Hs.44424	206376_at	10.7	11.9	15.2
	SLCO2B1	11309	NP_009187	NM_007256	Hs.7884	203473_at	9.7	6.0	6.8
	SYNGR3	9143	NP_004200	NM_004209	Hs.435277	205691_at	4.7	7.9	5.5

TABLE 6-continued

Without activation stimulation									
							Expression ratio		
Location of encoded protein	Gene symbol	Entrez Gene ID	Protein ID	Transcript ID	UniGene ID	Probe Set ID	Th17/ Th1	Th17/Th2	Th17/Treg
	TANC2	26115	NP_079461	NM_025185	Hs.410889	208425_s_at	4.7	9.0	7.3
						224952_at	6.1	5.8	7.5
	TJP1	7082	NP_003248,	NM_003257,	Hs.716406	202011_at	15.3	19.2	4.3
			NP_783297	NM_175610					
	TMEM163	81615	NP_112185	NM_030923	Hs.369471	1552626_a_at	16.1	32.5	16.4
						223503_at	28.8	47.9	29.7
	TNS3	64759	NP_073585	NM_022748	Hs.520814	217853_at	7.6	158.8	4.5
	UPK1B	7348	NP_008883	NM_006952	Hs.271580	210065_s_at	5.8	7.5	4.6
	WDFY3	23001	NP_055806,	NM_014991,	Hs.480116	212598_at	14.2	18.4	45.6
			NP_848698,	NM_178583,		212602_at	18.7	56.1	29.3
			NP_848700	NM_178585		212606_at	23.0	82.7	71.7
Extracellular/ secreted	C17orf99	100141515	NP_001156547	NM_001163075	Hs.633034	236981_at	29.1	10.9	4.1
	CXCL13	10563	NP_006410	NM_006419	Hs.100431	205242_at	57.7	20.1	4.6
	EBI3	10148	NP_005746	NM_005755	Hs.501452	219424_at	3.6	43.8	3.7
	IL17A	3605	NP_002181	NM_002190	Hs.41724	216876_s_at	340.3	618.9	21.8
	IL17F	112744	NP_443104	NM_052872	Hs.272295	234408_at	559.0	778.4	525.7
	IL1A	3552	NP_000566	NM_000575	Hs.1722	210118_s_at	38.1	13.8	6.5
	IL22	50616	NP_065386	NM_020525	Hs.287369	222974_at	7.5	26.0	13.6
	IL26	55801	NP_060872	NM_018402	Hs.272350	221111_at	11.6	13.5	53.7
	IL9	3578	NP_000581	NM_000590	Hs.960	208193_at	103.8	193.5	24.1
	PCOLCE2	26577	NP_037495	NM_013363	Hs.8944	219295_s_at	10.6	16.8	25.3
	PNOC	5368	NP_006219	NM_006228	Hs.88218	205901_at	36.8	27.3	69.3
	SMPDL3A	10924	NP_006705	NM_006714	Hs.486357	213624_at	4.0	3.8	7.9
	TGFBI	7045	NP_000349	NM_000358	Hs.369397	201506_at	54.7	476.7	33.8
	WNT3	7473	NP_110380	NM_030753	Hs.445884	229103_at	6.6	5.9	6.2
Intracellular	BCAT1	586	NP_005495	NM_005504	Hs.438993	214390_s_at	3.1	4.1	18.9
						214452_at	3.5	6.4	24.8
						225285_at	3.0	3.5	31.5
						226517_at	3.1	3.5	38.3
	BHLHE22	27319	NP_689627	NM_152414	Hs.591870	228636_at	18.9	24.7	40.5
	C13orf18,	80183,	NP_079389,	NM_025113,	Hs.98117	44790_s_at	3.2	11.2	32.0
	LOC728970	728970	XP_001132115,	XM_001132115,					
			XP_001133896,	XM_001133896,					
			XP_001720207	XM_001720155					
	CA2	760	NP_000058	NM_000067	Hs.155097	209301_at	6.3	452.7	103.6
	CCDC3	83643	NP_113643	NM_031455	Hs.498720	223316_at	16.3	106.1	42.1
	CDS1	1040	NP_001254	NM_001263	Hs.654899	205709_s_at	13.9	26.7	3.8
	CHN1	1123	NP_001020372,	NM_001025201,	Hs.654534	212624_s_at	6.9	12.3	6.4
			NP_001813	NM_001822					
	CLIC5,	53405,	NP_001107558,	NM_001114086,	Hs.485489	213317_at	6.7	53.5	13.3
	LOC100131610	100131610	NP_058625,	NM_016929,		217628_at	3.1	9.1	4.2
			XP_001723610	XM_001723558		243917_at	13.9	56.8	16.7
						219866_at	7.1	28.2	17.8
	CTSH	1512	NP_004381,	NM_004390,	Hs.148641	202295_s_at	4.7	10.4	5.6
			NP_683880	NM_148979					
	CYP7B1	9420	NP_004811	NM_004820	Hs.667720	207386_at	12.3	10.2	4.1
	DAPK2	23604	NP_055141	NM_014326	Hs.237886	206324_s_at	7.3	9.9	8.3
						215184_at	6.3	11.0	7.1
	DDIT4L	115265	NP_660287	NM_145244	Hs.480378	228057_at	3.1	5.2	106.8
	DHRS9	10170	NP_001135742,	NM_001142270,	Hs.179608	219799_s_at	8.3	14.6	11.9
			NP_001135743,	NM_001142271,		223952_x_at	5.3	7.8	7.7
			NP_005762,	NM_005771,		224009_x_at	6.3	7.9	7.0
			NP_954674	NM_199204					
	DMRT1	1761	NP_068770	NM_021951	Hs.98586	220493_at	3.6	16.6	6.4
	DSE	29940	NP_001074445,	NM_001080976,	Hs.486292	218854_at	13.9	41.8	26.2
			NP_037484	NM_013352					
	ERC2	26059	NP_056391	NM_015576	Hs.476389	213938_at	3.5	6.1	6.1
	FBXL17	64839	NP_073735	NM_022824	Hs.657225	227203_at	8.9	7.7	4.7
	FBXL21	26223	NP_036291	NM_012159	Hs.591275	1555412_at	22.9	29.2	13.0
	FERMT2	10979	NP_001128471,	NM_001134999,	Hs.509343	209210_s_at	3.1	9.5	5.8
			NP_001128472,	NM_001135000,					
			NP_006823	NM_006832					
	FHOD3	80206	NP_079411	NM_025135	Hs.436636	218980_at	7.2	10.3	7.8
	H2AFY2	55506	NP_061119	NM_018649	Hs.499953	218445_at	5.2	6.5	6.4
	HHEX	3087	NP_002720	NM_002729	Hs.118651	204689_at	3.6	5.9	6.4
	HLX	3142	NP_068777	NM_021958	Hs.74870	214438_at	4.1	8.4	26.3
	HS3ST1	9957	NP_005105	NM_005114	Hs.507348	205466_s_at	21.2	6.0	3.2
	IRAK3	11213	NP_001135995,	NM_001142523,	Hs.369265	213817_at	14.5	16.5	6.0
			NP_009130	NM_007199		220034_at	5.5	10.3	3.4

TABLE 6-continued

Without activation stimulation

							Expression ratio		
Location of encoded protein	Gene symbol	Entrez Gene ID	Protein ID	Transcript ID	UniGene ID	Probe Set ID	Th17/Th1	Th17/Th2	Th17/Treg
	MACC1	346389	NP_877439	NM_182762	Hs.598388	1566766_a_at	5.9	15.7	3.5
	MAML3	55534	NP_061187	NM_018717	Hs.586165	242794_at	5.4	5.7	4.1
	MYO10	4651	NP_036466	NM_012334	Hs.481720	201976_s_at	39.5	17.2	7.1
	NR5A2	2494	NP_003813, NP_995582	NM_003822, NM_205860	Hs.33446	208343_s_at	5.5	17.9	39.5
	OTUB2	78990	NP_075601	NM_023112	Hs.278815	219369_s_at	3.4	3.7	6.3
						222878_s_at	3.2	3.2	6.6
	PAPSS2	9060	NP_001015880,	NM_001015880,	Hs.524491	203058_s_at	4.4	5.1	19.5
			NP_004661	NM_004670		203060_s_at	6.6	17.0	14.3
	PCBP3	54039	NP_001123613, NP_065389	NM_001130141, NM_020528	Hs.474049	230486_at	4.1	3.6	4.8
	PDE4DIP	9659	NP_001002810,	NM_001002810,	Hs.654651	205872_x_at	4.3	33.4	3.3
			NP_001002811, NP_001002812, NP_055459, NP_071754	NM_001002811, NM_001002812, NM_014644, NM_022359	Hs.613082	209700_x_at	4.1	10.9	9.5
	PHLDA1	22822	NP_031376	NM_007350	Hs.602085	217999_s_at	3.6	5.0	10.3
						225842_at	3.3	3.2	8.0
	PLD1	5337	NP_001123553,	NM_001130081,	Hs.382865	177_at	3.5	3.4	10.3
			NP_002653	NM_002662		215723_s_at	3.9	3.4	11.4
						226636_at	5.7	3.6	13.1
	PPARG	5468	NP_005028, NP_056953, NP_619725, NP_619726	NM_005037, NM_015869, NM_138711, NM_138712	Hs.162646	208510_s_at	7.9	134.5	16.5
	PTPN13	5783	NP_006255, NP_542414, NP_542415, NP_542416	NM_006264, NM_080683, NM_080684, NM_080685	Hs.436142	243792_x_at	3.5	4.2	7.9
	RBM20	282996	NP_001127835, XP_001716171, XP_291671, XP_944430	NM_001134363, XM_001716119, XM_291671, XM_939337	Hs.715766	238763_at	8.0	3.5	3.0
	RGS18	64407	NP_570138	NM_130782	Hs.440890	223809_at	3.3	6.9	8.8
	RORC	6097	NP_001001523, NP_005051	NM_001001523, NM_005060	Hs.256022	228806_at	14.0	170.6	7.7
	NINL	22981	NP_079452	NM_025176	Hs.696157	207705_s_at	4.7	4.7	3.1
	RTN2	6253	NP_005610, NP_996783, NP_996784	NM_005619, NM_206900, NM_206901	Hs.47517	34408_at	3.7	4.6	4.5
	SH3RF2	153769	NP_689763	NM_152550	Hs.443728	243582_at	5.8	4.1	18.5
	SIM1	6492	NP_005059	NM_005068	Hs.520293	1556300_s_at	8.8	4.8	69.0
						206876_at	8.7	4.8	37.5
	SNAI2	6591	NP_003059	NM_003068	Hs.360174	213139_at	24.6	22.5	13.8
	SOX2	6657	NP_003097	NM_003106	Hs.518438	228038_at	9.6	8.3	3.4
	SPIRE1	56907	NP_001122098,	NM_001128626,	Hs.515283	1554807_a_at	4.7	6.1	3.8
			NP_001122099,	NM_001128627,		224995_at	8.0	9.0	4.7
			NP_064533	NM_020148		225018_at	6.6	9.2	6.3
	TBC1D12	23232	NP_056003	NM_015188	Hs.500598	221858_at	7.7	5.8	5.5
	TGM5	9333	NP_004236, NP_963925	NM_004245, NM_201631	Hs.129719	207911_s_at	3.6	6.6	5.1
	TMOD1	7111	NP_003266	NM_003275	Hs.494595	203661_s_at	7.0	14.7	5.1
						203662_s_at	7.8	14.5	4.5
	TSHZ2	128553	NP_775756	NM_173485	Hs.649877	220213_at	3.6	12.4	3.8
					Hs.271605	243940_at	3.1	10.6	4.1
	TUBB6	84617	NP_115914	NM_032525	Hs.193491	209191_at	4.1	12.7	4.7
Unknown	C1orf106	55765	NP_001136041, NP_060735	NM_001142569, NM_018265	Hs.518997	219010_at	78.5	111.8	3.3
	C6orf145	221749	NP_899229	NM_183373	Hs.484500	212923_s_at	10.4	3.8	5.2
	LOC401097	401097	XP_001717155, XP_001718614, XP_001718795	XM_001717103, XM_001718562, XM_001718743	Hs.710781	236738_at	6.8	3.3	24.9
	MAMLD1	10046	NP_005482	NM_005491	Hs.20136	205088_at	6.6	8.3	34.1
	ZC3H12C	85463	NP_203748	NM_033390	Hs.376289	231899_at	3.0	4.1	18.7
	—	—	—	AA579799, AA947186, AL049337, AW665328	Hs.663788	215768_at	4.1	6.1	6.7

TABLE 6-continued

Without activation stimulation									
							Expression ratio		
Location of encoded protein	Gene symbol	Entrez Gene ID	Protein ID	Transcript ID	UniGene ID	Probe Set ID	Th17/ Th1	Th17/Th2	Th17/Treg
	—	—	—	AK093229	Hs.586723	222900_at	5.9	3.0	4.5
	—	—	—	AK055628, uc001ljj.1	Hs.594351	226777_at	21.6	39.7	3.6
	—	—	—	AK129763, CR595588, uc002jiy.1, uc002jiz.1	Hs.157726	227452_at	4.6	4.2	4.5
	—	—	—	AA416573, AA628762, D53835, D53836, H24473, R37871, R40232, T10348, T23451, W56351, W57867, Z28733	Hs.654918	229951_x_at	4.7	15.0	7.1
	—	—	—	AI766299	—	236338_at	4.3	4.4	3.3
	—	—	—	AI262017, AI280978, AI284950, AI733224, AI733801	Hs.666775	237923_at	6.9	5.3	4.0

TABLE 7

Location of							Expression ratio		
encoded protein	Gene symbol	Entrez Gene ID	Protein ID	Transcript ID	UniGene ID	Probe Set ID	Th17/ Th1	Th17/ Th2	Th17/Treg
Without activation stimulation									
Unknown	—	—	—	AA687415, AA96901, AI291640, AI446064, AI634557, AI694948, AI701854, AI983938, AV745212, AV745909, AV746001, AW008696, AW511701, AW974416, BG149302, BG150103, N66771, R66991	Hs.434948	238009_at	4.0	19.0	27.6
	—	—	—	AI148241, AI735444, BE645654, BF510855, BF511636	Hs.659083	238151_at	50.6	21.1	24.4
	—	—	—	AK094629	Hs.594896	238623_at	4.9	4.8	3.4
	—	—	—	AI682088, AI951058, F06296, F13164, T77624, Z44722	Hs.606172	241726_at	5.4	5.7	9.5

TABLE 7-continued

Location of encoded protein	Gene symbol	Entrez Gene ID	Protein ID	Transcript ID	UniGene ID	Probe Set ID	Expression ratio		
							Th17/ Th1	Th17/ Th2	Th17/Treg
With activation stimulation									
Membrane	ADAM12	8038	NP__003465,	NM__003474,	Hs.594537	202952__s__at	19.5	71.0	3.5
			NP__067673	NM__021641					
	AKAP12	9590	NP__005091,	NM__005100,	Hs.371240	210517__s__at	9.8	4.5	12.8
			NP__653080	NM__144497		227529__s__at	8.9	5.7	45.5
	ANKS1B	56899	NP__064525,	NM__020140,	Hs.506458	227439__at	5.7	10.5	15.1
			NP__690001,	NM__152788,		227440__at	3.6	12.0	6.3
			NP__858056	NM__181670		240292__x__at	5.1	9.9	8.5
	ATP6V0A4	50617	NP__065683,	NM__020632,	Hs.98967	220197__at	9.0	96.4	64.8
			NP__570855,	NM__130840,					
			NP__570856	NM__130841					
	ATP9A	10079	NP__006036	NM__006045	Hs.714307	212062__at	7.5	55.4	46.4
	BVES	11149	NP__009004,	NM__007073,	Hs.221660	228783__at	3.4	5.9	9.8
			NP__671488	NM__147147					
	C5orf40	408263	NP__001001343	NM__001001343	Hs.437066	1554801__at	17.2	21.0	5.4
	C9orf125	84302	NP__115718	NM__032342	Hs.655738	224458__at	7.5	5.2	8.2
	CDH4	1002	NP__001785	NM__001794	Hs.473231	206866__at	7.4	13.7	11.6
	DIO2	1734	NP__000784,	NM__000793,	Hs.202354	203699__s__at	5.7	8.0	15.4
			NP__001007024,	NM__001007023,		203700__s__at	12.2	13.6	14.1
			NP__054644	NM__013989		231240__at	9.6	5.3	6.3
	DMD	1756	NP__000100,	NM__000109,	Hs.495912	203881__s__at	9.7	3.1	10.4
			NP__003997,	NM__004006,					
			NP__003998,	NM__004007,					
			NP__004000,	NM__004009,					
			NP__004001,	NM__004010,					
			NP__004002,	NM__004011,					
			NP__004003,	NM__004012,					
			NP__004004,	NM__004013,					
			NP__004005,	NM__004014,					
			NP__004006,	NM__004015,					
			NP__004007,	NM__004016,					
			NP__004008,	NM__004017,					
			NP__004009,	NM__004018,					
			NP__004010,	NM__004019,					
			NP__004011,	NM__004020,					
			NP__004012,	NM__004021,					
			NP__004013,	NM__004022,					
			NP__004014	NM__004023					
	DPY19L2	283417	NP__776173	NM__173812	Hs.533644	230158__at	12.5	13.0	3.4
	GPR34	2857	NP__001091048,	NM__001097579	Hs.495989	223620__at	7.2	12.6	22.1
	HRH4	59340	NP__001137300,	NM__001143828,	Hs.287388	221170__at	45.8	3.0	45.6
			NP__067637	NM__021624					
	IL23R	149233	NP__653302	NM__144701	Hs.677426	1561853__a__at	15.1	7.8	6.2
	IRS2	8660	NP__003740	NM__003749	Hs.442344	209185__s__at	3.3	6.4	5.1
	KCNE3	10008	NP__005463	NM__005472	Hs.523899	227647__at	14.9	5.0	3.7
	L1CAM	3897	NP__000416,	NM__000425,	Hs.522818	204584__at	10.3	6.6	5.9
			NP__076493	NM__024003					
	MCAM	4162	NP__006491	NM__006500	Hs.599039	210869__s__at	12.8	24.4	4.3
	MFAP3L	9848	NP__001009554,	NM__001009554,	Hs.593942	205442__at	25.8	22.6	10.5
			NP__067679	NM__021647		210492__at	3.5	4.7	6.7
	MUC20	200958	NP__001091986,	NM__001098516,	Hs.308992	231941__s__at	8.3	3.4	7.2
			NP__689886,	NM__152673,					
			XP__001726746	XM__001726694					
	MYO7A	4647	NP__000251,	NM__000260,	Hs.370421	208189__s__at	13.7	13.0	6.8
			NP__001120651,	NM__001127179,		211103__at	7.5	15.1	5.1
			NP__001120652	NM__001127180					
	POPDC3	64208	NP__071756	NM__022361,	Hs.458336	219926__at	4.5	12.9	12.8
				NR__024539					
	PTPRM	5797	NP__001098714,	NM__001105244,	Hs.49774	1555579__s__at	4.1	66.0	4.1
			NP__002836	NM__002845					
	SHROOM2	357	NP__001640	NM__001649	Hs.567236	204967__at	11.5	3.5	5.9
	SLC16A4	9122	NP__004687	NM__004696	Hs.351306	205234__at	29.8	16.6	6.8
	SLCO2B1	11309	NP__009187	NM__007256	Hs.7884	203473__at	11.0	5.9	5.9
	SORBS1	10580	NP__001030126,	NM__001034954,	Hs.713556	218087__s__at	37.9	4.7	12.8
			NP__001030127,	NM__001034955,		222513__s__at	14.4	3.6	8.2
			NP__001030128,	NM__001034956,					
			NP__001030129,	NM__001034957,					
			NP__006425,	NM__006434,					
			NP__056200,	NM__015385,					
			NP__079267	NM__024991					
	TANC1	85461	NP__203752	NM__033394	Hs.61590	225308__s__at	8.1	17.7	4.9
	TANC2	26115	NP__079461	NM__025185	Hs.410889	224952__at	5.3	4.9	6.4
	TJP1	7082	NP__003248,	NM__003257,	Hs.716406	202011__at	11.5	11.7	5.6
			NP__783297	NM__175610					

TABLE 7-continued

Location of encoded protein	Gene symbol	Entrez Gene ID	Protein ID	Transcript ID	UniGene ID	Probe Set ID	Expression ratio		
							Th17/ Th1	Th17/ Th2	Th17/Treg
	TMEM163	81615	NP_112185	NM_030923	Hs.369471	1552626_a_at	10.8	12.6	13.9
						223503_at	18.5	23.9	21.7
	TMEM44	93109	NP_001011655,	NM_001011655,	Hs.478729	228054_at	7.4	5.2	3.3
			NP_612408	NM_138399					
	TNS3	64759	NP_073585	NM_022748	Hs.520814	217853_at	7.8	27.1	6.4
	UNC13C	440279	NP_001074003	NM_001080534	Hs.657273	1556095_at	7.3	6.1	3.8
	UPK1B	7348	NP_008883	NM_006952	Hs.271580	210065_s_at	5.3	9.6	10.3
	WDFY3	23001	NP_055806,	NM_014991,	Hs.480116	212598_at	10.7	16.1	19.6
			NP_848698,	NM_178583,		212602_at	8.5	19.4	9.8
			NP_848700	NM_178585		212606_at	22.6	62.2	20.5
Extracellular/ secreted	CXCL13	10563	NP_006410	NM_006419	Hs.100431	205242_at	47.5	40.4	4.8
	IL17A	3605	NP_002181	NM_002190	Hs.41724	208402_at	16.5	11.1	3.2
						216876_s_at	404.7	50.0	7.6
	IL17F	112744	NP_443104	NM_052872	Hs.272295	234408_at	464.4	421.4	77.1
	IL22	50616	NP_065386	NM_020525	Hs.287369	221165_s_at	4.7	4.6	4.3
						222974_at	4.3	5.5	9.8
	IL26	55801	NP_060872	NM_018402	Hs.272350	221111_at	10.2	22.5	67.8
	IL9	3578	NP_000581	NM_000590	Hs.960	208193_at	729.7	174.0	35.8
	PCOLCE2	26577	NP_037495	NM_013363	Hs.8944	219295_s_at	10.8	19.3	6.2
	PNOC	5368	NP_006219	NM_006228	Hs.88218	205901_at	39.4	11.4	24.3
	SMPDL3A	10924	NP_006705	NM_006714	Hs.486357	213624_at	3.4	3.3	3.5
	TGFBI	7045	NP_000349	NM_000358	Hs.369397	201506_at	55.9	318.3	32.0
Intracellular	BCAT1	586	NP_005495	NM_005504	Hs.438993	214452_at	3.1	5.8	28.9
	BHLHE22	27319	NP_689627	NM_152414	Hs.591870	228636_at	11.6	14.2	18.7
	C13orf18,	80183,	NP_079389,	NM_025113,	Hs.98117	44790_s_at	3.2	18.8	12.4
	LOC728970	728970	XP_001132115,	XM_001132115,					
			XP_001133896,	XM_001133896,					
			XP_001720207	XM_001720155					
	CA2	760	NP_000058	NM_000067	Hs.155097	209301_at	5.2	61.3	167.6
	CCDC3	83643	NP_113643	NM_031455	Hs.498720	223316_at	11.2	52.3	43.4
	CDS1	1040	NP_001254	NM_001263	Hs.654899	205709_s_at	7.3	9.5	4.2
						226185_at	4.2	7.8	3.3
	CHN1	1123	NP_001020372,	NM_001025201,	Hs.654534	212624_s_at	11.5	21.3	9.1
			NP_001813	NM_001822					
	CLIC5,	53405,	NP_001107558,	NM_001114086,	Hs.485489	213317_at	7.1	22.1	9.6
	LOC100131610	100131610	NP_058625,	NM_016929,		217628_at	3.1	4.2	4.6
			XP_001723610	XM_001723558		243917_at	10.8	17.2	11.7
						219866_at	6.2	10.6	12.2
	CTSH	1512	NP_004381,	NM_004390,	Hs.148641	202295_s_at	4.6	12.1	6.9
			NP_683880	NM_148979					
	CYP7B1	9420	NP_004811	NM_004820	Hs.667720	207386_at	16.4	11.8	5.3
	DAPK2	23604	NP_055141	NM_014326	Hs.237886	206324_s_at	4.4	4.7	3.9
	DMRT1	1761	NP_068770	NM_021951	Hs.98586	220493_at	5.2	18.4	3.9
	DSE	29940	NP_001074445,	NM_001080976,	Hs.486292	218854_at	15.0	51.2	22.3
			NP_037484	NM_013352					
	EML1	2009	NP_001008707,	NM_001008707,	Hs.12451	204796_at	10.1	8.9	5.8
			NP_004425	NM_004434		204797_s_at	3.1	3.1	3.2
	FBXL17	64839	NP_073735	NM_022824	Hs.657225	227203_at	12.6	11.8	4.5
	FBXL21	26223	NP_036291	NM_012159	Hs.591275	1555412_at	26.5	35.3	22.3
	FHOD3	80206	NP_079411	NM_025135	Hs.436636	218980_at	7.0	9.9	6.7
	H2AFY2	55506	NP_061119	NM_018649	Hs.499953	218445_at	3.9	8.2	4.7
	HIST1H2BC	8347	NP_003517	NM_003526	Hs.658713	236193_at	3.8	4.4	3.3
	HLX	3142	NP_068777	NM_021958	Hs.74870	214438_at	3.3	5.2	39.3
	IRAK3	11213	NP_001135995,	NM_001142523,	Hs.369265	213817_at	9.4	18.8	6.5
			NP_009130	NM_007199					
	MACC1	346389	NP_877439	NM_182762	Hs.598388	1566764_at	5.6	12.8	3.5
						1566766_a_at	9.2	17.3	4.7
	MAML3	55534	NP_061187	NM_018717	Hs.586165	242794_at	6.4	5.7	4.6
	MAP3K4	4216	NP_005913,	NM_005922,	Hs.390428	204089_x_at	3.3	3.3	3.4
			NP_006715	NM_006724		216199_s_at	3.2	3.6	3.4
	MYO10	4651	NP_036466	NM_012334	Hs.481720	1554026_a_at	9.1	11.7	7.1
						201976_s_at	45.4	19.1	15.0
						216222_s_at	3.0	6.2	6.7
	OTUB2	78990	NP_075601	NM_023112	Hs.278815	219369_s_at	3.1	3.4	3.8
						222878_s_at	4.2	7.2	4.8
	PAPSS2	9060	NP_001015880,	NM_001015880,	Hs.524491	203058_s_at	5.5	11.0	11.1
			NP_004661	NM_004670		203060_s_at	6.3	47.2	17.3
	PCBP3	54039	NP_001123613,	NM_001130141,	Hs.474049	230486_at	4.5	3.1	5.0
			NP_065389	NM_020528					
	PDE4DIP	9659	NP_001002810,	NM_001002810,	Hs.654651	205872_x_at	5.2	33.6	4.3
			NP_001002811,	NM_001002811,	Hs.613082	209700_x_at	4.9	29.1	8.3
			NP_001002812,	NM_001002812,					
			NP_055459,	NM_014644,					
			NP_071754	NM_022359					
	PDK4	5166	NP_002603	NM_002612	Hs.8364	225207_at	5.3	3.0	4.1

TABLE 7-continued

Location of encoded protein	Gene symbol	Entrez Gene ID	Protein ID	Transcript ID	UniGene ID	Probe Set ID	Expression ratio		
							Th17/ Th1	Th17/ Th2	Th17/Treg
	PLD1	5337	NP_001123553, NP_002653	NM_001130081, NM_002662	Hs.382865	226636_at	3.7	3.2	8.2
	PPARG	5468	NP_005028, NP_056953, NP_619725, NP_619726	NM_005037, NM_015869, NM_138711, NM_138712	Hs.162646	208510_s_at	8.0	22.8	14.1
	PTPN13	5783	NP_006255, NP_542414, NP_542415, NP_542416	NM_006264, NM_080683, NM_080684, NM_080685	Hs.436142	204201_s_at 243792_x_at	3.1 7.9	4.5 5.5	19.7 11.7
	RGS18	64407	NP_570138	NM_130782	Hs.440890	223809_at	4.1	4.9	3.4
	RGS2	5997	NP_002914	NM_002923	Hs.78944	202388_at	3.3	3.5	8.1
	RGS20	8601	NP_003693, NP_733466	NM_003702, NM_170587	Hs.368733	210138_at	6.4	4.9	9.7
	RORC	6097	NP_001001523, NP_005051	NM_001001523, NM_005060	Hs.256022	228806_at	150.1	51.2	5.7
	SIM1	6492	NP_005059	NM_005068	Hs.520293	1556300_s_at 206876_at	14.5 10.9	5.8 5.2	99.6 26.9
	SNAI2	6591	NP_003059	NM_003068	Hs.360174	213139_at	8.2	15.0	6.8
	SOX2	6657	NP_003097	NM_003106	Hs.518438	228038_at	14.4	14.4	16.4
	SPIRE1	56907	NP_001122098, NP_001122099, NP_064533	NM_001128626, NM_001128627, NM_020148	Hs.515283	1554807_a_at 224995_at 225018_at	6.0 7.2 5.5	3.3 5.2 5.4	4.4 5.9 7.8
	TBC1D12	23232	NP_056003	NM_015188	Hs.500598	221858_at	4.2	3.2	3.1
	TGM5	9333	NP_004236, NP_963925	NM_004245, NM_201631	Hs.129719	207911_s_at	5.1	7.7	6.5
	TMOD1	7111	NP_003266	NM_003275	Hs.494595	203661_s_at 203662_s_at	6.2 6.2	10.7 9.5	4.0 3.7
	TUBB6	84617	NP_115914	NM_032525	Hs.193491	209191_at	3.5	11.2	6.4
Unknown	C12orf64	283310	NP_775862	NM_173591	Hs.355145	1553746_a_at	4.2	5.3	10.8
	C6orf168	84553	NP_115900	NM_032511	Hs.573245	232067_at	3.3	5.8	37.1
	CAMSAP1L1	23271	NP_982284	NM_203459	Hs.23585	217196_s_at	22.5	10.1	3.7
	MAGED4, MAGED4B	728239, 81557	NP_001092270, NP_110428, NP_803879, NP_803881	NM_001098800, NM_030801, NM_177535, NM_177537	Hs.571729	223313_s_at	16.3	8.6	3.5
	—	—	—	AK093612	Hs.663643	1556602_at	4.1	5.9	6.3
	—	—	—	BC010059	Hs.637648	1562957_at	6.6	3.6	4.6
	—	—	—	AK055628, uc001ljj.1	Hs.594351	226777_at	30.4	42.8	3.4
	—	—	—	GENSCAN00000030683	—	227985_at	13.4	19.2	3.6
	—	—	—	AA416573, AA628762, D53835, D53836, H24473, R37871, R40232, T10348, T23451, W56351, W57867, Z28733	Hs.654918	229951_x_at	4.2	13.5	4.9
	—	—	—	AK027107	Hs.655798	232331_at	3.5	3.5	9.0
	—	—	—	AI269134, AI312873, AI671475, AV656012, AW162011, BG151392, H69527, N43169, Z36958	Hs.657330	235438_at	73.9	22.0	3.3
	—	—	—	AA687415, AA96901, AI291640, AI446064, AI634557, AI694948, AI701854, AI983938, AV745212, AV745909, AV746001, AW008696,	Hs.434948	238009_at	4.6	15.9	15.0

TABLE 7-continued

Location of encoded protein	Gene symbol	Entrez Gene ID	Protein ID	Transcript ID	UniGene ID	Probe Set ID	Expression ratio Th17/Th1	 Th17/Th2	 Th17/Treg
				AW511701, AW974416, BG149302, BG150103, N66771, R66991					
	—	—	—	AI148241, AI735444, BE645654, BF510855, BF511636	Hs.659083	238151_at	37.6	48.1	29.9
	—	—	—	AK094629	Hs.594896	238623_at	7.0	5.6	6.8
	—	—	—	AI435469, BF111679, BF112253, R37814	Hs.656932	241022_at	6.1	10.7	12.4
	—	—	—	AA846423, AI022103, BF061333	Hs.665895	243922_at	16.7	12.8	6.0
	—	—	—	AA648972, AA879467, AI802768, AW974600	Hs.602350	244247_at	3.9	3.4	5.3

Among the above genes, those shown in Table 8 have been known for their specific expression in Th17 cells.

TABLE 8

SEQ ID NO:	Gene symbol (Gene title)	Entrez Gene ID	Protein ID	Transcript ID	UniGene ID	Probe Set ID	Expression ratio Th17/Th1	 Th17/Th2	 Th17/Treg
175	IL23R(interleukin 23 receptor)	149233	NP_653302	NM_144701	Hs.677426	1552912_a_at	7.6	11.7	4.5
176	IL17A(interleukin 17A)	3605	NP_002181	NM_002190	Hs.41724	216876_s_at	397.5	473.0	29.3
177	IL17F(interleukin 17F)	112744	NP_443104	NM_052872	Hs.272295	234408_at	611.6	951.0	383.6
178	IL22(interleukin 22)	50616	NP_065386	NM_020525	Hs.287369	222974_at	6.4	29.9	10.6
179	IL26(interleukin 26)	55801	NP_060872	NM_018402	Hs.272350	221111_at	10.1	13.0	39.4
180	RORC(RAR-related orphan receptor C)	6097	NP_001001523, NP_005051	NM_001001523, NM_005060	Hs.256022	228806_at	13.8	174.9	7.6

Expression levels of those known genes in Th1, Th2, Treg and Th17 cells obtained in the above step 2. were analyzed with microarray as described above. It was found that those genes were expressed 4 to 950 times higher in Th17 cells than in Th1, Th2 and Treg cells. These results are shown in FIG. **1**. These results indicated that the above cells are suitable for investigation of markers for detecting Th17 cells.

The present inventors have identified novel polynucleotide markers for detecting Th17 cells by excluding the genes shown in Table 8 from those obtained as above. These novel polynucleotide markers are shown in Table 9.

In this table, "Condition" means with or without activation stimulation of cells. The genes designated as "Common" in the column of "Condition" are the genes specifically expressed in both Th17 cells with stimulation and without stimulation. The genes designated as "With stimulation" and "Without stimulation" are the genes specifically expressed either in Th17 cells with stimulation or without stimulation, respectively.

TABLE 9

Location of encoded protein	Condition	No.	Gene symbol	Entrez Gene ID	Protein ID	Transcript ID	UniGene ID	Probe Set ID	SEQ ID NO:
Membrane	Common	1	ADAM12	8038	NP_003465, NP_067673	NM_003474, NM_021641	Hs.594537	202952_s_at	1
		2	ANKS1B	56899	NP_064525, NP_690001, NP_858056	NM_020140, NM_152788, NM_181670	Hs.506458	227439_at 240292_x_at	2 3
		3	ATP6V0A4	50617	NP_065683, NP_570855, NP_570856	NM_020632, NM_130840, NM_130841	Hs.98967	220197_at	4
		4	ATP9A	10079	NP_006036	NM_006045	Hs.714307	212062_at	5

TABLE 9-continued

Location of encoded protein	Condition	No.	Gene symbol	Entrez Gene ID	Protein ID	Transcript ID	UniGene ID	Probe Set ID	SEQ ID NO:
		5	BVES	11149	NP_009004, NP_671488	NM_007073, NM_147147	Hs.221660	228783_at	6
		6	C5orf40	408263	NP_001001343	NM_001001343	Hs.437066	1554801_at	7
		7	CDH4	1002	NP_001785	NM_001794	Hs.473231	206866_at	8
		8	DIO2	1734	NP_000784, NP_001007024, NP_054644	NM_000793, NM_001007023, NM_013989	Hs.202354	203700_s_at	9
		9	DMD	1756	NP_000100, NP_003997, NP_003998, NP_004000, NP_004001, NP_004002, NP_004003, NP_004004, NP_004005, NP_004006, NP_004007, NP_004008, NP_004009, NP_004010, NP_004011, NP_004012, NP_004013, NP_004014	NM_000109, NM_004006, NM_004007, NM_004009, NM_004010, NM_004011, NM_004012, NM_004013, NM_004014, NM_004015, NM_004016, NM_004017, NM_004018, NM_004019, NM_004020, NM_004021, NM_004022, NM_004023	Hs.495912	203881_s_at	10
		10	GPR34	2857	NP_001091048, NP_005291	NM_001097579, NM_005300	Hs.495989	223620_at	11
		11	IRS2	8660	NP_003740	NM_003749	Hs.442344	209184_s_at 209185_s_at	12 13
		12	KCNE3	10008	NP_005463	NM_005472	Hs.523899	227647_at	14
		13	L1CAM	3897	NP_000416, NP_076493	NM_000425, NM_024003	Hs.522818	204584_at	15
		14	MCAM	4162	NP_006491	NM_006500	Hs.599039	210869_s_at	16
		15	MFAP3L	9848	NP_001009554, NP_067679	NM_001009554, NM_021647	Hs.593942	205442_at	17
		16	MYO7A	4647	NP_000251, NP_001120651, NP_001120652	NM_00260, NM_001127179, NM_001127180	Hs.370421	208189_s_at	18
		17	PTPRM	5797	NP_001098714, NP_002836	NM_001105244, NM_002845	Hs.49774	1555579_s_at	19
		18	SHROOM2	357	NP_001640	NM_001649	Hs.567236	204967_at	20
		19	SLC16A4	9122	NP_004687	NM_004696	Hs.351306	205234_at	21
		20	SLCO2B1	11309	NP_009187	NM_007256	Hs.7884	203473_at	22
		21	TANC2	26115	NP_079461	NM_025185	Hs.410889	208425_s_at 224952_at	23 24
		22	TJP1	7082	NP_003248, NP_783297	NM_003257, NM_175610	Hs.716406	202011_at	25
		23	TMEM163	81615	NP_112185	NM_030923	Hs.369471	1552626_a_at 223503_at	26 27
		24	TNS3	64759	NP_073585	NM_022748	Hs.520814	217853_at	28
		25	UPK1B	7348	NP_008883	NM_006952	Hs.271580	210065_s_at	29
		26	WDFY3	23001	NP_055806, NP_848698, NP_848700	NM_014991, NM_178583, NM_178585	Hs.480116	212598_at 212602_at 212606_at	30 31 32
	w/o stimulation	27	DRD2	1813	NP_000786, NP_057658	NM_000795, NM_016574	Hs.73893	216938_x_at	33
		28	GJC1	10052	NP_001073852, NP_005488	NM_001080383, NM_005497	Hs.532593	228776_at 243502_at	34 35
	Without stimulation	29	PGBD5, LOC100134440	79605, 100134440	NP_078830, XP_001716155	NM_024554, XM_001716103	Hs.520463	219225_at	36
		30	MS4A7	58475	NP_067024, NP_996821, NP_996822, NP_996823	NM_021201, NM_206938, NM_206939, NM_206940	Hs.530735	223343_at	37
		31	ODZ4	26011	NP_001092286	NM_001098816	Hs.213087	213273_at	38
		32	PHKA1	5255	NP_001116142, NP_002628	NM_001122670, NM_002637	Hs.201379	229876_at	39
		33	RGS1	5996	NP_002913	NM_002922	Hs.75256	202988_s_at	40
		34	SHB	6461	NP_003019	NM_003028	Hs.521482	1557458_s_at	41
		35	SLC44A3	126969	NP_001107578, NP_689582	NM_001114106, NM_152369	Hs.483423	228221_at	42
		36	SLC6A15	55117	NP_060527, NP_877499	NM_018057, NM_182767	Hs.44424	206376_at	43
		37	SYNGR3	9143	NP_004200	NM_004209	Hs.435277	205691_at	44

TABLE 9-continued

Location of encoded protein	Condition	No.	Gene symbol	Entrez Gene ID	Protein ID	Transcript ID	UniGene ID	Probe Set ID	SEQ ID NO:
	With stimulation	38	AKAP12	9590	NP_005091, NP_653080	NM_005100, NM_144497	Hs.371240	210517_s_at 227529_s_at	45 46
		39	C9orf125	84302	NP_115718	NM_032342	Hs.655738	224458_at	47
		40	DPY19L2	283417	NP_776173	NM_173812	Hs.533644	230158_at	48
		41	HRH4	59340	NP_001137300, NP_067637	NM_001143828, NM_021624	Hs.287388	221170_at	49
		42	MUC20	200958	NP_001091986, NP_689886, XP_001726746	NM_001098516, NM_152673, XM_001726694	Hs.308992	231941_s_at	50
		43	POPDC3	64208	NP_071756	NM_022361, NR_024539	Hs.458336	219926_at	51
		44	SORBS1	10580	NP_001030126, NP_001030127, NP_001030128, NP_001030129, NP_006425, NP_056200, NP_079267	NM_001034954, NM_001034955, NM_001034956, NM_001034957, NM_006434, NM_015385, NM_024991	Hs.713556	218087_s_at 222513_s_at	52 53
		45	TANC1	85461	NP_203752	NM_033394	Hs.61590	225308_s_at	54
		46	TMEM44	93109	NP_001011655, NP_612408	NM_001011655, NM_138399	Hs.478729	228054_at	55
		47	UNC13C	440279	NP_001074003	NM_001080534	Hs.657273	1556095_at	56
Extra-cellular/ secreted	Common	48	CXCL13	10563	NP_006410	NM_006419	Hs.100431	205242_at	57
		49	IL9	3578	NP_000581	NM_000590	Hs.960	208193_at	58
		50	PCOLCE2	26577	NP_037495	NM_013363	Hs.8944	219295_s_at	59
		51	PNOC	5368	NP_006219	NM_006228	Hs.88218	205901_at	60
		52	SMPDL3A	10924	NP_006705	NM_006714	Hs.486357	213624_at	61
		53	TGFBI	7045	NP_000349	NM_000358	Hs.369397	201506_at	62
	w/o stimulation	54	C17orf99	100141515	NP_001156547	NM_001163075	Hs.633034	236981_at	63
		55	EBI3	10148	NP_005746	NM_005755	Hs.501452	219424_at	64
		56	IL1A	3552	NP_000566	NM_000575	Hs.1722	210118_s_at	65
		57	WNT3	7473	NP_110380	NM_030753	Hs.445884	229103_at	66
Intracellular	Common	58	BCAT1	586	NP_005495	NM_005504	Hs.438993	214390_s_at 214452_at 225285_at 226517_at	67 68 69 70
		59	BHLHE22	27319	NP_689627	NM_152414	Hs.591870	228636_at	71
		60	C13orf18, LOC728970	80183, 728970	NP_079389, XP_001132115, XP_001133896, XP_001720207	NM_025113, XM_001132115, XM_001133896, XM_001720155	Hs.98117	44790_s_at	72
		61	CA2	760	NP_000058	NM_000067	Hs.155097	209301_at	73
		62	CCDC3	83643	NP_113643	NM_031455	Hs.498720	223316_at	74
		63	CDS1	1040	NP_001254	NM_001263	Hs.654899	205709_s_at	75
		64	CHN1	1123	NP_001020372, NP_001813	NM_001025201, NM_001822	Hs.654534	212624_s_at	76
		65	CLIC5, LOC100131610	53405, 100131610	NP_001107558, NP_058625, XP_001723610	NM_001114086, NM_016929, XM_001723558	Hs.485489	213317_at 217628_at 243917_at 219866_at	77 78 79 80
		66	CTSH	1512	NP_004381, NP_683880	NM_004390, NM_148979	Hs.148641	202295_s_at	81
		67	CYP7B1	9420	NP_004811	NM_004820	Hs.667720	207386_at	82
		68	DAPK2	23604	NP_055141	NM_014326	Hs.237886	206324_s_at 215184_at	83 84
		69	DMRT1	1761	NP_068770	NM_021951	Hs.98586	220493_at	85
		70	DSE	29940	NP_001074445, NP_037484	NM_001080976, NM_013352	Hs.486292	218854_at	86
		71	FBXL17	64839	NP_073735	NM_022824	Hs.657225	227203_at	87
		72	FBXL21	26223	NP_036291	NM_012159	Hs.591275	1555412_at	88
		73	FHOD3	80206	NP_079411	NM_025135	Hs.436636	218980_at	89
		74	H2AFY2	55506	NP_061119	NM_018649	Hs.499953	218445_at	90
		75	HLX	3142	NP_068777	NM_021958	Hs.74870	214438_at	91
		76	IRAK3	11213	NP_001135995, NP_009130	NM_001142523, NM_007199	Hs.369265	213817_at 220034_at	92 93
		77	MACC1	346389	NP_877439	NM_182762	Hs.598388	1566766_a_at	94
		78	MAML3	55534	NP_061187	NM_018717	Hs.586165	242794_at	95
		79	MYO10	4651	NP_036466	NM_012334	Hs.481720	201976_s_at	96
		80	OTUB2	78990	NP_075601	NM_023112	Hs.278815	219369_s_at 222878_s_at	97 98
		81	PAPSS2	9060	NP_001015880, NP_004661	NM_001015880, NM_004670	Hs.524491	203058_s_at 203060_s_at	99 100
		82	PCBP3	54039	NP_001123613, NP_065389	NM_001130141, NM_020528	Hs.474049	230486_at	101

TABLE 9-continued

Location of encoded protein	Condition	No.	Gene symbol	Entrez Gene ID	Protein ID	Transcript ID	UniGene ID	Probe Set ID	SEQ ID NO:
		83	PDE4DIP	9659	NP_001002810, NP_001002811, NP_001002812, NP_055459, NP_071754	NM_001002810, NM_001002811, NM_001002812, NM_014644, NM_022359	Hs.654651 Hs.613082	205872_x_at 209700_x_at	102 103
		84	PLD1	5337	NP_001123553, NP_002653	NM_001130081, NM_002662	Hs.382865	177_at 215723_s_at 226636_at	104 105 106
		85	PPARG	5468	NP_005028, NP_056953, NP_619725, NP_619726	NM_005037, NM_015869, NM_138711, NM_138712	Hs.162646	208510_s_at	107
		86	PTPN13	5783	NP_006255, NP_542414, NP_542415, NP_542416	NM_006264, NM_080683, NM_080684, NM_080685	Hs.436142	243792_x_at	108
		87	RGS18	64407	NP_570138	NM_130782	Hs.440890	223809_at	109
		88	SIM1	6492	NP_005059	NM_005068	Hs.520293	1556300_s_at 206876_at	110 111
		89	SNAI2	6591	NP_003059	NM_003068	Hs.360174	213139_at	112
		90	SOX2	6657	NP_003097	NM_003106	Hs.518438	228038_at	113
		91	SPIRE1	56907	NP_001122098, NP_001122099, NP_064533	NM_001128626, NM_001128627, NM_020148	Hs.515283	1554807_a_at 224995_at 225018_at	114 115 116
		92	TBC1D12	23232	NP_056003	NM_015188	Hs.500598	221858_at	117
		93	TGM5	9333	NP_004236, NP_963925	NM_004245, NM_201631	Hs.129719	207911_s_at	118
		94	TMOD1	7111	NP_003266	NM_003275	Hs.494595	203661_s_at 203662_s_at	119 120
		95	TUBB6	84617	NP_115914	NM_032525	Hs.193491	209191_at	121
	Without stimulation	96	DDIT4L	115265	NP_660287	NM_145244	Hs.480378	228057_at	122
		97	DHRS9	10170	NP_001135742, NP_001135743, NP_005762, NP_954674	NM_001142270, NM_001142271, NM_005771, NM_199204	Hs.179608	219799_s_at 223952_x_at 224009_x_at	123 124 125
		98	ERC2	26059	NP_056391	NM_015576	Hs.476389	213938_at	126
		99	FERMT2	10979	NP_001128471, NP_001128472, NP_006823	NM_001134999, NM_001135000, NM_006832	Hs.509343	209210_s_at	127
		100	HHEX	3087	NP_002720	NM_002729	Hs.118651	204689_at	128
		101	HS3ST1	9957	NP_005105	NM_005114	Hs.507348	205466_s_at	129
		102	NR5A2	2494	NP_003813, NP_995582	NM_003822, NM_205860	Hs.33446	208343_s_at	130
		103	PHLDA1	22822	NP_031376	NM_007350	Hs.602085	217999_s_at 225842_at	131 132
		104	RBM20	282996	NP_001127835, XP_001716171, XP_291671, XP_944430	NM_001134363, XM_001716119, XM_291671, XM_939337	Hs.715766	238763_at	133
		105	NINL	22981	NP_079452	NM_025176	Hs.696157	207705_s_at	134
		106	RTN2	6253	NP_005610, NP_996783, NP_996784	NM_005619, NM_206900, NM_206901	Hs.47517	34408_at	135
		107	SH3RF2	153769	NP_689763	NM_152550	Hs.443728	243582_at	136
		108	TSHZ2	128553	NP_775756	NM_173485	Hs.649877 Hs.271605	220213_at 243940_at	137 138
	With stimulation	109	EML1	2009	NP_001008707, NP_004425	NM_001008707, NM_004434	Hs.12451	204796_at 204797_s_at	139 140
		110	HIST1H2BC	8347	NP_003517	NM_003526	Hs.658713	236193_at	141
		111	MAP3K4	4216	NP_005913, NP_006715	NM_005922, NM_006724	Hs.390428	204089_x_at 216199_s_at	142 143
		112	PDK4	5166	NP_002603	NM_002612	Hs.8364	225207_at	144
		113	RGS2	5997	NP_002914	NM_002923	Hs.78944	202388_at	145
		114	RGS20	8601	NP_003693, NP_733466	NM_003702, NM_170587	Hs.368733	210138_at	146
Unknown	Common	115	—	—	—	AK055628, uc001ljj.1	Hs.594351	226777_at	147
		116	—	—	—	AA416573, AA628762, D53835, D53836, H24473, R37871, R40232, T10348, T23451,	Hs.654918	229951_x_at	148

TABLE 9-continued

Location of encoded protein	Condition	No.	Gene symbol	Entrez Gene ID	Protein ID	Transcript ID	UniGene ID	Probe Set ID	SEQ ID NO:
						W56351, W57867, Z28733			
		117	—	—	—	AA687415, AA96901, AI291640, AI446064, AI634557, AI694948, AI701854, AI983938, AV745212, AV745909, AV746001, AW008696, AW511701, AW974416, BG149302, BG150103, N66771, R66991	Hs.434948	238009_at	149
		118	—	—	—	AI148241, AI735444, BE645654, BF510855, BF511636	Hs.659083	238151_at	150
		119	—	—	—	AK094629	Hs.594896	238623_at	151
	Without stimulation	120	C1orf106	55765	NP_001136041, NP_060735	NM_001142569, NM_018265	Hs.518997	219010_at	152
		121	C6orf145	221749	NP_899229	NM_183373	Hs.484500	212923_s_at	153
		122	LOC401097	401097	XP_001717155, XP_001718614, XP_001718795	XM_001717103, XM_001718562, XM_001718743	Hs.710781	236738_at	154
		123	MAMLD1	10046	NP_005482	NM_005491	Hs.20136	205088_at	155
		124	ZC3H12C	85463	NP_203748	NM_033390	Hs.376289	231899_at	156
		125	—	—	—	AA579799, AA947186, AL049337, AW665328	Hs.663788	215768_at	157
		126	—	—	—	AK093229	Hs.586723	222900_at	158
		127	—	—	—	AK129763, CR595588, uc002jiy.1, uc002jiz.1	Hs.157726	227452_at	159
		128	—	—	—	AI766299	—	236338_at	160
		129	—	—	—	AI262017, AI280978, AI284950, AI733224, AI733801	Hs.666775	237923_at	161
		130	—	—	—	AI682088, AI951058, F06296, F13164, T77624, Z44722	Hs.606172	241726_at	162
	With stimulation	131	C12orf64	283310	NP_775862	NM_173591	Hs.355145	1553746_a_at	163
		132	C6orf168	84553	NP_115900	NM_032511	Hs.573245	232067_at	164
		133	CAMSAP1L1	23271	NP_982284	NM_203459	Hs.23585	217196_s_at	165
		134	MAGED4, MAGED4B	728239, 81557	NP_001092270, NP_110428, NP_803879, NP_803881	NM_001098800, NM_030801, NM_177535, NM_177537	Hs.571729	223313_s_at	166
		135	—	—	—	AK093612	Hs.663643	1556602_at	167
		136	—	—	—	BC010059	Hs.637648	1562957_at	168
		137	—	—	—	GENSCAN00000030683	—	227985_at	169
		138	—	—	—	AK027107	Hs.655798	232331_at	170
		139	—	—	—	AI269134, AI312873, AI671475, AV656012, AW162011, BG151392, H69527, N43169, Z36958	Hs.657330	235438_at	171

TABLE 9-continued

Location of encoded protein	Condition	No.	Gene symbol	Entrez Gene ID	Protein ID	Transcript ID	UniGene ID	Probe Set ID	SEQ ID NO:
		140	—	—	—	AI435469, BF111679, BF112253, R37814	Hs.656932	241022_at	172
		141	—	—	—	AA846423, AI022103, BF061333	Hs.665895	243922_at	173
		142	—	—	—	AA648972, AA879467, AI802768, AW974600	Hs.602350	244247_at	174

It is believed that detection of the polynucleotide markers shown in Table 9 by well-known methods in the art such as PCR or detection of proteins encoded by these polynucleotide markers by well-known methods in the art such as ELISA or flow cytometry allows specific detection of human Th17 cells.

EXAMPLE 2

Expression Analysis of Protein Markers for Detecting Human Th17 Cells

1. Preparation of Measurement Samples

(1) Preparation of MCAM Measurement Samples

To Th17 cells "without activation stimulation" (5x10^6 cells/ml) prepared in Example 1 under the paragraph "2. Cell culture" was added a phycoerythrin (PE)-labeled anti-MCAM antibody (BioLegend) to a final concentration of 1.25 μg/ml and reaction was carried out at 4° C. for 20 minutes.

After the reaction, Th17 cells were washed by adding phosphate buffered saline (PBS) containing 0.5% BSA and centrifuging to collect the cells. The washed Th17 cells were suspended in PBS containing 0.5 μg/ml 7-amino-actinomycin D (7-AAD) and 0.5% BSA to prepare a MCAM measurement sample of Th17 cells (5x10^6 cells/ml).

MCAM measurement samples of Th1 cells (5x10^6 cells/ml), of Th2 cells (5x10^6 cells/ml) and of Treg cells (5x10^6 cells/ml) were prepared in the similar manner as above except that Th1, Th2 and Treg cells "without activation stimulation", respectively, were used instead of Th17 cells "without activation stimulation".

A negative control sample (5x10^6 cells/ml) was prepared by adding a PE-labeled mouse IgG2a isotype control (BioLegend) to a final concentration of 1.0 μg/ml instead of the PE-labeled MCAM antibody and reacting at 4° C. for 20 minutes.

(2) Preparation of PTPRM Measurement Samples

To Th17 cells "without activation stimulation" (5x10^6 cells/ml) prepared in Example 1 under the paragraph "2. Cell culture" was added an anti-PTPRM antibody (Abcam) to a final concentration of 2.0 μg/ml and reaction was carried out at 4° C. for 20 minutes.

After the reaction, Th17 cells were added with PBS containing 0.5% BSA and centrifuged to collect the cells. The collected Th17 cells were suspended in PBS containing 0.5% BSA. The suspension was added with a PE-labeled anti-mouse IgG antibody (BioLegend) to a final concentration of 1.0 μg/ml and reaction was carried out at 4° C. for 20 minutes.

After reaction with the PE-labeled anti-mouse IgG antibody, Th17 cells were washed by adding PBS containing 0.5% BSA and centrifuging to collect the cells. The washed Th17 cells were suspended in PBS containing 0.5 μg/ml 7-amino-actinomycin D (7-AAD) and 0.5% BSA to prepare a PTPRM measurement sample of Th17 cells (5x10^6 cells/ml).

PTPRM measurement samples of Th1 cells (5x10^6 cells/ml), of Th2 cells (5x10^6 cells/ml) and of Treg cells (5x10^6 cells/ml) were prepared in the similar manner as above except that Th1, Th2 and Treg cells "without activation stimulation", respectively, were used instead of Th17 cells "without activation stimulation".

A negative control sample (5x10^6 cells/ml) was prepared by adding a mouse IgG2a isotype control (BioLegend) to a final concentration of 1.0 μg/ml instead of the anti-PTPRM antibody and reacting at 4° C. for 20 minutes.

(3) Preparation of CCR6 Measurement Samples

CCR6 measurement samples of Th17 cells (5x10^6 cells/ml), of Th1 cells (5x10^6 cells/ml), of Th2 cells (5x10^6 cells/ml) and of Treg cells (5x10^6 cells/ml) were prepared in the similar manner as the above paragraph "(1) Preparation of MCAM measurement samples" except that a PE-labeled anti-CCR6 antibody (BD Bioscience) was used at a final concentration of 1.0 μg/ml instead of the PE-labeled anti-MCAM antibody.

A negative control sample (5x10^6 cells/ml) was prepared by adding a PE-labeled mouse IgG1 isotype control (BioLegend) to a final concentration of 1.0 μg/ml instead of the PE-labeled anti-CCR6 antibody and reacting at 4° C. for 20 minutes.

(4) Preparation of FOXP3 Measurement Samples

Th17 cells "without activation stimulation" (5x10^6 cells/ml) prepared in Example 1 under the paragraph "2. Cell culture" were fixed and permeability of the cell membranes was increased using FOXP3 staining buffer set (eBioscience) before addition of a PE-labeled anti-FOXP3 antibody (BioLegend) to a final concentration of 3.125 μg/ml and reaction at 4° C. for 20 minutes.

After the reaction, Th17 cells were washed by adding phosphate buffered saline (PBS) containing 0.5% BSA and centrifuging to collect the cells. The washed Th17 cells were suspended in PBS containing 0.5% BSA to prepare a FOXP3 measurement sample of Th17 cells (5x10^6 cells/ml).

FOXP3 measurement samples of Th1 cells (5x10^6 cells/ml), of Th2 cells (5x10^6 cells/ml) and of Treg cells (5x10^6 cells/ml) were prepared in the similar manner as above except that Th1, Th2 and Treg cells "without activation stimulation", respectively, were used instead of Th17 cells "without activation stimulation".

A negative control sample (5x10^6 cells/ml) was prepared by adding a PE-labeled mouse IgG1 isotype control (BioLegend) to a final concentration of 1.0 μg/ml instead of the PE-labeled FOXP3 antibody and reacting at 4° C. for 20 minutes.

(5) Preparation of GRP34 Measurement Samples

Th17 cells "without activation stimulation" prepared in Example 1 under the paragraph "2. Cell culture" were prepared in 5% FBS/RPMI at 2.5×10^5 cells/ml. Phorbol myristate acetate at a final concentration of 50 ng/ml and ionomycin at a final concentration of 1 μM were added and incubated at 37° C. for 4 hours to stimulate Th17 cells. Then, brefeldin A was added to a final concentration of 10 μg/ml and incubated at 37° C. for 2 hours.

After cultivation, Th17 cells were washed twice by adding phosphate buffered saline (PBS) containing 0.5% BSA and centrifuging to collect the cells. The washed Th17 cells were added with 2% paraformaldehyde to fix the cells. After fixing the cells, a saponin buffer (0.5% saponin, 0.5% bovine serum albumin (BSA), 1 mM sodium azide (in PBS)) was added to accelerate cell membrane permeability of Th17 cells.

The sample after saponin treatment was added with an anti-GPR34 antibody (Lifespan Biosciences) to a final concentration of 25.0 μg/ml and reaction was carried out at 4° C. for 20 minutes. After the reaction, the saponin buffer was added and Th17 cells were collected by centrifugation. The collected Th17 cells were suspended in the saponin buffer. The suspension was added with a PE-labeled anti-mouse IgG antibody (BioLegend) to a final concentration of 1.0 μg/ml and reaction was carried out at 4° C. for 20 minutes.

After the reaction with the PE-labeled anti-mouse IgG antibody, Th17 cells were washed twice by adding the saponin buffer and centrifuging to collect the cells. The washed Th17 cells were suspended in PBS containing 0.5% BSA to prepare a GRP34 measurement sample of Th17 cells (2.5×10^5 cells/ml).

GRP34 measurement samples of Th1 cells, of Th2 cells and of Treg cells were prepared in the similar manner as above except that Th1, Th2 and Treg cells "without activation stimulation", respectively, were used instead of Th17 cells "without activation stimulation".

A negative control sample (2.5×10^6 cells/ml) was prepared by adding a mouse IgG2a isotype control (BioLegend) to a final concentration of 1.0 μg/ml instead of the anti-GPR34 antibody and reacting at 4° C. for 20 minutes.

(6) Preparation of IL-17a Measurement Samples

Th17 cells "without activation stimulation" prepared in Example 1 under the paragraph "2. Cell culture" were prepared in 5% FBS/RPMI at 2.5×10^5 cells/ml. Phorbol myristate acetate at a final concentration of 50 ng/ml and ionomycin at a final concentration of 1 μM were added and incubated at 37° C. for 4 hours to stimulate Th17 cells. Then, brefeldin A was added to a final concentration of 10 μg/ml and incubated at 37° C. for 2 hours.

After cultivation, Th17 cells were washed by adding phosphate buffered saline (PBS) containing 0.5% BSA and centrifuging to collect the cells. The washed Th17 cells were added with 2% paraformaldehyde to fix the cells. After fixing the cells, a saponin buffer (0.5% saponin, 0.5% bovine serum albumin (BSA), 1 mM sodium azide (in PBS)) was added to accelerate cell membrane permeability of Th17 cells.

The sample after saponin treatment was added with a PerCP-Cy5.5-labeled anti-IL-17A antibody (eBioscience) to a final concentration of 0.15 μg/ml and reaction was carried out at 4° C. for 20 minutes.

After the reaction, Th17 cells were washed by adding the saponin buffer and centrifuging to collect cells. The washed Th17 cells were suspended in PBS containing 0.5% BSA to prepare a IL-17A measurement sample of Th17 cells (2.5×10^5 cells/ml).

A negative control sample (2.5×10^6 cells/ml) was prepared by adding a PerCP-Cy5.5-labeled mouse IgG1 isotype control (eBioscience) to a final concentration of 1.0 μg/ml instead of the PerCP-Cy5.5-labeled anti-IL-17A antibody.

(7) Preparation of IFN-γ Measurement Samples

IFN-γ measurement samples of Th17 cells (2.5×10^5 cells/ml), of Th1 cells (2.5×10^5 cells/ml), of Th2 cells (2.5×10^5 cells/ml) and of Treg cells (2.5×10^5 cells/ml) were prepared in the similar manner as the above paragraph "(6) Preparation of IL-17A measurement samples" except that an Alexa488-labeled anti-IFN-γ antibody (BioLegend) was used at a final concentration of 1.0 μg/ml instead of the PerCP-Cy5.5-labeled anti-IL-17A antibody.

A negative control sample (2.5×10^6 cells/ml) was prepared by adding an Alex488-labeled mouse IgG 1 isotype control (BioLegend) to a final concentration of 1.0 μg/ml instead of the Alexa488-labeled anti-IFN-γ antibody and reacting at 4° C. for 20 minutes.

(8) Preparation of IL-4 Measurement Samples

IL-4 measurement samples of Th17 cells (2.5×10^5 cells/ml), of Th1 cells (2.5×10^5 cells/ml), of Th2 cells (2.5×10^5 cells/ml) and of Treg cells (2.5×10^5 cells/ml) were prepared in the similar manner as the above paragraph "(6) Preparation of IL-17A measurement samples" except that an APC-labeled anti-IL-4 antibody (eBioscience) was used at a final concentration of 0.2 μg/ml instead of the PerCP-Cy5.5-labeled anti-IL-17A antibody.

A negative control sample (2.5×10^6 cells/ml) was prepared by adding an APC-labeled rat IgG1 isotype control (BioLegend) to a final concentration of 1.0 μg/ml instead of the APC-labeled anti-IL-4 antibody and reacting at 4° C. for 20 minutes.

2. Expression Analysis of Protein Markers in Measurement Samples Using Flow Cytometer

The prepared measurement samples were analyzed by FACSCanto II (BD Bioscienct) and FACS DIVA software (BD Bioscience). Histograms (particle size distribution) of fluorescent intensities obtained by the analysis are shown in FIGS. **2** to **9**, which correspond respectively to the histograms obtained from MCAM measurement samples, PTPRM measurement samples, GPR34 measurement samples, CCR6 measurement samples, IL-17A measurement samples, IFN-γ measurement samples, IL-4 measurement samples, and FOXP3 measurement samples. In FIGS. **2** to **9**, the vertical axis of the histograms shows the number of cells and the horizontal axis shows the fluorescent intensity. The numbers at the upper right of the histograms correspond to the ratio (%) of positive cells for the marker gene relative to the number of total cells in the respective measurement samples. The cells were determined as positive or negative based on the maximal fluorescent intensity in the negative control. Namely, the cells having higher fluorescent intensity than the maximal fluorescent intensity of the negative control were determined as positive, while the cells having a fluorescent intensity equal to or lower than the maximal fluorescent intensity of the negative control were determined as negative. The ratio of positive cells was calculated as the ratio of the number of positive cells relative to the number of total cells.

CCR6 and IL-17A are known markers for Th17 cells. FIGS. **5** and **6** show that the expression levels of CCR6 and IL-17A proteins are high in Th17 cells. IFN-γ is a known marker for Th1 cells. FIG. **7** shows that the expression level of IFN-γ protein is high in Th1 cells. IL-4 is a known marker for Th2 cells. FIG. **8** shows that the expression level of IL-4 protein is high in Th2 cells. FOXP3 is a known marker for Treg cells. FIG. **9** shows that the expression level of FOXP3 protein is high in Treg cells. Thus, it is indicated that these measurement samples are suitable for expression analysis of protein markers.

FIGS. **2** to **4** show that the expression levels of MCAM, PTPRM and GPR34 proteins are high in Th17 cells. It is also found that the ratios of positive cells in the MCAM measurement sample, PTPRM measurement sample and GPR34 measurement sample of Th17 cells were equal to or higher than the ratios of positive cells in the CCR6 measurement sample and IL-17A measurement sample. This reveals that the proteins encoded by the genes MCAM, PTPRM and GPR34 which were identified in Example 1 as the polynucleotide markers for detecting Th17 cells can also be used as protein markers for detecting Th17 cells.

EXAMPLE 3

Expression Analysis of Polynucleotide Markers for Detecting Th17 Cells by Real-Time PCR

1. Preparation of cDNA

(1) Preparation of cDNA from Cells "without Activation Stimulation"

Total RNA (0.1 μg) of Th17 cells "without activation stimulation" extracted in Example 1 under the paragraph "3. Extraction of total RNA" was reverse-transcribed with a poly dT primer (Hokkaido System Science Co., Ltd.), random primers (Hokkaido System Science Co., Ltd.) and Superscript III reverse transcriptase (Invitrogen Corporation) to obtain cDNA of Th17 cells "without activation stimulation". Reverse transcription was carried out according to the attached instructions.

cDNAs of Th1 cells "without activation stimulation", of Th2 cells "without activation stimulation" and of Treg cells "without activation stimulation" were prepared in the similar manner as above except that total RNAs (0.1 μg) of Th1 cells, Th2 cells and Treg cells "without activation stimulation" were used instead of total RNA (0.1 μg) of Th17 cells "without stimulation".

The number of samples of the cells "without activation stimulation" used for preparation of cDNA is shown in Table 10.

TABLE 10

	Th1 cells	Th2 cells	Th17 cells	Treg cells
w/o activation stimulation	5	5	5	4

(2) Preparation of cDNA from Cells "with Activation Stimulation"

Th17 cells "without activation stimulation" prepared in Example 1 under the paragraph "2. Cell culture" were prepared in 5% FBS/RPMI at 2.5×10^5 cells/ml. Th17 cells were stimulated by incubating the cells at 37° C. for 3 hours with T cell activation/expansion kit (Miltenyi Biotec). These Th17 cells "with activation stimulation" were subjected to extraction of total RNA in the same manner as Example 1, "3. Extraction of total RNA". The extracted total RNA (0.1 μg) of Th17 cells "with activation stimulation" was reverse-transcribed with a poly dT primer (Hokkaido System Science Co., Ltd.), random primers (Hokkaido System Science Co., Ltd.) and Superscript III reverse transcriptase (Invitrogen Corporation) to obtain cDNA of Th17 cells "with activation stimulation". Reverse transcription was carried out according to the attached instructions.

cDNAs of Th1 cells "with activation stimulation", of Th2 cells "with activation stimulation" and of Treg cells "with activation stimulation" were prepared in the similar manner as above except that total RNAs (0.1 μg) of Th1 cells, Th2 cells and Treg cells "with activation stimulation" were used instead of total RNA (0.1 μg) of Th17 cells "with activation stimulation".

The number of samples of the cells "with activation stimulation" used for preparation of cDNA is shown in Table 11.

TABLE 11

	Th1 cells	Th2 cells	Th17 cells	Treg cells
w/ activation stimulation	5	5	5	3

2. Design of Primer Sets

The following primer sets were designed with Primer3 software.

(1) Primer Sets for Detecting Th17 Cells

Primer sets were designed for the genes ADAM12, ATP6V0A4, ATP9A, BVES, C5orf40, CDH4, DIO2, L1CAM, MCAM, SHROOM2, TMEM163, UPK1B, DRD2, PGBD5 (LOC100134440), ODZ4, SLC6A15, AKAP12, C9orf125, POPDC3, UNC13C, PCOLCE2, PNOC, TGFBI, IL1A, BHLHE22, PPARG, SIM1 and SNAI2, which were detected in Example 1 as the polynucleotide markers for detecting Th17 cells.

(2) Primer Sets for Known Markers for Th17 Cells

Primer sets were designed for known gene markers for Th17 cells, CCR6, RORC and IL-17A.

(3) Primer Sets for Known Markers for Th1 Cells

Primer sets were designed for known gene markers for Th1 cells, TBX21 and IFN-γ.

(4) Primer Sets for Known Markers for Th2 Cells

Primer sets were designed for known gene markers for Th2 cells, GATA3 and IL-4.

(5) Primer Sets for Known Markers for Treg Cells

Primer sets were designed for a known gene marker for Treg cells, FOXP3.

(6) Primer Sets for Internal Controls

Primer sets were designed for internal control genes, Gapdh, ACTB, B2M and UBC.

Designed primer sets are shown in Table 12.

TABLE 12

Gene symbol	Forward primer	SEQ ID NO:	Reverse primer	SEQ ID NO:
ADAM12	TCTCCCTCGCTCGAAATTACA	181	CAGAATATCCCCGTACATGTCCAT	182
ATP6V0A4	TCCTTGAACATCTTTGGCTCTTC	183	TCCATGTGCCGTTTCTGAAC	184
ATP9A	AGAGGAGCAGTATCAGGACTTTGAA	185	AGCGGTCGTGCACACTCA	186

TABLE 12-continued

Gene symbol	Forward primer	SEQ ID NO:	Reverse primer	SEQ ID NO:
BVES	CGGCTTGCACCAGTTTCTTC	187	GCTCCTTCTTCTATCGGTTTCATC	188
C5orf40	TCGGAGGGCAGAGCTCTAAC	189	CCTCGATGTTCATCCCGATT	190
CDH4	GATCAGCCCCACTCTCCAAA	191	GATGGATCCCCACTGATGATG	192
DIO2	CATGATGCTAAGAGTCCTGGGTAA	193	TTCTGCAACTGAGAAGCACATATG	194
L1CAM	CAAGGAGGGCCAGTGCAA	195	GAAGCCCCACCCTTCTCTTC	196
MCAM	GGGCATCCCTGTGAACAGTAA	197	GGTACCCGTTCCTCCCTACAC	198
SHROOM2	TGCATGTTAATGGTGAGTGAATCC	199	TTGATCCAACAAATGCCCTAATAC	200
TMEM163	GGTCAAACTCCTCATCGACATG	201	CCCCTTCACTCAAACATCTCGTA	202
UPK1B	CCAGTGGAAAAACAATGGAGTCA	203	ACAGCAATTGTCCTGGAGCAT	204
DRD2	CTGCTCATCGCTGTCATCGT	205	CGGGACACAGCCATGCA	206
PGBD5	AGAGTTTGAGAAGCAAGGGATTTACT	207	GGCCGGTGCAGTCACTCTT	208
ODZ4	GCCCACAGACTTAGCCATCA	209	TCCCGGCGACAATGC	210
SLC6A15	TGCCACCACCTATTACTGGTACA	211	AGTTTAAGCCCCCACTTTCAGAA	212
AKAP12	TCCATAGCTGGGTCTGGTGTAGA	213	TTCTTGATTGAGACCCAGGATTC	214
C9orf125	GAGAGGCTCCAGCACTACATCA	215	CTACACCAACCCATTCCAGGAT	216
POPDC3	TTCAGTTCCTGGATTCTCCTGAGT	217	CAGTGAGGGTTACCTGAAAAATGC	218
UNC13C	TCAGGGACCAACCACCAAGA	219	CAGGACAGGTGTGTAGGCAGTTT	220
PCOLCE2	CCACCACATTCCCTGTAACCA	221	TCCGTCTACACTTTTGTTGACACA	222
PNOC	CTCAGTCTCTTCTCCAGTGTGTTCA	223	GGAGCTTCTCCTGGCATGTG	224
TGFBI	GGGCGGCAAAAAACTGAGA	225	CCGCGATGCAGGTGTTCT	226
IL1A	CAATTGTATGTGACTGCCCAAGA	227	TGGGTATCTCAGGCATCTCCTT	228
BHLHE22	TGCTCCCCACCCCCTTTA	229	CTGCTTTGTTTGCTCTGCAAGT	230
PPARG	CCTGAGCCACTGCCAACATT	231	AGGTGTCAGATTTTCCCTCAGAAT	232
SIM1	CATGCCTCACATCGCTTCAG	233	CCACACTATCTTCATCCCAATGAC	234
SNAI2	CTTGCCCTCACTGCAACAGA	235	TCTGCAGATGAGCCCTCAGA	236
TBX21	GATGCGCCAGGAAGTTTCA	237	GACGCCCCCTTGTTGTTTG	238
GATA3	GCGGGCTCTATCACAAAATGA	239	GCCTTCGCTTGGGCTTAAT	240
FOXP3	CACCTGGCTGGGAAAATGG	241	GGAGCCCTTGTCGGATGAT	242
CCR6	GGCAGTTCTCCAGGCTATTTGT	243	GGAGGCCAAAGACACAGATCA	244
RORC	CCAAGGCTCAGTCATGAGAACA	245	GCGGAAGAAGCCCTTGCA	246
IFNG	CCAACGCAAAGCAATACATGA	247	CGAAACAGCATCTGACTCCTTTT	248
IL4	TGGGTCTCACCTCCCAACTG	249	GCCGGCACATGCTAGCA	250
IL17A	CCCAAAAGGTCCTCAGATTACTACA	251	CATTGCGGTGGAGATTCCA	252
GAPDH	ACCCACTCCTCCACCTTTGA	253	TTGCTGTAGCCAAATTCGTTGT	254
ACTB	CAGCAGATGTGGATCAGCAAG	255	GCATTTGCGGTGGACGAT	256
B2M	TGCTGTCTCCATGTTTGATGTATCT	257	TCTCTGCTCCCCACCTCTAAGT	258
UBC	GTCGCAGCCGGGATTTG	259	GCATTGTCAAGTGACGATCACA	260

3. Expression Analysis of Gene Markers by Real-Time PCR

(1) Real-Time PCR Using cDNAs of Cells "Without Activation Stimulation" as Templates

cDNAs of Th17 cells "without activation stimulation" obtained from samples in the above "1. Preparation of cDNA" were respectively used as a template. The primer sets used were the primer sets for ADAM12, ATP6V0A4, ATP9A, BVES, C5orf40, CDH4, DIO2, L1CAM, MCAM, SHROOM2, TMEM163, UPK1B, DRD2, PGBD5, ODZ4, SLC6A15, AKAP12, C9orf125, POPDC3, UNC13C, PCOLCE2, PNOC, TGFBI, IL1A, BHLHE22, PPARG, SIM1, SNAI2, TBX21, GATA3, FOXP3, CCR6, RORC, GAPDH, ACTB, B2M and UBC, which were designed as described in "2. Design of primer sets". Real-time PCR was carried out with the template, primer sets and Power SYBR Green PCR Master Mix (Applied Biosystems) in 7300 Real Time PCR System (Applied Biosystems) and Ct value of each gene was measured. PCR was carried out at 50° C. for 2 minutes, 95° C. for 10 minutes followed by 45 cycles of 95° C. for 15 seconds and 60° C. for 1 minute and two cycles of 95° C. for 15 seconds and 60° C. for 1 minute. Ct value was measured by automatic calculation on 7300 Fast SDS software (Applied Biosystems).

Real-time PCR was also carried out in the similar manner as above except that cDNAs of Th1 cells "without activation stimulation" obtained from 5 samples, cDNAs of Th2 cells "without activation stimulation" obtained from 5 samples and cDNAs of Treg cells "without activation stimulation" obtained from 4 samples were used as a template instead of cDNAs of Th17 cells "without activation stimulation", and Ct values for the genes were measured.

(2) Real-Time PCR Using cDNAs of Cells "with Activation Stimulation" as Templates

cDNAs of Th17 cells "with activation stimulation" obtained from 5 samples in the above "1. Preparation of cDNA" were used as a template. The primer sets used were the primer sets for AKAP12, C9orf125, POPDC3, UNC13C, PCOLCE2, PNOC, TGFBI, IFNG, IL4, IL17A, GAPDH, ACTB, B2M and UBC, which were designed as described in "2. Design of primer sets". Real-time PCR was carried out with the template, primer sets and Power SYBR Green PCR Master Mix (Applied Biosystems) in 7300 Real Time PCR System (Applied Biosystems) and Ct value of each gene was measured. PCR was carried out at 50° C. for 2 minutes, 95° C. for 10 minutes followed by 45 cycles of 95° C. for 15 seconds and 60° C. for 1 minute and two cycles of 95° C. for 15 seconds and 60° C. for 1 minute. Ct value was measured by automatic calculation on 7300 Fast SDS software (Applied Biosystems).

Real-time PCR was also carried out in the similar manner as above except that cDNAs of Th1 cells "with activation stimulation" obtained from 5 samples, cDNAs of Th2 cells "with activation stimulation" obtained from 5 samples and cDNAs of Treg cells "with activation stimulation" obtained from 3 samples were used as a template instead of cDNAs of Th17 cells "with activation stimulation", and Ct values for the genes were measured.

(3) Analysis of Expression Level

Based on the Ct values obtained from real-time PCR, expression levels of the gene markers were calculated according to the formula (I):

$$(\text{Expression level of a gene})=100000\times 2^{-y} \tag{I}$$

wherein: y=(Ct value of a gene)−(((Ct value of Gapdh gene)+(Ct value of ACTB gene)+(Ct value of B2M gene)+(Ct value of UBC gene))/4)

The expression level of each gene marker in Th17 cells "without activation stimulation" was obtained as an average of the expression levels of the gene marker in question obtained from five cDNAs used as templates. The expression level of each gene marker in Th17 cells "with activation stimulation" was also obtained as an average of the expression levels of the gene marker in question obtained from five cDNAs used as templates.

Similarly, the expression level of each gene marker in Th1 cells or Th2 cells "without activation stimulation" or "with activation stimulation" was obtained as an average of the expression levels of the gene marker in question obtained from five cDNAs used as templates. The expression level of each gene marker in Treg cells "without activation expression" was obtained as an average of the expression levels of the gene marker in question obtained from four cDNAs used as templates. The expression level of each gene marker in Treg cells "with activation stimulation" was obtained as an average of the expression levels of the gene marker in question obtained from three cDNAs used as templates.

Expression levels of the gene markers are shown in Tables 13 and 14. Table 13 shows expression levels of gene markers in Th1, Th2, Treg and Th17 cells "without activation stimulation" and Table 14 shows expression levels of gene markers in Th1, Th2, Treg and Th17 cells "with activation stimulation"

Expression levels of gene markers in the cells "without activation stimulation"

TABLE 13

Location of encoded protein	Gene symbol	Expression level			
		Th1	Th2	Treg	Th17
Membrane	ADAM12	9.95	0.55	22.08	193.83
	ATP6V0A4	35.21	2.55	7.17	625.03
	ATP9A	125.11	9.08	41.42	407.43
	BVES	23.85	3.58	6.84	77.99
	C5orf40	0.74	0.00	33.36	107.84
	CDH4	4.93	7.47	29.44	143.90
	DIO2	0.46	1.25	0.91	10.40
	L1CAM	41.95	45.03	72.77	220.54
	MCAM	62.69	18.93	159.46	500.64
	SHROOM2	0.22	0.46	0.90	11.44
	TMEM163	13.77	8.78	24.25	249.56
	UPK1B	2.94	0.12	0.55	22.59
	DRD2	51.14	49.86	58.21	884.06
	PGBD5	10.30	11.96	19.04	157.52
	ODZ4	1.14	0.44	0.39	41.82
	SLC6A15	0.50	3.46	2.65	27.71
	AKAP12	29.57	30.67	46.71	110.16
	C9orf125	1.31	0.50	3.43	39.73
	POPDC3	0.23	0.00	0.52	10.19
	UNC13C	0.08	0.08	0.27	12.10
Extracellular/ secreted	PCOLCE2	0.60	0.00	2.59	15.64
	PNOC	8.01	25.75	5.43	335.81
	TGFBI	58.45	31.18	253.89	1427.38
	IL1A	13.47	47.92	128.89	502.06
Intracellular	BHLHE22	32.48	13.80	29.69	247.81
	PPARG	120.16	16.40	92.84	456.67
	SIM1	143.63	229.39	40.78	837.78
	SNAI2	0.15	0.03	4.20	69.35

TABLE 13-continued

Location of encoded protein	Gene symbol	Expression level			
		Th1	Th2	Treg	Th17
Known markers	TBX21	4851.97	21.94	513.23	26.92
	GATA3	1820.22	5684.93	4811.71	1353.37
	FOXP3	471.34	250.11	21799.93	334.68
	CCR6	102.73	42.69	939.98	401.01
	RORC	96.77	3.75	328.99	788.05

Expression levels of gene markers in the cells “with activation stimulation

TABLE 14

Location of encoded protein	Gene symbol	Expression level			
		Th1	Th2	Treg	Th17
Membrane	AKAP12	34.55	59.13	40.36	201.43
	C9orf125	0.51	0.00	1.92	35.77
	POPDC3	7.28	2.60	3.42	28.09
	UNC13C	0.04	0.36	1.76	11.11
Extracellular/ secreted	PCOLCE2	1.01	0.36	2.04	20.82
	PNOC	10.33	28.87	0.63	289.07
	TGFBI	39.99	6.24	86.85	861.02
Known markers	IFNG	191944.46	393.70	1593.07	1118.25
	IL4	4011.14	8401.51	329.94	108.98
	IL17A	84.43	458.57	1600.38	34052.24

Expression levels of gene markers in Th17 cells and ratios thereof relative to the expression levels of the gene markers in Th1, Th2 and Treg cells are shown in Tables 15 and 16. Table 15 shows expression levels of gene markers in Th17 cells “without activation stimulation” and ratios thereof relative to the expression levels of the gene markers in Th1, Th2 and Treg cells “without activation stimulation”. Table 16 shows expression levels of gene markers in Th17 cells “with activation stimulation” and ratios thereof relative to the expression levels of the gene markers in Th1, Th2 and Treg cells “with activation stimulation”. The values shown in the columns of Th17/Th1, Th17/Th2 and Th17/Treg in Tables 15 and 16 were calculated as follows:

$$\mathit{Th}17/\mathit{Th}1=\text{(Expression level in }\mathit{Th}17\text{ cells)/(Expression level in }\mathit{Th}1\text{ cells)}$$

$$\mathit{Th}17/\mathit{Th}2=\text{(Expression level in }\mathit{Th}17\text{ cells)/(Expression level in }\mathit{Th}2\text{ cells)}$$

$$\mathit{Th}17/\mathit{Treg}=\text{(Expression level in }\mathit{Th}17\text{ cells)/(Expression level in }\mathit{Treg}\text{ cells)}$$

TABLE 15

Location of encoded protein	Gene symbol	Expression ratio		
		Th17/Th1	Th17/Th2	Th17/Treg
Membrane	ADAM12	19.49	352.65	8.78
	ATP6V0A4	17.75	245.31	87.13
	ATP9A	3.26	44.86	9.84
	BVES	3.27	21.80	11.41
	C5orf40	144.92	∞	3.23
	CDH4	29.17	19.26	4.89
	DIO2	22.83	8.34	11.42
	L1CAM	5.26	4.90	3.03
	MCAM	7.99	26.44	3.14
	SHROOM2	53.13	24.85	12.71
	TMEM163	18.13	28.42	10.29
	UPK1B	7.69	191.37	41.23
	DRD2	17.29	17.73	15.19
	PGBD5	15.30	13.17	8.27
	ODZ4	36.59	94.68	106.41
	SLC6A15	55.24	8.01	10.47
	AKAP12	3.72	3.59	2.36
	C9orf125	30.34	79.90	11.59
	POPDC3	44.01	∞	19.75
	UNC13C	152.73	157.50	44.10
Extracellular/ secreted	PCOLCE2	25.86	4097.03	6.04
	PNOC	41.93	13.04	61.86
	TGFBI	24.42	45.77	5.62
	IL1A	37.28	10.48	3.90
Intracellular	BHLHE22	7.63	17.96	8.35
	PPARG	3.80	27.85	4.92
	SIM1	5.83	3.65	20.54
	SNAI2	466.76	2536.05	16.52
Known markers	TBX21	0.01	1.23	0.05
	GATA3	0.74	0.24	0.28
	FOXP3	0.71	1.34	0.02
	CCR6	3.90	9.39	0.43
	RORC	8.14	210.37	2.40

TABLE 16

Location of encoded protein	Gene symbol	Expression ratio		
		Th17/Th1	Th17/Th2	Th17/Treg
Membrane	AKAP12	5.83	3.41	4.99
	C9orf125	69.61	∞	18.59
	POPDC3	3.86	10.79	8.20
	UNC13C	266.35	31.25	6.30
Extracellular/ secreted	PCOLCE2	20.54	58.21	10.22
	PNOC	27.99	10.01	456.13
	TGFBI	21.53	138.01	9.91
Known markers	IFN-γ	0.01	2.84	0.70
	IL-4	0.03	0.01	0.33
	IL-17A	403.31	74.26	21.28

Table 15 shows that the expression levels of ADAM12, ATP6V0A4, ATP9A, BVES, C5orf40, CDH4, DIO2, L1CAM, MCAM, SHROOM2, TMEM163, UPK1B, DRD2, PGBD5, ODZ4, SLC6A15, AKAP12, C9orf125, POPDC3, UNC13C, PCOLCE2, PNOC, TGFBI, IL1A, BHLHE22, PPARG, SIM1 and SNAI2 in Th17 cells “without activation stimulation” are two or more times higher than that in Th1, Th2 and Treg cells “without activation stimulation”.

Table 16 shows that the expression levels of AKAP12, C9orf125, POPDC3, UNC13C, PCOLCE2, PNOC and TGFBI in Th17 cells “with activation stimulation” are two or more times higher than that in Th1, Th2 and Treg cells “with activation stimulation”.

Thus, it is demonstrated that these genes are useful as polynucleotide markers for detecting Th17 cells.

EXAMPLE 4

Expression Analysis of Polynucleotide Markers in Healthy Subjects and Patients with Rheumatoid Arthritis

1. Isolation of CD4 Positive Cells from Peripheral Blood of Healthy Subjects and Patients with Rheumatoid Arthritis

Peripheral blood from healthy adults (healthy subjects) and patients with rheumatoid arthritis was collected in blood collecting tubes NP-HE0557 (NIPRO) and peripheral blood CD4 positive cells were isolated with magnetic beads bound to anti-CD4 antibody (Miltenyi Biotec). Isolation of CD4 positive cells using anti-CD4 antibody beads was carried out according to the attached instruction.

2. Preparation of cDNA from Peripheral Blood CD4 Positive Cells

Total RNA was extracted from the isolated peripheral blood CD4 positive cells in the same manner as Example 1, "3. Extraction of total RNA". The extracted total RNA (0.1 μg) of peripheral blood CD4 positive cells were reverse-transcribed with a poly dT primer (Hokkaido System Science Co., Ltd.), random primers (Hokkaido System Science Co., Ltd.) and Superscript III reverse transcriptase (Invitrogen Corporation) to obtain cDNA of peripheral blood CD4 positive cells. Reverse transcription was carried out according to the attached instructions.

The number of samples of peripheral blood CD4 positive cells used for preparation of cDNA is shown in Table 17.

TABLE 17

	Healthy subject	Patient with rheumatoid arthritis
w/o activation stimulation	9	9

3. Expression Analysis of Gene Markers by Real-Time PCR

(1) Real-Time PCR Using cDNAs of Peripheral Blood CD4 Positive Cells as Templates

cDNAs of peripheral blood CD4 positive cells obtained from nine healthy subjects and nine patients with rheumatoid arthritis as prepared in the above "2. Preparation of cDNA from peripheral blood CD4 positive cells" were used as templates. The primer sets used were the primer sets for ATP6V0A4, BVES, C5orf40, UPK1B, DRD2, PCOLCE2, PNOC, TGFBI, BHLHE22, SIM1, CCR6, RORC, GAPDH, ACTB, B2M, and UBC, which were designed as described in "2. Design of primer sets". Real-time PCR was carried out with the template, primer sets and Power SYBR Green PCR Master Mix (Applied Biosystems) in 7300 Real Time PCR System (Applied Biosystems) and Ct value of each gene was measured. PCR was carried out at 50° C. for 2 minutes, 95° C. for 10 minutes followed by 45 cycles of 95° C. for 15 seconds and 60° C. for 1 minute and two cycles of 95° C. for 15 seconds and 60° C. for 1 minute. Ct value was measured by automatic calculation on 7300 Fast SDS software (Applied Biosystems).

(2) Analysis of Expression Level

Expression levels of the gene markers were calculated according to the above formula (I). The expression level of each gene marker in peripheral blood CD4 positive cells of the patients with rheumatoid arthritis was obtained as an average of the expression levels of the gene marker in question obtained from nine cDNAs used as templates. Similarly, the expression level of each gene marker in peripheral blood CD4 positive cells of the healthy subjects was obtained as an average of the expression levels of the gene marker in question obtained from nine cDNAs used as templates.

Expression levels of the gene markers in peripheral blood CD4 positive cells from healthy subjects and patients with rheumatoid arthritis and expression ratios of the gene markers between peripheral blood CD4 positive cells of healthy subjects and patients with rheumatoid arthritis are shown in Table 18. In Table 18, "RA" denotes patients with rheumatoid arthritis and "HC" denotes healthy subjects. The values shown in the column RA group/HC group were calculated as follows:

RA group/*HC* group=(Expression level in peripheral blood *CD*4 positive cells of patients with rheumatoid arthritis)/(Expression level in peripheral blood *CD*4 positive cells of healthy subjects)

TABLE 18

Location of encoded protein	Gene symbol	Expression level HC group	Expression level RA group	Expression ratio RA group/HC group
Membrane	ATP6V0A4	6.44	52.16	8.10
	BVES	0.08	32.79	403.57
	C5orf40	0.04	21.60	496.29
	UPK1B	0.31	39.65	126.98
	DRD2	59.42	243.55	4.10
Extracellular/ secreted	PCOLCE2	0.07	4.94	70.29
	PNOC	18.89	73.38	3.88
	TGFBI	1651.40	5413.26	3.28
Intracellular	BHLHE22	3.15	27.75	8.81
	SIM1	4.75	20.73	4.36
Known markers	CCR6	3136.22	4316.17	1.38
	RORC	528.64	421.20	0.80

Table 18 shows that the expression levels of ATP6V0A4, BVES, C5orf40, UPK1B, DRD2, PCOLCE2, PNOC, TGFBI, BHLHE22 and SIM1 in the RA group were three or more times higher than that in the HC group. This indicates that these genes are useful as polynucleotide markers for screening of patients with rheumatoid arthritis.

EXAMPLE 5

Analysis of Expression Ratios of Polynucleotide Markers in Cultured Th17 and Th22 Cells Derived from Human Peripheral Blood

1. Isolation of Th17 and Th22 Cells from Human Peripheral Blood

Buffy coat obtained from peripheral blood of a healthy adult was overlaid on Ficoll-paque plus solution (GE Healthcare Bioscience) and centrifuged to obtain a monocyte fraction. Crude CD4 positive cells were purified from the fraction by using magnetic beads bound to anti-CD4 antibody (Miltenyi Biotec).

The obtained CD4 positive cells were stained with the fluorescence labeled antibodies shown in Table 19 and then Th17 and Th22 cells were separated by a cell sorter (FACS Aria: Becton Dickinson). The separation was carried out with the gating shown in Table 20.

TABLE 19

Antigen	Fluorescent labeling substance	Clone	Manufacturer
CD4	APC-Cy7	RPA-T4	BD Biosciences
CD25	PE-Cy7	BC96	eBioscience
CXCR3	Alexa Fluor ™ 488	1C6/CXCR3	BD Biosciences
CCR4	APC	FAB1567A	R&D systems
CCR6	PE	11A9	BD Biosciences
CD45RA	APC	HI100	BioLegend
CCR10	PE	6588-5	BioLegend

TABLE 20

Cell	Gating
Th17	$CD4^{high}$ $CD25^{low\text{-}negative}$ $CXCR3^{-}$ $CCR6^{+}$ $CCR4^{+}$
Th22	$CD4^{high}$ $CD25^{low\text{-}negative}$ $CD45RA^{-}$ $CXCR3^{-}$ $CCR10^{+}$

The above gating is described in detail in the reference by Acosta-Rodriguez E V et al. (Surface phenotype and antigenic specificity of human interleukin 17-producing T helper memory cells, Nat Immunol., vol. 8, p. 639-646 (2007)).

2. Th17 and Th22 Cell Cultures

Th17 and Th22 cells derived from adult peripheral blood obtained in the above step 1. were respectively plated in a 96-well plate at the density of 1.5×10^5 cells/0.3 ml/well. The medium used was Yssel medium (IMDM, 1% human serum of AB-type, 0.25% BSA, 1.8 mg/l 2-aminomethanol, 40 mg/l transferrin, 5 mg/l insulin, 2 mg/l linoleic acid, 2 mg/l oleic acid, 2 mg/l palmitic acid, 1% penicillin/streptomycin).

For activation and proliferation of the above cells, magnetic beads coated with anti-CD2/3/28 antibody (Miltenyi Biotec) (hereinafter also referred to as “antibody beads”) were added at 0.75×10^5 per well. After addition of cytokines and neutralizing antibodies suitable for differentiation culture of respective Th17 and Th22 cells, cells were incubated in an incubator at 37° C. with 5% CO_2. Cytokines and neutralizing antibodies used are shown in Table 21.

TABLE 21

Cell	Cytokine	Neutralizing antibody (clone)
Th17	TGF-β1, IL-6, IL-23, IL-21, IL-1β, TNFα, IL-2	Anti-IL-4 antibody (MP4-25D2), Anti-IFN-γ antibody (R4-6A2),
Th22	IL-6, TNFα, IL-2	Anti-IL-4 antibody (MP4-25D2), Anti-IFN-γ antibody (R4-6A2), Anti-TGFβ antibody (9016)

The concentrations of the above cytokines were 50 ng/ml for IL-6 and 10 ng/ml for other than IL-6. The concentrations of antibodies were 10 μg/ml for anti-IFN-γ antibody, 2.5 μg/ml for anti-IL-4 antibody and 2.5 μg/ml for anti-TGF-β antibody.

The cytokines and neutralizing antibodies were obtained from R&D systems and eBioscience, respectively.

After three days from the start of culture, cells were diluted three-fold with the medium containing the above cytokines and antibodies and cultured for further seven days (10 days in total).

After ten days from the start of culture, the obtained Th17 and Th22 cells were respectively divided into two equal parts, and one was washed with Yssel medium and PBS before centrifugation to collect cells, which were stored at −80° C. until the subsequent RNA extraction step. These cells were designated as Th17 and Th22 cells “without activation stimulation”. The other half was added with the antibody beads and cultured for three more hours to re-activate the cells. The cells were collected by centrifugation and similarly stored at −80° C. These cells were designated as Th17 and Th22 cells “with activation stimulation”.

3. Extraction of Total RNA

The cells obtained as the above step 2. were subjected to extraction of total RNAs using RNeasy Plus Mini kit and RNeasy micro kit (QIAGEN). The specific procedures were according to the attached instructions of the kits.

4. Expression Analysis by Microarray

Total RNAs (10 to 100 ng) extracted from the cells as the above step 3. were reverse-transcribed to cDNAs with Two-Cycle Target Labeling and Control Reagents (Affymetrix), and further transcribed to biotinylated-cRNAs. The amplified biotinylated-cRNAs (20 μg) were fragmented. The specific procedures were according to the attached instructions of the kit.

The biotinylated-cRNAs derived from the cells as obtained above (15 μg) were applied to GeneChip Human Genome U-133 Plus 2.0 Array (Affymetrix) as samples, transferred to GeneChip Hybridization Oven 640 (Affymetrix) and hybridized under the conditions of 45° C. and 60 rpm for 16 hours.

After completion of the hybridization, the microarray was washed and fluorescence-labeled in GeneChip Fluidic Station 450 (Affymetrix), and scanned in GeneChip Scanner 3000 7G (Affymetrix) to obtain fluorescent intensity data.

The fluorescent data obtained were standardized with the expression analysis software GeneSpring Ver.11 (Agilent Technologies) based on MAS5 algorithm to obtain relative fluorescent intensities of the genes in the cells. The relative fluorescent intensities correspond to the expression levels of the genes in these cells.

Tables 22 and 23 show the results of the relative fluorescent intensities of the genes corresponding to the polynucleotide markers in Th17 cells obtained in Example 1 compared to those in Th22 cells. Table 22 shows expression ratios of the polynucleotide markers in Th17 and Th22 cells “without activation stimulation” and Table 23 shows expression ratios of the polynucleotide markers in Th17 and Th22 cells “with activation stimulation”. In the tables, values in the column “Th17/Th22” correspond to the values obtained by dividing the relative fluorescent intensity of a gene corresponding to a polynucleotide marker in Th17 cells by that in Th22 cells.

TABLE 22

Location of encoded protein	Gene symbol	Expression ratio Th22/Th17
Membrane	ADAM12	11.1
	ATP6V0A4	521.3
	ATP9A	33.9
	BVES	3.5
	C5orf40	7.7
	CDH4	12.5
	DIO2	10.6
	MCAM	10.5
	SHROOM2	5.2
	TMEM163	5.6
		3.8
	UPK1B	9.2
	DRD2	5.8
	LOC100134440, PGBD5	14.5
	ODZ4	8.2
	SLC6A15	12.2
	AKAP12	17.2
		36.1
	C9orf125	3.3
Extracellular/ secreted	PCOLCE2	9.0
	PNOC	38.5
	TGFBI	182.0
	IL1A	17.7

TABLE 22-continued

Location of encoded protein	Gene symbol	Expression ratio Th22/Th17
Intracellular	BHLHE22	108.3
	PPARG	13.6
	SIM1	4.6
		5.0
	SNAI2	8.2
Membrane	PTPRM	36.3

TABLE 23

Location of encoded protein	Gene symbol	Expression ratio Th17/Th22
Membrane	AKAP12	12.8
		22.9

TABLE 23-continued

Location of encoded protein	Gene symbol	Expression ratio Th17/Th22
	C9orf125	6.8
	POPDC3	5.4
Extracellular/ secreted	PCOLCE2	11.9
	PNOC	8.5
	TGFBI	367.4
Membrane	GPR34	28.2

Tables 22 and 23 clearly indicate that the polynucleotide markers in Th17 cells obtained in Example 1 are expressed three or more times higher in Th17 cells than in Th22 cells. Thus, it is demonstrated that the polynucleotide markers shown in Tables 22 and 23 are useful for detection of Th17 cells.

SEQUENCE LISTING

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<160> NUMBER OF SEQ ID NOS: 260

<210> SEQ ID NO 1
<211> LENGTH: 500
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 1

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agtgttttat gagaaagcct tcttttgggg tcaacagttt tcctatgctt tgaaacagaa     120

aaatatgtac caagaatctt ggtttgcctt ccagaaaaca aaactgcatt tcactttccc     180

ggtgttcccc actgtatcta ggcaacatag tattcatgac tatggataaa ctaaacacgt     240

gacacaaaca cacacaaaag ggaacccagc tctaatacat tccaactcgt atagcatgca     300

tctgtttatt ctatagttat taagttcttt aaaatgtaaa gccatgctgg aaaataatac     360

tgctgagata catacagaat tactgtaact gattacactt ggtaattgta ctaaagccaa     420

acatatatat actattaaaa aggtttacag aattttatgg tgcattacgt gggcattgtc     480

tttttagatg cccaaatcct                                                 500


<210> SEQ ID NO 2
<211> LENGTH: 541
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (42)..(43)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (45)..(49)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (418)..(419)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (496)..(496)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 2

cacctccaaa gcatctgtaa aatcattcta tcattgagta tnntnnnnng caaaaggaca      60

aaaacaactc ccgtgatatg attgccagga gattctgttt ccccatttct atatttgtgg     120
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attttatatg taatcaccta tgtcagagaa agaaaacctt tcaaccaaat gattggttca 180

aaaggaaaga atgattcaaa gcagaggaat ttattatgca cagcaaaatg tgtcttgtat 240

taaatatttt tattaaaaga atgtttcatt aatgcattga taagaaaact aggttagttg 300

cgagggatgt ttctggtttc atttcaaata attaaatttc tactgctact accaagagga 360

ctggctcagt ggtggcaaaa tactggtgat gctccctaga gcaggaggcc cggaagtnnt 420

gacgcagcca tcagcctgcc aagattgttt tttaatcttc acagtgtttt aaagaacatg 480

ttaaaaaaaa aaaaantcta gtgctcctgc tgtcaagatt tctgtcatgg aaaccttgtt 540

t 541

<210> SEQ ID NO 3
<211> LENGTH: 361
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (247)..(247)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 3

actgacatta ttttaaacct aactgagatg atcagttaca ttcatcagtt ggtgagtttt 60

gaagaataac tacattttat ttcaaactaa caaatgtata cggttttagt tcagtgttga 120

agaattttaa tacaatatta aattacttga actgaacagt tccttgtata tattttgcct 180

attcactgtt gatatgtatg tagcaaaatg agagttaaat aacactaaaa tatggtacca 240

ggaggcnaat tgtataggag caaagttaat aggagctttg ctgaaacaga agcatatgtg 300

taaataagct tgggcttcca gttataaatt ttgtaatttt tgtcattatt tatatcctat 360

a 361

<210> SEQ ID NO 4
<211> LENGTH: 424
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

tggtgatgaa cagcggcctt cagacgcgag gctggggagg aatcgtcggg gtttttatta 60

tttttgccgt atttgctgtc ctgacagtag ccatccttct gatcatggag ggcctctctg 120

ctttcctgca cgccctgcga ctgcactggg ttgagttcca gaacaagttc tatgtcgggg 180

atggttacaa gttttctcca ttctccttta aacacatcct ggatggcaca gccgaggagt 240

aggctgaggg ctgcacctcc cacggtggtc accatgccaa tgaaggaagt tcagtcttgt 300

ctttgatatc agcccctgca aggcgctcaa tgggaaggtt gttcttggct cacctgaagc 360

atgaaactgt gtattatttg gacgtcagcc tgtggatttg atacgactta accacgtcag 420

agga 424

<210> SEQ ID NO 5
<211> LENGTH: 463
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 5

aaagcatcct gcagcgtgag cagctcctcc acctggagct ccgaagcatc ttctcaggcc 60

aaagcggcat tacccgtgaa tctgtcttct ccgccacagc atggtttgag gcgcagtctg 120

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ttaatatagc tgggccatgt cagtgactgt tgtgtttgtg gggtcaggtg gggggcatgg    180

tatttgcaaa aaaaacaaat tatggctaat ttattatttt gttgcagtgg ggttaactgt    240

aaactcatgt aagagtctgt gatttcctca ttggttgatc tctctctctg taatcctcat    300

tgcaaatttt caccaggaca gcgtttttg attagagggg agctctggca cagtatgctt    360

taatttagca ggaacttcca gatgatttaa attctcgatg ctgtgatgac acacatatga    420

tctttcgtgt ttctgagcga ctctactttc attgtttgcc agc                      463


<210> SEQ ID NO 6
<211> LENGTH: 529
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (38)..(38)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (203)..(203)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 6

gcctcaccat tttgcgtttt ttagaaaccc attttctntg gtcatttata aagctgcttt     60

atagatatct ttgatcctgg catgccttgg tttcctctcc cttccctctt tccaatcctg    120

gtttcctaac ctcctcttgt agtaattctc aactcaactc aaagtcccaa gaatttggaa    180

tggtaggatg ctgtgcgggg agntcgaggc tgaggcataa tcactgcttc ggttctgctc    240

atcaggggac acgctccctt actcatggca gccatgtttg attgtcacag agccccccga    300

atactctgtc tatagtgaca cactgtaggt gtcataaatt ttaagaaacc tgcttttaag    360

tactatttat aggtttttct gttatacttg caacctagtt ttaaaataca tgaggatttt    420

atgaaagctt tatacagaca tttataggaa actcattctt tgattttagg tgccatttaa    480

attgataaca cttactttat aaaaagatgc tttttgtctg gatagagcc                529


<210> SEQ ID NO 7
<211> LENGTH: 421
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 7

gttacaagta ggctctcaga ggtacacttt tgggcaaagg tagatgtcca gtttcctctg     60

cccttgaggg gattatttgg aaataatttg ggattatttg gaaataattt gtgagaaccc    120

ttgctctgga gtgttttcca acttttaggc aatcacatac caccgctctc tattttttaa    180

aaccatggat tatcttcact attattaata atactttcct ttaaattgac tcatttttta    240

agcgtaaact tattttcaaa gacagcctta tattactcca taagtgaaaa accagcaccc    300

tcctgctgca aacagaaggg aagagacata agaataaaca tcatgaaaac aagataatat    360

taaataatct gacttagctt ctattgcctg ccagtgattc tgagcttaat gcctgcttgc    420

t                                                                    421


<210> SEQ ID NO 8
<211> LENGTH: 483
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 8

cacccaggcg acatcggtga cttcatcaat gagggactcc gcgctgctga caacgacccc     60
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acggcacccc cctatgactc cctgctggtc ttcgactacg aggggagcgg ctccaccgca 120

ggctccgtca gctccctgaa ctcatccagt tccggggacc aagactacga ttacctcaac 180

gactggggcc ccagattcaa gaagctggcg gacatgtatg gaggtggtga agaggattga 240

ctgacctcgc atcttcggac cgaagtgaga gccgtgctcg gacgccggag gagcaggact 300

gagcagaggc ggccggtctt cccgactccc tgcggctgtg tccttagtgc tgttaggagg 360

ccccccaatc cccacgttga gctgtctagc atgagcaccc acccccacag cgccctgcac 420

ccggccgctg cccagcaccg cgctggctgg cactgaagga cagcaagagg cactctgtct 480

tca 483

<210> SEQ ID NO 9
<211> LENGTH: 491
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 9

cccatgtcac tggtcagcgt ggtttttatg tgtattagga ttgggggatg tgaagaaata 60

agtatccagt actttataac caaagcaatt aaatgatatt ggggtaggga atgttggcca 120

gttttgttta gttttgccat cacattgtca cccagacctc acctagcccc aagtaatcgg 180

gcgccccgaa gagggagaca gagatgtgcc agagttgacc cagtgtgcgg atgataacta 240

ctgacgaaag agtcatcgac ctcagttagt ggttggatgt agtcacatta gtttgcctct 300

ccccatcttt gtctccctgg caaggagaat atgcgggaca tgatgctaag agccctgggt 360

aaatgtggtg agaatgcacg cgtgcatatg ctacacatat gtgcttctca gttgcagaaa 420

atgaactgct ttgggagatt atcagtagaa agagtgttat catattggtg ctgagtgcta 480

tgtgtgctta t 491

<210> SEQ ID NO 10
<211> LENGTH: 484
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 10

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ggttacttta catcctacta agaagtttaa gtaagtaagt ttcattctaa aatcagaggt 120

aaatagagtg cataaataat tttgttttaa tctttttgtt tttcttttag acacattagc 180

tctggagtga gtctgtcata atatttgaac aaaaattgag agctttattg ctgcatttta 240

agcataatta atttggacat tatttcgtgt tgtgttcttt ataaccaccg agtattaaac 300

tgtaaatcat aatgtaactg aagcataaac atcacatggc atgttttgtc attgttttca 360

ggtactgagt tcttacttga gtatcataat atattgtgtt ttaacaccaa cactgtaaca 420

tttacgaatt atttttttaa acttcagttt tactgcattt tcacaacata tcagacttca 480

ccaa 484

<210> SEQ ID NO 11
<211> LENGTH: 482
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 11

aatatgccac tacagctcgt aactccttta ttgtacttat catttttact atatgttttg 60

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ttccctatca tgcctttcga ttcatctaca tttcttcaca gctaaatgta tcatcttgct 120

actggaaaga aattgttcac aaaaccaatg agatcatgct ggttctctca tctttcaata 180

gttgcttaga tccagtcatg tatttcctga tgtccagtaa cattcgcaaa ataatgtgcc 240

aacttctttt tagacgattt caaggtgaac caagtaggag tgaaagcact tcagaattta 300

aaccaggata ctccctgcat gatacatctg tggcagtgaa aatacagtct agttctaaaa 360

gtacttgagg taaacatact aaaatgaatt atataatgca gcctcttaat tctttgaaga 420

actaaaaaat taggaaacaa agttctagca tttacaaaac tcagatctca aagctctgct 480

tg 482

<210> SEQ ID NO 12
<211> LENGTH: 504
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (63)..(63)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 12

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ttnaaatggt ccaagtagac agctgcttgt tggattccag tgcaggtacc tgcgatgttt 120

acgtccacac cgagcccagt gtgggactga catttctcaa tggaagtgaa atttgggatt 180

ggactttgaa gacggattac taaataataa ttattatatg taactgaagc aacctacttt 240

tgaaaatcaa ctgtattggg tagtgggagg tgggagggaa gggctttggg aaggggatga 300

atatctcttt ttacctttaa cagacttgtt taatcttctc gatgtagatg tttatgtagg 360

tacttcacat tgcaaacgcc ttttattcta tttacaagct cagatgtctc tgctctcctg 420

aatcttgggc atgcctttct gtaaccaaaa atccctgtag gcgtgctagc aattccaggg 480

tggtccgggt ttggcagatt tgat 504

<210> SEQ ID NO 13
<211> LENGTH: 538
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 13

attgacgcat atttaactcg ccctctatcc gtagagtagt catgacacta tacagatggt 60

tcgtgttcat actgcagctt aaaacaagca aaatacacag atgataatat gctaaatttt 120

cctctatcct gtacatttca caaaaaggca tatgcaatat ttacattttt aatttagttt 180

acagaatgga accaaaatgt ataaatgtta tgtttgctaa aacttcacaa tgtatattgg 240

gtctttgtac attttgcctg acttacctta aatttaaaat attttttgct atataaactt 300

taacagttat taaacagtgt tttccttttg ggtacgtatt gtttctggat atcaagatgt 360

taaatatatt tcttgctatt gtgatatgac aagagactta acttatcttg ctctgtcttc 420

cactgtacac gctgtatata ggggtcaatg tgatgctgct ggagacgaga ataaactgga 480

ctagaatagt gcattgtatt tagtctgtat tgatcatgga tgccctcctt aatagcca 538

<210> SEQ ID NO 14
<211> LENGTH: 459
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature

<222> LOCATION: (45)..(45)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (360)..(360)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (402)..(402)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 14

agccctgatt ctaccactta aggtgatgta tgatcttagg ctggncactt ctctccctca 60

tccgttttcc tcttcaacat aatgaaatag acttgaaagt ctctaaggct ctatcagttc 120

tgacattcta ggcttcatat acattaagtt gagccatatg taatcactgt gtttgtaggt 180

tagaaacagc tgagtatcgt agtttcatat atggttccag ctaatacatg caatgtggct 240

ggtgaacact tctgaattca gaaactatcc cagatctcag ctagaaccat ccactgttct 300

gtttgtccag tttcaactta agggatctcc atgcggtccc tggaagtacc cattgaaacn 360

tgcgtatttg tgtatagcag aactctgaaa taatattctg anagcagtta tctctgagga 420

attgggttat aggtgatttt ccctttccgc atgataaat 459

<210> SEQ ID NO 15
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 15

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taaatacacc gtgactttga aagtttgtac ccctgtcctt ccctttacgc cactagtgtg 120

taggcagatg tctgagtccc taggtggttt ctaggattga tagcaattag ctttgatgaa 180

cccatcccag gaaaaataaa aacagacaaa aaaaaaggaa agattggttc tcccagcact 240

gctcagcagc cacagcctcc ctgtatgcct gtgcttggtc tactgataag ccctctacaa 300

aa 302

<210> SEQ ID NO 16
<211> LENGTH: 397
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 16

caggtgcacc actgaagtga ggacacaccg gagccaggcg cctgctcatg ttgaagtgcg 60

ctgttcacac ccgctccgga gagcacccca gcagcatcca gaagcagctg cagtgcaagc 120

ttgcatgcct gcgtgttgct gcaccaccct cctgtctgcc tcttcaaagt ctcctgtgac 180

atttttcttt tggtcagagg ccaggaactg tgtcattcct taaagatacg tgccggggcc 240

aggtgtggct cacgcctgta atcccagcac tttgggaggc cgaggcggcg gatcacaaag 300

tcagacgaga ccatcctggc taacacggtg aaaccctgtc tctactaaaa atacaaaaaa 360

aaattagcta ggcgtagtgg ttggcaccta tagtccc 397

<210> SEQ ID NO 17
<211> LENGTH: 571
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 17

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gtttcttcat tgatcaacca ggtttgggtt acacaaatca attgtggggg aaaaatcaaa 60

taaaacaatt gcttattata ttttccaaag gactgagcat ttatctttta ttcacgaaga 120

tatcatatga ggatgataat gatctttaac agatttttta gagatagaat ttataaagag 180

gctgatacta agaatactac aatcaaaatt gaagctagag aatgtaaaaa tagaaagtaa 240

atagttctaa gaatattctg gcataaatta tttttattta gccaataaaa tagcctccaa 300

atgtatatct cagacaccat agagctgcta acaatgagaa tcaaggaaga tgcttgcact 360

tagatttcgt ttgttgtatt tcagtagttc tggatgtcct ttgttaaaat tggaaaatgg 420

aaaaatgtct cgacagaaat gtcaatctgg tgattctgtg aactgtaaaa tgttcacttt 480

taaaaataaa gttgtaaaca agttactcat ataagttggt attacagtag caaaaacaga 540

aaaccatgtg atccatcctg tattttgatt g 571

<210> SEQ ID NO 18
<211> LENGTH: 469
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 18

catgcctgct ctcgaggcag cagtgggttc aggcccatca gctacccctg cagctgggga 60

agacttatgc catcccggca gcgaggctgg gctggccagc caccactgac tataccaact 120

gggcctctga tgttcttcca gtgaggcatc tctctgggat gcagaacttc cctccatcca 180

cccctctggc acctgggttg gtctaatcct agtttgctgt ggccttcccg gttgtgagag 240

cctgtgatcc ttagatgtgt ctcctgtttc agaccagccc caccatgcaa cttcctttga 300

ctttctgtgt accactggga tagaggaatc aagaggacaa tctagctctc catactttga 360

acaaccaaat gtgcattgaa tactctgaaa ccgaagggac tggatctgca ggtgggatga 420

gggagacaga ccacttttct atattgcagt gtgaatgctg ggcccctgc 469

<210> SEQ ID NO 19
<211> LENGTH: 383
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 19

gagcagcgta gacagctggt aaactgaaga gcacaactat attcttatga aggaatttgt 60

acctttgggg tattattttg tggcccgtga ccctcgttat tgttacagct gagtgtatgt 120

ttttgttctg tggagaatgc tatctggcat tatggtaata tattatttta ggtaatattt 180

gtactttaac atgttgcata atatatgctt atgtagcttt ccaggactaa cagataaatg 240

tgtaatgaac aaagatatgt tgtatgagtc gtcgtttctg tcagatttgt attgtttcca 300

agggaaaagc ttgggggagg actcagttca caaaatgcaa aactcaacga tcagattcac 360

ggacccagag cttttccatg tgt 383

<210> SEQ ID NO 20
<211> LENGTH: 480
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 20

gcttttacct gttattcttt gccctcaaat acagtattgt ggtcattttg atgatatgtg 60

tgtaaaatgt gaataatcca attggtgtct gtactcagcc ttttgatgtc tttttaggac 120

tttctcttct acacagcaat acgtcgtgct cgagtatcct tgtagcaaag cacatagagc 180 cagctgtcct gtcagttccc ctgtttgcct ctgaaacgtc tggttagtgg ggacccaaag 240

attctagtga gtcaacatcc ataactctgt atctagttgt attattcata gaaaatcaat 300

ctggtgctaa tggttggccc tggtgttgtt gggtggcagc tgctccttcg ccctcttgta 360

gtgtggctgt ggagggctct gcctatgggg ggtggcctgt ggcttgtatc cttcagtcca 420

ccacagcaaa tgtgtgtaga tttcatgctc gacacttacc actcacctat caacagatca 480

<210> SEQ ID NO 21
<211> LENGTH: 389
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 21

ccactgggcg cggccagata agtttttaag gttccttctt gctttagcat tctgagaaat 60

gtctaattgg tagtaagaca agagtaatag caacctgtat tgttagtatt taaccaaata 120

ggctaaaatt ttaatcaggt accttatgta ttaaatagaa atcggaatgt accataataa 180

atccaaactc tcaattacgc catggtaatt cagtcactaa aatatgtaaa gatagaaaat 240

tttttaattt aaagaagtgt gaaacatagc cattgattga tcagaattct ggaatctgaa 300

tattaaaacc ttacttagtg actggaatgg tatatgctcc ctccaaaagt ttatctttgt 360

ttattgatta aaggtaatcc ttactttct 389

<210> SEQ ID NO 22
<211> LENGTH: 497
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 22

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tttgttttat ggctagtctt atctggcctg gttatttcct tgcggggagg agagggtttg 120

ctaatctgct cccagcccaa cctattacca ccccacctcg ctgggaccta ctgctcggga 180

ggcagcagac agggagccac cagcagtggc ttcctggccc tgtgctgggg gtggggggaa 240

gctgggggca catgtggccc ttgccttctg agcagctccc agtgccaggg ctttgagact 300

ttcccacatg ataaaagaaa agggaggtac agaagttcca attccctttt tattttgctg 360

gttggtatct gtaaatgttt aataaatatc tgagcatgta tctatcaacg ccaagaattt 420

caaagtctcc ttcaacaata tgaggctttt aggatgttta tattccttca tccctcttgt 480

ttcccaggtt ttgcagg 497

<210> SEQ ID NO 23
<211> LENGTH: 309
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 23

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atgaaactta ctcaattcat accaccctga aatggaggac agaggtgaca aacttcagtt 120

taataggttt ctcaccaagt tgtatgttcc attggcccag gattcttgca ctaatgggtt 180

tctatcacat tatgtctata aatgggtgca ctttactgtt tgaatttgta actgaagtac 240

tggatattta agtgtgagta atgtcttcat tagaaaatag cagaaccgct cttgtctttt 300

agtgtattt 309

<210> SEQ ID NO 24
<211> LENGTH: 362
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 24

aatatgattt tgattcttcc tcctctttgc tgtcctttca agacacttgc tggaaaaagc 60

tttaatgcac ttagttttcc tttaggtttt ctatgactca gatgtaaagg actttctctg 120

tacagtatat tatccaatgc atgtttgttc tctctcctga tatattgaac accacacagt 180

tgtgaagccg tgcagtgggg atgccccaca ccccacagag gcatctaccc ctgtgtataa 240

ggaaagacat tttcctttgc tgtacttgct tgagcagttt tattgtctgt acatgtgagc 300

tgtgtgagat agatgtgaaa agttcaaatg aatgcatttt cctgccccat gtatacagat 360

tg 362

<210> SEQ ID NO 25
<211> LENGTH: 485
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 25

aggggcagtg gtggttttct gttctttctg gctatgcatt tgaaaatttt gatgttttaa 60

ggatgcttgt acataatgcg tgcataccac ttttgttctt ggtttgtaaa ttaactttta 120

taaactttac ctttttttata cataaacaag accacgtttc taaaggctac ctttgtattc 180

tctcctgtac ctcttgagcc ttgaactttg acctctgcag caataaagca gcgtttctat 240

gacacatgca aggtcatttt ttttaagaaa aaggatgcac agagttgtta catttttaag 300

tgctgcattt aaaagataca gttactcaga attctctagt ttgattaaat tcttgcaaag 360

tatccctact gtaatttgtg atacaatgct gtgccctaaa gtgtattttt ttactaatag 420

acaatttatt atgacacatc agcacgattt ctgtttaaat aatacaccac tacattctgt 480

taatc 485

<210> SEQ ID NO 26
<211> LENGTH: 498
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 26

catcaaacat gttgggacaa tgcccatagg aatggacctc cttccccgtc tccagctggg 60

actggtgttt ttttagtctc tggagtatga tggttctcat gggtaggatg agatctttgg 120

cagaaaggtc ttcggtggtg ctctgagcct gcgctgcata ggactgagca gacccacctc 180

ctccagcttg ggtggccctg ccactcctgg ttccaagtct ctcctttcct ggcaggtctt 240

aagggaagat tgtacccctc accctttaca tacccagaat catcagtatg tcacttccta 300

atttctatca gtgtatctca ttatttcata ctgttttact aatcctaagt ctaaacagat 360

ttgctcaaaa ggagaccatt ctatttttta aagtacttag tgatacacgt ataagctttg 420

catggacgaa ttaaataagc acattgacct tttcttgtac attcagaacc tgaacatcca 480

tgtgaaaact gggtccat 498

<210> SEQ ID NO 27
<211> LENGTH: 485
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 27

acccttaca tacccagaat catcagtatg tcacttccta atttctatca gtgtatctca 60

ttatttcata ctgttttact aatcctaagt ctaaacagat ttgctcaaaa ggagaccatt 120

ctatttttta aagtacttag tgatacacgt ataagctttg catggacgaa ttaaataagc 180

acattgacct tttcttgtac attcagaacc tgaacatcca tgtgaaaact gggtccattt 240

ttgagagatg tgaaactaca gtttatttgt aataaataaa tataatctat ccggtatatg 300

catatatcta tatgctgtgt taagtggtaa tgggtacatt acagtctgtg agagatggat 360

cgctccctct gtaaggaaca agacgttctc agctgatgtc acggtaggtt tagattctgt 420

agagtgttcc ccaacccgca ccgttctgta cctctcacac cactgcttgc ccgggcagta 480

gtggc 485

<210> SEQ ID NO 28
<211> LENGTH: 520
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 28

gaagcaagtt tccatgattt ctgaagagct ggtataggaa gtttctttct tccttttgtg 60

ttacatgtgc attaaacaga acaagctgtg tgtcatcaca gattgtactg tgggctcaga 120

aaccgtgaga gagcccccac cgtggacacc ggctctatgg ccacaggaaa aggaacgttt 180

ccaggcattt tgtctccagg gctcccgctg gacaggcacg tactgccccg gggagtaaat 240

gcggagagtt cacgaactgt gcccaacgca tgttatagcc agggtcctac taactactca 300

gtaaaagaac gtattgttgt attcctccag tgttaagcta tagccatgtt aaaagtcact 360

gtgcatttat tctcagcatc aaataccttg taacgtcttc tctgccttgt tagtgcatat 420

ttttactttt ctgatactgt aaagaatata tccagtatgt aaatgaatgt tctataaatc 480

ttttgtatag tcattttctc tgctccttaa atatcatctc 520

<210> SEQ ID NO 29
<211> LENGTH: 565
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 29

gtttagtagc ctcaattctc cattaattaa aagtgtgggc tgggcgtggg ggctcatgcc 60

tgtaatccca gcactttggg aggccgaggt gggcagatca cctgaggtca ggagttcaag 120

accagcctgg ccaacatggt gaaaccccgt ctctacaaaa atacaaaaat tagccaggcg 180

tgatggcagg tgcctgtaat cctagctact tggcaggcta acgcaggaga atcacttgac 240

cgggagacag aggttgcagt gagctgagat cgtacctatt gcactccatc ctggatgaaa 300

gagccagact ctgtctcaaa acaaacaaaa aagcgtgggg acttctgggg acagacaagg 360

tgcctgttat atatttactc agtctttgcc ctgaatggtc tcagcttgag accatttcaa 420

actggagaga agcaagccag ccaatagaat ggggtgattt acagggattt ctgtttactg 480

tcaaaatatt tctcatctgc actatgtttc catttgtggt cctgaaggaa attcttataa 540

ctcaacattt gtctggtctt ataag 565

<210> SEQ ID NO 30
<211> LENGTH: 401
<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 30

gaacaattct aaaagccctg tgatttgaaa aatatagaat cattaatggc ccaagatagg 60

ccttcacacc ttcacaggtg cgaaaggaaa ggccttcaca ccctcacaga ggcatcatgc 120

aaaggacagc ggctttggct tttccaattt tccatcttta ggccctggtg agaggcacac 180

ttatgcacta aaatgcacat atatgcacat gcattcaaaa ataggcattt ggtacaatgg 240

tgatcttgta cctgatgggc tgaaaccagc ttaagaacaa atttgttctt cctgatatga 300

taactaggtc tccaagagaa aatagaaagg ctgctttagt gccttacgct tactaaattt 360

aaatctttat ttacctgggt ttgagcctac agtctattta t 401

<210> SEQ ID NO 31
<211> LENGTH: 518
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 31

gagaccatgg tctgtagacc ccttcccgat tctcctgtcc cagcttggaa ggcattgaaa 60

acagtctccg tttacacatc tcttcatacc acgtgtttga agtgttaaaa ttcaaaggga 120

tcattgaata aaacgggtgt agagtacagg aatggggcag acgcgattca ggtgaacagc 180

acaagaagaa tatgaggtgg ttcctaggag caacactttc gacctccagt tctccctgat 240

gacagtagct gtctccaaga gaaaaatcct cacttattaa ctctcttttc ttgcatctca 300

tttttataga gctactcatc cttatttgga aaaaccaaca acaaaaaagg cttttagaaa 360

atggttgtaa atctgacttc tttgcaagta actatgtata ttgtaaatag atataaaagg 420

cctttttttct aaataaggac ttaactgcct gtaacatgaa acttcaaact aaaccactaa 480

ctcaatgaac tacttatggt ttgtctgaca tccctcac 518

<210> SEQ ID NO 32
<211> LENGTH: 531
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 32

tatctttctg tgttccatgt aaatttattt accaacatct attgtcaaca tgtacatcta 60

ccttagtatg gtctgcattc tttttctgag agtacctcat agggctcctg cctgatcttt 120

gtagtttgtt cattcatcca tccacctgtt catttgttca tccatgtatt ctaacatttc 180

tatgtagtgt gcaactctaa tgtcatgctt ttgaagaaga gaatagctgc ccatagcagc 240

catccgtctg gataatagca aaacactcta gataagttat tttgcacttt cttatgtata 300

aagttggtag aaacttattt ttgctttgta tcatttaaat acattttgtt ttggtaaatg 360

aactgtgtat aaaatattta tgccgttaaa actgttttta gaaagtattt ttaatttcag 420

caagtttggt tacttgttgc atgactctta acacagctga ctttttgtgt cagtgcaatg 480

tatatttttt gtcctgttat taacttgtaa gccctagtaa tggccaatta t 531

<210> SEQ ID NO 33
<211> LENGTH: 459
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 33

gtggtttcca catgctctga gaagaggagc cctcatcttg aagggccagg agggtctatg 60 gggagaggaa ctccttggcc tagcccaccc tgctgccttc tgacggccct gcaatgtatc 120

ccttctcaca gcacatgctg gccagcctgg ggcctggcag ggaggtcagg ccctggaact 180

ctatctgggc ctgggctagg ggacatcaga ggttctttga gggactgcct ctgccacact 240

ctgacgcaaa accactttcc ttttctattc cttctggcct ttcctctctc ctgtttccct 300

tcccttccac tgcctctgcc ttagaggacc cacggctaag aggctgctga aaaccatctg 360

gcctggcctg gccctgccct gaggaaggag gggaagctgc agcttgggag agcccctggg 420

gcctagactc tgtaacatca ctatccatgc accaaacta 459

<210> SEQ ID NO 34
<211> LENGTH: 380
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 34

aaaaggtact agttctgcat ttcagagttg gcttgttgaa ccaggctata tgcttccaag 60

atttaaatgt ttttctgtat tatactctca attgtgtttt aaaaaaatct cttacagaaa 120

tctctacctc aggcactaag tgttatgaca tgggtagcat attgatattg aaaacttagc 180

taggacttcc agccttttaa gataatttaa atgtaaaatt aaatggttaa ccagcaatct 240

aatgtcatgt ggtgtgcagt ttggatattg catgaacagc taaggaatca cctgttctag 300

tgccaaagat cactcattgc taattttgtt ctgtacagct tatgtaatat tttcatggtg 360

gagacggact ctgtgtgctc 380

<210> SEQ ID NO 35
<211> LENGTH: 286
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (63)..(63)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (121)..(121)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 35

ttaatttctg tgaagagtgc ccctggtgtt tcatcttggc ctgttttgat gagaatgtta 60

tcntttgtgt ctggataacg cgtcagcttc ttaaagtaca tataaagata ttctgtcacc 120

nccccacatg cacacacttt taaaatctat ttttattctc ttgctaaagt tgtaattatg 180

tcaagaattt tccagctcta actgccttct tagtacatgt ctttctgcct ttgaagcata 240

tgagtttgcc aaagtcattc tcccctaatg acatattgtg gactta 286

<210> SEQ ID NO 36
<211> LENGTH: 486
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 36

gcactggcag cgaggctcgt gtgtccccca ggcagatctg ggcactttcc caacccaggt 60

ttatgcgtct ccagggaagc ctcggtgcca gagtggtggg cagatctgac catccccaca 120

gaccagaaac aaggaatttc tgggattacc cagtccccct tcaacccagt tgatgtaacc 180

acctcatttt ttacaaatac agaatctatt ctactcaggc tatgggcctc gtcctcactc 240

-continued

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agttattgcg agtgttgctg tccgcatgct ccgggcccca cgtggctcct gtgctctaga    300

tcatggtgac tcccccgccc tgtggttgga atcgatgcca cggattgcag gccaaatttc    360

agatcgtgtt tccaaacacc cttgctgtgc cctttaatgg gattgaaagc acttttacca    420

catggagaaa tatattttta atttgtgatg cttttctaca aggtccacta ttcctgagtt    480

taatgt                                                                486


<210> SEQ ID NO 37
<211> LENGTH: 521
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (96)..(96)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (102)..(102)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (354)..(354)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 37

gagtccaaat gtcatcagtg ctcattttga gataccctgc tatcgatggt cgctacaaac     60

caggaaatac tcaagttatt atgtgtatac attggnttta gntttatgaa acaatttacc    120

ttcatgatct catagttaaa attgtaataa atttaggaat ataaaggatc aatatgggaa    180

gcaaaatttc taaaggcagt ttctgttgtt ttaattagta tttgtgtagt tcaaaccagg    240

aaggatttga ctatcattag attttgctta actttatgaa agctaaaata ttctctgtta    300

taaaggggca actccatctg gtcctatagc atctttacta ctgatttttt tttngtttaa    360

tttgaaaatg caaagaattg ttaaatgttc ttaaatgttc tcactacaaa aaaagaaaaa    420

agataactac gtgaggtgat ggatatgtta attagctgga ttgtggtaat cattttggaa    480

tgtatatgta tatcaaaaca tgtagtacac cctaaatata t                        521


<210> SEQ ID NO 38
<211> LENGTH: 518
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (102)..(102)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (360)..(360)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 38

caggcgaggg ccaatgttgt gtttcttacc ccctctggaa tgccaaaggc aaggtactag     60

gtgacctcct ggtccccaag aaaatgtgat ttattctgag gncgaacagc caagggagga    120

ctagtctgga gcacgctcgg ccgtcctggc aggagctgag cctcaggtgt ctggcggtgc    180

cccagcagcc ctggattcac ccaacaccag aatcccactt ttctaaatcc acctgttgtt    240

ctgagcacct ctgaacccgc agcttcggca aaaggagtct gtaccaagct gcttctggat    300

gaccaacact ggagactctg gccttaccat gtggaaatca ttttcctgaa gtctggaacn    360

aattttgaga agttttttc tcaacacttt tgtgtttcta acactgtatc ttgactgtgt    420

aaataccaac aaggctgtaa ataaatgcag atgtagatac cttctagaaa aaaaaaagca    480
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taaaaacaaa accagaagtg atcccgtgta gccttcgt 518

<210> SEQ ID NO 39
<211> LENGTH: 462
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (177)..(177)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 39

gaggacagca aaccttttca gcacttctct cagagcaaat ggaaacacac agtaagtagc 60

tttctgacta cattattttc tggtcacttt taaagaaagt ttacaacctg ttctgaaact 120

atttgtcttt tcactggttg taagtgtacc ccaatctcag ggagtatatc tgtagtncca 180

caggcaaaag atccactcct tcccacactc atttgcctga acttactcga agggctgcat 240

ttctctgagt ttacgaaatt gtgtcattat ggtccccata cagtggtatt taacttttaa 300

agcaactttt aagaaaactc gacttgtttt ttgttcattt taagtgtgtg gtactaaaaa 360

gacatgttag actttttta aaaaagcact tatgttttga aaatagaata aataataaga 420

atttccaatt aaatcatgtc tggtgccaat gtgcaaaact tc 462

<210> SEQ ID NO 40
<211> LENGTH: 470
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 40

gtgaacagct tggccttttt tgggtgtctt gacaggccaa gaagaacaaa tgactcagaa 60

ccggattaac atgaaagtta tccaggcgca gagttgaaga agcataagca agcaagacaa 120

aaacagagag accgcaagga ggaagatctg tggtactgtc ataaaaaaca gtggagctct 180

gtattagaaa agcccctcag aactgggaag gccaggtaac tctagttaca cagaaactgg 240

tactaaagtc tatcaaactg attacacaga ctgtaagaat tcaaagtcaa ctgacatcta 300

tgctacatat attatatagt ttgtacttga ctatgagcca ttaacttaaa gcatatgttt 360

caaatagcca ttgctactat tccttgtccg gtgtaatttt attttattgt ttttactttg 420

gaagagatga actgtgtatt taacttaagc tattgctctt aaaaccaggg 470

<210> SEQ ID NO 41
<211> LENGTH: 298
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (42)..(42)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (45)..(45)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (47)..(53)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (55)..(55)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (57)..(60)

<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (64)..(83)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (85)..(85)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 41

accctctcct tgagtttctg tgaattaaaa tatttgcaaa tncanannnn nnnanannnn 60

aaannnnnnn nnnnnnnnnn nnncnactga tgctgggagc caaatgctgg tgctttgaga 120

gtcccggagg ccccggggtt cccgccccgc tggtgtgtat atgtgtgtct gtgtgagtgt 180

gtgtgtgagt acagatgtga gaaggtggtc acacacagat gggtaagccc actgatctac 240

ttgtagtcac tcagtgtaat cattaggcta tcttcaagga atcattgtgc agtcaaaa 298

<210> SEQ ID NO 42
<211> LENGTH: 407
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (238)..(238)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 42

gtccaagaac tcaagtcact ttacatctat taactgcttt ggagacttca taatttttct 60

aggaaaggtg ttagtggtgt gtttcactgt ttttggagga ctcatggctt ttaactacaa 120

tcgggcattc caggtgtggg cagtccctct gttattggta gctttttttg cctacttagt 180

agcccatagt tttttatctg tgtttgaaac tgtgctggat gcacttttcc tgtgtttngc 240

tgttgatctg gaaacaaatg atggatcgtc agaaaagccc tactttatgg atcaagaatt 300

tctgagtttc gtaaaaagga gcaacaaatt aaacaatgca agggcacagc aggacaagca 360

ctcattaagg aatgaggagg gaacagaact ccaggccatt gtgagat 407

<210> SEQ ID NO 43
<211> LENGTH: 375
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 43

agggtaactt ccagtgtcac aatgagcagt tctgtaagtg ggtgcctctc agcacatttc 60

tatgaatata ttatgtagat aggctgtatt gattttggta gcattgacac cttcttaggc 120

aattagttga agaaaactgc aaaatatttt cttatgtaat agctgtatag agcaatagca 180

atcaaagcat gagaaggcac taacgctggg atgaaagatg agattcagag gtgactgaga 240

atcatgtgag tgatggctgt atattttgtg taaaatatat gtgtgaaaat gaactaagag 300

tgagttactc agcactctca agaattatgc agattctgca tttttcttat gccgtgtgcc 360

taaaaaccta cttga 375

<210> SEQ ID NO 44
<211> LENGTH: 527
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 44

gggtggttct ggccaggaag gcacaaggta gctgtgggcc aagacaccag ccctgtccta 60 gcccttcagt aagaccttgc caggagagga gaaggatgcc tgggtgccag gcaagacaag 120

cccctcagca ggagagaggc ccagaggctc cagctggcca ccgtgcccca caagatggcc 180

cctgtgtggt tccctttacc ttggcttcct ggcccagtcc ctgcctctcc acctgcaccc 240

tgcttcctgg cccagtccca ggttggagtc cctctgcata gctgactact catgcattgc 300

tcaaagctgg cttttcacat taagtcaaca ccaaacgtgg ttgccacatt tcatcagaca 360

gacacctccc tctggagatg cagttgagtg acaaccttgt tacattgtag cctagaccaa 420

ttctgtgtgg atatttaagt gaacatgttt acaattttg tatatatcac tctctccctc 480

tcctgaaaga ccagagattg tgtattttca gtgtcccatg ttccgac 527

<210> SEQ ID NO 45
<211> LENGTH: 518
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 45

gtgccatagt gcaggcttgg ggagctttaa gcctcagtta tataacccac gaaaaacaga 60

gcctcctaga tgtaacattc ctgatcaagg tacaattctt taaaattcac taatgattga 120

ggtccatatt tagtggtact ctgaaattgg tcactttcct attacacgga gtgtgctaaa 180

actaaaaagc attttgaaac atacagaatg ttctattgtc attgggaaat ttttctttct 240

aacccagtgg aggttagaaa gaagttatat tctggtagca aattaacttt acatcctttt 300

tcctacttgt tatggttgtt tggaccgata agtgtgctta atcctgaggc aaagtagtga 360

atatgtttta tatgttatga agaaaagaat tgttgtaagt ttttgattct actcttatat 420

gctggactgc attcacacat ggcatgaaat aagtcaggtt ctttacaaat ggtattttga 480

tagatactgg attgtgtttg tgccatattt gtgccatt 518

<210> SEQ ID NO 46
<211> LENGTH: 233
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 46

gccatcacag ttgcgattcc atgagtagct gctttatgac tgctttttgt actatctgga 60

tgtgcccaga gttacttctg tacaagctct gtatctatgt ccgttgagaa cattatttta 120

acaagaagaa caccaacagt agcatgaaat ataatactgt tttataattc taaagctgct 180

gttaatttat gaagtacata ataatctaat gtaaactgca gaagtcagag caa 233

<210> SEQ ID NO 47
<211> LENGTH: 548
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 47

agggtgccaa gagatgcctt tctgaagttg gccacttctt gaagattcaa atatttatct 60

ctttatttag acatggttgc ctgcaggtat ttcactgttt actgttgtta gagatatagg 120

cactggggca gctgaggaac ctcaatatgt taagagcctt ggctttggta gcctcctggc 180

aggagcagca gtttgccaca ggtccggacc tctccctcca cacagccaca ctgcctcatg 240

cagtctgacc cacccagtga gggtgcattt gaacactgat tatattctcc atttgttttt 300

aagctctgct ttgtgttaga gcttgtgact gccaaaaatt ttgtgcacag tgatatgact 360

-continued

gttttaggat cttaagggta gaattttgtg aaaggtgaga tcctttggaa ttgagttctt 420

tctcattggg tatgaaaatg gatgtatgtt tagaatatat gcccaacgag gcaggaccat 480

gtggatagat tccatttgtt tccttgacct gatgtaataa aaactgataa aagccgtgca 540

gtgcccgg 548

<210> SEQ ID NO 48
<211> LENGTH: 352
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 48

atgaaatatg ccagatctat agtattttaa tgtgcatcta ctttaaatga gtcatcttgg 60

ggtttttata attcccttat gttcttgccc ctctacactt gaaataacaa aatgccttaa 120

ttttatggat tagttctctt atagtagaca ggcagctata tgcagcaaaa ccaataaagt 180

tatttttcaa ctttcatagt tgtaaaatat cttataacag aatacaaaac agctaagaaa 240

acatgccaca ttttatttta gcattttcaa ataatttgtt tttggtgtaa gcacaggata 300

aaaaaggaga gcgtcaaaga aaagagacat aacacctaac attcataaaa at 352

<210> SEQ ID NO 49
<211> LENGTH: 488
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 49

ataggttata ctttgctgac gattcacatt ttattagttt ggttatgttt tgtcctttta 60

aaacattttc ttttgagatg ggggtcttgc tctgttgccc acgcaggagt gcagtggcat 120

gctctcagct cactgcagcc ctgactgcct aggctccagc aatcttctta cgtcagcctc 180

cagagtagct gggaccgcag gcacttgcca ccacgcccca ctaaaaattt tttaaattgt 240

tgcctttctt gaagtgttct ctgcctgtct ttgtcacaaa atttcatttt tctcatagtt 300

aatttcatct ctccggtaag attttattgg tgtttctttt ataactttgc agttcttaca 360

ccgtttggtg attttcatgt ttcttagaaa ctttaaacct ttaacttcaa acattaaaat 420

acaagtcttt taagtacatg agtgcttaga aatgtacata atgtttatat acacttatgc 480

cttacatt 488

<210> SEQ ID NO 50
<211> LENGTH: 297
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (117)..(118)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (120)..(120)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (122)..(122)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (165)..(165)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (177)..(177)
<223> OTHER INFORMATION: n is a, c, g, t or u

<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (193)..(193)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (240)..(241)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (254)..(254)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (256)..(260)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 50

caccaagtta cgtcaaagtc tcaggagcag ctccggtctc catagaggct gggtcagcag 60

tgggcaaaac aacttccttt gctgggagct ctgcttcctc ctacagcccc tcggaanncn 120

cnctcaagaa cttcacccct tcagagacac cgaccatgga catcncaacc aaggggncct 180

tccccaccag canggaccct cttccttctg tccctccgac tacaaccaac agcagccgan 240

ngacgaacag cacntnnnnn aagatcacaa cctcagcgaa gaccacgatg aagcccc 297

<210> SEQ ID NO 51
<211> LENGTH: 539
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 51

gttgatggcg aatttctgca ttacatttcc ccccttcagt tcctggattc tcctgagtgg 60

gattcactga gacccacaga ggaaggcatt tttcaggtaa ccctcactgc agaaactgat 120

tgtcgatatg tgtcttggag gagaaagaaa ttatatctgc tctttgctca gcatcgctac 180

atctcccgcc ttttttcagt gctaattggc agtgacattg cagataaact ctatgccttg 240

aatgacaggg tatatatagg aaaaagatat cactatgata ttcggctacc caacttctat 300

caaatgtcaa ctccagaaat acgcagatca cccctgacac aacattttca gaattccaga 360

cgatactgtg ataaatgaca tcaaagtctg aaatttataa gtataaaaaa agactctctc 420

ttcatcattc cccagtgaaa tagcaaaata caaaaaaaga gctccctaat gtttttataa 480

atcaaattca gaagcgagat gccattgcca actgttttat tcctttcaac aactgcatt 539

<210> SEQ ID NO 52
<211> LENGTH: 520
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 52

aactttgtat agcccatgta cctaccttgt atagaaaaat aattttaaaa atttgaatgg 60

aaggggggtaa aggaagtcat gaagtttttt tgcattttta tttaaatgaa ggaattccaa 120

ataactcacc tacagatttt tagcacaaaa atagccattg taaagtgtta aaatttacga 180

taagtattct attggggagg aaaggtaact ctgatctcag ttacagtttt tttttccttt 240

ttaatttcat tattttgggt ttttggtttt tgcagtccta tttatctgca gtcgtattaa 300

gtcctattgc tagaataggt tactacaaaa aaggttatat tctgaaagaa aaataactga 360

cattatatat aaccaattaa tttaaagtat tgccatttaa attacacact gagagcatgt 420

cctatgcaga catagatttt tctgttcatt tatttttctt cattgcagtg gattgatttg 480 ataaatagat gtgttgaatt actacatttg ctgtacatat 520

<210> SEQ ID NO 53
<211> LENGTH: 577
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 53

tgccactaat tcattcacac taaggtgtaa atgattgata ataggaatga gttacctctt 60

cccacagaca tttgttttta agtatgacag agcagggcct taatcccaag ggaaaaggtt 120

atggaactgg agggggtgag ctttctgggt agaaggagac ttcctgaatt tccttaaaac 180

ccagtaagag taagacctgt tgttttggaa ggtctgctcc accatctaag agcactgttt 240

ttttttttt gttgttgttg ttgttttacg gtctctgagg gaatatagta aaaatgcata 300

tgcacgtgca atttgcacgg cagcatttca ccgattgtgg actgtattgg ctaatgtgtt 360

tcctggtctt tagatgcaaa ccattaataa cactatctta tctcatagtt ttttcagggg 420

tgcttcttga ttagtaggga attttgaaca cctctttaaa tacagctaga aaataaaacc 480

aatttgtaaa gccacatttg catatgatgc cagcctcacg catttgtata tctccagaaa 540

ttcaggtatg cctcaccaat ttgcccgtct ttaataa 577

<210> SEQ ID NO 54
<211> LENGTH: 539
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (179)..(179)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 54

agggcatgtt aacagtatac cagtaacagc actttatctc atttatatga acacctttga 60

ggtgctactt aagtccaagc tctgatgtat tattcatttg taaagataag gtacaggaat 120

gaaccttggt ttaaaggtat ttttatatga aaatggtgtg ttattggaag atgttaaant 180

gctaatttga gagaagtagg agtgtatctg ttttatatgt tgggatgtga aatttatttt 240

ctaaaattga ggagaaggaa gttatatatt tgcagaatgt tttaaagtga attgttgtaa 300

tgaagttcct gtgaacatca ttatggtttt gtacaaatag gaacctctga tgtcattctt 360

caacgtttgt tcctgtgtgt acaattgtac tttgtatgaa cagctttatc atttttatag 420

gctttccatg agttttgctg taactactat ggcttattta ttttctttaa tatttgtgaa 480

agtcttactc ctttgttagt tttgtttctg cacaactact gtacttttcc atatggaat 539

<210> SEQ ID NO 55
<211> LENGTH: 480
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (45)..(45)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (133)..(133)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 55

aacggaatac ctgctaggtt ccaggaatga gctcacctaa caganagcaa atgtgtctgg 60

ttagatctca gcagagccca ttctgcaaga cctggctgag ccagatgaga gggtgggccc 120 tgtgctgggg ggnccttggg tcacacacag gaaccgagac ctggcttcca ccccccagtc 180

acccacttgg gttatctgct ggaagttatc gataggactg tgtggccaac caagtgcttg 240

tgagatcact gacactgcaa aaacaaagca aactgctccg ggtaccagga cttcctccaa 300

cctggcaagg gtgtgcgctg aggcggggct tgcaggtgag gggctgtat gcttcaggaa 360

ctaactaaat gcatgcagaa ggtaagaggc atgatgggag gtgttcaagc acagcaatcc 420

catttgggag ttattttgat actgcgatga gtaagggtaa gggcgcatgg aatggggcta 480

<210> SEQ ID NO 56
<211> LENGTH: 273
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (163)..(163)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (197)..(197)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 56

tactatatat tgtactgatg ccaaaagtca tgttttcatc cacttagtga aaaaatagta 60

aaattaagtc ggaagaaatt gcttaaaatt ttgtaatttg tatttataag ccccaaatgc 120

atcaaatgca gtaggagaac aatgtaatac agcttggtac ctnaaaaata tagctaagtt 180

ggtttttgaa tataaancag tttatgaata tgtgcatttt ctgtattgtt atgatttgac 240

tttttagagt ctatgccaaa atatatggct gta 273

<210> SEQ ID NO 57
<211> LENGTH: 544
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 57

ggagtttgca ttcttattca tcagggagga aagtttcttt gaaaatagtt attcagttat 60

aagtaataca ggattatttt gattatatac ttgttgttta atgtttaaaa tttcttagaa 120

aacaatggaa tgagaattta agcctcaaat ttgaacatgt ggcttgaatt aagaagaaaa 180

ttatggcata tattaaaagc aggcttctat gaaagactca aaaagctgcc tgggaggcag 240

atggaacttg agcctgtcaa gaggcaaagg aatccatgta gtagatatcc tctgcttaaa 300

aactcactac ggaggagaat taagtcctac ttttaaagaa tttctttata aaatttactg 360

tctaagatta atagcattcg aagatcccca gacttcatag aatactcagg gaaagcattt 420

aaagggtgat gtacacatgt atcctttcac acatttgcct tgacaaactt ctttcactca 480

catctttttc actgactttt tttgtggggg cggggccggg gggactctgg tatctaattc 540

ttta 544

<210> SEQ ID NO 58
<211> LENGTH: 507
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 58

tgtcaagatg cttctggcca tggtccttac ctctgccctg ctcctgtgct ccgtggcagg 60

ccaggggtgt ccaaccttgg cggggatcct ggacatcaac ttcctcatca acaagatgca 120 ggaagatcca gcttccaagt gccactgcag tgctaatgtg accagttgtc tctgtttggg 180

cattccctct gacaactgca ccagaccatg cttcagtgag agactgtctc agatgaccaa 240

taccaccatg caaacaagat acccactgat tttcagtcgg gtgaaaaaat cagttgaagt 300

actaaagaac aacaagtgtc catatttttc ctgtgaacag ccatgcaacc aaaccacggc 360

aggcaacgcg ctgacatttc tgaagagtct tctggaaatt ttccagaaag aaaagatgag 420

agggatgaga ggcaagatat gaagatgaaa tattatttat cctatttatt aaatttaaaa 480

agctttctct ttaagttgct acaattt 507

<210> SEQ ID NO 59
<211> LENGTH: 533
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 59

gaagatgggc gaggcaaaat catgccaaac agctttatca tgatgttcaa gaccaagaat 60

cagaagctcc tggatgcctt aaaaaataag caatgttaac agtgaactgt gtccatttaa 120

gctgtattct gccattgcct ttgaaagatc tatgttctct cagtagaaaa aaaaatactt 180

ataaaattac atattctgaa agaggattcc gaaagatggg actggttgac tcttcacatg 240

atggaggtat gaggcctccg agatagctga gggaagttct ttgcctgctg tcagaggagc 300

agctatctga ttggaaacct cccgacttag tgcggtgata ggaagctaaa agtgtcaagc 360

gttgacagct tggaagcgtt tatttataca tctctgtaaa aggatatttt agaattgagt 420

tgtgtgaaga tgtcaaaaaa agatttttaga agtgcaatat ttatagtgtt atttgtttca 480

ccttcaagcc tttgccctga ggtgttacaa tcttgtcttg cgttttctaa atc 533

<210> SEQ ID NO 60
<211> LENGTH: 537
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (209)..(209)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 60

gcccggaagt cggccaggaa gttggccaat cagaagcggt tcagtgagtt tatgaggcaa 60

tacttggtcc tgagcatgca gtccagccag cgccggcgca ccctgcacca gaatggtaat 120

gtgtagccgg aaggggcgct cctcccagct gtaccggcca ctgcaaccca tgagcgtcca 180

ggtgatcccc caaacagcat gtgctcagnc ccagacctgc cgcctgggaa tcaggattcc 240

ttcttcccca aggcactgag cgcctgcaga tcccgcaggc ttcgtttgcc tccagaacct 300

tcccgtctga ttgttcctcc ccagccccct ggcatgtttc accacaaccc tgttgctaca 360

tcagagtgta tttttgtaat tcctctagct accatttcaa tagccccatc tctcctgctc 420

acccgcctct tgccccttct aggggcaggt gaaaggaata ggaaattgaa cctggggttt 480

tgacttgcca ctgccataac ttgtttgtaa aagagctgtt ctttttgact gattgtt 537

<210> SEQ ID NO 61
<211> LENGTH: 557
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (464)..(464)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 61

gggagagtcc atctggaagc tggagtatat cctgacccag acctacgaca ttgaagattt 60

gcagccggaa agtttatatg gattagctaa acaatttaca atcctagaca gtaagcagtt 120

tataaaatac tacaattact tctttgtgag ttatgacagc agtgtaacat gtgataagac 180

atgtaaggcc tttcagattt gtgcaattat gaatcttgat aatatttcct atgcagattg 240

cctcaaacag ctttatataa agcacaatta ctagtatttc acagtttttg ctaatagaaa 300

atgctgattc tgattctgag atcaatttgt gggaatttta cataaatctt tgttaattac 360

tgagtgggca agtagacttc ctgtctttgc tttcttttttt tttttctttt tgatgcctta 420

atgtagatat ctttatcatt ctgaattgta ttatatattt aaantgctca ttaatagaat 480

gatggatgta aattggatgt aaatattcag tttatataat tatatctaat ttgtaccctt 540

gttgaaattg tcattta 557

<210> SEQ ID NO 62
<211> LENGTH: 545
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 62

acaggaggaa tgcaccacgg cagctctccg ccaatttctc tcagatttcc acagagactg 60

tttgaatgtt ttcaaaacca agtatcacac tttaatgtac atgggccgca ccataatgag 120

atgtgagcct tgtgcatgtg ggggaggagg gagagagatg tactttttaa atcatgttcc 180

ccctaaacat ggctgttaac ccactgcatg cagaaacttg gatgtcactg cctgacattc 240

acttccagag aggacctatc ccaaatgtgg aattgactgc ctatgccaag tccctggaaa 300

aggagcttca gtattgtggg gctcataaaa catgaatcaa gcaatccagc ctcatgggaa 360

gtcctggcac agtttttgta aagcccttgc acagctggag aaatggcatc attataagct 420

atgagttgaa atgttctgtc aaatgtgtct cacatctaca cgtggcttgg aggcttttat 480

ggggccctgt ccaggtagaa aagaaatggt atgtagagct tagatttccc tattgtgaca 540

gagcc 545

<210> SEQ ID NO 63
<211> LENGTH: 288
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 63

cacccgccgt ctgagtgaag aggagtttgg ggggttcagg atagggaatg gggaggtcag 60

aggacgcaaa gcagcagcca tgtagaatga accgtccaga gagccaagca cggcagagga 120

ctgcaggcca tcagcgtgca ctgttcgtat ttggagttca tgcaaaatga gtgtgtttta 180

gctgctcttg ccacaaaaaa aaaaaaaaaa aaaaaaaagg gtaactatga gagatggtgg 240

atatgttaac ttgcttcgct ataggaacct ttgtgctatc tatattat 288

<210> SEQ ID NO 64
<211> LENGTH: 468
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 64

caggtactac gtccaagtgg cggctcagga cctcacagac tacggggaac tgagtgactg 60 gagtctcccc gccactgcca caatgagcct gggcaagtag caagggcttc ccgctgcctc 120

cagacagcac ctgggtcctc gccaccctaa gccccgggac acctgttgga gggcggatgg 180

gatctgccta gcctgggctg gagtccttgc tttgctgctg ctgagctgcc gggcaacctc 240

agatgaccga cttttccctt tgagcctcag tttctctagc tgagaaatgg agatgtacta 300

ctctctcctt tacctttacc tttaccacag tgcagggctg actgaactgt cactgtgaga 360

tatttttat tgtttaatta gaaaagaatt gttgttgggc tgggcgcagt ggatcgcacc 420

tgtaatccca gtcactggga agccgacgtg ggtgggtagc ttgaggcc 468

<210> SEQ ID NO 65
<211> LENGTH: 515
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 65

aaagactcta cccatattac agatgggcaa attaaggcat aagaaaacta agaaatatgc 60

acaatagcag ttgaaacaag aagccacaga cctaggattt catgatttca tttcaactgt 120

ttgccttctg cttttaagtt gctgatgaac tcttaatcaa atagcataag tttctgggac 180

ctcagtttta tcattttcaa aatggaggga ataataccta agccttcctg ccgcaacagt 240

tttttatgct aatcagggag gtcattttgg taaaatactt ctcgaagccg agcctcaaga 300

tgaaggcaaa gcacgaaatg ttattttta attattattt atatatgtat ttataaatat 360

atttaagata attataatat actatattta tgggaacccc ttcatcctct gagtgtgacc 420

aggcatcctc cacaatagca gacagtgttt tctgggataa gtaagtttga tttcattaat 480

acagggcatt ttggtccaag ttgtgcttat cccat 515

<210> SEQ ID NO 66
<211> LENGTH: 360
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (51)..(51)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 66

ttcacttcta aatctgctgg ccacaagccc tgctaaagat acacatctca ncccctccg 60

ccaagtctga aatgcccctc cccatctcac cttagactga aaagttttaa atcatgtcaa 120

ctggataata cttgctttat gtgagaatac ttcagcagaa tggatacgaa ttttcaaaac 180

aatcttttca tatctatgta ttctatatta aaagtgataa agtcatgttt ctggggcgta 240

ttcaagtagc tgacaagtaa ttatttaata atagtacatg agtgcattgt aatgattctc 300

gccgtagtca ggtaatagta tccaaccgaa atttcctacc aacctgctgt atccaaagtt 360

<210> SEQ ID NO 67
<211> LENGTH: 448
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 67

gtcccatatt caacatctgc tagtctgtat attcgtccta cattcattgg aactgagcct 60

tctcttggag tcaagaagcc taccaaagcc ctgctctttg tactcttgag cccagtggga 120

ccttattttt caagtggaac ctttaatcca gtgtccctgt gggccaatcc caagtatgta 180

agagcctgga aaggtggaac tggggactgc aagatgggag ggaattacgg ctcatctctt 240

```
tttgcccaat gtgaagcagt agataatggg tgtcagcagg tcctgtggct ctatggagag    300

gaccatcaga tcactgaagt gggaactatg aatctttttc tttactggat aaatgaagat    360

ggagaagaag aactggcaac tcctccacta gatggcatca ttcttccagg agtgacaagg    420

cggtgcattc tggacctggc acatcagt                                       448


<210> SEQ ID NO 68
<211> LENGTH: 523
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (41)..(41)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (440)..(440)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (442)..(442)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (485)..(486)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (488)..(491)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (493)..(498)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 68

gacaacagcc ctggagggga acagagtgag agagatgttt ngctctggta cagcctgtgt     60

tgtttgccca gtttctgata tactgtacaa aggcgagaca atacacattc caactatgga    120

gaatggtcct aagctggcaa gccgcatctt gagcaaatta actgatatcc agtatggaag    180

agaagagagc gactggacaa ttgtgctatc ctgaatggaa aatagaggat acaatggaaa    240

atagaggata ccaactgtat gctactggga cagactgttg catttgaatt gtgatagatt    300

tctttggcta cctgtgcata atgtagtttg tagtatcaat gtgttacaag agtgattgtt    360

tcttcatgcc agagaaaatg aattgcaatc atcaaatggt gtttcataac ttggtagtag    420

taacttacct taccttaccn anaaaaatat taatgtaagc catataacat gggattttcc    480

tcaannannn nannnnnncc ttttgtactt cactcagata cta                      523


<210> SEQ ID NO 69
<211> LENGTH: 427
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (207)..(207)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 69

aacctgttct cttgtatctg aatctgattg caattactat tgtactgata gactccagcc     60

attgcaagtc tcagatatct tagctgtgta gtgattcttg aaattctttt taagaaaaat    120

tgagtagaaa gaaataaacc ctttgtaaat gaggcttggc ttttgtgaaa gatcatccgc    180

aggctatgtt aaaaggattt tagctcncta aaagtgtaat aatggaaatg tggaaaatat    240
```

```
cgtaggtaaa ggaaactacc tcatgctctg aaggttttgt agaagcacaa ttaaacatct    300

aaaatggctt tgttacacca gagccatctg gtgtgaagaa ctctatattt gtatgttgag    360

agggcatgga ataattgtat tttgctggca atagacacat tctttattat ttgcagattc    420

ctcatca                                                               427


<210> SEQ ID NO 70
<211> LENGTH: 397
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (345)..(345)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 70

aacttatatt gcatgttctc ttcctttcac ttttttcagt gtctacattt cagaccgagt     60

ttgtcagctt ttttgaaaac acatcagtag aaaccaagat tttaaaatga agtgtcaaga    120

cgaaggcaaa acctgagcag ttcctaaaaa gatttgctgt tagaaatttt ctttgtggca    180

gtcatttatt aaggattcaa ctcgtgatac accaaaagaa gagttgactt cagagatgtg    240

ttccatgctc tctagcacag gaatgaataa atttataaca cctgctttag cctttgtttt    300

caaaagcaca aaggaaaagt gaaagggaaa gagaaacaag tgacngagaa gtcttgttaa    360

ggaatcaggt tttttctacc tggtaaacat tctctat                              397


<210> SEQ ID NO 71
<211> LENGTH: 466
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 71

ccaggctgtg ctgtgcattt ttaaaaggtc taatttaatt gcttttaata tatatgtaca     60

tatatgttat tttaactgtg gagaattatt taagttaaaa gactggtttg atttgcctat    120

ggtgtgaaat cctttgttat ttttctaaaa aaataaaatt taaaaagaaa gaaaactaag    180

gaagaacaag aagctattta cccaaagtga gctttcagtt ttagttttgc atggctgttt    240

gactgccttt ccgccctatg aaaatcaaga aaatcttttt taaaaatgga gtcctgctat    300

tttccactcc ttgcagataa tacaaattca gtttgtcagg ttggatggtg agttgggagc    360

tgtgatggat ctgttggcgg gttttggatg tgtaaagaat gatatatata ttaaataggt    420

caatcagact atgacagcta tgtacgacca tttgtatgtg tatcta                    466


<210> SEQ ID NO 72
<211> LENGTH: 298
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 72

ccgatttgtg tctattattg gtgacattgt tttagatatt gggtattgta tattaaggaa     60

aaagatggtc tatattctct ttattgcata tacttaatgt ttcaaaagaa tgcagattct    120

gtgtttaagc acagggctga tagttgtggt tttgtttaca aatgttctgt tttggctgct    180

attggttttt taaagaggtt ttttatactt ttgtatttga atagttatgt ttcactgatg    240

ctgagccagt ttgtatgtgt gtgcatatat gtgaactgta actgacaaga tgaattac      298


<210> SEQ ID NO 73
<211> LENGTH: 293
```

```
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 73

tgaatcttcg ggtgtttccc tttagctaag cacagatcta ccttggtgat ttggaccctg     60

gttgctttgt gtctagtttt ctagaccctt catctcttac ttgatagact tactaataaa    120

atgtgaagac tagaccaatt gtcatgcttg acacaactgc tgtggctggt tggtgctttg    180

tttatggtag tagtttttct gtaacacaga atataggata agaaataaga ataaagtacc    240

ttgactttgt tcacagcatg tagggtgatg agcactcaca attgttgact aaa           293


<210> SEQ ID NO 74
<211> LENGTH: 537
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 74

tgatcatggc ctttcaaccc aacaagggcc cttccctgct cttccaccag taaaggctcc     60

tggcctctca tcaggatctg ccccccagag accccccag acactgcagg gcctggtgat    120

gctgtcctct gtaccggaaa tggcaggcac tgtcagattt ccactcttct gcctttagga    180

aggctgggtg cttcttgctc tgacagccag tctggggaga tgactcttac gttgcttgag    240

tcttggtggc aggctgctgt ccacgggggga gaagtctctg ctctggactg gacagaagag    300

agacttttac cctggggcac tcacacggcc aagcttctgc caccacttca ttagctgtat    360

tctccatagt atggtgaaat agcaggtgcg tcttctagtt tattcctcct ggggacattt    420

cctcaaagca gttttgcgcc cccgcaaggg aatggtcagc ctaagggtaa tgtacagccc    480

gtgcttggag aaccatggaa gctacacccc tacaggtgca tactgttctg cttttcc       537


<210> SEQ ID NO 75
<211> LENGTH: 533
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 75

atcctacaac ccaccttgaa ggtataactg gatccagaga gggaaggact gacaagaagg     60

aattattcag aaaaacactg acagatgttt tataaattgt acagaaaaat agttaaaaat    120

gcaataggtt gaagttttcc agatatgttt ctctctgaaa ttactgtgaa tatttaacaa    180

acacttactt gatctatgtt atgaaataag tagcaaattg ccagcaaaat gtcttgtacc    240

ttttctaaag tgtattttct gatgtgaact tccttcccct tacttgctag gtttcaataa    300

tttaaaagag tcaaacacta taaatgagta agttgacgat gttttaagat tgcacctggc    360

agtgtgcctt tttgcaacaa atatttacct ggcagtgtgc ctttttgcaa caaatattta    420

ctttgcactt ggagctgctt ttaattttag caaaatgttt tatgcaaggc acaataggaa    480

gtcagttctc ctgcacttcc tcctcatgta gtctggagta ctttctaaag ggc           533


<210> SEQ ID NO 76
<211> LENGTH: 486
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 76

gctcctgtag ctgcattatt tcttgattag aggtttgggc atataaccag attaaagtga     60

aggaactttc tgttgttttt gtagcaccgc tcagctgtct tgtaaaacag tgaacacacg    120
```

```
ctttctggtt ctagtaatcc tgggtgttta tcacgttcag agaaactcaa gctattgcat    180

gattagcccc ctatctggca aggaaacccc atacagaaga aacaacaaac ctgcgcctgc    240

accgcctctg cgtcctgggt agtctgtgct tgtaatccag catgtttcac agagtaagcc    300

tgttgtgact ttgcttttgg ggtctatgtc attggtttct gatgcttgta caaacacgca    360

cacacaaatg gataaaacag cacctctggc tgttacatta ccataaacca tatcacatgc    420

ctacatttta caaatgattt ctggtttctc ttagttcttc tctaacatag tactttcttt    480

ccagca                                                                486


<210> SEQ ID NO 77
<211> LENGTH: 530
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 77

aagtgtgcat aatttcattt aacgttaaag aaatagatcc aattcctttc ttgcaaccaa     60

aaataaataa aatacgttgc ctcaatataa ggtttgggct attctgtgtt tctatagaag    120

caatctgttt ttggtaaaat gtacttttaa ggatccagtc atctgaagta ttttatgtag    180

agttagagat ttcacaatat tgactataca tatatttaaa atataaatta tccagctgat    240

gtttgaattt gtcttacttt cctggccacc tcgttgtcct attttataag ctggggagtt    300

aactagctta acaaaagatg cttagctttt gtaaaagaac aagtgtttca ttttacaaag    360

acactccaaa tgatagttac ttgattttct cgagaccttt aactatggtg atgaataaca    420

ggacttgctt tcaagcctta ataaatgtaa aatgcctttt aatgaagata cagctgagtg    480

ttttcctcat gaatctgaac caattaccaa tttgtgttcc agtcttgatt                530


<210> SEQ ID NO 78
<211> LENGTH: 557
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (477)..(477)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 78

ctaagaggca gtttacttcc ctgagaccca cagttgggct gttctggaaa cacatctgtg     60

aatcatagcc aattgccaca gagaaaacag aaccaagcct ccggtgaggc cactccaccc    120

cagagaagtc tgcagaattc caaggactcg gattggatgt tcagaattca gcaactggaa    180

agtccttaaa aacaaacagg ccaaaccaaa tcaatattgc tgtttctaga tgtcccttct    240

gtggttgagc tagttttaca gagataaata tattaagaca aggaggtggg ggtgttatat    300

gatcaatgat agccatttga aagagaggga ggagtacaga aggaaggcac ttctgggtac    360

ttaattcaga aatttcttta tatttcagca ctggattatc atataatgca agtgactatg    420

gactaagagt tagttatggt gtcttatgac tagatttatt atggtatatt aaagtancaa    480

taatattaat attaccttcc ttgtttttg gtttcaaaaa gagatctttt ccagatgttc     540

agctgttggg cttctta                                                    557


<210> SEQ ID NO 79
<211> LENGTH: 291
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
```

```
<222> LOCATION: (87)..(87)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (94)..(94)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (102)..(102)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (110)..(110)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (123)..(123)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 79

ctttcaggtt tatctccatc cctggaagca gagttgctct ggcccaggct ctccatgaga     60

gtttggcttg aacattcatt gtctggnccc cctncctagt tnctcatctn cccaaagtca    120

agnccaatgt gtgaagaaat gaccagctca gcagccaagg cccagggtgc acaggtcttc    180

gttgggagag gcatctgcag gcctttcctt gcccactggg atccttgcct agcatagtga    240

cgatgttcag ccctggagac aaacaagaag gggaacacca acatcaatag a             291


<210> SEQ ID NO 80
<211> LENGTH: 477
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 80

gttgatgcca aaatacccac ggggtctacc agccatgggg tttgcttgct taggagtagt     60

tgtttcagag gtgattacag gcctgggttt gactgtgctt accaatgagt ggtttttgag    120

ctatgagaaa gtggatggga gtgggaggag gagagatggg tgaagacaaa agagttcttt    180

atgagcctcg atgttccctg gtaaactttt aaaaaggcct tctctcatga tctaagtctt    240

ggactggtgg catcatgtaa ctgctaacct tacagtaaaa acccaagaat gggtcaaaaa    300

tgtcttccca gtttctccaa gctgcttctg gaatgcaggt ctgtcggctg ggtgctctcc    360

agcagctgct cctgcctgat tcaactgtag cctgtaatgg gtaaaagcca catttaggag    420

gtggtctgat catagaacac cttaggaaga aagtccatga gactttctga ctaggaa       477


<210> SEQ ID NO 81
<211> LENGTH: 540
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 81

tagaacgggc atctactcca gtacttcctg ccataaaact ccagataaag taaaccatgc     60

agtactggct gttgggtatg gagaaaaaaa tgggatccct tactggatcg tgaaaaactc    120

ttggggtccc cagtggggaa tgaacgggta cttcctcatc gagcgcggaa agaacatgtg    180

tggcctggct gcctgcgcct cctaccccat ccctctggtg tgagccgtgg cagccgcagc    240

gcagactggc ggagaaggag aggaacgggc agcctgggcc tgggtggaaa tcctgccctg    300

gaggaagttg tggggagatc cactgggacc cccaacattc tgccctcacc tctgtgccca    360

gcctggaaac ctacagacaa ggaggagttc caccatgagc tcacccgtgt ctatgacgca    420

aagatcacca gccatgtgcc ttagtgtcct tcttaacaga ctcaaaccac atggaccacg    480
```

aatattcttt ctgtccagaa gggctacttt ccacatatag agctccaggg actgtctttt 540

<210> SEQ ID NO 82
<211> LENGTH: 503
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 82

aggactaaac tacagccgct tgttgtttgg tattcagtat ccagattctg atgttttatt 60

tagatacaaa gtgaaatctt agagaagcta aaaggaaaga aaataaatct atcaaaatta 120

ccctaaacat cctaagctca tctatttctt tttaatttct gcaaagtaat tgatttattt 180

gtttaaaaag cgctaatttc tatttgatct gatatcagtc cagtttgtcc ttagtcacaa 240

agcccatata atataaaaca ggatggtggc aggaaaatgg acatcaaaat caacttaagg 300

gtaggctcaa aacagggttg ttgttgtttt tttagtttct ccttgttgtg attttcacct 360

gttataataa atgtaccttc acaccaatag attgggcact gtggaattta aatcactcaa 420

attgttctct aatatgtaaa attacacttt gaactactag aaaattgtgc tggaaatgga 480

cacagtctaa caaattccaa att 503

<210> SEQ ID NO 83
<211> LENGTH: 375
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 83

tgggcccaag gaattcagaa gagcttgcag gcaagccagg agaccctggg agctgtggct 60

gtcttctgtg gaggaggctc cagcattccc aaagctctta attctccata aaatgggctt 120

tcctctgtct gccatcctca gagtctgggg tgggagtgtg gacttaggaa aacaatataa 180

aggacatcct catcatcacg gggtgaaggt cagagtaagg cagccttctt cacaggctga 240

gggggttcag aaccagcctg gccaaaaatt acaccagaga gacagagtcc tccccattgg 300

gaacagggtg attgaggaaa gtgaaccttg ggtgtgaggg accaatcctg tgacctccca 360

gaaccatgga agcca 375

<210> SEQ ID NO 84
<211> LENGTH: 485
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 84

gctactccag ggctgaggt gacagcattg cttaagccca gaaggtcgag gctgcagtga 60

gctgagatca cgccactgca ctccagtctg ggtgacagag agagaccata tccaaaaaaa 120

aaaaaagttg ccagagacga gtatgcccat gctccctcta cctcactgcc accactcctg 180

cttttaggag ctgagtgtgt ctccctaaaa tttctatgtt gaagtcttaa cccttggtac 240

cacagaatat cactgtattt ggagatgggg tctttagaaa ggcacttaaa ttaaaatgag 300

ctcactgata tgggccccga tgcaatataa ttggtgtcct tataagaagg ggaggttagg 360

acacgcagga aagaccacat gaaggcccag gagtgggagg gggaatagcc atcgacaaac 420

taagggggcc tcagaggaaa ccaaccctgc tgacacctca atcttagact ctggcctcaa 480

aaatt 485

<210> SEQ ID NO 85
<211> LENGTH: 566

<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 85

tgaaatctta ggtgccttag gggttttttt tttttaagta ttttttaaaa acctgcaaag 60

atataaattt agccaagtta cctgacgggt gagaagaaaa gagcaggcaa aattagtgat 120

tttttagaa gtctgctaaa tggatatatt gtgtgtgttg ctgttggaaa tagccccacc 180

ccatcctccc aatccaaaac gtaactgaaa tataatcaga aacattaaag cctgtaaaaa 240

aaaattgctg cgtttttggt aaagggtgta atttaacagt gcaatttaaa gtgaccttag 300

tgatgcagag ttcctgagtg gtgtttgtag aatgagttta tcatacattc tttctactac 360

tggaaaaaaa tggatgcagt ctggactgtt gtaaccttag gttgtaatct gatttggaaa 420

taagtacatc tttaaaagtt gctacagatt tgagttcatg attttgttaa aaattgctat 480

ggagtacttt gttatataac agaagccatc ctgaaatgaa actagtctaa aaaaattcat 540

tgttctactt agttgcagct gtacct 566

<210> SEQ ID NO 86
<211> LENGTH: 317
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 86

aaatgttgct aagtcctggt atgatggtgt gagcttcctt ggggaagtac ttcttgagtt 60

atgtaactaa caggatgttt tactacagat ctggatggct attcagataa catggcaaaa 120

aatgatagca gaagatcatt aaaaacttaa aatatatttt attagaaaac atttatctat 180

gaatgaatat ttccttgatg ctggtctctg cacacatatg cttggttact tgcatgcatt 240

cattggttgt tcaataagtg agatgattac agataatact gtattttcct tatatggaaa 300

accgttatag acccaat 317

<210> SEQ ID NO 87
<211> LENGTH: 317
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 87

gaagggagag ccatctatga tatagatggt accatttcag ttcaaagttg taataacctt 60

tggagtgtta cagtttggtt gtcaaatggt ttcagaatgt ataattgatt tttttaaatg 120

ttgcattgtt tgaatctaaa gtacagcact ataacatgct ttagcttggg ggggtggggg 180

tggggtgggg acttgcactt attctctaaa atgttgacta atccagaaag cctgatgcaa 240

cataatctgg aaaactgctt tggtacattt gtagaaatcc gtagaaatac catatccagc 300

ctcaaagcat taatctc 317

<210> SEQ ID NO 88
<211> LENGTH: 128
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 88

attgctgtaa atagggcaca agccctgtat atggattaga tggtcgatat gccaaaaact 60

acagatggtt tctaagtaga tttctcacct ttccttggag gcatattgta gcttgctaag 120

ttttatca 128

<210> SEQ ID NO 89
<211> LENGTH: 402
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 89

gcacctcgga gttgcagctg tgacactcat aggttactcc caggagtgtg ctgagcagaa 60

ggcaagctct tgctggatga aacccctcca ggtggggttg gggagacttg atattcacat 120

ccaacagttt gaaaagggag agctcaattc ccagcgtcac cccatggctt gtgttgcctg 180

ctacgcattg acttggatct ccaggagtcc cctgcacata ccttctccat cgtgtcagct 240

gtgtttctct tgattccgtg acacccggtt tattagttca aaagtgtgac acctttctg 300

ggcaaggaac agcccctta aggagcaaat cacttctgtc acagttatta tggtaatatg 360

aggcaatctg attagcttca cagactgagt ctccacaaca cc 402

<210> SEQ ID NO 90
<211> LENGTH: 475
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 90

cagggatcgg aggacgaccc gagtcccaag agtggggttt tgctttttaa aaggagagag 60

gaggggtgat ggcaggggag tggagggtgg ccgggcaggt cctgccggcg cagggagccc 120

tctgcccttc acactctcct ccaaaagagc ctccatctgt aaggaagcag gtctccgcga 180

ggggtttctt tccatgtgtt ttcctcctgt tgttaaaaga actttttaa aaaaacagac 240

ctcgttttag atttatagca ttgactttta cacacattca cacaagaaaa aaatcctttc 300

aaaattctta aatcttctgt tcctcctttt tccaagggaa gagggcaaaa agtggcctgg 360

gctctgttgg tgtgcgtgtt ccgtggcgga gagaagaaaa tgggaaagac atctcactgg 420

tgcttttctc ttttgtttta gtgccccccg cccccatccc tataatatct gtaac 475

<210> SEQ ID NO 91
<211> LENGTH: 491
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (314)..(314)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 91

ggcggcaata gtttcagctt cagcagcgcc agcagtctta gtagcagcag caccagtgcg 60

ggttgcgcca gcagccttgg cggcggcggc gcctcggagc ttctccctgc aacacagccc 120

acagccagca gcgctcccaa aagccccgag ccagcccaag gcgcgcttgg ctgcttatag 180

actgtactag ggcggagggg atccgggcct tgcgtgcagc ctcccaacca tgggctgggt 240

tttgtgctta ctgtatgttg gcgacttggt agggcaggag acgcagcgtg gagcctacct 300

cccgacattc acgnttcgcc ccacgctgct ccgactggct gcagcggaca ctgcccaaag 360

cagaggggag tctcagtgtc ctgctagcca gccgaacact tctctccgga agcaggctgg 420

ttcgactgtg aggtgtttga ctaaactgtt tctctgactc gccccagagg tcgtggctca 480

aaggcactta g 491

<210> SEQ ID NO 92
<211> LENGTH: 483

<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (48)..(48)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (212)..(212)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 92

ggaattcttg ttcaatactg gcaggagtga aaattggtag aacctttnta gaaggcaatt 60

tggcaacatg tatgaaaacc taaatgttga tacaccttta cccagcagtt tgtttaggaa 120

tttatcctaa tgaataaaag ttgtccaagt cttcaaacat gagcccaaag gtatatttca 180

tgatgtttat gatattaaaa cattggaaac anctgaaaca tccttcagta aaagatggat 240

taaataaatt ccatgcagtt gtcatttaaa aatatttaga tatatgttta ttgctatgga 300

tatatgttcc caaaatatta ttgaatcaaa aagtagacta caggatatat gttgaatatg 360

agctcattta taacattgaa tattttaaga taatgtatgt ttcatagaga gatcttcacc 420

aaatgttaag gatttttttt tctgggctgt ggtatttggg tgatctttac attcttcaga 480

ctc 483

<210> SEQ ID NO 93
<211> LENGTH: 560
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 93

tcccaaagta tatagttcca tcccaggact taaggcccta taaggtaaat atagatcctt 60

cttcagaagc tccagggcat tcttgcagga gcaggccagt ggagagcagc tgttcctcca 120

aattttcctg ggatgaatat gaacagtaca aaaaagaata aattctacca gaagataaag 180

aaaaaagcaa gtattgcata ggcacctgag cataggtatg accttgggaa gacattggct 240

ccataagcaa tgccaagaga atgatcaata gtgagtttgg gtgatgcaga taaacaatct 300

ggataattcc atttcttttt tcccaaaccc tcaaacagag tgccttaaaa aattgtttta 360

tcaggataat tgtctcatga ccaaatccac gctcaattag agccattcaa aattccttaa 420

gatcatgggt tctgacttca gccaaacaaa acaatcaaaa cctaccaaaa agggactgga 480

ttgtaatgtc ctctccatca tcctcagtgt gagtcctcag agcctccatc tgccaagaac 540

attcagttgg attccatcgt 560

<210> SEQ ID NO 94
<211> LENGTH: 532
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 94

gtttcttgca tatgtattta ctggtccaca gcacaaaata aagtgaccac atatacatag 60

gaaagttgaa tttgtacaca tacagcatct gaaatgtatc tgatgttcag catcaagatt 120

tcactgaaca ttgtagaaat gtgtatcttt tgcatgtata ttttacattg attttctatt 180

tatgtacatc tagaaagttt taaccctaat aaatagtttt gtaattttga ataatagtgt 240

cagtttatat gtgagggagt agagacagag aggttagcac tggataataa ttagtaaggc 300

caaaggagaa aatttcatag aaaatattgt tgttgtcata atgagtacag catgaaaggc 360 ttcctctaca agacactagt caaagagttg agagctgcgg tttctaatct ttgtccatta 420

ctcccttact ccctatgaga ctgtggacct gtcacttggc ctctctggtc ttcagttttc 480

tcaccagtaa aacaaggaac ttgaaccaaa tgacctctag tgttcccctt gg 532

<210> SEQ ID NO 95
<211> LENGTH: 311
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 95

gttttgtttt tactacggtg ctgatgtata tgtaatgtct aaaaaaagtt atttgtacat 60

aagtttttac aatactgcag atatcactgg gtctactatc tgtaaaaaat atacatataa 120

atatatatat actgtttgtt taaaatagag tatttttatt tcattcctta actcatcatc 180

acagcagtgg tattgcactt cagatgacat ctaattacta atttgtactg tatgacctct 240

ggcaacttgc tccattttat tcagattttt ctagttttct gtttttactt tgtacattga 300

gcattgctta t 311

<210> SEQ ID NO 96
<211> LENGTH: 546
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 96

acacgtgttg actccattgt tttacatgta gcaaagtctg ccatctgtgt ctgctgtatt 60

ataaacagat aagcagccta caagataact gtatttataa accactcttc aacagctggc 120

tccagtgctg gttttagaac aagaatgaag tcattttgga gtctttcatg tctaaaagat 180

ttaagttaaa aacaaagtgt tacttggaag gttagcttct atcattctgg atagattaca 240

gatataataa ccatgttgac tatgggggag agacgctgca ttccagaaac gtcttaacac 300

ttgagtgaat cttcaaagga ccctgacatt aaatgctgag gctttaatac acacatattt 360

tatcccaagt ttataatggt ggtctgaaca aggcacctgt aaataaatca gcatttatga 420

ccagaagaaa aataatctgg tcttggactt tttattttta tatggaaaag ttttaaggac 480

ttgggccaac taagtctacc cacacgaaaa aagaaatttg ccttgtccct ttgtgtacaa 540

ccatgc 546

<210> SEQ ID NO 97
<211> LENGTH: 457
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 97

cagtccctgc ttttgactgg gttcctattt taagcacaaa tgagagctct ggagccagaa 60

tgccagggtt ctaacttcag cattcactta ctagctgtat gatcttggcc aagtcacttc 120

acctccctga gccccaattc ccaagtttgt gaaatggcaa caatacctat gtgtcactgg 180

attattggtt aaaacagaat gagattcctt gtgtgaaaat agctattata cctgacacac 240

tcatcgtatg ggctctgcaa agggatattc cccaacctgt ccttcccgac aggaagcata 300

gggcactgca gatggggaag catgtcacct tggcagtgac tcggtggctt cccaagcagg 360

agtgtcaggg gaaccatgag agagagtcta ggagccaaac acatcaccac cctgagcaga 420

tacaggagtg gggaggggc tgtaactcag tgagtgg 457

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<210> SEQ ID NO 98
<211> LENGTH: 530
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 98

tcaaagaacg cgtactgcag accccaaatg accttctggc tgctggcttt gaggagcaca     60

agttcagaaa cttcttcaat gctttttaca gtgtggtgga actggtagag aaggacggct    120

cagtgtccag cctgctgaag gtgttcaacg accagagtgc ctcggaccac atcgtgcagt    180

tcctgcgcct gctcacgtcg gccttcatca ggaaccgagc agacttcttc cggcacttca    240

ttgatgagga gatggacatc aaagacttct gcactcacga agtagagccc atggccacgg    300

agtgtgacca catccagatc acggcgttgt cgcaggccct gagcattgcc ctgcaagtgg    360

agtacgtgga cgagatggat accgccctga accaccacgt gttccctgag gccgccaccc    420

cttccgttta cctgctctat aaaacatccc actacaacat cctttatgca gccgataaac    480

attgattaat tttaggccat gcagtggaac ctgtcaccta atgggactgc               530


<210> SEQ ID NO 99
<211> LENGTH: 510
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 99

atggcctctg tgaataatgt aactccagtt acacggtgac ttttaatagc atacagtgat     60

ttgatgaaag gacgtcaaac aatgtggcga tgtcgtggaa agttatcttt cccgctcttt    120

gctgtggtca ttgtgtcttg cagaaaggat ggccctgatg cagcagcagc gccagctgta    180

ataaaaaata attcacacta tcagactagc aaggcactag aactggaaaa gaccacagaa    240

aacaaagaat ccaacccttt catcttacag gtgaacaaac tgtgatgatg cacatgtatg    300

tgttttgtaa gctgtgagca ccgtaacaaa atgtaaattt gccattatta ggaaagtgct    360

ggtggcagtg aagaagcacc caggccactt gactcccagt ctggtgccct gtctacacca    420

gacaacacag gagctgggtc agattcccct cagctgctta acaaagttcc tcgaacagaa    480

agtgcttaca aagctgcctt ctcggatact                                     510


<210> SEQ ID NO 100
<211> LENGTH: 560
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 100

agctgccttc tcggatactg aaaggtcgag ttttctgaac tgcactgatt ttattgcagt     60

tgaaaaaccc aaagctattc caaagatttc aagctgttct gagacatctt ctgatggctt    120

tacttcctga gaggcaatgt ttttacttta tgcataattc attgttgcca aggaataaag    180

tgaagaaaca gcaccttttt aatatatagg tctctctgga agagacctaa atttagaaag    240

agaaaactgt gacaattttc atattctcat tcttaaaaaa cactaatctt aactaacaaa    300

agttcttttg agaataagtt acacacaatg gccacagcag tttgtcttta atagtatagt    360

gcctatactc atgtaatcgg ttactcacta ctgcctttaa aaaaaaccag catatttatt    420

gaaaacatga gacaggatta tagtgcctta accgatatat tttgtgactt aaaaaataca    480

tttaaaactg ctcttctgct ctagtaccat gcttagtgca aatgattatt tctatgtaca    540

actgatgctt gttcttattt                                                 560
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-continued

<210> SEQ ID NO 101
<211> LENGTH: 392
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 101

atcggccatg ccatcctgag atgaatgaac acattggcca tgctgtcttg agatgaatga 60

acacctgggc catgctgtct tgagatgaat gaacacctgg gccatgctgt cctgagacga 120

atgaacacct gggccatgct gtcttgagat gaatgaacac atcagccatg ctctcctgag 180

agggatgaac acctgggcct tgccgtcctg agatgaatga acacattgac catgctgtcc 240

tgagatgatt gtcctggtta tgcagacatt tctttatatt atttgcttaa ctttaatgcc 300

ctcctaggaa gatttcccat actttcctcc cttcaatcaa aatatcccaa gttcaacagg 360

tctggctcac tcctctctat tcatctaagg tc 392

<210> SEQ ID NO 102
<211> LENGTH: 348
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 102

tgaagctgag ctccgacggc agtttgagga gcgacagcag gagatggagc atgtttatga 60

gctcttggag aataagatgc agcttctgca ggaggaatcc aggctagcaa agaatgaagc 120

tgcgcggatg gcagctctgg tggaagcaga gaaggagtgt aacctggagc tctcagagaa 180

actgaaggga gtcaccaaaa actgggaaga tgtaccagga gaccaggtca agcccgacca 240

atacactgag gccctggccc agagggacaa gatctaaaaa aaataatgct gggaagtcct 300

aaccacatca agaatgcctc agatcagtga cccaaggacc ttccagaa 348

<210> SEQ ID NO 103
<211> LENGTH: 460
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 103

cttgggccac aaaatatcag tttaatcaga tggtttatgt taacaagtat gatttatggc 60

aaacatagat ctctaatctc catttctctc tcatatatct atatttatct atccatatat 120

atgtacctat atatatcaaa tataaagata tgtttatagc aattgtatat acgtagagag 180

ataatatgta gtatgaagag agacatagat attattcttc attttagaat gttatcttgg 240

tatgtttaaa aggaaaaact taagatgtgt tgcaattgca gtatgagttt caggtatgta 300

catgttatgt gtgtgtgtga gagacacaca caaacacatt tcaaacatgt tttatgttta 360

agctcaatat tcaaacacag aaatataaca tctattctta atatgtttta tgtaagtaca 420

gcagcagcat tattaaatac tgtatttcta tggtgattga 460

<210> SEQ ID NO 104
<211> LENGTH: 601
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 104

ccttggctat cttgatgacc caagtgagga cattcaggat ccagtgagtg acaaattctt 60

caaggaggtg tgggtttcaa cagcagctcg aaatgctaca atttatgaca aggttttccg 120

gtgccttccc aatgatgaag tacacaattt aattcagctg agagacttta taaacaagcc 180 cgtattagct aaggaagatc ccattcgagc tgaggaggaa ctgaagaaga tccgtggatt 240

tttggtgcaa ttccccttt atttcttgtc tgaagaaagc ctactgcctt ctgttgggac 300

caaagaggcc atagtgccca tggaggtttg gacttaagag atattcattg gcagctcaaa 360

gacttccacc ctggagacca cactgcacac agtgacttcc tggggatgtc atagccaaag 420

ccaggcctga cgcattctcg tatccaaccc aaggaccttt tggaatgact ggggagggct 480

gcagtcacat tgatgtaagg actgtaaaca tcagcaagac tttataattc cttctgccta 540

acttgtaaaa agggggctgc attcttgttg gtagcatgta ctctgttgag taaaacacat 600

a 601

<210> SEQ ID NO 105
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 105

accggcggag gaaatgctct acaggcaatc atgcacttca actacagaac catgtgcaga 60

ggagaaaatt ccatccttgg acagttaaaa gcagagcttg gtaatcagtg gataaattac 120

atatcattct gtggtcttag aacacatgca gagctcgaag gaaacctagt aactgagctt 180

atctatgtcc acagcaagtt gttaattgct gatgataaca ctgttattat tggctctgcc 240

aacataaatg accgcagcat gctgggaaag cgtgacagtg aaatggctgt cattgtgcaa 300

gatacagaga ctgttccttc agtaatggat ggaaaagagt accaagctgg ccggtttgcc 360

cgaggacttc ggctacagtg c 381

<210> SEQ ID NO 106
<211> LENGTH: 409
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 106

aactggctct tgattttcag caccctactc tcatgaaaaa agcctgaaag gaccctttcc 60

cttataagta atttaatcca atttctcccc attttataga tgaggaaact gaggctcaga 120

tcagatgaga actcacttaa atccactcaa tgtgtagatg gtagagctgg gactagcaac 180

attgctgcag cccattgttg gcctctctct tcactttatc attgcccaag aatgaggata 240

tgcagtaaac agaattcagg caagatacct ctaagctgtt ttgaaccctc tgatattttg 300

tatttatgtg tttgtctgtc tccccctact agaatgtaag ctccatgggg cagggacttc 360

actgtatttt gttcatagtg tatccccaga gcctggacca gtgcttggc 409

<210> SEQ ID NO 107
<211> LENGTH: 564
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 107

catctttcag ggctgccagt ttcgctccgt ggaggctgtg caggagatca cagagtatgc 60

caaaagcatt cctggttttg taaatcttga cttgaacgac caagtaactc tcctcaaata 120

tggagtccac gagatcattt acacaatgct ggcctccttg atgaataaag atggggttct 180

catatccgag ggccaaggct tcatgacaag ggagtttcta aagagcctgc gaaagccttt 240

tggtgacttt atggagccca agtttgagtt tgctgtgaag ttcaatgcac tggaattaga 300 tgacagcgac ttggcaatat ttattgctgt cattattctc agtggagacc gcccaggttt   360

gctgaatgtg aagcccattg aagacattca agacaacctg ctacaagccc tggagctcca   420

gctgaagctg aaccatcctg agtcctcaca gctgtttgcc aagctgctcc agaaaatgac   480

agacctcaga cagattgtca cggaacacgt gcagctactg caggtgatca agaagacgga   540

gacagacatg agtcttcacc cgct   564

<210> SEQ ID NO 108
<211> LENGTH: 370
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (140)..(140)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (166)..(166)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (200)..(200)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 108

ggtttagcat ttagttctct ttattatagt ggatctttat tgttcattta tgtatgaaac   60

ctgtgctagg gattatagaa gatacaaatt tgaataaaat atttgatcta ggagctctta   120

tctaaaatgc cataaccatn tgcttaatta taaaatgaaa gaaggnctat aaaatgatac   180

atagtaaaaa ttttaacagn ctatgagagt ttaaaggaaa aggatacaaa ttatgactgc   240

attgaaaaat agcactttga agctgagcat ggtgatgcat gcctttagtc ccagctactc   300

aggaggctga gatgggagga ctacttgagc ctgggaggtc gaggctgtag tgaggcatga   360

ttgcaccact   370

<210> SEQ ID NO 109
<211> LENGTH: 456
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 109

atacaaagta cttctgttgg tcacagaaac atgaccagat tttgcatatc tccaggtagg   60

gaactaagta gactacctta tcaccggcta agaaaacttg ctactaaact attaggccat   120

caatggcttg aataaaaacc agagaaggtt tttcccagga cgtctcatgt ttggcccttt   180

agaattgggg tagaaatcag aaatgagatg aggggaagaa gcaaggagtc taaggcccta   240

gcgatttggg catctgccac attggttcat attcagaaag tgttatctca ttgattatat   300

tcttgttaag caaatctcct taagtaatta ttattcaaat aagattatac tcatacatct   360

atatgtcact gttttaaaga gatatttaat ttttaatgtg tgttacatgg tctgtaaata   420

tttgtattta aaaatgccat gcattaggct ttggaa   456

<210> SEQ ID NO 110
<211> LENGTH: 257
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 110

atttgttttt tgactaatgt gctataaaaa ggattatatt tgtgagaaaa gatactgatc   60

gccaatattt caaataccgt cttgcaatgt atagttttta gtgacattgt agtataaagc   120 tgtaatttga aattttactt tggaatgtaa agtagaaaat attagctatg tcaatgatat 180

cttgcaaagt gttcccattt ataattattt atattgtaaa tagctttctg aagtaaattc 240

gaagttaatg tgcataa 257

<210> SEQ ID NO 111
<211> LENGTH: 474
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 111

gtttattgca actttgctgc atgggacttt gctttcataa atctatatgg ggttggggtt 60

aatttgccct aatttgctga cctgggacac atgtaatcac tgttaaactt acacccggta 120

accctgatgt gtttacattt caaaagaaat gaaattggcc tggaaaaaaa ttttggaagt 180

actgtaagtc ttttttcttt ttttttccga agggaaatat ttcaaaaaag gaaacattat 240

gagtagacac ttcaaaaaag ataaaatatt ttacatttgt tttttgacta atgtgctata 300

aaaaggatta tatttgtgag aaaagatact gatcgccaat atttcaaata ccgtcttgca 360

atgtatagtt tttagtgaca ttgtagtata aagctgtaat ttgaaatttt actttggaat 420

gtaaagtaga aaatattagc tatgtcaatg atatcttgca aagtgttccc attt 474

<210> SEQ ID NO 112
<211> LENGTH: 501
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (116)..(116)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 112

gtattccaag tttactccat tacatgtcgg ttgtctggtt gccattgttg aactaaagcc 60

ttttttgat tacctgtagt gctttaaagt atatttttaa aagggaggaa aaaaantaac 120

aagaacaaaa cacaggagaa tgtattaaaa gtatttttgt tttgttttgt ttttgccaat 180

taacagtatg tgccttgggg gaggagggaa agattagctt tgaacattcc tggcgcatgc 240

tccattgtct tactatttta aaacatttta ataatttttg aaaattaatt aaagatggga 300

ataagtgcaa aagaggattc ttacaaattc attaatgtac ttaaactatt tcaaatgcat 360

accacaaatg caataataca atacccttc caagtgcctt tttaaattgt atagttgatg 420

agtcaatgta aatttgtgtt tatttttata tgattgaatg agttctgtat gaaactgaga 480

tgttgtctat agctatgtct a 501

<210> SEQ ID NO 113
<211> LENGTH: 536
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (54)..(57)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (60)..(71)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (73)..(76)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:

<221> NAME/KEY: misc_feature
<222> LOCATION: (79)..(83)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (85)..(87)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (89)..(91)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (93)..(94)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (96)..(96)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 113

ggagaggctt cttgctgaat tttgattctg cagctgaaat ttaggacagt tgcnnnngtn 60

nnnnnnnnnn nannnntcnn nnntnnncnn ntnnantgtt taaaaattgt acaaaaggaa 120

aaaattagaa taagtactgg cgaaccatct ctgtggtctt gtttaaaaag ggcaaaagtt 180

ttagactgta ctaaatttta taacttactg ttaaaagcaa aaatggccat gcaggttgac 240

accgttggta atttataata gcttttgttc gatcccaact ttccattttg ttcagataaa 300

aaaaaccatg aaattactgt gtttgaaata ttttcttatg gtttgtaata tttctgtaaa 360

tttattgtga tattttaagg ttttcccccc tttattttcc gtagttgtat tttaaaagat 420

tcggctctgt attatttgaa tcagtctgcc gagaatccat gtatatattt gaactaatat 480

catccttata acaggtacat tttcaactta agtttttact ccattatgca cagttt 536

<210> SEQ ID NO 114
<211> LENGTH: 356
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 114

gactatttcc cctgagtggc cgtgttgtcc cagtgccctg gttcagtgtc tcctgagtgg 60

atgacaggtc ttcattctct atcttgaatg tattatggtt actaatagtt ttataatgga 120

ggtctaagaa ttaaagttgt gtgggagttt caggacaaag gaaggctaaa agtttgtcaa 180

gacgttgagc gtattttggt tacctatgag aagggttgtg acagtgtaca gtggcagctg 240

ttggccacgc tgcagaaatg agctggagct catgggtttt cagctacatt tttcataact 300

ttgtagtaca tccatcttga gtaaattaag ccacaatttg gtacctaggg tctcaa 356

<210> SEQ ID NO 115
<211> LENGTH: 498
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 115

ccctgtcagt gtcggagtgt ataagaatgc ttgtaaatac tgtaatatat ttattaatat 60

ttgaaaggca ttcattcagt ggacagtggg aattaactct cccaaggcaa gtgaaaatga 120

atgattgacg tacgttgatt taacaatctt actagatttt aattcttaag gatttcaaat 180

gaaaccagaa ggtggttatg taagaggctt aaaatgatct tatgtttaaa gagattctgt 240

tattagcacc atgaactcgt actatgaaat ttttaagcct tttatttttc taactatatt 300

actgtaggac tggatattag gtgtcatata ggaaacacaa aagttattgc tgtttgctaa 360 agcaaaatag cagaaaattt tgtatatgca aaactgttga aggaccatag agaaatgtgt 420

actactgacg gggcttttac taggcttcct gcgtgtgtaa aagtcgaggt attgctggca 480

ttcagggtga catgatgg 498

<210> SEQ ID NO 116
<211> LENGTH: 487
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (257)..(257)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 116

gccacaattt ggtacctagg gtctcaaact aaaatttatt tttataaatg aattttaaaa 60

gaaaaaatat ctacttcttt taaagttaga agaaaattaa cctgctgaca ggcaacattt 120

ttggggtgct ttctgcacta gttttccttg taaatgattt gagtgagtag gtttggtttc 180

tgacgaaagt agactggagg gtagcattgt atgcctcaaa tgtctcagtg tgtttggctc 240

atacgtgggc tatactntat tattttggta tgcttacaaa tgactaacca atcaaattgt 300

cattaatgtt tggaaaatct gttaatgcac atgcacaata atttcctgaa agccatagga 360

catgtctgta gtcagcacca cgatagcacc gtttcatgaa aggcatggcg gctgcatttc 420

ataccacatc aaaatacagt aacatttcta tactaaatta acagtaatac ctcaaaactg 480

ctccggt 487

<210> SEQ ID NO 117
<211> LENGTH: 411
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 117

acaacactta agcacactat ttctgttagt gtatatagtt ttcaaactaa caagcctgcg 60

atccttgtta gtgtagtgac tgcctcttta ggagtatggg gccctagggt gtccatatat 120

ttttacccca tgggtcattc tagtctaagg actactagta gaaccctcaa aaggtaattg 180

ctattatagg gacttactta ttggagactg gtaatataat aaaatattga aggagtggcc 240

atggtcttag caggttttag aatgaccttt taactccagt aactacttcc ttggtattgg 300

tatccttgat agagggaata taacatctgg cagtaatctc attcaggtta tactacctga 360

ctaaatttaa tcatactttc atgtatttgt ttcctcagtt ggacctaagt t 411

<210> SEQ ID NO 118
<211> LENGTH: 461
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 118

aaagtgaacc tgagtgccca gtctctgctg cacgatggca gccccctgtc cccattctgg 60

caggacacag cgttcatcac actctctcct aaagaagcaa agacctaccc ctgcaaaatc 120

tcctattccc agtacagcca gtacctgtca acagacaagc tgatccgcat cagtgccctg 180

ggtgaagaga aaagcagtcc tgagaaaatc ctggtgaaca agatcatcac cttatcttat 240

ccaagcatca cgattaatgt tctaggagca gccgttgtga accagccact ctccatacag 300

gtgatatttt caaacccccct ctcggagcag gttgaggact gtgtgctgac tgtggaagga 360

-continued

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agtggcctct tcaagaaaca gcagaaagtc ttccttggag tcctcaaacc ccaacaccaa    420

gcaagcatca ttctggagac cgtccccttc aagagtggac a                        461


<210> SEQ ID NO 119
<211> LENGTH: 484
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 119

gcttcgggca tccaacgcaa tgatgaacaa caatgacctt gtgaggaaga ggaggcttgc     60

ggacctgact gggcccatca ttcccaagtg ccggagtggt gtctagtgtg tggcggtgga    120

gtccatgcct ttgaactgga tgtgttctat tgatgacctg tgctctgcag gggaaaccag    180

aaggcaaaat gctggcagca tgaaaccctt ttgtggttca gttctttatg cactaaggtt    240

ttaggttgac tagtggttgt agttgaaaat tttataaaat accgttaatg tgaagttttt    300

ctttagtcac agaagttgaa tctggttatt atttaaaaac tagaagcccc caaaccagca    360

gatcttactg aagatgatgt tccagcagca gcgacttagc cccaggagcc cagtttcaat    420

ggccttgctg tgtggtgttt caagtgcatt taaaatgtgt gacacagaaa cggcacactc    480

ttcc                                                                 484


<210> SEQ ID NO 120
<211> LENGTH: 504
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 120

agacaaattg ctgctgacct tacgcctgta tattaagcct ccgcaggatg ccggacaatg     60

gtgaagaaac tccagatatc aaggaattgg gaaatcctgg ccaaaccacc ccaagatgat    120

tacactgaaa tgtagtatta gtactgctgc cagatctctt tttaacatca tgtgcgtctc    180

ttgggatcca gcaaaagtgt taagccacaa tgcccttgtg ccttttaata taccacagtg    240

ccagttaaac taatattttt gtttgttgct tttgggagtt attttcatta gtgatttcag    300

caaatctcat gataaaggac aaggtcaaga actccagagc actgagcaga gaggctggtg    360

atgaaaaggt gaaggcctgc gcactgaact gtaaggcagt gggcagtaca gggtaactgg    420

aggcggggcc agggcctcag cgctatggaa gagtgtccac tgaggctgca catggcccag    480

gagtggcacc atgttgcagg gaca                                           504


<210> SEQ ID NO 121
<211> LENGTH: 389
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 121

gatagtcgga atagagccgc cccaactcag atcctacaac acgcaagttc cttcttgaac     60

cctggtgcct cctaccctat ggccctgaat ggtgcactgg tttaattgtg ttggtgtcgg    120

cccctcacaa atgcagccaa gtcatgtaat tagtcatctg gaacaaagac taaaaacagc    180

agagaattgc gggttctacc cagtcagaag atcacaccat ggagactttc tactagagga    240

cttgaaagag aactgagggg ccacaaaata aacttcacct tccattaagt gttcaagcat    300

gtctgcaaat taggagggag ttagaaacag tctttttcat cctttgtgat gaagcctgaa    360

attgtgccgt gttgccttat atgaatatg                                      389
```

<210> SEQ ID NO 122
<211> LENGTH: 427
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (81)..(81)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (86)..(86)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (117)..(117)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (176)..(176)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (258)..(258)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (274)..(274)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (359)..(359)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (382)..(382)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 122

ctgtgggtcg tggataagga gcttattcag gtttcctgcc ctagctatta gctccacttc 60

acatgctgga gaccggcgta nggacngatg tattcatcct ggtgttactg aaaaacnggt 120

gtgatcctgt tactgatact ataagtgacc taaaatgtca ctgttcaaat tagccngtgt 180

tctaacaaac taaactcttc aaatgcttgg aaagatacta caaagccaat ctttatagaa 240

ttgggccaag ataaatcnat gttgttttgc atgnctattg ttaagctcca aaggttcact 300

gtgtttctgc cgctgtcctg gagttgtcac cactgactgg gcaaggcttc ttgggcatng 360

atgtagaact gttgtccttt tnccactaac agttatcttt gactctcttg cctgttatgc 420

ttacaaa 427

<210> SEQ ID NO 123
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 123

accatcgctg gtggtatccc agggtccctg ctcaagtttt ctttgaaaag gagggctgga 60

atggtacatc acataggcaa gtcctgccct gtatttaggc tttgcctgct tggtgtgatg 120

taagggaaat tgaaagactt gcccattcaa aatgatcttt accgtggcct gccccatgct 180

tatggtcccc agcatttaca gtaacttgtg aatgttaagt atcatctctt atctaaatat 240

t 241

<210> SEQ ID NO 124
<211> LENGTH: 392
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 124

ggggctatac tccatccaaa tatgcagtgg aaggtttcaa tgacagctta agacgggaca 60

tgaaagcttt tggtgtgcac gtctcatgca ttgaacgtct agacaaactg aaaggcaata 120

aatcctatgt gaacatggac ctctctccgg tggtagagtg catggaccac gctctaacaa 180

gtctcttccc taagactcat tatgccgctg gaaaagatgc caaaattttc tggatacctc 240

tgtctcacat gccagcagct ttgcaagact ttttattgtt gaaacagaaa gcagagctgg 300

ctaatcccaa ggcagtgtga ctcagctaac cacaaatgtc tcctccaggc tatgaaattg 360

gccgatttca agaacacatc tccttttcaa cc 392

<210> SEQ ID NO 125
<211> LENGTH: 512
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 125

ggggctatac tccatccaaa tatgcagtgg aaggtttcaa tgacagctta agacgggacc 60

tgaaagcttt tggtgtgcac gtctcatgca ttgaaccagg attgttcaaa acaaacttgg 120

cagatccagt aaaggtaatt gaaaaaaaac tcgccatttg ggagcagctg tctccagaca 180

tcaaacaaca atatggagaa ggttacattg aaaaaagtct agacaaactg aaaggcaata 240

aatcctatgt gaacatggac ctctctccgg tggtagagtg catggaccac gctctaacaa 300

gtctcttccc taagactcat tatgccgctg gaaaagatgc caaaattttc tggatacctc 360

tgtctcacat gccagcagct ttgcaagact ttttattgtt gaaacagaaa gcagagctgg 420

ctaatcccaa ggcagtgtga ctcagctaac cacaaatgtc tcctccaggc tatgaaattg 480

gccgatttca agaacacatc tccttttcaa cc 512

<210> SEQ ID NO 126
<211> LENGTH: 502
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (224)..(224)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (238)..(238)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (269)..(269)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 126

aagcaggctt gtgctttata ccccatttga tttcgatgta cagtctcaat tttgtattta 60

atgatttttg tgtatccagt atgcacgtta acagcgtgtc aactttcatt tgaaagtggg 120

tttcaattta ctttttaaac agtgtttatg acgagacctc agatgtgttg acgtaagctc 180

tatctgcaat gtttttgtgt agagtggcga ttgaatgctg cccngggtca gtgtatcnta 240

attccccgag accctcgttt gatagtgcnt cttgtaatat ttcttcaagt gagtggcatg 300

tgggttgtga tattgaccat gtgattatgg acatcgatat gaaaaataaa taaataaaac 360

taaggaaccc tggaaactac cagtgggcat gtattagcca gtcattgtaa cctcgtgtct 420

agtagaacaa tgtacaaggt atgtacagtt cataaatttg ttgtcatgtg tatgagaagt 480

actttgtgct gatcgcctta tt 502

<210> SEQ ID NO 127
<211> LENGTH: 536
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (26)..(26)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (64)..(64)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (124)..(124)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 127

aaaatgctat tagtccgtcg tgcttnattt gtttttgtcc ttgaataagc atgttatgta 60

tatngtctcg tgtttttatt tttacaccat attgtattac acttttagta ttcaccagca 120

taancactgt ctgcctaaaa tatgcaactc tttgcattac aatatgaagt aaagttctat 180

gaagtatgca ttttgtgtaa ctaatgtaaa aacacaaatt ttataaaatt gtacagtttt 240

ttaaaaacta ctcacaacta gcagatggct taaatgtagc aatctctgcg ttaattaaat 300

gcctttaaga gatataatta acgtgcagtt ttaatatcta ctaaattaag aatgacttca 360

ttatgatcat gatttgccac aatgtcctta actctaatgc ctggactggc catgttctag 420

tctgttgcgc tgttacaatc tgtattggtg ctagtcagaa aattcctagc tcacatagcc 480

caaaagggtg cgagggagag gtggattacc agtattgttc aataatccat ggttca 536

<210> SEQ ID NO 128
<211> LENGTH: 304
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 128

cttttctgta atctgtttat ctcccactta atggaaaggc aaaggggtac cccaaatcca 60

gaggtgccta catttcaggc agccttggag tattttaaaa ggaaaacatt ctttactttt 120

atatgacatt cttatactgc tgtctcaaat ccttttttcat ttcagagctc ttgtctcaga 180

gatgtgtgtt ctttttgtca gagatatggt tgatgagaat cttaaatgct tgttttgcac 240

tatcacttag tacctgtttg accaaggtgt taagggatag tacctcccat cagcagagaa 300

actg 304

<210> SEQ ID NO 129
<211> LENGTH: 408
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 129

gatcaatgct tcgaacttct actttaacaa aaccaagggc ttttactgcc tgcgggacag 60

cggccgggac cgctgcttac atgagtccaa aggccgggcg cacccccaag tcgatcccaa 120

actactcaat aaactgcacg aatattttca tgagccaaat aagaagttct tcgagcttgt 180

tggcagaaca tttgactggc actgatttgc aataagctaa gctcagaaac tttcctactg 240

taagttctgg tgtacatctg aggggaaaaa gaattttaaa aaagcattta aggtataatt 300

tatttgtaaa atccataaag tacttctgta cagtattaga ttcacaattg ccatatatac 360 tagttatatt tttctacttg ttaaatggag ggcattttgt attgtttt 408

<210> SEQ ID NO 130
<211> LENGTH: 399
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 130

ggatgtcaaa tagtcacagt tctaagtagt tggaaacaaa attgacgcat gttaatctat 60

gcaaagagaa aggaaaggat gaggtgatgt attgactcaa ggttcattct tgctgcaatt 120

gaacatcctc aagagttggg atggaaatgg tgatttttac atgtgtcctg gaaagatatt 180

aaagtaattc aaatcttccc caaaggggaa aggaagagag tgatactgac ctttttaagt 240

catagaccaa agtctgctgt agaacaaata tgggaggaca aagaatcgca aattcttcaa 300

atgactatta tcagtattat taacatgcga tgccacaggt atgaaagtct tgccttattt 360

cacaatttta aaaggtagct gtgcagatgt ggatcaaca 399

<210> SEQ ID NO 131
<211> LENGTH: 268
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (172)..(173)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (176)..(176)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 131

cagtggctct attctacctg taagaaaatg atacaaaacc acctaagata ttttgaagcc 60

tgacaaatca gcttcatgga aaaaggtaaa aaatgcattt ttcaaccgaa agggcagatc 120

caatagaaga cccgctcctt aaataaacat aaaatgtaaa aagttggaaa annaanagta 180

atgttccatc tggaaactga acttttgtcc ttgaacttgt gttggcacca agcctcatac 240

acagtgagct caataactgt tgggacaa 268

<210> SEQ ID NO 132
<211> LENGTH: 433
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 132

ggcttattga cttgcacggt tgggcagata atccagattt acctaagatt gggtaaaaaa 60

gtcatctgtg actttgctgg cagggcattt gctaagtgga gtacaggatc taaaagggtt 120

ttcttagaaa gggcaatatt gtccaatgaa gtaagcagaa ggactctggg ttagaagcat 180

ctgcacaaaa actggtgaga cctactctcc actgctctgc agctggatgg ctgatggcag 240

gctgagcagt ggggaagcag gttttaacaa cagggagtcc ttccaggtca ctgtatattg 300

agaagaaaca taaaactatt gtctgttaca ttccgaggtc agccttcttc ttaacgtttt 360

ataatatgca aatgccagct tctggaaagc aagtatcatc atgtaccaaa tgctttatac 420

accatcacat tca 433

<210> SEQ ID NO 133
<211> LENGTH: 497
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 133

cttttattt ctatgtgtgc cacacacaat gcagtattaa tggcaaccag gtaaatattg 60

atttattttt taaagctttt cttcagtgtt ttgtcaacca tttcaaagtg tctcccaaaa 120

aaggatgctg aagagcaatt gctcccttaa gcaacagatt catatttacc ctgggttaat 180

acaacaaaag gcctgtataa ttgtcttttc attgttaaca cccaaaatag catctatcta 240

gacagtatcc ccaaagaatt tggaaaatct gatggtgtga gcagcagccg ttagtatcag 300

ggtttcccat tcttggacag tccgaggctg tgacctgtta gataattaga ttatacttga 360

actggaccag agtttgtttt ttgaatttat gagaaaaacc aaaacactaa gttaagtttg 420

aacttgtaaa gtattgaaat ttgttgagtg tcctataaat tgtcactact tttcctgatc 480

tgtataactg actgcaa 497

<210> SEQ ID NO 134
<211> LENGTH: 533
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 134

ctgccttaga ttccgtgggt catgagccat gagtcctggg acatctgagg attgggattc 60

tttgttcacc ccgcagatag ttaatgaatg gtctgccctg ggcaagatgg aggtgggggc 120

tgggggaata tgcatgttgc agaagccggc gtttttatta gcggtcctga gtaatttccc 180

ttggcaaaat tcccagtttt gccactcgct ggagccagat cctgggagct gtcagcaagg 240

agcaggtaag tgagcagtta tggacagcac tttccatgtg gtgcttccga ccctggctgt 300

cagagtgaaa tgtaaagtca gggctctgta cagttttgcc atttcactgt tctgctttaa 360

gcttagctta ttagaactct tggtggaggg tgcgtacaca cattccagaa aaggcttcac 420

tcgctgggaa cgtcaaccca gcgagaaagg aggggaagcc ccttctccgg ggaccttatc 480

tgtggactca gggatgatgg tgtttattgc aaatgcacaa tctttttccc att 533

<210> SEQ ID NO 135
<211> LENGTH: 485
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (55)..(55)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (57)..(83)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (123)..(123)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (173)..(173)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (213)..(231)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (380)..(380)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (382)..(383)

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<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (417)..(417)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 135

tccgagctaa aatcccaggg accggagccc tggcctctgc agcagccgca gtctncnnnn     60

nnnnnnnnnn nnnnnnnnnn nnnacggtgt ctctgcccgc aggacgcctg cccccagccc    120

ccngcagccc tctggccccc tccatctctt gtccgttccc acccaccccc ctncctcggc    180

ccgagccttt tcccggtggg tgtcaggatc acnnnnnnnn nnnnnnnnnn nctaattacc    240

tgagcgacca ggactacatt tcccaagagg ctctgctcca ggagtccagg aaagacgagg    300

caccttggcc gcggggcctg ctgggacttg tagttgccta gacagggcac caccctgcac    360

ttccggaccc gccgctggan gnnccgtgag gcgttggtgt ctcctggatg ctactanccc    420

caacgccggg gctttgcatg gggcccaggg gaggcctgag cttggattta cactgtaata    480

aagac                                                                485


<210> SEQ ID NO 136
<211> LENGTH: 287
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 136

gattctgtgg tagactcagt gctttcagag tccagagctt gacttgggtt agtggcctta     60

atgaagtgct aaatttgctc tttaccgcga gactgatcag aagaagcaaa aggggaaagg    120

gggctagagg tccactcgca ccttttacat cagacaagag gaggactgtg ccagaaatct    180

gtgcatgaaa caccatctgc tcttcatgca gggaggggtc aaccgtgtga acgtgcagag    240

attactcgag ccttctttgc caaaaatatg cattcttccc agctgta                  287


<210> SEQ ID NO 137
<211> LENGTH: 508
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 137

tgaagtgcca gcactcatcc atcaatcaat cacccacaag gaaaaatagc aacagtacaa     60

cggggtggct tttatgggat ttactcatgg gcatagggaa tagcggctca aatgtagttc    120

tgacatgaaa agcaaggtgc tgatattatt ttttatgatg ggaggatcat aaagtgaatt    180

gagaacagtg aggtctgtct ttgcttaacc tattcaacca gaaatgaatg gagctcgact    240

ggaaaggaac agtcttcaga tgggttaaga ttgaagggtg gactggactc tactgagcac    300

cgtccttcaa caaggaaatt ctattaaagg aaaatcaatg cattagtatt ggggttcttg    360

tagcttgtta aaaattgtct gctccaatcc agggttatta ggccaaagtt acataattca    420

gatctcactg caaccatcca aaagtggatt ctcgagccct tgctccaatg gggggaggag    480

atcaatacaa ttccccaatt tccatgga                                       508


<210> SEQ ID NO 138
<211> LENGTH: 515
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (382)..(382)
<223> OTHER INFORMATION: n is a, c, g, t or u
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (393)..(393)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (402)..(402)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 138

aagtcttgca tacctagtgc acagtttgga gacgcaagga tagatctgtt tactctagtt 60

gaacattttc tatacaattg aaagcaacct ataatagata aatccatcat tgcatttaaa 120

caatgaattt ccttattctc aaaggacaaa tacgtctgga ttatgtggta aattgctact 180

cagctatggt gaaatattta tactattcta ggcacaacac taggaactag gtgattctga 240

aacaaaagga atattttctg ttgttgcttt aattaccaag gttatttttt tttaatctca 300

acactgacaa aatgaaacca aatatctctt cctcaccatt tctcaaggag gctgcctgtt 360

ggaattgttt tggaaatttt gnacatgatc ccntaaattc ancattggga ttaaaaaaaa 420

aaaaaacttc ttatttacct cctaagggaa ggttgccctt atgccacata taataccaaa 480

ttgctttttt atgggctgcc ataacctgaa gggaa 515

<210> SEQ ID NO 139
<211> LENGTH: 388
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 139

tgcagatttt attctcacct gggccatttg cagatgagac tgtagtttgc agatgagact 60

gtagtttgca gatggcgtgg aagcattcat caggggagat aaccataaag gatttggcct 120

aattaccata ctcaattgtc agtttacgtg gttttgtgaa tactggcaaa agcaattgtt 180

tttaaattaa caatggagag aatgataaga tgagggaagg aaaaggcatt cattattgac 240

ttacatgtca gtaaggtctg cttttatttc tatgtactcc tgtttgccaa gctcaataat 300

ggacaaagga tacaaacaca cacacatcta ctattttaga taaatgtact gttatatata 360

tatgtaaact actattgctc tctttata 388

<210> SEQ ID NO 140
<211> LENGTH: 544
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 140

taggctttac tgtcttatgc ttatggacat tgtatatttg tattttatga ccaagtagac 60

caagtcagaa agatctctct cgagcgcacc ataaacctgc agagagaagt ctcgaaaggc 120

tccaccaagg taccaagggc agctgctttt cctgtctttt gtgcatgggc gacccattac 180

agtatgagat aagattgagt tctgatgcgt taaacggagg tggcagaaat ttgtcaagaa 240

ggccttatcc atttcgattg tgtgacagat tgaaatttat tgtttacatt ggggaatgta 300

tctcaaattt ttaaatagaa gagtaataaa cagactttaa agcaaatatt aagattttta 360

ctcattcaag gcaagtaaat gaatggaatt atctgagctc tatggcactg gttgtttaga 420

gtgactgatg aagtgcacct ttcaaaaaca tttttgatgc catcaccagc ctactgcaga 480

agtgcagggc acagtaaaca ccatgtatta ttgaagatga tctgttttgt atgtatcctt 540

gtca 544

<210> SEQ ID NO 141
<211> LENGTH: 392
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (198)..(198)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 141

atgtttcttg ttagccatga ccctataaga aataaactgc actgcaaaat gataaacatg 60

atatcaatca ttacatggga aggcactata taaagaataa taccttaggt taaggccaca 120

taaatattta tcaggtgcct tttctgcgga ggactctgaa gggatactaa actgcattta 180

gctgcatgca actgaaanta cttttaccta cattgtctct tataaacatt ataactactc 240

tttgagaaag tgtttactat ggactgaatt gtctccccat ccccccaaat tcatatattg 300

aagccataaa ccccaatatg actctattcc tagacaggac ttataagagg taattaaggt 360

taaatgaggt cattaggatg ggttcctaac tg 392

<210> SEQ ID NO 142
<211> LENGTH: 508
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 142

ttcctttctc actgccttga gagtgaccca aagatgagat ggaccgccag ccagctcctc 60

gaccattcgt ttgtcaaggt ttgcacagat gaagaatgaa gcctagtaga atatggactt 120

ggaaaattct cttaatcact actgtatgta atatttacat aaagactgtg ctgagaagca 180

gtataagcct ttttaacctt ccaagactga agactgcaca ggtgacaagc gtcacttctc 240

ctgctgctcc tgtttgtctg atgtggcaaa aggccctctg gagggctggt ggccacgagg 300

ttaaagaagc tgcatgttaa gtgccattac tactgtacac ggaccatcgc ctctgtctcc 360

tccgtgtctc gcgcgactga gaaccgtgac atcagcgtag tgttttgacc tttctaggtt 420

caaaagaagt tgtagtgtta tcaggcgtcc cataccttgt tttaatctc ctgtttgttg 480

agtgcactga ctgtgaaacc tttacctt 508

<210> SEQ ID NO 143
<211> LENGTH: 502
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 143

ctggagtctg ggtgtgttg tcatagagat ggtgactggc aaggtttgca cagatgaaga 60

atgaagccta gtagaatatg gacttggaaa attctcttaa tcactactgt atgtaatatt 120

tacataaaga ctgtgctgag aagcagtata agccttttta accttccaag actgaagact 180

gcacaggtga caagcgtcac ttctcctgct gctcctgttt gtctgatgtg gcaaaaggcc 240

ctctggaggg ctggtggcca cgaggttaaa gaagctgcat gttaagtgcc attactactg 300

tacacggacc atcgcctctg tctcctccgt gtctcgcgcg actgagaacc gtgacatcag 360

cgtagtgttt tgacctttct aggttcaaaa gaagttgtag tgttatcagg cgtcccatac 420

cttgtttta atctcctgtt tgttgagtgc actgactgtg aaacctttac ctttttgtt 480

gttgttggca agctgcaggt tt 502

<210> SEQ ID NO 144
<211> LENGTH: 500
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (299)..(299)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (456)..(456)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 144

ttgtgtgtaa tttcatggtg gcctagtgtt gtggtgcttc tggtaatggt aatagaagct 60

caactatttt tttgtggatt tcagttttta tcatcagaag tcctagacag tgacatttct 120

taatggtggg agtccagctc atgcatttct gattatacaa aacagtttgc agtaggttat 180

ttgtcatttc agtttttac tgaaatttga gctaaacatt tttacatgta aatacttgta 240

tttaccaaag atttaaatca gttgattaat taattaactc aaatactgtg aactatctnt 300

aaaacactag aaaaaagaaa tgttagtatc tcaattacac caactgtgca aatgaacttt 360

gataaaatag aaataatcta cattggcctt tgtgaaatct ggggaagagc tttaggattc 420

tagtagatgg atactgaata ctcaggccca cttaanttat taatgtatac attgtgtttt 480

tgtctttatg ctatgtacag 500

<210> SEQ ID NO 145
<211> LENGTH: 450
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 145

gctggtatca gaacagcttc cctcactgtg tacagaacgc aagaagggaa taggtggtct 60

gaacgtggtg tctcactctg aaaagcagga atgtaagatg atgaaagaga caatgtaata 120

ctgttggtcc aaaagcattt aaaatcaata gatctgggat tatgtggcct taggtagctg 180

gttgtacatc tttccctaaa tcgatccatg ttaccacata gtagttttag tttaggattc 240

agtaacagtg aagtgtttac tatgtgcaag ggtattgaag ttcttatgac cacagatcat 300

cagtactgtt gtctcatgta atgctaaaac tgaaatggtc cgtgtttgca ttgttaaaaa 360

tgatgtgtga aatagaatga gtgctatggt gttgaaaact gcagtgtccg ttatgagtgc 420

caaaaatctg tcttgaaggc agctacactt 450

<210> SEQ ID NO 146
<211> LENGTH: 386
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 146

gtagcatgtt gtcagtggcc aaggctacac agaaggctcc ctgctgcccg gagcaggtac 60

atccaccaga gcaaagggaa ccacttttat tttgcatgag tttggtaact gattactctc 120

ccctcaaaga aaagacattc aggtgtttct caacgacatc ttctgtccag caagctcggt 180

ttgaatacgt cacttaccag tgccattgca ggacccaaat tcacagttca taaaagatgt 240

gaccactaca tgtaaaaata gcattctact tgatcttaca gtatgtatgt atgtatgtat 300

ggagacatat gtgtgtgtgt ggatgtctac atggttaatg gaaagcactg tgctctgaag 360

tggatcagtc tcaagtgtct ggtaac 386

```
<210> SEQ ID NO 147
<211> LENGTH: 487
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (296)..(296)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 147

tataaggtaa ctctttagtc ctccatttag cacattttaa atcctccaaa gaataagtat     60

catgtgatta ttttagcttt acaaaaaaaa agttgaatgg cgttttattt tcatggccta    120

taagcaggta ccttagtagg gcagatatag gaaaaacaaa ttagagcaaa acaaatcctc    180

tacaaatcca aggcaggaaa agtggtggca gagtgactca ttctcctgtc cctcccatca    240

ggtcaaatca ggaggctgca gtgaatgcct gttctttgaa tgtgtagcag ttgttncctg    300

taactcttta aaacttggct ataggctgtt tagcacagta cagattaaag atacagttac    360

gtaaacagca aagtaatttt atagtgcttc atccatttat catgctttgg tttgctaatt    420

ttttcacata ccttttttcta tcacagtctg ttgcttttgt acacatttct catattgggg    480

ttcgaca                                                              487


<210> SEQ ID NO 148
<211> LENGTH: 400
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (120)..(120)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (373)..(375)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 148

gcagtatgag tttcaggtat gtacatgtta tgtgtgtgtg tgagagacac acacaaacac     60

atttcaaaca tgttttatgt ttaagctcaa tattcaaaca cagaaatata acatctattn    120

cttaatatgt tttatgtaag tacagcagca gcattattaa atactgtatt tctatggtga    180

ttgaaaatta gtaggcagag aatttttgta atggttctta ataatttttg taatagtaaa    240

tgattacttt ttgtttagta tagttttata atctatacat gaataaagtg gatatttcta    300

ttcatataga aatgtgattt actctcatgt acttatctac atgctaaaac cataagttat    360

caattttagt tcnnngccaa ggcactttta ctgaataaaa                          400


<210> SEQ ID NO 149
<211> LENGTH: 518
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (199)..(199)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 149

gtatcctata actatcaact tcccaggttg aagacgatgt gttgagtttc ctactgattg     60

attgattcct gtcctcccca gtgtttccgt cactggttca ctaaaacagt atttatatag    120

ctccactggc tctaaagctc ttagtccttc taatattttg gattttacaa gtaaaaatgg    180

aaaaaaaata gaaaagagnc aatcaaatgc ctggagctta aaacaaagta tgtgcaacct    240
```

accatctcac ttgaaattta ataaaataat aagtaattat gtaaatataa catagagtta 300

tagatttata ttttgttcat aacacatagt gtaatataag ttgtatattt tcatgttttt 360

ggttttatgt tatcattcat gccacaataa aaataaaaca ggagtttatg tgctcttaaa 420

aaaaagatgt gggttgccac caacctgttt ttcgtttttg ttttttgttt attttatttt 480

atttttttgc attctccttt ttcagtatta ctgccatg 518

<210> SEQ ID NO 150
<211> LENGTH: 343
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 150

gtttcagtca atgatgggcc acatgtagat ggtggtcccg taagattata ataccttatt 60

ttaactgtac cttttctatg tttagatgtg tttagatacc attgtgttac aatggcctga 120

agcattcagt acagtcacat gcgagcaggt atgcagccta ggagcaatag gccacaccac 180

acagcctagg tgtgcggcag gtgtagcgca ctctgatgcc tgcacgacga caaaatcaac 240

taacagcaaa ctcctcagac cgtatcccca tcattaagca acacatgact gcagtttctt 300

tctttgcttc taggctcagc ctacaaaagc ttgctgctca tgc 343

<210> SEQ ID NO 151
<211> LENGTH: 388
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (172)..(172)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 151

gcctgatagt gctgaatttc tgaattgacc ttcatcttat ttactcaata atattcattt 60

gacaaatact tattaagtgc atatatgtgt caggaactgt actagatgct gaggatatag 120

cagtaagcgc aacagaccaa gctaacagct tagtaaaggg tgaggtaaaa cnaaaacaaa 180

aaagtattca aaaaaataaa ctaattttta tcttaattta aaaaattaca aatttttaaa 240

aatcacaaat tggtatccat gtataattca tttccgtgca ttttcttgtg tgaagaaagc 300

tcagtaaaag tatttcttag gtttctgtaa ttctagttct ctactcgatt ttcttctgca 360

attttctgag ccagaaccct tcttagaa 388

<210> SEQ ID NO 152
<211> LENGTH: 493
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 152

cccccatgtt acctggactg gaacagactg tgaatatagc agaaggttcc aagaactctg 60

gtgtctgacc tagaagaggc acagttctct ctactggaaa gaaaacgatg tagccgattg 120

cacaagggtg ccaagggaag acccaggatg gcccatcaaa ggaacctggg ggaggatgca 180

ggaggctgaa gggatgcacc tggcatttct ctcactgtgc tcttaccgca tcagcaaccc 240

ccaacttttg ggcctactct gccccccatg cgtgaatacc ctgcttggat gctgtgcttt 300

tccggtttgt ctctaagccc ctttctccag ggcatgttgg tttccctggc ctctcagtgt 360

cctaactgga gcccagagtg ccttgttctg agccaggaga cggctgagca ctggccctcc 420

-continued

acacctaagc gtcctttaca ttaacttatt ggtcttgtat aacacctggt gccattgcca 480

agtggctgtg tcc 493

<210> SEQ ID NO 153
<211> LENGTH: 398
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (141)..(141)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 153

gggtcaaccc caggagtatt tgcagaaggc ccagcacagt ggggggtatt ggctgcaggg 60

cagggaaggc attgccgact agataaccgt gtgagcttgg actgagcgtt ggtggttctt 120

cccaaaggaa aggaatttct ncccggcctg ccaggtctct gggccttcag cgcgggtcct 180

ggtgctgcgg ccacaccacc ctggggtgct cattgacaga gctgccataa tgaacttgaa 240

aggacgggaa tcacgaggga agctggggct cccctgccca caggagagga tccccgttct 300

tcaagcttct ctgctcagtg tctactaacg accgacattt gctaatgtaa ataatagtaa 360

attattgaga attctaattc ttttacacag tctgtttt 398

<210> SEQ ID NO 154
<211> LENGTH: 380
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (161)..(161)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (173)..(173)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 154

gtaatgtaca tatgcatatt gtctatgtac tatatacaca ttgtttataa tattgttatt 60

acagtttgtc attcacctga aaggagaagg aaaagtacga aaggtttctc tgcttgggaa 120

aaggtgaatg ttgttatatc aagaacgatt acacacatgg ntctcataca tgnttttaga 180

acattgttct tctgattgaa gaagtctgat gctcctgaaa aatcttaaaa tatctgactt 240

gtattgaaga aaattattta attaaatttt taaaggctgg ttgaaaaagt ctgacagttc 300

tgagaatttt ttaaatgtct gaattgtaat aaaaaaatgg tttactttaa acttctaaaa 360

actaatgacc ttgtgactaa 380

<210> SEQ ID NO 155
<211> LENGTH: 495
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 155

cttttgcgaa cctttcagtc tccgctagct ctttcctaat gagctttaca gcagaagctg 60

ttttatcgtt aagtgcccca cagagacact ttaccaggag gctgggagag ttctccagat 120

ttgggagagg cgcagagaca gtgtgtgagc cgagccctgt ctcagcaatc cacctggagg 180

agctagagta tcctcctccc tttaccattc agaccgagag aaaaagccca gcttgtgtgc 240

accctcgtgg ggttaaggcg agctgttcct ggtttaaagc ctttcagtat ttgttttgat 300

gtaaggctct gtggtttggg ggggaacatc tgtaaacatt attagttgat ttggggtttg 360

-continued

tctttgatgg tttctatctg caattatcgt catgtatatt taagtgtctg ttatagaaaa 420

cccacaccca ctgtcctgta aacttttctc agtgtccaga ctttctgtaa tcacatttta 480

attgccacct cgtat 495

<210> SEQ ID NO 156
<211> LENGTH: 540
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (111)..(111)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (333)..(334)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (344)..(344)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (354)..(354)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (392)..(392)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 156

aaatattcac aaacgtgcac acttctgcag agacaaagca tttcactgca cgtgtaccag 60

gttattgatt ttatcttttc ctttcagggt tttgtcctcc caaaccagag ncatatgctg 120

ctagtagaat tttttatttg atcctgcgaa cttttcttat aggaaaagta aggcaaagga 180

tgtgtagtgc aaccatctga taaactagtg tgattgtatt tatcctctgt tctgtgtatt 240

tctgtaatgg aatctttaca attcccaaaa cggtatttta gacctactgg aaatctgtat 300

cgaaacagct atgtgattct gccactgaga aannaaaatt tttnaattcg tttntcttat 360

gctggtttgt ttttctttaa tgaagaaatt gntctcatat ggcatcatag atgctaaata 420

aataaaagca tcatacttct ctagtttgcc tgcattcagt ggctaacatt atgagcattg 480

tgtaagataa acacatggtc agtatcaatg taaatgttag agccatgatt aattcctatg 540

<210> SEQ ID NO 157
<211> LENGTH: 460
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 157

gatcagttga aagcccttca gtgatagagg aagactggga gttttaaatg tttgaatact 60

ttttaatgaa ttcaatgaga cattttcttt gcttcttcaa agccagaaat aagatatagg 120

gggactatca aacatattat gatagaataa atatatttta tatggtcttg agaaatagta 180

agcttatttt atttatttat ttatttattt ttttacttct tgcatcgtat tctatgaact 240

cactttcaag agagagagac gttgtctatc cacaggtttt ctgcagtcct aattaaaaag 300

aactgcagtg agaagttttt catttcaact tccaacccaa gcttgagggc atagcagtaa 360

ctgcagagta tattgtgttc attttgctgt ttgagtagtt caggaaaaag gagttgcctt 420

tcaaacacca aacaactaat atgattccct gcggacactg 460

<210> SEQ ID NO 158

<211> LENGTH: 543
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 158

gttgattatt ctcctagctc atatctcctt gatgtgcatg agggagcact gggtctaatt 60

tttgggggct gagaaggtaa gaaggtgagg tcagtttttc ccaggagtcc taaaaaattc 120

tggtacctta cattgagggt gtgggagaaa gggtgtcata gttctgaaaa taggcagtag 180

catgaagcac cagacctgtc tcattcctta ttagatgtct atctcaaatg acagagtttg 240

aaaaatattg gttttatcat ttgatatttc catgcctgac tcgggaaaat aacattttct 300

gactttttc tattttcttg ccctgcacag accctacctg gtacaatttt ctatttctta 360

gctcaaagtg tctatacaat gggttgcctg gtatgtcagc tgccctcact cttgtgtaat 420

agaaatatat tgccaggctg gggacgtgga ggagacgaac tggattcctc cctcctcctg 480

ttgccaggcc tctctgcatt ggcactttat cctttcagtg tttctggctg tgttgggttc 540

att 543

<210> SEQ ID NO 159
<211> LENGTH: 431
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (136)..(136)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 159

ctctcggacc ttagggctgt tggagaaggc ttcagcagca gaactgatgg tgaaggctcg 60

tgttctccat cctcaacttt ctttgcttcg atcatacaca agaatacatt tggaagggca 120

aaaaatgaac actgtngttc attgcagccg tgttttgtga cacagatgca cagtctgctg 180

tgaagacctt ctctcaagtg gcatttggga gtccatgcca gatcatggtg cttcatgaga 240

gactgacagc tatcaggggt tgtggcactt agtgaggact ctcctccccc agtgtgtgct 300

gatgacacat acacacctga caatagcttg agtcttctct gttcctttta ctctgtagcc 360

aacatacaca tgatttaaaa ccctttctaa atatctatca tggttcatcc ttgtccaaat 420

gcagagtcag a 431

<210> SEQ ID NO 160
<211> LENGTH: 396
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 160

ggtgggacaa acctggactg ggtggagctg gggccccagc agtgggctct gccatagcag 60

gcgccataag ctggaatttg tgcctccagg cctggaggga cgcaaggcgt ttctgatgaa 120

gccgatacat tcagaattgg ggtccaaata ggaaataatg ccctttttcag gctagtgaaa 180

atgttgaact ctaagagata agtttattta gagactggat tgagcttttg tttaagattt 240

cccacctgcg taaaattcct ttcagcccat aggattcttg attctgaagt ccagacagaa 300

gcctgtgttc tgtagctgct gaacaaagat gagagatcac tggggctgct gtttgtccga 360

agtttgtgtg ggtatcatga tgaaccctct tctaag 396

<210> SEQ ID NO 161
<211> LENGTH: 393

<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 161

tggaacacca caggtttagt tgggaaaata ttttgcagct gagttagaaa cttgaaagtt 60

aggcttataa tcaagatgct gattttcaac cttagcatcg gggaaggtaa tgatagttta 120

gttggcaaag actttttgca gcaaactgta tttgagacag cagaatccaa ggatatcttt 180

caagattcac ttatactaca ttctttttag ccccctctct aggggtggag ggggtggctt 240

agaaaaacca aaggtaatct ggtttcaatt acatgctgta aaaatagaat ttgtggccag 300

aaattaattt ggaatatttt ttatgggggc aacattgtgg gttgtatgag tctttcacca 360

actttattgc ttttctttgg ttctggatct aaa 393

<210> SEQ ID NO 162
<211> LENGTH: 519
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (297)..(297)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 162

ggaggtttaa tacggccaat ggatcttgta taaagtctac gtaagtttta atttaccaga 60

gctataagat ggttaaggta gactagtggg gactgctaca gataaaatga gatacaaaga 120

acatttgcaa ataaatgcca taaaattaca gtagcttgga attttagtga atcatggccc 180

ttgtgttatc tagaatgcta attattcaag ctgttcctaa acttaagtat gacatataag 240

attaaaatct tggggggaaa aactgttcag atgaaaagtc aagtcaagaa gtttccncaa 300

aagaaaagaa aaatcctaaa aaccatctag ctgttgttac attaaattta tttctcacct 360

ccattaaaag ggtttttgct ttggagtttt gttaactttc gttctttgga gtaataatat 420

ttctcttgtg tatggcgctg aatacatttg tcaataatac gtcaaaaaaa aaaacacttg 480

gcttcttaat acttggaaat acgtacatat tccttacta 519

<210> SEQ ID NO 163
<211> LENGTH: 503
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 163

gaggatgtac ttgcatactg ttgaagttga gtgctgtttt gctgttaatg ctgctgcttt 60

gccaatgaag aatgaaataa atttatctga atgtatcaat aactttaaaa tggaatgctg 120

cacttttaaa atatggtaga ttattgacat ttgcaagaag aatgtattga ggtctttgga 180

aatgcccaaa ttctttgcca cctataatta aaaattgtct gaattttctc ctcagtataa 240

aggagtgaat gccctactta gtgtaattgt atcaagtgaa gtcaaacatc aacaaaagaa 300

cagtaaagtc tcattgcaaa gcagatactg ggcctcaagg gtgggcttag gcttaaacta 360

gattatctgc tttcatatac taatgttttc atttcaaaat catgtgtccc caaaatattg 420

caacttactg aatattttag atctcttggg ttacttaaat atgtgtgaaa aaatcaacat 480

tgcattgcaa atcccagtgt tta 503

<210> SEQ ID NO 164
<211> LENGTH: 519
<212> TYPE: DNA

<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (100)..(100)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (219)..(219)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 164

gacactcact ctttgattcg gatgtggaca tggatgacta tacagaccac gaacagtgca 60

agtgacgtcc agcctcactg accctcttcc ttgggacctn ccactccctg ggtcggtcca 120

ttttcccagg tagcaatcca tccgagctgg gaggagatct tcgtgcttgg cagagttttc 180

acatgctaac tggactatag cagccttatt tcttttttng tacaaacaaa acacagaacc 240

attcagatga ctccattgaa aacaaacagg caaaaaaataa tgtcagcatg gttcctgaaa 300

tccatttttg ttttcattag aaaactatta ataatattgt gtggtagagc aggtgtaaga 360

gctggttgtc agctgatagt ttttatgatg atcctcttca accctgaggt cttaattgtg 420

agatggattc ttgaacctcc ttcctccacc aggatttgaa gtaatgagag atatcatcag 480

aaaaatgttt tacggtggct gcttgtactt tatgtgtgt 519

<210> SEQ ID NO 165
<211> LENGTH: 470
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 165

acttgaatga ttatgtgacc ctgttatatt tcagtgttgt gacaaatgtg taaactagcg 60

ggggaagaca gtattgtatc ataaatgaga tgcgtagttt gttttctttc atgggaagta 120

gagataaaaa tatatacatt tctctaattg agttgtttag agaaagaact aatgtctcat 180

atgatgtatt tacttatttt aaaaaaaaga ataggaatga gatgtccctg agctgtactt 240

ttctattatt ataaggcctt taggcatcag tgcatctggg ttatcaacat tttctcaaat 300

gctgtcaata ttttactgta atttatgttc ttatatttat gtatatttgt taaaactgta 360

aaaaaatttc acagattttt ttccaatacc tgtgcaagat acatgtgtag ctcaaaacta 420

tttgtgatct actgtttgca tgtaagagac caggatatgt aactcttata 470

<210> SEQ ID NO 166
<211> LENGTH: 458
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 166

gaacatgcca gggcccagat gagggcccag atgaatatcg gggatgaagc gctgattgga 60

cggtggagct gggatgacat acaagtcgag ctcctgacct gggatgagga cggagatttt 120

ggcgatgcct gggccaggat ccccctttgct ttctgggcca gataccatca gtacattctg 180

aatagcaacc gtgccaacag gagggccacg tggagagctg gcgtcagcag tggcaccaat 240

ggaggggcca gcaccagcgt cctagatggc cccagcacca gctccaccat ccggaccaga 300

aatgctgcca gagctggcgc cagcttcttc tcctggatcc agcaccgttg acgaactgca 360

gcgatcttac tggccaagcc agagcgcctc ctctcagatt ccttctcgac acagcaccct 420

aggcggcttc ttcctgtcag tcggaggtgg catgcaag 458

<210> SEQ ID NO 167
<211> LENGTH: 131
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 167

gaattgacag tgattccgtt ttcaaagcat ttattgaata gtatcttcca aacagtatgc 60

tggcttttag acaggttata caggtgaatg taggggtcta tccttaaaaa gcctataagg 120

cagttgttct c 131

<210> SEQ ID NO 168
<211> LENGTH: 338
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 168

gtccctggtg ccaaatctgt gggagatcac tggcttagaa tcttcaaaag agtattgccc 60

ccaatgtaaa ctatggactt tgtgtgataa tgacatgtca atgtaagttc atcaactgta 120

acaaatgtgc cattctggag agagatgttg atagtctagg aggctatgca tgtgtggagg 180

caggggtat atgggaactt tctgtacttc ctgctcaatt ttgctgtgaa tctgaaacta 240

ctctaaaaaa taaggtctat tttcttaaag gtcattttgc ctccatagtg ggaaagaaaa 300

tagcagttga ctaatagctg ctcttatcct gcctaaaa 338

<210> SEQ ID NO 169
<211> LENGTH: 459
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 169

gaagtgaacc ttctagatcc tgctgactca tacaatgagt tttgtgtgga ccatcagaca 60

aaagggctgg ctggtgaagg tggctgttgt ctggaaattc ctcccagctc tcctctaatt 120

atgtcataag gactggaggc cccttagcct gcttgtgata acacgcaagg aaatatgggc 180

caactcttca catgaacaca agatatttcc atgctagcct tttgcaagta acaacagaga 240

gagctctgtg cagttttcac tggaatgcct gtggattgct tgtgtcataa ctgtaatcta 300

aagagttgtc catttgttga ttcctttgta tttgtattgg tagaattgcc actatcaaac 360

caagatcttt agctgccttt gtatcaactt ctttggagct tatgtgattt tccagaaaat 420

ttccaaggca tagttttgtc cctaagtccc atgaatatg 459

<210> SEQ ID NO 170
<211> LENGTH: 484
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (42)..(42)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (81)..(81)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (144)..(144)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (260)..(260)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:

<221> NAME/KEY: misc_feature
<222> LOCATION: (263)..(263)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 170

ctcctgtatc ttattcccta gggccacttg cacctttcaa antggataaa ttaaattccc 60

ctgctcccct tctaccaact ntaacatcat atccttggtg tatgatgccc tacttttcat 120

tgttttgcct aaataagagt atgnttggga attttaggct tagggctggg aaaagatggg 180

atatggaatc gtcagctata gattgccgga caagaaattt taggagcagt agacctttca 240

accgccctca ataggatggn acntgactgt ccccacaacc tatttccctt tcagtggctt 300

gctccagcca aggcccctta tttaagagat ctttgtgcgc tctgaaaacc atgcatatgc 360

cagaactagg tgctctgttt catgaaggca gtttgataac tgaatggact ttggaagtgc 420

ccagtgtttg actattaccc tggtgcgatg atcacactgg gcgtatcatt gtcacatgat 480

ccca 484

<210> SEQ ID NO 171
<211> LENGTH: 536
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (60)..(61)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 171

acatgccctt agaatgtgca ttttttaacc tattaaattt gccaatcttg caaactattn 60

nttacttgta ttgcataatt agatactcat attaacatat tgaattcaga aaaagttagc 120

aagccaagat gacattctct gtagcactat tttaaattat aatgaatgat cacataaaac 180

tctttagtat ttatctaaag taattattac tctacttcat ttgtttatct aaatcagtga 240

tcattgatgt ttgaactttt tggcttaaat gtttattttg tttatactac ttgctagagt 300

aaaataaatt taatacatga aaaactctac acaatttaaa ataggttata atttgtcaat 360

acttatgttt taaaatattt ttagaaggag gagtgctgta tattattaaa acaattttct 420

gaaattgttt aatattatct ttgattttaa aatgacatat atgtggattt acaatgaatc 480

aaattgtcct aaaagatgtc agataagaaa tgcaagtgct ttgcaagtct aatact 536

<210> SEQ ID NO 172
<211> LENGTH: 311
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 172

aaacacagtc catgctattc taccactggc tgtgtcttag aaggcctcag aggccactcc 60

aaaaacaatg ctctgtgctt ttataatatt ttaatgtccc tggttatatc agtaagcata 120

cattagaaag tattagctta aaacattcta caccaaaatg aagtacattc acatattttg 180

tgctgcatct tacaggtctt ctagtacctt ctatcccctt ctatgattgg tcgtacacat 240

agtacgtaag agcctcttcc catatagaag aagggggaaa gctaagctgc tttcagctat 300

caacccagga c 311

<210> SEQ ID NO 173
<211> LENGTH: 370
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (92)..(92)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 173

aaccatgcct ctttataaca tttagatcac cgtccttata atgcgccttt ctgtctcttt     60

ttaaaccttg agcaccttga aggcaaaaat tncaactttc tttccctagt gtcttgcact    120

ccctggtatc tagcacatag agagctcaat aaatgttttt tgaatgagta aatcattgca    180

cgaatttata acttcatgaa cccatggaac ccattgactg gtctgccctc atctccgatc    240

cttggctgaa aagcctaaca agccattatc tgtccgtact gaaacactcc tcctgatgtc    300

aagaaccttc taaacataaa accacctggt gcacggatca tttcttcttc caagatgtat    360

ctgccattga                                                           370


<210> SEQ ID NO 174
<211> LENGTH: 463
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (384)..(388)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (390)..(390)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 174

aattaacctt agcattattc ctgtgcttta ttattcactg ataggttctt attcaactaa     60

tgtttatttc ttgcctaata tgtgccagaa accgtgaagt gtttaggata tgcagtgagt    120

ggttaatgag acaagtatga tccaacttgt gtttgcaatt aagcagggat acaggtactg    180

aataaatact gaaaataatt aaaatggtaa taagtgattt gttaatactg atgcatgtag    240

atctaattca ttttaaatgt tacaaaataa gttacaaaat ggtatatgcc atatgatgct    300

atttttgtac atctataata aactttatga gacacaaata tgcaatgtag ttactaataa    360

aactataaga acaagaacac caannnnnan ataaagctta ctgccaggag ggaatggaat    420

ggatgcagag agcatggtta gctgtatctt taatgtttca ttt                      463


<210> SEQ ID NO 175
<211> LENGTH: 263
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (28)..(28)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (50)..(50)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (54)..(54)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (77)..(77)
<223> OTHER INFORMATION: n is a, c, g, t or u
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<400> SEQUENCE: 175

catgtaagaa ttcccgggag ctccatgncn ttttaatttt agccattctn ctgncctcat 60

ttcttaaaat tagagantta aggtcccgaa ggtggaacat gcttcatggt cacacataca 120

ggcacaaaaa cagcattatg tggacgcctc atgtattttt tatagagtca actatttcct 180

ctttattttc cctcattgaa agatgcaaaa cagctctcta ttgtgtacag aaagggtaaa 240

taatgcaaaa tacctggtag taa 263

<210> SEQ ID NO 176
<211> LENGTH: 421
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 176

gcttcagagg taacacttgg ccaagatatg agatctgaat tacctttccc tctttccaag 60

aaggaaggtt tgactgagta ccaatttgct tcttgtttac ttttttaagg gctttaagtt 120

atttatgtat ttaatatgcc ctgagataac tttggggtat aagattccat tttaatgaat 180

tacctacttt attttgtttg tctttttaaa gaagataaga ttctgggctt gggaatttta 240

ttatttaaaa ggtaaaacct gtatttattt gagctattta aggatctatt tatgtttaag 300

tatttagaaa aaggtgaaaa agcactatta tcagttctgc ctaggtaaat gtaagataga 360

attaaatggc agtgcaaaat ttctgagtct ttacaacata cggatatagt atttcctcct 420

c 421

<210> SEQ ID NO 177
<211> LENGTH: 170
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 177

cccctcggaa gttgtacagg cccagtgtag gaacttgggc tgcatcaatg ctcaaggaaa 60

ggaagacatc tccatgaatt ccgttcccat ccagcaagag accctggtcg tccggaggaa 120

gcaccaaggc tgctctgttt ctttccagtt ggagaaggtg ctggtgactg 170

<210> SEQ ID NO 178
<211> LENGTH: 439
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 178

gggaagccaa actccatcat gatgggtgga ttccaaatga acccctgcgt tagttacaaa 60

ggaaaccaat gccacttttg tttataagac cagaaggtag actttctaag catagatatt 120

tattgataac atttcattgt aactggtgtt ctatacacag aaaacaattt attttttaaa 180

taattgtctt tttccataaa aaagattact ttccattcct ttaggggaaa aaacccctaa 240

atagcttcat gtttccataa tcagtacttt atatttataa atgtatttat tattattata 300

agactgcatt ttatttatat cattttatta atatggattt atttatagaa acatcattcg 360

atattgctac ttgagtgtaa ggctaatatt gatatttatg acaataatta tagagctata 420

acatgtttat ttgacctca 439

<210> SEQ ID NO 179
<211> LENGTH: 529
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 179

ggaatctaca aagccatcag tgaactggat attcttcttt cctggattaa aaaattattg 60

gaaagcagtc agtaaaccaa agccaagtac attgatttta cagttatttt gaaatacaat 120

aagaactgct agaaatatgt ttataacagt ctatttcttt taaaaacttt ttaacataat 180

actgacggca tgttaggtga ttcagaatag acaagaagga tttagtaaat taacgttttg 240

gatataagtt gtcactaatt tgcacatttt ctgtgttttc aaataatgtt tccattctga 300

acatgttttg tcattcacaa gtacattgtg tcaacttaat ttaaagtatg taacctgaat 360

taactcgtgt aatatttgtg tgtggagtgg gatgtggggg gtggaggggg aatgacagat 420

ttctggaatg caatgtaatg ttactgagac ttaaatagat gttatgtata tgattgtctg 480

tttaagtgtt tgaaaattgt taattatgcc cagtgtgaac ttagtactt 529

<210> SEQ ID NO 180
<211> LENGTH: 335
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (216)..(216)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 180

ggcaagatca gatcctggag gactttcctg gcctgcccgc cagccctgct cttgttgtgg 60

agaaggaagc agatgtgatc acatcacccc gtcattgggc accgctgact ccagcatgga 120

ggacaccagg gagcagggcc tgggcctgtt tccccagctg tgatcttgcc cagaacctct 180

cttggcttca taaacagctg tgaaccctcc cctganggat taacagcaat gatgggcagt 240

cgtggagttg ggggggttgg gggtgggatt gtgtcctcta aggggacggg ttcatctgag 300

taaacataaa ccccaacttg tgccattctt tataa 335

<210> SEQ ID NO 181
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 181

tctccctcgc tcgaaattac a 21

<210> SEQ ID NO 182
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 182

cagaatatcc ccgtacatgt ccat 24

<210> SEQ ID NO 183
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 183

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tccttgaaca tctttggctc ttc                                              23


<210> SEQ ID NO 184
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 184

tccatgtgcc gtttctgaac                                                  20


<210> SEQ ID NO 185
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 185

agaggagcag tatcaggact ttgaa                                            25


<210> SEQ ID NO 186
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 186

agcggtcgtg cacactca                                                    18


<210> SEQ ID NO 187
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 187

cggcttgcac cagtttcttc                                                  20


<210> SEQ ID NO 188
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 188

gctccttctt ctatcggttt catc                                             24


<210> SEQ ID NO 189
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 189

tcggagggca gagctctaac                                                  20


<210> SEQ ID NO 190
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 190

cctcgatgtt catcccgatt                                                  20


<210> SEQ ID NO 191
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 191

gatcagcccc actctccaaa                                                  20


<210> SEQ ID NO 192
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 192

gatggatccc cactgatgat g                                                21


<210> SEQ ID NO 193
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 193

catgatgcta agagtcctgg gtaa                                             24


<210> SEQ ID NO 194
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 194

ttctgcaact gagaagcaca tatg                                             24


<210> SEQ ID NO 195
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 195

caaggagggc cagtgcaa                                                    18


<210> SEQ ID NO 196
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 196

gaagccccac ccttctcttc                                                  20
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<210> SEQ ID NO 197
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<400> SEQUENCE: 197

gggcatccct gtgaacagta a                                              21


<210> SEQ ID NO 198
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<400> SEQUENCE: 198

ggtacccgtt cctccctaca c                                              21


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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 199

tgcatgttaa tggtgagtga atcc                                           24


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<400> SEQUENCE: 200

ttgatccaac aaatgcccta atac                                           24


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<220> FEATURE:
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<400> SEQUENCE: 201

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<220> FEATURE:
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<400> SEQUENCE: 202

ccccttcact caaacatctc gta                                            23


<210> SEQ ID NO 203
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ccagtggaaa aacaatggag tca                                              23


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<400> SEQUENCE: 204

acagcaattg tcctggagca t                                                21


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<400> SEQUENCE: 205

ctgctcatcg ctgtcatcgt                                                  20


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cgggacacag ccatgca                                                     17


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<400> SEQUENCE: 207

agagtttgag aagcaaggga tttact                                           26


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<212> TYPE: DNA
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 208

ggccggtgca gtcactctt                                                   19


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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 209

gcccacagac ttagccatca                                                  20


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tcccggcgac aatgc                                                     15


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<400> SEQUENCE: 211

tgccaccacc tattactggt aca                                            23


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<400> SEQUENCE: 212

agtttaagcc cccactttca gaa                                            23


<210> SEQ ID NO 213
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<400> SEQUENCE: 213

tccatagctg ggtctggtgt aga                                            23


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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 214

ttcttgattg agacccagga ttc                                            23


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gagaggctcc agcactacat ca                                             22


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ctacaccaac ccattccagg at                                          22


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<400> SEQUENCE: 217

ttcagttcct ggattctcct gagt                                        24


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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 218

cagtgagggt tacctgaaaa atgc                                        24


<210> SEQ ID NO 219
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 219

tcagggacca accaccaaga                                             20


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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 220

caggacaggt gtgtaggcag ttt                                         23


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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 221

ccaccacatt ccctgtaacc a                                           21


<210> SEQ ID NO 222
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<400> SEQUENCE: 222

tccgtctaca cttttgttga caca                                        24


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ctcagtctct tctccagtgt gttca 25

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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 224

ggagcttctc ctggcatgtg 20

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<400> SEQUENCE: 225

gggcggcaaa aaactgaga 19

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<400> SEQUENCE: 226

ccgcgatgca gctgttct 18

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<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 227

caattgtatg tgactgccca aga 23

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<400> SEQUENCE: 228

tgggtatctc aggcatctcc tt 22

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tgctccccac cccctttta 18

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ctgctttgtt tgctctgcaa gt                                            22


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<400> SEQUENCE: 231

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<400> SEQUENCE: 232

aggtgtcaga ttttccctca gaat                                          24


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<400> SEQUENCE: 233

catgcctcac atcgcttcag                                               20


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ccacactatc ttcatcccaa tgac                                          24


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<400> SEQUENCE: 235

cttgccctca ctgcaacaga                                               20


<210> SEQ ID NO 236
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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 236

tctgcagatg agccctcaga                                                  20


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<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 237

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<400> SEQUENCE: 238

gacgcccccct tgttgtttg                                                  19


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gcgggctcta tcacaaaatg a                                                21


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<220> FEATURE:
<223> OTHER INFORMATION: synthetic oligonucleotide

<400> SEQUENCE: 242

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<400> SEQUENCE: 244

ggaggccaaa gacacagatc a                                                21


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<220> FEATURE:
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<400> SEQUENCE: 245

ccaaggctca gtcatgagaa ca                                               22


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ccaacgcaaa gcaatacatg a                                                21


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cgaaacagca tctgactcct ttt                                              23


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tgggtctcac ctcccaactg                                                  20


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gccggcacat gctagca                                                     17


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cccaaaaggt cctcagatta ctaca                                            25


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cattgcggtg gagattcca                                                   19


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<400> SEQUENCE: 254

ttgctgtagc caaattcgtt gt                                               22


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cagcagatgt ggatcagcaa g                                                21


<210> SEQ ID NO 256
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gcatttgcgg tggacgat                                                   18


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tgctgtctcc atgtttgatg tatct                                           25


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tctctgctcc ccacctctaa gt                                              22


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gtcgcagccg ggatttg                                                    17


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gcattgtcaa gtgacgatca ca                                              22
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What is claimed is:

1. A method for detecting human IL-17-producing helper T-cells comprising:

- isolating CD4-positive cells from a blood sample with an anti-CD4 antibody;
- mixing at least some of said CD4-positive cells with a labeling substance and with an antibody that specifically binds to a protein encoded by a PTPRM gene, wherein one or more of the CD4-positive cells, the antibody that specifically binds to a protein encoded by a PTPRM gene, and the labeling substance, form a complex;
- applying said complex to a flow cytometer; and
- detecting the presence of an IL-17-producing helper T-cell by detecting the label of the complex using the flow cytometer, wherein said sample is determined to contain a human IL-17-producing helper T-cell when the label is detected with the flow cytometer in the detecting step.

2. The method according to claim **1**, further comprising detecting a protein encoded by a MCAM gene.

3. The method according to claim **1**, further comprising detecting a protein encoded by a L1CAM gene.

4. The method according to claim **1**, further comprising detecting a protein encoded by a GPR34 gene.

5. The method according to claim **1**, further comprising detecting a protein encoded by a gene,

- wherein the gene is selected from the group consisting of:
- genes encoding membrane proteins consisting of: ADAM12, ANKS1B, ATP6V0A4, ATP9A, BVES, C5orf40, CDH4, DIO2, DMD, IRS2, KCNE3, MFAP3L, MYO7A, SHROOM2, SLC16A4, SLCO2B1, TANC2, TJP1, TMEM163, TNS3, UPK1B, WDFY3, DRD2, GJC1, PGBD5 (LOC100134440), MS4A7, ODZ4, PHKA1, RGS1, SHB, SLC44A3,

SLC6A15, SYNGR3, AKAP12, C9orf125, DPY19L2, HRH4, MUC20, POPDC3, SORBS1, TANC1, TMEM44 and UNC13C;

genes encoding secretory proteins consisting of: CXCL13, PCOLCE2, PNOC, SMPDL3A, TGFBI, C17orf99, EBI3, IL1A and WNT3;

genes encoding intracellular proteins consisting of: BCAT1, BHLHE22, C13orf18 (LOC728970), CA2, CCDC3, CDS1, CHN1, CLIC5 (LOC100131610), CTSH, CYP7B1, DAPK2, DMRT1, DSE, FBXL17, FBXL21, FHOD3, H2AFY2, HLX, IRAK3, MACC1, MAML3, MYO10, OTUB2, PAPSS2, PCBP3, PDE4DIP, PLD1, PPARG, PTPN13, RGS18, SIM1, SNAI2, SOX2, SPIRE1, TBC1D12, TGM5, TMOD1, TUBB6, DDIT4L, DHRS9, ERC2, FERMT2, HHEX, HS3ST1, NR5A2, PHLDA1, RBM20, NINL, RTN2, SH3RF2, TSHZ2, EML1, HIST1H2BC, MAP3K4, PDK4, RGS2 and RGS20;

genes consisting of: C1orf106, C6orf145, LOC401097, MAMLD1, ZC3H12C, C12orf64, C6orf168, CAMSAP1L1 and MAGED4 (MAGED4B); and

genes comprising at least one nucleic acid sequence selected from SEQ ID NO: 147 to 151, 157 to 162 and 167 to 174.

6. The method according to claim **5**, wherein the gene is selected from the group consisting of:

genes encoding membrane proteins consisting of: ADAM12, ATP6V0A4, ATP9A, BVES, C5orf40, CDH4, DIO2, SHROOM2, TMEM163, UPK1B, DRD2, PGBD5 (LOC100134440), ODZ4, SLC6A15, AKAP12, C9orf125, POPDC3 and UNC13C;

genes encoding secretory proteins consisting of: PCOLCE2, PNOC, TGFBI and IL1A; and

genes encoding intracellular proteins consisting of BHLHE22, PPARG, SIM1 and SNAI2.

* * * * *

专利名称(译)	用于检测产生人IL-17的辅助性T细胞的标记和试剂，以及用于检测产生人IL-17的辅助性T细胞的方法		
公开(公告)号	US9410208	公开(公告)日	2016-08-09
申请号	US13/868638	申请日	2013-04-23
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[标]发明人	TANAKA SATOSHI UGA HITOSHI IKEDA MASAFUMI MIYAMOTO YOSHIAKI YANAGIDA MASATOSHI KADOWAKI MASAKAZU OKAZAWA TAKAHIRO KURATA HIROKAZU		
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IPC分类号	G01N33/537 C07K14/54 G01N33/50 G01N33/68 C12Q1/68		
CPC分类号	C07K14/54 C12Q1/6881 G01N33/505 C12Q1/6888 G01N33/68 C12Q2600/158 G01N2333/54		
代理机构(译)	萨格鲁MION，PLLC		
优先权	2009176755 2009-07-29 JP		
其他公开文献	US20130267435A1		
外部链接	Espacenet USPTO		

摘要(译)

本发明涉及能够特异性检测产生人IL-17的辅助T细胞（人Th17细胞）的标记，特异性检测人Th17细胞的方法和检测人Th17细胞的试剂。

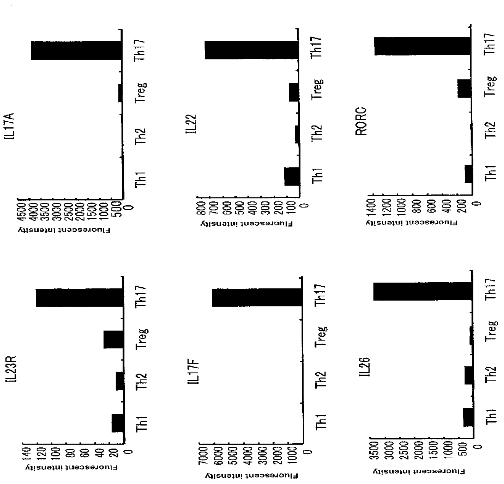

FIG. 1