



US 20120039900A1

(19) **United States**(12) **Patent Application Publication**
Stuhlmüller et al.(10) **Pub. No.: US 2012/0039900 A1**(43) **Pub. Date: Feb. 16, 2012**(54) **BIOMARKERS PREDICTIVE OF THE
RESPONSIVENESS TO TNF α INHIBITORS IN AUTOIMMUNE DISORDERS**(75) Inventors: **Bruno Stuhlmüller**, Berlin (DE);
Gerd-Reudiger Burmester, Berlin (DE)(73) Assignee: **Abbott Laboratories**, Abbott Park, IL (US)(21) Appl. No.: **13/282,850**(22) Filed: **Oct. 27, 2011****Related U.S. Application Data**

(63) Continuation of application No. 12/130,373, filed on May 30, 2008.

(60) Provisional application No. 60/932,888, filed on May 31, 2007.

Publication Classification(51) **Int. Cl.**
A61K 39/395 (2006.01)
C12Q 1/68 (2006.01)
A61P 37/06 (2006.01)**G01N 33/573** (2006.01)
C40B 40/06 (2006.01)
A61P 29/00 (2006.01)
C40B 30/04 (2006.01)
G01N 33/566 (2006.01)(52) **U.S. Cl. 424/142.1; 506/9; 435/6.11; 435/7.1; 435/7.4; 506/16; 435/6.12; 435/7.24**(57) **ABSTRACT**

The invention provides methods for predicting responsiveness to TNF α inhibitors in a subject suffering from an autoimmune disorder, such as rheumatoid arthritis. The methods involve assaying for expression of one or more biomarkers in the subject that are predictive of responsiveness to TNF α inhibitors. A preferred biomarker of the invention is CD11c. The methods can further comprise selecting a treatment regimen with a TNF α inhibitor in an autoimmune disorder subject based upon expression of the biomarker(s) in the subject. The methods can further comprise administering a TNF α inhibitor to the subject according to the selected treatment regimen. Kits that include means for measuring expression of one or more biomarkers that are predictive of responsiveness to TNF α inhibitors for an autoimmune disorder are also provided. Methods of preparing and using databases, and computer program products therefore, for selecting an autoimmune disorder subject for treatment with a TNF α inhibitor are also provided.

Figure 1

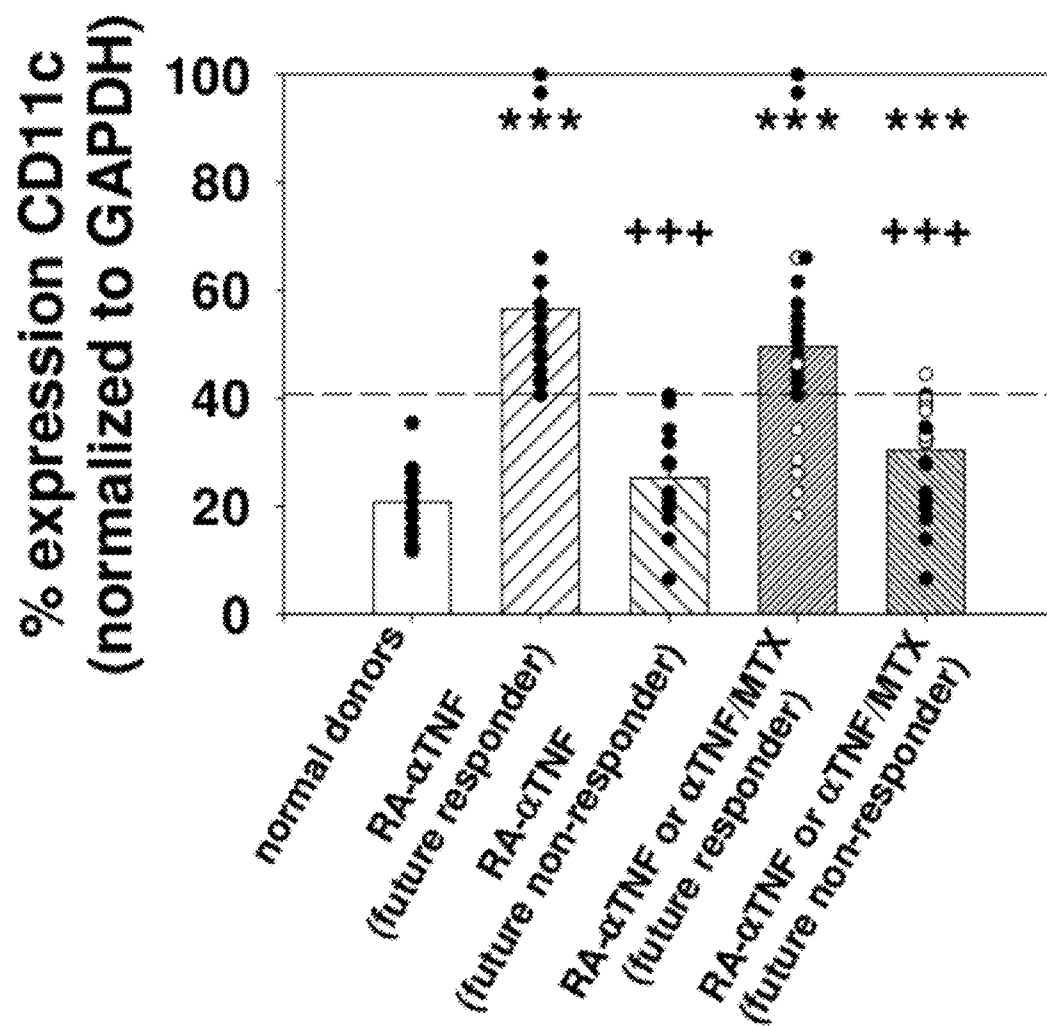


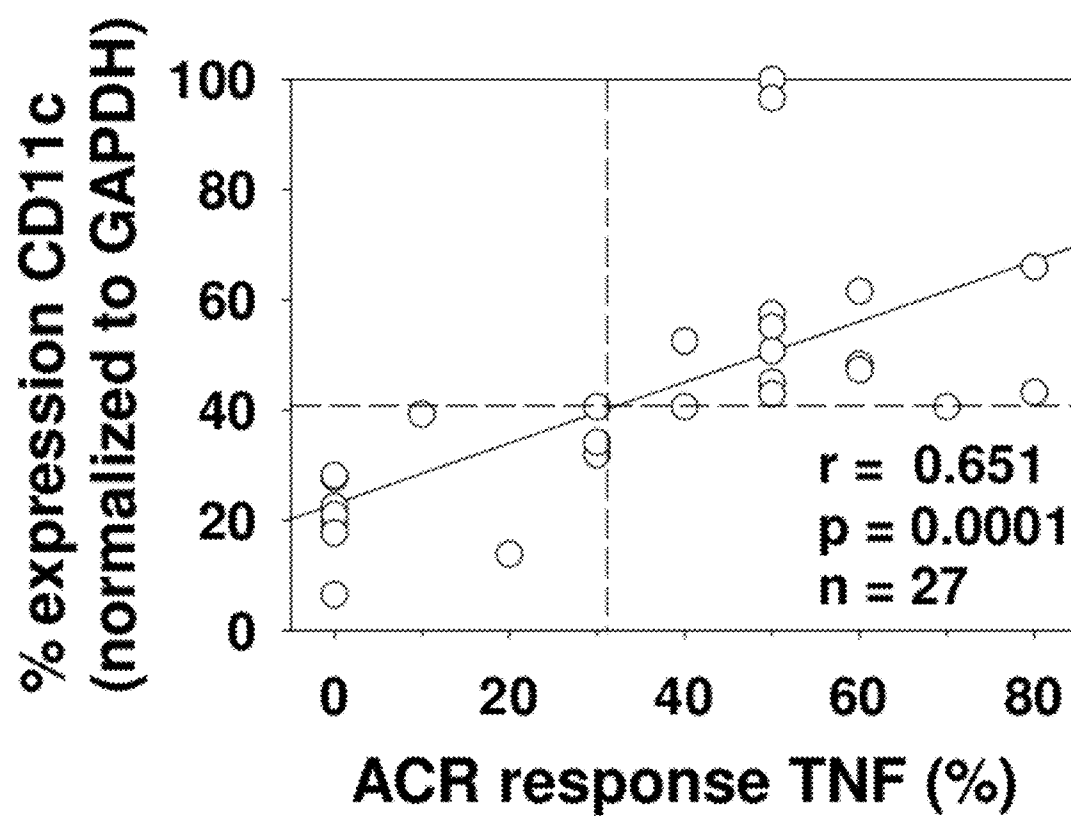
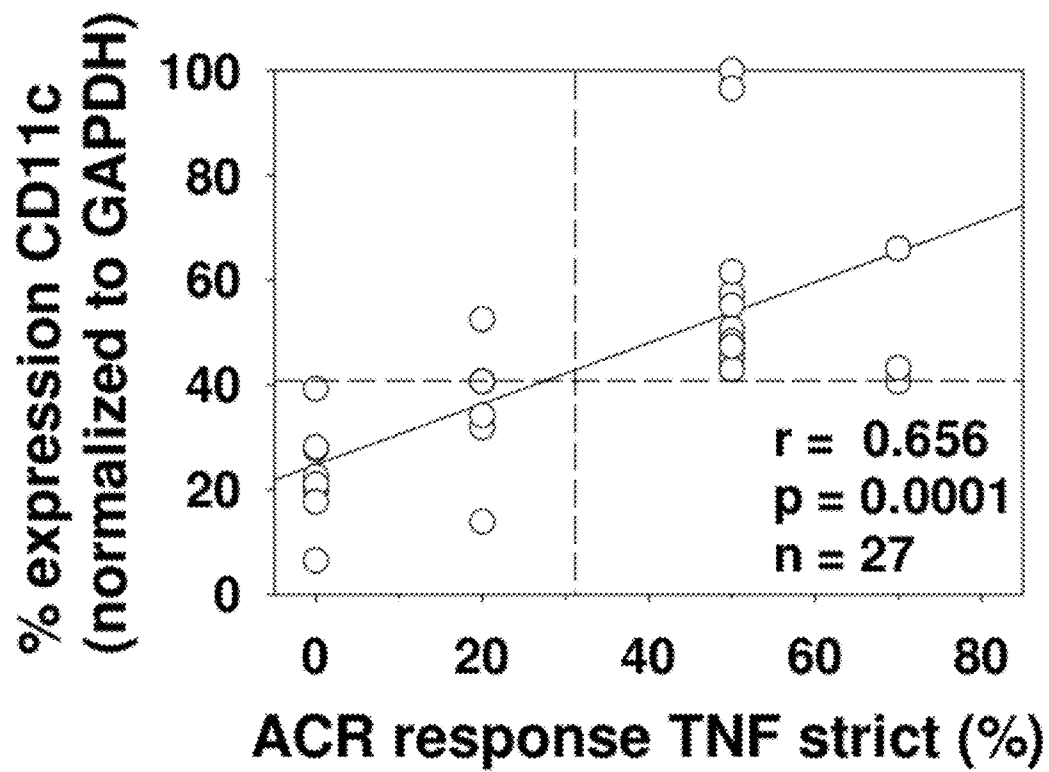
Figure 2

Figure 3

BIOMARKERS PREDICTIVE OF THE RESPONSIVENESS TO TNF α INHIBITORS IN AUTOIMMUNE DISORDERS

RELATED APPLICATIONS

[0001] This application is a continuation application of U.S. patent application Ser. No. 12/130,373, filed on May 30, 2008, which claims the benefit of priority to U.S. provisional patent application No. 60/932,888 filed on May 31, 2007. The contents of the above-mentioned priority application is hereby incorporated by reference in its entirety.

BACKGROUND OF THE INVENTION

[0002] Autoimmune disorders are a significant and widespread medical problem. For example, rheumatoid arthritis (RA) is an autoimmune disease affecting more than two million people in the United States. RA causes chronic inflammation of the joints and typically is a progressive illness that has the potential to cause joint destruction and functional disability. The cause of rheumatoid arthritis is unknown, although genetic predisposition, infectious agents and environmental factors have all been implicated in the etiology of the disease. In active RA, symptoms can include fatigue, lack of appetite, low grade fever, muscle and joint aches and stiffness. Also during disease flare ups, joints frequently become red, swollen, painful and tender, due to inflammation of the synovium. Furthermore, since RA is a systemic disease, inflammation can affect organs and areas of the body other than the joints, including glands of the eyes and mouth, the lung lining, the pericardium, and blood vessels.

[0003] Traditional treatments for the management of RA and other autoimmune disorders include fast acting "first line drugs" and slower acting "second line drugs." The first line drugs reduce pain and inflammation. Example of such first line drugs include aspirin, naproxen, ibuprofen etodolac and other nonsteroidal anti-inflammatory drugs (NSAIDs), as well as corticosteroids, given orally or injected directly into tissues and joints. The second line drugs promote disease remission and prevent progressive joint destruction and are also referred to as disease-modifying anti-rheumatic drugs or DMARDs. Examples of second line drugs include gold, hydrochloroquine, azulfidine and immunosuppressive agents, such as methotrexate, azathioprine, cyclophosphamide, chlorambucil and cyclosporine. Many of these drugs, however, can have detrimental side-effects. Thus, additional therapies for rheumatoid arthritis and other autoimmune disorders have been sought.

[0004] More recently, biological therapies have been applied to the treatment of autoimmune disorders such as rheumatoid arthritis. For example, three TNF α inhibitors, REMICADE™ (infliximab), a chimeric anti-TNF α mAb, ENBREL™ (etanercept), a TNFR-Ig Fc fusion protein, and HUMIRA™ (adalimumab), a human anti-TNF α mAb, have been approved by the FDA for treatment of rheumatoid arthritis. While such biologic therapies have demonstrated success in the treatment of rheumatoid arthritis and other autoimmune disorders, not all subjects treated respond, or respond well, to a TNF α inhibitor. The use of TNF α inhibitors such as TNF α inhibitors typically is more expensive than traditional treatments and usually requires administration by injection, which, at least for certain agents, may require that the patient visit a medical office on a frequent basis. Thus, it would be very helpful to predict in advance of treatment whether a

rheumatoid arthritis patient is likely to be responsive to treatment with a TNF α inhibitor. Accordingly, ways for predicting responsiveness to a TNF α inhibitor in patients having autoimmune disorders, such as rheumatoid arthritis patients, are of particular interest.

SUMMARY OF THE INVENTION

[0005] This invention provides methods and compositions for predicting responsiveness to a TNF α inhibitor in a subject having an autoimmune disorder, such as rheumatoid arthritis, based on the discovery that the expression patterns of particular biomarkers in the subject correlate with responsiveness to a TNF α inhibitor. Using microarray analysis of monocytes from representative rheumatoid arthritis (RA) patients treated with an anti-TNF α monoclonal antibody, 82 differentially expressed genes predictive of responsiveness to TNF α inhibitor treatment were identified by pairwise comparisons between future RA responders and future RA non-responders to anti-TNF α therapy. Furthermore, hierarchical clustering and TaqMan®-PCR of RA responders/non-responders pretreatment identified one gene of particular interest, CD11c, which was fully predictive of future response to anti-TNF α treatment.

[0006] Accordingly, in one aspect, the invention pertains to a method for predicting responsiveness to a TNF α inhibitor in a subject having an autoimmune disorder (e.g., rheumatoid arthritis). The method comprises: (i) assaying the subject for expression of one or more biomarkers predictive of responsiveness to a TNF α inhibitor in an autoimmune disorder, and (ii) predicting responsiveness of the subject to the TNF α inhibitor based on expression of the one or more biomarkers in the subject, wherein the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-82 (corresponding to the sequences set forth in Table 9)

[0007] Within SEQ ID NOs: 1-82, certain genes were found to be upregulated in RA responders to TNF α inhibitors. Accordingly, in one embodiment, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 6, 7, 10, 15-17, 19, 22, 24, 27, 31, 34-39, 43-47, 49, 51, 54, 55, 57, 59, 61, 62, 64, 70, 75, 79 and 82 (corresponding to sequences from Table 9 that are increased in $\geq 80\%$ of responders vs. non-responders). More preferably, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 31, 37, 44, 47, 62 and 70 (corresponding to sequences from Table 9 that are increased in $\geq 90\%$ of responders vs. non-responders). Even more preferably, the one or more biomarkers is encoded by a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 44. (corresponding to CD11c, from Table 9, which is increased in 100% of responders vs. non-responders). In each of these embodiments, increased expression of the one or more biomarkers is predictive of responsiveness of the subject to a TNF α inhibitor.

[0008] Within SEQ ID NOs: 1-82, certain genes were found to be downregulated in RA responders to TNF α inhibitors. Accordingly, in one embodiment, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-5, 8, 9, 11-14, 18, 20, 21, 23, 25, 26, 28-30, 32, 33, 40-42, 48, 50, 52, 53, 56, 58, 60, 63, 65-69, 71-74, 76-78, 80 and 81. (corresponding to sequences from Table 9

that are decreased in $\geq 80\%$ of responders vs. non-responders). More preferably, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 11, 29, 65, 73 and 74 (corresponding to sequences from Table 9 that are decreased in $\geq 90\%$ of responders vs. non-responders). Even more preferably, the one or more biomarkers is encoded by a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 11 or SEQ ID NO: 74 (corresponding to sequences from Table 9 that are decreased in 100% of responders vs. non-responders). In each of these embodiments, decreased expression of the one or more biomarkers is predictive of responsiveness of the subject to a TNF α inhibitor.

[0009] In another aspect, the invention provides a method for predicting responsiveness to a TNF α inhibitor in a subject having an autoimmune disorder, the method comprising: (i) assaying the subject for expression of one or more biomarkers predictive of responsiveness to a TNF α inhibitor in an autoimmune disorder, and (ii) predicting responsiveness of the subject to the TNF α inhibitor based on expression of the one or more biomarkers in the subject, wherein the one or more biomarkers is selected from the group consisting of Aquaporin 3 (Genbank Accession No. NM_004925); Similar to ribosomal protein S24, clone MGC:8595 (Genbank Accession No. NM_033022); Transmembrane emp24 domain trafficking protein 2 (Genbank Accession No. NM_006815); Superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (Genbank Accession No. NM_000454); Calmodulin 1 (phosphorylase kinase, delta) (Genbank Accession No. NM_006888); Guanine nucleotide binding protein (G protein), beta polypeptide 1 (Genbank Accession No. NM_002074); Prothymosin, alpha (gene sequence 28) (Genbank Accession No. NM_002823); *Homo sapiens* isocitrate dehydrogenase 1 (NADP+) soluble (IDH1) (Genbank Accession No. NM_005896); Tumor protein D52 (Genbank Accession Nos. NM_001025252, NM_001025253, NM_005079); Early growth response 1 (Genbank Accession No. NM_001964); *Homo sapiens* predicted osteoblast protein (GS3786) (Genbank Accession Nos. NM_014888, NM_001040020); Cytochrome c oxidase subunit VIIb (Genbank Accession No. NM_001866); CUG triplet repeat, RNA binding protein 2 (Genbank Accession No. NM_001025077, NM_001025076, NM_006561); Ubiquinol-cytochrome c reductase hinge protein (Genbank Accession No. NM_006004); *Homo sapiens* leptin receptor gene-related protein (HS0BRGRP) (Genbank Accession No. NM_017526); Wiskott-Aldrich syndrome protein interacting protein (Genbank Accession Nos. NM_001077269, NM_003387); CD97 antigen (Genbank Accession Nos. NM_001025160, NM_001784, NM_078481); Glutamate-cysteine ligase, catalytic subunit (Genbank Accession No. NM_001498); Crystallin, zeta (quinone reductase) (Genbank Accession No. NM_001889); Rap guanine nucleotide exchange factor (GEF) 2 (Genbank Accession No. NM_014247); Ataxin 1 (Genbank Accession No. NM_000332); Adaptor-related protein complex 1, sigma 2 subunit (Genbank Accession No. NM_003916); Ectonucleotide pyrophosphatase/phosphodiesterase 4 (Genbank Accession No. NM_014936); Desmocollin 2 (Genbank Accession Nos. NM_024422, NM_004949); MAL, T-cell differentiation protein (Genbank Accession Nos. NM_002371, NM_022438, NM_022439, NM_022440); Glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylman-

nosamine kinase (Genbank Accession No. NM_005476); Chemokine (C—C motif) ligand 3 (Genbank Accession Nos. NM_001001437, NM_021006); Carboxypeptidase A3 (Genbank Accession No. NM_001870); Charcot-Leyden crystal protein (Genbank Accession No. NM_001828); NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7 kDa (Genbank Accession No. NM_004545); Interleukin 8 receptor, beta (Genbank Accession No. NM_001557); Platelet factor 4 variant 1 (Genbank Accession No. NM_002620); Poly(A) binding protein interacting protein 1 (Genbank Accession No. NM_006451); ATP-binding cassette, subfamily C (CFTR/MRP), member 3 (Genbank Accession No. NM_003786); Actinin, alpha 1 (Genbank Accession No. NM_001102); NAD kinase (Genbank Accession No. NM_023018); Platelet/endothelial cell adhesion molecule (CD31 antigen) (Genbank Accession No. NM_000442); Esterase D/formylglutathione hydrolase (Genbank Accession No. NM_001984); Chromosome 20 open reading frame 111 (Genbank Accession No. NM_016470); Sterol-C4-methyl oxidase-like (Genbank Accession Nos. NM_001017369, NM_006745); PIM-1 oncogene (Genbank Accession No. NM_002648); GATA binding protein 2 (Genbank Accession No. NM_032638); Cathepsin Z (Genbank Accession No. NM_001336); Integrin alpha-X (antigen CD11c) (Genbank Accession No. NM_000887); Lectin, galactoside-binding, soluble, 8 (galectin 8) (Genbank Accession Nos. NM_006499, NM_201545); CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) (Genbank Accession Nos. NM_006889, NM_175862); Interleukin 8 (Genbank Accession No. NM_000584); Fc fragment of IgE, high affinity 1, receptor for alpha polypeptide (Genbank Accession No. NM_002001); Actin, gamma 1 (Genbank Accession No. NM_001614); KIAA0746 protein (Genbank Accession No. NM_015187); Glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID) (Genbank Accession No. NM_002076); Transcription factor 4 (Genbank Accession Nos. BF592782, CR612521); Major histocompatibility complex, class II, DQ alpha 1 (Genbank Accession Nos. NM_002122, NM_020056); Cell division cycle 2-like 6 (CDK8-like) (Genbank Accession No. NM_015076); Major histocompatibility complex, class II, DQ beta 1 (Genbank Accession No. XM_942240); Phospholipase C-like 2 (Genbank Accession No. NM_015184); Coagulation factor II (thrombin) receptor-like 1 (Genbank Accession No. NM_005242); TM2 domain containing 1 (Genbank Accession No. NM_032027); Splicing factor 3b, subunit 1, 155 kDa (Genbank Accession No. NM_012433); SUB1 homolog (*S. cerevisiae*) (Genbank Accession No. NM_006713); MRNA; cDNA DKFZp564O0862 (Genbank Accession No. AI278204); Amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer disease) (Genbank Accession Nos. NM_201413, NM_000484, NM_201414); Cytochrome b-5 (Genbank Accession Nos. NM_001914, NM_148923); Cold autoimmune syndrome 1 (Genbank Accession No. NM_183395); Neugrin, neurite outgrowth associated (Genbank Accession Nos. NM_016645, NM_001033088); Ribosomal protein S26, 40S ribosomal protein (Genbank Accession No. XM_941927); CCR4-NOT transcription complex, subunit 6 (Genbank Accession No. NM_015455); Ubiquinol-cytochrome c reductase complex (7.2 kD) (Genbank Accession Nos. NM_013387, NM_001003684); Hepatocellular carcinoma-associated antigen 112 (Genbank Accession No. NM_018487); Kruppel-like factor 11 (Genbank Accession No. XM_001129527); GGA binding partner

(Genbank Accession No. NM_018318); Cornichon homolog 4 (*Drosophila*) (Genbank Accession No. NM_014184); Hypothetical protein FLJ21616 (Genbank Accession No. NM_024567); *Homo sapiens* hypothetical protein FLJ10134 (Genbank Accession No. NM_018004); Nuclear prelamin A recognition factor (Genbank Accession Nos. NM_012336, NM_001038618); Erythroblast membrane-associated protein (Genbank Accession Nos. NM_018538, NM_001017922); LR8 protein (Genbank Accession No. NM_014020); Likely ortholog of mouse limb-bud and heart gene (LBH) (Genbank Accession No. NM_030915); Calmin (calponin-like, transmembrane) (Genbank Accession No. NM_024734); Chromosome 14 open reading frame 156 (Genbank Accession No. NM_031210); Guanine nucleotide binding protein (G protein) alpha 12 (Genbank Accession No. NM_007353); and SRY (sex determining region Y)-box 18 (Genbank Accession No. NR_003287) (corresponding to biomarkers listed in Table 9).

[0010] Within the above-listed biomarkers, certain genes were found to be upregulated in RA responders to TNF α inhibitors. Accordingly, in one embodiment, the one or more biomarkers is selected from the group consisting of Guanine nucleotide binding protein (G protein), beta polypeptide 1; Prothymosin, alpha (gene sequence 28); Early growth response 1; *Homo sapiens* leptin receptor gene-related protein (HS0BRGRP); Wiskott-Aldrich syndrome protein interacting protein; CD97 antigen; Crystallin, zeta (quinone reductase); Adaptor-related protein complex 1, sigma 2 subunit; Desmocollin 2; Chemokine (C—C motif) ligand 3; Interleukin 8 receptor, beta; ATP-binding cassette, sub-family C (CFTR/MRP), member 3; Actinin, alpha 1; NAD kinase; Platelet/endothelial cell adhesion molecule (CD31 antigen); Esterase D/formylglutathione hydrolase; Chromosome 20 open reading frame 111; Cathepsin Z; Integrin alpha-X (antigen CD11c); Lectin, galactoside-binding, soluble, 8 (galectin 8); CD86 antigen (CD28 antigen ligand 2, B7-2 antigen); Interleukin 8; Actin, gamma 1; Glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID); Cell division cycle 2-like 6 (CDK8-like); Major histocompatibility complex, class II, DQ beta 1; Coagulation factor II (thrombin) receptor-like 1; Splicing factor 3b, subunit 1, 155 kDa; mRNA; cDNA DKEZp564O0862; Amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer disease); Cold autoimmune syndrome 1; Kruppel-like factor 11; Nuclear prelamin A recognition factor; Calmin (calponin-like, transmembrane); and SRY (sex determining region Y)-box 18 (corresponding to biomarkers from Table 9 that are increased in $\geq 80\%$ of responders vs. non-responders). More preferably, the one or more biomarkers is selected from the group consisting of Interleukin 8 receptor, beta; Platelet/endothelial cell adhesion molecule (CD31 antigen); Integrin alpha-X (antigen CD11c); Interleukin 8; Amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer disease); and Kruppel-like factor 11 (corresponding to biomarkers from Table 9 that are decreased in $\geq 80\%$ of responders vs. non-responders). Even more preferably, the one or more biomarkers is Integrin alpha-X (antigen CD11c) (corresponding to a biomarker from Table 9 that is increased in 100% of responders vs. non-responders). In each of these embodiments, increased expression of the one or more biomarkers is predictive of responsiveness of the subject to a TNF α inhibitor.

[0011] Within the above-listed biomarkers, certain genes were found to be downregulated in RA responders to TNF α

inhibitors. Accordingly, in one embodiment, the one or more biomarkers is selected from the group consisting of Aquaporin 3; Similar to ribosomal protein S24, clone MGC:8595; Transmembrane emp24 domain trafficking protein 2; Superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1; Calmodulin 1 (phosphorylase kinase, delta); *Homo sapiens* isocitrate dehydrogenase 1 (NADP+) soluble (IDH1); Tumor protein D52; *Homo sapiens* predicted osteoblast protein (GS3786); Cytochrome c oxidase subunit VIIb; CUG triplet repeat, RNA binding protein 2; Ubiquinol-cytochrome c reductase hinge protein; Glutamate-cysteine ligase, catalytic subunit; Rap guanine nucleotide exchange factor (GEF) 2; Ataxin 1; Ectonucleotide pyrophosphatase/phosphodiesterase 4; MAL, T-cell differentiation protein; Glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase; Carboxypeptidase A3; Charcot-Leyden crystal protein; NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7 kDa; Platelet factor 4 variant 1; Poly(A) binding protein interacting protein 1; Sterol-C4-methyl oxidase-like; PIM-1 oncogene; GATA binding protein 2; Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide; KIAA0746 protein; Transcription factor 4; Major histocompatibility complex, class II, DQ alpha 1; Phospholipase C-like 2; TM2 domain containing 1; SUB1 homolog (*S. cerevisiae*); Cytochrome b-5; Neugrin, neurite outgrowth associated; Ribosomal protein S26, 40S ribosomal protein; CCR4-NOT transcription complex, subunit 6; Ubiquinol-cytochrome c reductase complex (7.2 kD); Hepatocellular carcinoma-associated antigen 112; GGA binding partner; Cornichon homolog 4 (*Drosophila*); Hypothetical protein FLJ21616; *Homo sapiens* hypothetical protein FLJ10134; Erythroblast membrane-associated protein; LR8 protein; Likely ortholog of mouse limb-bud and heart gene (LBH); Chromosome 14 open reading frame 156; and Guanine nucleotide binding protein (G protein) alpha 12 (corresponding to biomarkers from Table 9 that are decreased in $\geq 80\%$ of responders vs. non-responders). More preferably, the one or more biomarkers is selected from the group consisting of *Homo sapiens* predicted osteoblast protein (GS3786); Charcot-Leyden crystal protein; Neugrin, neurite outgrowth associated; Hypothetical protein FLJ21616; and *Homo sapiens* hypothetical protein FLJ10134 (corresponding to biomarkers from Table 9 that are decreased in $\geq 90\%$ of responders vs. non-responders). Even more preferably, the one or more biomarkers is *Homo sapiens* predicted osteoblast protein (GS3786) or *Homo sapiens* hypothetical protein FLJ10134 (corresponding to biomarkers from Table 9 that are decreased in 100% of responders vs. non-responders). In each of these embodiments, decreased expression of the one or more biomarkers is predictive of responsiveness of the subject to a TNF α inhibitor.

[0012] In yet another aspect, the invention provides a method for predicting responsiveness to a TNF α inhibitor in a subject having an autoimmune disorder, the method comprising: (i) assaying the subject for increased expression of a biomarker, which biomarker is CD11c, and (ii) predicting responsiveness of the subject to the TNF α inhibitor based on increased expression of CD11c in the subject.

[0013] In yet another aspect, the invention provides a method for predicting responsiveness to a TNF α inhibitor, which TNF α inhibitor is adalimumab, in a subject having an autoimmune disorder, the method comprising: (i) assaying the subject for expression of one or more biomarkers predictive of responsiveness to adalimumab in an autoimmune disorder, and (ii) predicting responsiveness of the subject to

adalimumab based on expression of the one or more biomarkers in the subject. Preferably, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-82 (corresponding to biomarkers set forth in Table 9).

[0014] In one embodiment of the methods of the invention, a sample from the subject is assayed for expression of mRNA encoding the one or more biomarkers. In another embodiment of the methods of the invention, a sample from the subject is assayed for protein expression of the one or more biomarkers.

[0015] In one embodiment, the methods of the invention further comprise selecting a treatment regimen with the TNF α inhibitor based upon expression of the one or more biomarkers in the subject. In another embodiment, the methods of the invention further comprise administering the TNF α inhibitor to the subject according to the treatment regimen such that autoimmune disorder is inhibited in the subject.

[0016] A preferred TNF α inhibitor of the invention is an anti-tumor necrosis factor-alpha (TNF α) antibody, or antigen-binding portion thereof. The anti-TNF α antibody, or antigen-binding portion thereof, can be, for example, a humanized antibody, a chimeric antibody or a multivalent antibody. For example, the anti-TNF α antibody, or antigen-binding portion thereof, can be infliximab or golimumab. In another embodiment, the anti-TNF α antibody, or antigen-binding portion thereof, is a human antibody. For example, the anti-TNF α antibody, or antigen-binding portion thereof, can be an isolated human antibody that dissociates from human TNF α with a K_d of 1×10^{-8} M or less and a K_{off} rate constant of 1×10^{-3} s $^{-1}$ or less, both determined by surface plasmon resonance, and neutralizes human TNF α cytotoxicity in a standard in vitro L929 assay with an IC_{50} of 1×10^{-7} M or less. In another embodiment, the anti-TNF α antibody, or antigen-binding portion thereof, is an isolated human antibody with the following characteristics:

[0017] a) dissociates from human TNF α with a K_{off} rate constant of 1×10^{-3} s $^{-1}$ or less, as determined by surface plasmon resonance;

[0018] b) has a light chain CDR3 domain comprising the amino acid sequence of SEQ ID NO: 305, or modified from SEQ ID NO: 305 by a single alanine substitution at position 1, 4, 5, 7 or 8 or by one to five conservative amino acid substitutions at positions 1, 3, 4, 6, 7, 8 and/or 9;

[0019] c) has a heavy chain CDR3 domain comprising the amino acid sequence of SEQ ID NO: 306, or modified from SEQ ID NO: 306 by a single alanine substitution at position 2, 3, 4, 5, 6, 8, 9, 10 or 11 or by one to five conservative amino acid substitutions at positions 2, 3, 4, 5, 6, 8, 9, 10, 11 and/or 12.

[0020] In another embodiment, the anti-TNF α antibody, or antigen-binding portion thereof, is an isolated human antibody with a light chain variable region (LCVR) comprising the amino acid sequence of SEQ ID NO: 303 and a heavy chain variable region (HCVR) comprising the amino acid sequence of SEQ ID NO: 304. In yet another embodiment, the anti-TNF α antibody, or antigen-binding portion thereof, is adalimumab. Yet another example of a TNF α inhibitor is etanercept.

[0021] Preferably, in the methods of the invention, the subject is a human.

[0022] In another aspect, the invention pertains to a kit for predicting responsiveness to a TNF α inhibitor in a subject having an autoimmune disorder (e.g., rheumatoid arthritis). The kit comprises:

[0023] a) means for isolating monocytes;

[0024] b) means for measuring expression in the subject of one or more biomarkers predictive of responsiveness to a TNF α inhibitor in an autoimmune disorder;

[0025] c) means for measuring expression of at least one housekeeping gene; and

[0026] d) instructions for use of the kit to predicting responsiveness to a TNF α inhibitor in a subject having an autoimmune disorder, wherein the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-82.

[0027] In one embodiment of the kit, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 6, 7, 10, 15-17, 19, 22, 24, 27, 31, 34-39, 43-47, 49, 51, 54, 55, 57, 59, 61, 62, 64, 70, 75, 79 and 82, more preferably the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 31, 37, 44, 47, 62 and 70, even more preferably the one or more biomarkers is encoded by a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 44 (CD11c). In each of these embodiments, the instructions for use of the kit instruct that increased expression of the one or more biomarkers is predictive of responsiveness of the subject to a TNF α inhibitor.

[0028] In another embodiment of the kit, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-5, 8, 9, 11-14, 18, 20, 21, 23, 25, 26, 28-30, 32, 33, 40-42, 48, 50, 52, 53, 56, 58, 60, 63, 65-69, 71-74, 76-78, 80 and 81, more preferably the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 11, 29, 65, 73 and 74, even more preferably the one or more biomarkers is encoded by a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 11 or SEQ ID NO: 74. In each of these embodiments, the instructions for use of the kit instruct that decreased expression of the one or more biomarkers is predictive of responsiveness of the subject to a TNF α inhibitor.

[0029] In one embodiment of the kit, the means for measuring expression in the subject of one or more biomarkers predictive of responsiveness to a TNF α inhibitor in an autoimmune disorder comprises a nucleic acid preparation sufficient to detect expression of mRNA encoding the biomarker in a sample from the subject. In another embodiment of the kit, the means for measuring expression in the subject of one or more biomarkers predictive of responsiveness to a TNF α inhibitor in an autoimmune disorder comprises an antibody preparation sufficient to detect protein expression of the biomarker in a sample from the subject. The kit can further comprise a TNF α inhibitor for treating the autoimmune disorder in the subject.

[0030] In another aspect, the invention pertains to methods of monitoring an autoimmune disorder (e.g., RA) in a subject having the autoimmune disorder (e.g., RA). These methods are based, at least in part, on microarray analysis of monocytes from representative rheumatoid arthritis (RA) patients treated with an anti-TNF α monoclonal antibody, including (i) hierarchical clustering with the genes resulting from a simultaneous comparison between RA versus ND and RA responders pre- versus post-anti-TNF α therapy, (ii) prediction analy-

sis of microarrays (PAM); and (iii) hierarchical clustering based on the comparison between RA responders and non-responders post-treatment.

[0031] Accordingly, in another aspect, the invention provides a method of monitoring an autoimmune disorder in a subject having the autoimmune disorder, the method comprising: assaying the subject for expression of one or more biomarkers, wherein the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 83-133 (corresponding to biomarkers set forth in Table 3), thereby monitoring the autoimmune disorder in the subject.

[0032] In another aspect, the invention provides a method of monitoring an autoimmune disorder in a subject having the autoimmune disorder, the method comprising: assaying the subject for expression of one or more biomarkers, wherein the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 134-177, 110, 112, 118, 123 and 131 (corresponding to biomarkers set forth in Table 4), thereby monitoring the autoimmune disorder in the subject. In one embodiment, preferably the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 134-150, 112, 118 and 131 (upregulated biomarkers from Table 4), wherein expression of the one or more biomarkers is increased in the subject. In another embodiment, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 151-177, 110 and 123 (downregulated biomarkers from Table 4), wherein expression of the one or more biomarkers is decreased in the subject.

[0033] In another aspect, the invention provides a method of monitoring an autoimmune disorder in a subject having the autoimmune disorder, the method comprising: assaying the subject for expression of one or more biomarkers, wherein the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 178-292, 91 and 97 (corresponding to biomarkers set forth in Table 5), thereby monitoring the autoimmune disorder in the subject. In one embodiment, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 178-185; 187-200, 202, 203, 205-207; 211, 213, 214, 216, 220, 221, 226, 228, 229, 231, 232, 234, 235, 238-247, 249, 250, 253, 262-265, 268-282 and 285-288 (upregulated biomarkers from Table 5), wherein expression of the one or more biomarkers is increased in the subject. In another embodiment, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 186, 201, 204, 208, 209, 91, 210, 212, 97, 215, 217-219, 222-225, 227, 230, 233, 236, 237, 248, 251, 252, 254-261, 266, 267, 283, 284 and 289-292 (downregulated biomarkers from Table 5), wherein expression of the one or more biomarkers is decreased in the subject.

[0034] In another aspect, the invention provides a method of monitoring an autoimmune disorder in a subject having the autoimmune disorder, the method comprising: assaying the subject for expression of one or more biomarkers, wherein the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 87, 97, 101, 293, 92, 272, 93, 107, 108, 121 and 123 (corresponding to pre-treatment biomarkers

set forth in Table 6), and wherein the subject is monitored prior to treatment with a TNF α inhibitor, thereby monitoring the autoimmune disorder in the subject.

[0035] In another aspect, the invention provides a method of monitoring an autoimmune disorder in a subject having the autoimmune disorder the method comprising: assaying the subject for expression of one or more biomarkers, wherein the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 290, 209, 98, 112, 116, 121, 130, 155, 92, 289, 216 and 131 (corresponding to post-treatment biomarkers set forth in Table 6), and wherein the subject is monitored after treatment with a TNF α inhibitor, thereby monitoring the autoimmune disorder in the subject.

[0036] In yet another aspect, the invention provides a method of monitoring an autoimmune disorder in a subject having the autoimmune disorder, the method comprising: assaying the subject for expression of one or more biomarkers, wherein the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 97, 102, 29, 294, 295, 91, 131, 290, 100, 134, 296, 297, 298, 299, 136, 174 and 300 (corresponding to biomarkers set forth in Table 7), thereby monitoring the autoimmune disorder in the subject.

[0037] In yet another aspect, the invention pertains to a method of building a database for use in selecting a subject having an autoimmune disorder (e.g., RA) for treatment with a TNF α inhibitor. The method comprises: receiving, in a computer system, biomarker expression patterns from a plurality of subjects having an autoimmune disorder; and storing the biomarker expression pattern from each subject such that the biomarker expression pattern is associated with an identifier of the subject, wherein the biomarker expression pattern reports expression in the subject of one or more biomarkers encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-82. The identifier of the subject can be, for example, a numerical identifier coded to an identity of the subject. In a preferred embodiment, the method further comprises receiving, in the computer system, one or more treatment regimens for treatment of the autoimmune disorder in a subject such that the treatment regimen is associated with the biomarker expression pattern of the subject and the identifier of the subject.

[0038] The invention also pertains to a computer program product containing executable instructions that when executed cause a processor to perform operations comprising: receiving, in a computer system, a biomarker expression pattern of a subject at one or more biomarkers predictive of responsiveness to a TNF α inhibitor in an autoimmune disorder; and storing the biomarker expression pattern such that the biomarker expression pattern is associated with an identifier of the subject, wherein the biomarker expression pattern reports expression in the subject of one or more biomarkers encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-82. The computer program can further cause the processor to perform an operation comprising: receiving, in the computer system, a treatment regimen for treatment of the autoimmune disorder in the subject such that the treatment regimen is associated with the biomarker expression pattern of the subject and the identifier of the subject.

[0039] In yet another aspect, the invention pertains to a method of selecting an autoimmune disorder subject for treatment with a TNF α inhibitor, the method comprising: (i) identifying, in a database comprising a plurality of autoimmune disorder subjects, a subject whose database entry is associated with a biomarker expression pattern that is predictive of responsiveness to treatment with a TNF α inhibitor; and (ii) selecting the subject for treatment with a TNF α inhibitor, wherein the biomarker expression pattern reports expression in the subject of one or more biomarkers encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-82. The method can further comprise selecting a treatment regimen by identifying, in the database, a treatment regimen that has been associated with the biomarker expression pattern of the subject and with an identifier of the subject.

[0040] The invention also pertains to a computer program product containing executable instructions that when executed cause a processor to perform operations comprising: (i) identifying, in a database including a plurality of autoimmune disorder subjects associated with biomarker expression patterns, a subject that is associated with a biomarker expression pattern that is predictive of responsiveness to treatment with a TNF α inhibitor; and (ii) outputting the identified subject as a subject to be treated with a TNF α inhibitor; wherein the biomarker expression pattern reports expression in the subject of one or more biomarkers encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-82. In one embodiment, the computer program further causes the processor to perform an operation comprising outputting a treatment regimen that is associated with the subject to be treated with the TNF α inhibitor.

BRIEF DESCRIPTION OF THE DRAWINGS

[0041] FIG. 1 is a bar graph showing the results of experiments validating the predictive gene CD11c by quantitative real-time PCR. mRNA expression was compared in monocytes from normal donors (n=16), as well as future responders and future non-responders to therapy with anti-TNF α (RA-ATNF; filled circles ●; 15 responders and 12 non-responders) or to combination therapy with anti-TNF α /methotrexate (RA- α TNF/MTX; empty circles ○; 7 responders and 9 non-responders). The expression of CD11c is expressed as the means $\pm$ standard error of the mean normalized to that of the house keeping gene glycerol-aldehyd-3-phosphate dehydrogenase (GAPDH; % expression). Except for 1 RA patient with a borderline ACR response of 30 and a CD11c mRNA level directly at the distinction threshold (who was therefore classified as a false negative), the threshold level (40%) almost fully distinguished future responders from non-responders (100% specificity, 94% sensitivity, and 96% power). The threshold level to distinguish future responders from non-responders is indicated by a broken line (----); * P $\leq$ 0.05, ** P $\leq$ 0.01 as compared to normal donors; +++ P $\leq$ 0.005 as compared to future responders to anti-TNF α therapy.

[0042] FIG. 2 is a graph showing the correlation between the mRNA expression of predictive CD11c in pre-treatment RA patients and their individual future ACR response (continuous ACR score). The horizontal and vertical broken lines indicate the thresholds for the separation between RA-responders and RA-non-responders, both in terms of the pre-treatment CD11c mRNA levels (40%) and their ACR

response (continuous ACR score $\leq$ 30). Responders (continuous American College of Rheumatology [ACR] score $\geq$ 40; clustered as ND) and non-responders to anti-TNF therapy (continuous ACR score $\leq$ 30; clustered as RA) were defined according to the criteria of the ACR.

[0043] FIG. 3 is a graph showing the correlation between the mRNA expression of predictive CD11c in pre-treatment RA patients and their individual future strict ACR response in the following conventional used steps: $\geq$ 0%, $\geq$ 20%, $\geq$ 50%, and $\geq$ 70% (continuous ACR score).

DETAILED DESCRIPTION OF THE INVENTION

[0044] This invention provides methods for predicting responsiveness to a TNF α inhibitor in a subject suffering from an autoimmune disorder, and methods for selecting a treatment regimen with a TNF α inhibitor, based on expression of particular biomarkers in the subject to be treated. The invention is based, at least in part, on the observation that altered expression of particular biomarkers in a subject suffering from rheumatoid arthritis is associated with increased or decreased responsiveness to therapy with a TNF α inhibitor. Microarray analysis, hierarchical clustering and Taq-Man ® -PCR analysis were used to examine normal donors (NA) and rheumatoid arthritis (RA) patients, who were categorized as being responsive to treatment with an anti-TNF α antibody (RA responders) or nonresponsive to treatment with an anti-TNF α antibody (RA nonresponders). A panel of 82 genes were identified whose expression was altered (upregulated or downregulated) in patients identified as either future RA responders or future RA nonresponders, demonstrating the ability of these genes to act as biomarkers for predicting responsiveness to TNF α inhibitor treatment. In particular, one gene, encoding the antigen CD11c, was identified as fully predicting the future response to anti-TNF α treatment. Accordingly, the expression pattern of one or more biomarkers can be assessed in RA subjects for which TNF α inhibitor therapy is being considered, or subjects suffering from other autoimmune disorders amenable to TNF α inhibitor therapy, to thereby predict responsiveness of the subject to such therapy and/or to aid in the selection of an appropriate treatment regimen.

[0045] Furthermore, additional patterns of biomarker expression were identified by (i) hierarchical clustering with the genes resulting from a simultaneous comparison between RA versus ND and RA responders pre- versus post-anti-TNF α therapy; (ii) prediction analysis of microarrays; and (iii) hierarchical clustering based on the comparison between RA responders and non-responders post-treatment. Accordingly, the biomarker expression patterns described herein also can be using in monitoring an autoimmune disorder in a subject, e.g., monitoring the responsiveness of the subject to a particular therapy or assisting in the diagnosis or prognosis of the autoimmune disorder (e.g., RA) in the subject.

[0046] In order that the present invention may be more readily understood, certain terms are first defined. Additional definitions are set forth throughout the detailed description.

[0047] The term “predicting responsiveness to a TNF α inhibitor”, as used herein, is intended to refer to an ability to assess the likelihood that treatment of a subject with a TNF α inhibitor will or will not be effective in (e.g., provide a measurable benefit to) the subject. In particular, such an ability to assess the likelihood that treatment will or will not be effective typically is exercised before treatment with the TNF α inhibitor is begun in the subject. However, it is also possible

that such an ability to assess the likelihood that treatment will or will not be effective can be exercised after treatment has begun but before an indicator of effectiveness (e.g., an indicator of measurable benefit) has been observed in the subject.

[0048] The term “TNF α inhibitor” as used herein is intended to encompass agents including proteins, antibodies, antibody fragments, fusion proteins (e.g., Ig fusion proteins or Fc fusion proteins), multivalent binding proteins (e.g., DVD Ig), small molecule TNF α antagonists and similar naturally- or nonnaturally-occurring molecules, and/or recombinant and/or engineered forms thereof, that, directly or indirectly, inhibits TNF α activity, such as by inhibiting interaction of TNF α with a cell surface receptor for TNF α , inhibiting TNF α protein production, inhibiting TNF α gene expression, inhibiting TNF α secretion from cells, inhibiting TNF α receptor signaling or any other means resulting in decreased TNF α activity in a subject. The term “TNF α inhibitor” also includes agents which interfere with TNF α activity. Examples of TNF α inhibitors include etanercept (ENBREXTM, Amgen), infliximab (REMICADETM, Johnson and Johnson), human anti-TNF monoclonal antibody adalimumab (D2E7/HUMIRATM, Abbott Laboratories), CDP 571 (Celltech), and CDP 870 (Celltech), as well as other compounds which inhibit TNF α activity, such that when administered to a subject suffering from or at risk of suffering from a disorder in which TNF α activity is detrimental (e.g., RA), the disorder is treated. The term also includes each of the anti-TNF α human antibodies and antibody portions described herein as well as those described in U.S. Pat. Nos. 6,090,382; 6,258,562; 6,509,015, and in U.S. patent application Ser. Nos. 09/801,185 (U.S. Publication No. 20030092059) and 10/302,356 (U.S. Publication No. 20030219438), each incorporated by reference herein.

[0049] The term “antibody” as referred to herein includes whole antibodies and any antigen binding fragment (i.e., “antigen-binding portion”) or single chains thereof. An “antibody” refers to a glycoprotein comprising at least two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds, or an antigen binding portion thereof. Each heavy chain is comprised of a heavy chain variable region (abbreviated herein as V_H) and a heavy chain constant region. The heavy chain constant region is comprised of three domains, C_{H1}, C_{H2} and C_{H3}. Each light chain is comprised of a light chain variable region (abbreviated herein as V_L) and a light chain constant region. The light chain constant region is comprised of one domain, C_L. The V_H and V_L regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDR), interspersed with regions that are more conserved, termed framework regions (FR). Each V_H and V_L is composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. The variable regions of the heavy and light chains contain a binding domain that interacts with an antigen. The constant regions of the antibodies may mediate the binding of the immunoglobulin to host tissues or factors, including various cells of the immune system (e.g., effector cells) and the first component (C1q) of the classical complement system.

[0050] The term “antibody” is also intended to encompass dual-specific antibodies and bispecific antibodies. The term “dual-specific antibody”, as used herein, refers to full-length antibodies that can bind two different antigens (or epitopes) in each of its two binding arms (a pair of HC/LC) (see e.g., PCT

publication WO 02/02773). Accordingly a dual-specific binding protein has two identical antigen binding arms, with identical specificity and identical CDR sequences, and is bi-valent for each antigen it binds to. The term “bispecific antibody”, as used herein, refers to full-length antibodies that are generated by quadroma technology (see Milstein, C. and A. C. Cuello (1983) *Nature*, 305:537-40), by chemical conjugation of two different mAbs (see Staerz, U. D., et al. (1985) *Nature* 314: 628-31), or by knob-into-hole or similar approaches which introduces mutations in the Fc region (see Holliger, P., T. Prospero, and G. Winter (1993) *Proc. Natl. Acad. Sci. USA* 90:6444-8), resulting in multiple different immunoglobulin species of which only one is the functional bispecific antibody. By molecular function, a bispecific antibody binds one antigen (or epitope) on one of its two binding arms (one pair of HC/LC), and binds a different antigen (or epitope) on its second arm (a different pair of HC/LC). By this definition, a bispecific antibody has two distinct antigen binding arms (in both specificity and CDR sequences), and is mono-valent for each antigen it binds to. Thus, when used herein, a “bispecific” antibody of the invention has one binding arm that is specific for an epitope of TNF α and a second binding arm that is specific for a different antigen or epitope.

[0051] The term “antigen-binding portion” of an antibody (or simply “antibody portion”), as used herein, refers to one or more fragments of an antibody that retain the ability to specifically bind to an antigen. It has been shown that the antigen-binding function of an antibody can be performed by fragments of a full-length antibody. Examples of binding fragments encompassed within the term “antigen-binding portion” of an antibody include (i) a Fab fragment, a monovalent fragment consisting of the V_L, V_H, C_L and C_{H1} domains; (ii) a F(ab')₂ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the V_H and C_{H1} domains; (iv) a Fv fragment consisting of the V_L and V_H domains of a single arm of an antibody, (v) a dAb fragment (Ward et al., (1989) *Nature* 341:544-546), which consists of a V_H domain; and (vi) an isolated complementarity determining region (CDR). Furthermore, although the two domains of the Fv fragment, V_L and V_H, are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the V_L and V_H regions pair to form monovalent molecules (known as single chain Fv (scFv); see e.g., Bird et al. (1988) *Science* 242:423-426; and Huston et al. (1988) *Proc. Natl. Acad. Sci. USA* 85:5879-5883). Such single chain antibodies are also intended to be encompassed within the term “antigen-binding portion” of an antibody. These antibody fragments are obtained using conventional techniques known to those with skill in the art, and the fragments are screened for utility in the same manner as are intact antibodies.

[0052] The terms “monoclonal antibody” or “monoclonal antibody composition” as used herein refer to a preparation of antibody molecules of single molecular composition. A monoclonal antibody composition displays a single binding specificity and affinity for a particular epitope.

[0053] The terms “chimeric antibody” or “chimeric monoclonal antibody” are intended to refer to antibodies in which the variable region sequences are derived from one species and the constant region sequences are derived from another species, such as an antibody in which the variable region sequences are derived from a mouse antibody and the constant region sequences are derived from a human antibody.

Such “chimeric antibodies” can be prepared by standard recombinant technology well established in the art. For example, a nucleic acid encoding a V_H region from a mouse antibody can be operatively linked to a nucleic acid encoding the heavy chain constant regions from a human antibody and, likewise, a nucleic acid encoding a V_L region from a mouse antibody can be operatively linked to a nucleic acid encoding the light chain constant region from a human antibody.

[0054] The terms “humanized antibody” or “humanized monoclonal antibody” are intended to refer to antibodies in which CDR sequences derived from the germline of a non-human mammalian species, such as a mouse, have been grafted onto human framework sequences. Additional framework region modifications may be made within the human framework sequences. Such “humanized antibodies” can be prepared by standard recombinant technology well established in the art. For example, nucleic acids encoding the CDR1, CD2 and CDR3 regions from a V_H region of a mouse antibody can be operatively linked to nucleic acids encoding the FR1, FR2, FR3 and FR4 regions of a human V_H region, and the entire “CDR-grafted” V_H region can be operatively linked to nucleic acid encoding the heavy chain constant regions from a human antibody. Likewise, nucleic acids encoding the CDR1, CD2 and CDR3 regions from a V_L region of a mouse antibody can be operatively linked to nucleic acids encoding the FR1, FR2, FR3 and FR4 regions of a human V_L region, and the entire “CDR-grafted” V_L region can be operatively linked to nucleic acid encoding the light chain constant region from a human antibody.

[0055] The term “human antibody”, as used herein, is intended to refer to antibodies having variable regions in which both the framework and CDR regions are derived from human germline immunoglobulin sequences. Furthermore, if the antibody contains a constant region, the constant region also is derived from human germline immunoglobulin sequences. Human antibodies may include amino acid residues not encoded by human germline immunoglobulin sequences (e.g., mutations introduced by random or site-specific mutagenesis in vitro or by somatic mutation in vivo).

[0056] The term “human monoclonal antibody” refers to antibodies displaying a single binding specificity which have variable regions in which both the framework and CDR regions are derived from human germline immunoglobulin sequences. Human monoclonal antibodies can be produced by a hybridoma which includes a B cell obtained from a transgenic nonhuman animal, e.g., a transgenic mouse, having a genome comprising a human heavy chain transgene and a light chain transgene fused to an immortalized cell. The term “human monoclonal antibody”, as used herein, also includes all human antibodies that are prepared, expressed, created or isolated by recombinant means, such as (a) antibodies isolated from an animal (e.g., a mouse) that is transgenic or transchromosomal for human immunoglobulin genes or a hybridoma prepared therefrom, (b) antibodies isolated from a host cell transformed to express the human antibody, e.g., from a transfectoma, (c) antibodies isolated from a recombinant, combinatorial human antibody library, and (d) antibodies prepared, expressed, created or isolated by any other means that involve splicing of human immunoglobulin gene sequences to other DNA sequences. Such recombinant human antibodies have variable regions in which the framework and CDR regions are derived from human germline immunoglobulin sequences. Such recombinant human antibodies, however, can be subjected to in vitro mutagenesis

(or, when an animal transgenic for human Ig sequences is used, in vivo somatic mutagenesis) and thus the amino acid sequences of the V_H and V_L regions of the recombinant antibodies are sequences that, while derived from and related to human germline V_H and V_L sequences, may not naturally exist within the human antibody germline repertoire in vivo.

[0057] The terms “Ig fusion protein” and “Fc fusion protein” are intended to refer to a recombinant, composite protein comprising a polypeptide of interest operatively linked to a constant region portion of immunoglobulin, typically the hinge, CH_2 and CH_3 domains of heavy chain constant region, more typically the human IgG1 hinge, CH_2 and CH_3 domains. The polypeptide of interest operatively linked to the Fc portion can be, for example, a full-length protein or only a portion of a full-length protein, such as one or more extracellular domains of a protein, e.g., one or more extracellular domains of a cell-surface protein. Such “Ig fusion proteins” can be prepared by standard recombinant technology well established in the art. For example, a nucleic acid encoding the polypeptide of interest can be operatively linked to a nucleic acid encoding the hinge, CH_2 and CH_3 domains of a heavy chain constant region.

[0058] The term “multivalent binding protein”, as a form of TNF α inhibitor, is used in this specification to denote a binding protein comprising two or more antigen binding sites. Examples of multivalent binding proteins include dual variable domain (DVD) binding proteins. The multivalent binding protein is preferably engineered to have three or more antigen binding sites, and is generally not a naturally occurring antibody. A multivalent binding protein also can be a “multispecific binding protein.” The term “multispecific binding protein” refers to a binding protein capable of binding two or more related or unrelated targets (wherein, with respect to this specification at least one of the targets is TNF α). Dual variable domain (DVD) binding proteins, as used herein, are binding proteins that comprise two or more antigen binding sites and are tetravalent or multivalent binding proteins. Such DVDs may be monospecific, i.e., capable of binding one antigen (e.g., TNF α) or multispecific, i.e., capable of binding two or more antigens (e.g., TNF α and one or more other antigens). DVD binding proteins comprising two heavy chain DVD polypeptides and two light chain DVD polypeptides are referred to as “DVD Ig.” Each half of a DVD Ig comprises a heavy chain DVD polypeptide, and a light chain DVD polypeptide, and two antigen binding sites. Each binding site comprises a heavy chain variable domain and a light chain variable domain with a total of 6 CDRs involved in antigen binding per antigen binding site. DVD binding proteins and methods of making DVD binding proteins are disclosed in US. Publication No. 20070071675, the entire contents of which are specifically incorporated herein by reference.

[0059] As used herein, the term “biomarker” is intended to encompass a substance that is used as an indicator of a biologic state and includes genes (and nucleotide sequences of such genes), mRNAs (and nucleotide sequences of such mRNAs) and proteins (and amino acid sequences of such proteins). A “biomarker expression pattern” is intended to refer to a quantitative or qualitative summary of the expression of one or more biomarkers in a subject, such as in comparison to a standard or a control.

[0060] The terms “increased” or “increased expression” and “decreased” or “decreased expression”, with respect to the expression pattern of a biomarker(s), are used herein as

meaning that the level of expression is increased or decreased relative to a constant basal level of expression of a housekeeping, gene, whose expression level does not significantly vary under different conditions. A nonlimiting example of such a housekeeping, gene is GAPDH. Other suitable housekeeping, gene are well-established in the art.

[0061] As used herein, the term “CD11c” refers to a protein having a full-length amino acid sequence as set forth at Genbank Accession No. NP_000878 (also shown as SEQ ID NO: 302) and encoded by a full-length nucleotide sequence as set forth at Genbank Accession No. NM_000887 (also shown as SEQ ID NO: 301). CD11c is also known in the art as CD11C, CD11c antigen, Integrin alpha X, complement component 3 receptor 4 subunit, ITGAX, LeuM5, Integrin alpha X precursor, Leukocyte adhesion glycoprotein p150,p95 alpha chain, and Leukocyte adhesion receptor p150 subunit, which terms may be used interchangeably herein to refer to CD11c.

[0062] As used herein, the term “Affymetrix ID” refers to a numerical identifier that corresponds to a sequence entry in an Affymetrix database, which entry includes the sequence as well as additional information relating to the sequence and corresponding protein. The sequence entries, and additional information in the entries, for each Affymetrix ID are publicly available (e.g., by entering the Affymetrix ID number into the Affymetrix database search engine, e.g., at <https://www.affymetrix.com/analysis/netaffx/index.affx>). All sequence entries (such as Genbank Accession numbers), and additional information provided for each entry, corresponding to each of the Affymetrix ID numbers disclosed herein are hereby specifically incorporated by reference in their entirety.

[0063] As used herein, the term “subject” includes humans, and non-human animals amenable to TNF α inhibitor therapy, e.g., preferably mammals, such as non-human primates, sheep, dogs, cats, horses and cows.

[0064] As used herein, the term “autoimmune disorder subject” or “AD subject” is intended to refer to a subject (e.g., human patient) suffering from an autoimmune disorder.

[0065] As used herein, the term “rheumatoid arthritis subject” or “RA subject” is intended to refer to a subject (e.g., human patient) suffering from rheumatoid arthritis.

[0066] As used herein, the term “treatment regimen” is intended to refer to one or more parameters selected for the treatment of a subject, e.g., with a TNF α inhibitor, which parameters can include, but are not necessarily limited to, the type of agent chosen for administration, the dosage, the formulation, the route of administration and the frequency of administration.

[0067] Various aspects of the invention are described in further detail in the following subsections.

Prediction of Responsiveness to a TNF α Inhibitor for Autoimmune Disorders

[0068] In one aspect, the invention pertains to a method for predicting responsiveness to a TNF α inhibitor in a subject having an autoimmune disorder, such as rheumatoid arthritis. Typically, the method comprises (i) assaying the subject for the expression of one or more biomarkers predictive of responsiveness to a TNF α inhibitor in an autoimmune disorder, and (ii) predicting responsiveness of the subject to the TNF α inhibitor based on expression of the one or more biomarkers in the subject. As used herein, the term “one or more biomarkers” is intended to mean that at least one biomarker in a disclosed list of biomarkers is assayed and, in various

embodiments, more than one biomarker set forth in the list may be assayed, such as two, three, four, five, ten, twenty, thirty, forty, fifty, more than fifty, or all the biomarkers in the list may be assayed.

[0069] Predicting responsiveness of the subject to the TNF α inhibitor “based on expression of the one or more biomarkers in the subject” typically involves comparing the level, or pattern, of expression of the one or more biomarkers in the subject to a known standard or control (which known standard or control may be derived from, for example, a normal subject, a pre-established TNF α inhibitor responder or a pre-established TNF α inhibitor non-responder). In a preferred embodiment, the level of expression of the biomarker(s) is measured in parallel with measurement of the level of expression of one or more “housekeeping” genes, such as GAPDH, whose expression level is not altered by the autoimmune disorder. The level of expression of the biomarker(s) is determined to be “increased” or “decreased” relative to a constant basal level of expression of the housekeeping gene. Examples of suitable housekeeping genes, such as GAPDH, that can be used for comparison purposes are well known in the art.

[0070] Preferably, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-82 (corresponding to sequences of the biomarkers set forth in Table 9). Thus, at least one of the biomarkers encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-82 is assayed and, in various embodiments, for example, two, three, four, five, ten, twenty, thirty, forty, fifty, more than fifty, or all the biomarkers in the list may be assayed.

[0071] In a preferred embodiment, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 6, 7, 10, 15-17, 19, 22, 24, 27, 31, 34-39, 43-47, 49, 51, 54, 55, 57, 59, 61, 62, 64, 70, 75, 79 and 82 (corresponding to sequences from Table 9 that are increased in $\geq 80\%$ of responders vs. non-responders). More preferably, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 31, 37, 44, 47, 62 and 70 (corresponding to sequences from Table 9 that are increased in $\geq 90\%$ of responders vs. non-responders). Even more preferably, at least one of the biomarkers to be assayed is encoded by a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 44 (corresponding to the biomarker CD11c, which, as set forth in Table 9, is increased in 100% of responders vs. non-responders). In each of these embodiments, increased expression of the one or more biomarkers is predictive of responsiveness of the subject to a TNF α inhibitor (e.g., increased expression relative to a standard or control level of expression, which standard or control level of expression can be based, for example, on the level of expression in previously established TNF α inhibitor non-responder RA subjects).

[0072] In another preferred embodiment, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-5, 8, 9, 11-14, 18, 20, 21, 23, 25, 26, 28-30, 32, 33, 40-42, 48, 50, 52, 53, 56, 58, 60, 63, 65-69, 71-74, 76-78, 80 and 81 (corresponding to sequences from Table 9 that are decreased in $\geq 80\%$ of responders vs. non-responders). More preferably, the one or more biomarkers is encoded

by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 11, 29, 65, 73 and 74 (corresponding to sequences from Table 9 that are decreased in $\geq 90\%$ of responders vs. non-responders). Even more preferably, the one or more biomarkers is encoded by a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 11 or SEQ ID NO: 74 (corresponding to sequences from Table 9 that are decreased in 100% of responders vs. non-responders). In each of these embodiments, decreased expression of the one or more biomarkers is predictive of responsiveness of the subject to a TNF α inhibitor (e.g., decreased expression relative to a standard or control level of expression, which standard or control level of expression can be based, for example, on the level of expression in previously established TNF α inhibitor non-responder RA subjects).

[0073] In another aspect, the invention provides a method for predicting responsiveness to a TNF α inhibitor in a subject having an autoimmune disorder, the method comprising: (i) assaying the subject for expression of one or more biomarkers predictive of responsiveness to a TNF α inhibitor in the autoimmune disorder, and (ii) predicting responsiveness of the subject to the TNF α inhibitor based on expression of the one or more biomarkers in the subject, wherein the one or more biomarkers is selected from the group consisting of Aquaporin 3 (Genbank Accession No. NM_004925); Similar to ribosomal protein S24, clone MGC:8595 (Genbank Accession No. NM_033022); Transmembrane emp24 domain trafficking protein 2 (Genbank Accession No. NM_006815); Superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (Genbank Accession No. NM_000454); Calmodulin 1 (phosphorylase kinase, delta) (Genbank Accession No. NM_006888); Guanine nucleotide binding protein (G protein), beta polypeptide 1 (Genbank Accession No. NM_002074); Prothymosin, alpha (gene sequence 28) (Genbank Accession No. NM_002823); *Homo sapiens* isocitrate dehydrogenase 1 (NADP⁺) soluble (IDH1) (Genbank Accession No. NM_005896); Tumor protein D52 (Genbank Accession Nos. NM_001025252, NM_001025253, NM_005079); Early growth response 1 (Genbank Accession No. NM_001964); *Homo sapiens* predicted osteoblast protein (GS3786) (Genbank Accession Nos. NM_014888, NM_001040020); Cytochrome c oxidase subunit VIIb (Genbank Accession No. NM_001866); CUG triplet repeat, RNA binding protein 2 (Genbank Accession No. NM_001025077, NM_001025076, NM_006561); Ubiquinol-cytochrome c reductase hinge protein (Genbank Accession No. NM_006004); *Homo sapiens* leptin receptor gene-related protein (HS0BRGRP) (Genbank Accession No. NM_017526); Wiskott-Aldrich syndrome protein interacting protein (Genbank Accession Nos. NM_001077269, NM_003387); CD97 antigen (Genbank Accession Nos. NM_001025160, NM_001784, NM_078481); Glutamate-cysteine ligase, catalytic subunit (Genbank Accession No. NM_001498); Crystallin, zeta (quinone reductase) (Genbank Accession No. NM_001889); Rap guanine nucleotide exchange factor (GEF) 2 (Genbank Accession No. NM_014247); Ataxin 1 (Genbank Accession No. NM_000332); Adaptor-related protein complex 1, sigma 2 subunit (Genbank Accession No. NM_003916); Ectonucleotide pyrophosphatase/phosphodiesterase 4 (Genbank Accession No. NM_014936); Desmocollin 2 (Genbank Accession Nos. NM_024422, NM_004949); MAL, T-cell differentiation protein (Genbank Accession Nos.

NM_002371, NM_022438, NM_022439, NM_022440); Glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase (Genbank Accession No. NM_005476); Chemokine (C—C motif) ligand 3 (Genbank Accession Nos. NM_001001437, NM_021006); Carboxypeptidase A3 (Genbank Accession No. NM_001870); Charcot-Leyden crystal protein (Genbank Accession No. NM_001828); NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7 kDa (Genbank Accession No. NM_004545); Interleukin 8 receptor, beta (Genbank Accession No. NM_001557); Platelet factor 4 variant 1 (Genbank Accession No. NM_002620); Poly(A) binding protein interacting protein 1 (Genbank Accession No. NM_006451); ATP-binding cassette, subfamily C (CFTR/MRP), member 3 (Genbank Accession No. NM_003786); Actinin, alpha 1 (Genbank Accession No. NM_001102); NAD kinase (Genbank Accession No. NM_023018); Platelet/endothelial cell adhesion molecule (CD31 antigen) (Genbank Accession No. NM_000442); Esterase D/formylglutathione hydrolase (Genbank Accession No. NM_001984); Chromosome 20 open reading frame 111 (Genbank Accession No. NM_016470); Sterol-C4-methyl oxidase-like (Genbank Accession Nos. NM_001017369, NM_006745); PIM-1 oncogene (Genbank Accession No. NM_002648); GATA binding protein 2 (Genbank Accession No. NM_032638); Cathepsin Z (Genbank Accession No. NM_001336); Integrin alpha-X (antigen CD11c) (Genbank Accession No. NM_000887); Lectin, galactoside-binding, soluble, 8 (galectin 8) (Genbank Accession Nos. NM_006499, NM_201545); CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) (Genbank Accession Nos. NM_006889, NM_175862); Interleukin 8 (Genbank Accession No. NM_000584); Fc fragment of IgE, high affinity I, receptor for alpha polypeptide (Genbank Accession No. NM_002001); Actin, gamma 1 (Genbank Accession No. NM_001614); KIAA0746 protein (Genbank Accession No. NM_015187); Glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID) (Genbank Accession No. NM_002076); Transcription factor 4 (Genbank Accession Nos. BF592782, CR612521); Major histocompatibility complex, class II, DQ alpha 1 (Genbank Accession Nos. NM_002122, NM_020056); Cell division cycle 2-like 6 (CDK8-like) (Genbank Accession No. NM_015076); Major histocompatibility complex, class II, DQ beta 1 (Genbank Accession No. XM_942240); Phospholipase C-like 2 (Genbank Accession No. NM_015184); Coagulation factor II (thrombin) receptor-like 1 (Genbank Accession No. NM_005242); TM2 domain containing 1 (Genbank Accession No. NM_032027); Splicing factor 3b, subunit 1, 155 kDa (Genbank Accession No. NM_012433); SUB1 homolog (*S. cerevisiae*) (Genbank Accession No. NM_006713); mRNA; cDNA DKFZp564O0862 (Genbank Accession No. AI278204); Amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer disease) (Genbank Accession Nos. NM_201413, NM_000484, NM_201414); Cytochrome b-5 (Genbank Accession Nos. NM_001914, NM_148923); Cold autoinflammatory syndrome 1 (Genbank Accession No. NM_183395); Neugrin, neurite outgrowth associated (Genbank Accession Nos. NM_016645, NM_001033088); Ribosomal protein S26, 40S ribosomal protein (Genbank Accession No. XM_941927); CCR4-NOT transcription complex, subunit 6 (Genbank Accession No. NM_015455); Ubiquinol-cytochrome c reductase complex (7.2 kD) (Genbank Accession Nos. NM_013387, NM_001003684); Hepatocellular carcinoma-associated antigen 112 (Genbank

Accession No. NM_018487); Kruppel-like factor 11 (Genbank Accession No. XM_001129527); GGA binding partner (Genbank Accession No. NM_018318); Cornichon homolog 4 (*Drosophila*) (Genbank Accession No. NM_014184); Hypothetical protein FLJ21616 (Genbank Accession No. NM_024567); *Homo sapiens* hypothetical protein FLJ10134 (Genbank Accession No. NM_018004); Nuclear prelamin A recognition factor (Genbank Accession Nos. NM_012336, NM_001038618); Erythroblast membrane-associated protein (Genbank Accession Nos. NM_018538, NM_001017922); LR8 protein (Genbank Accession No. NM_014020); Likely ortholog of mouse limb-bud and heart gene (LBH) (Genbank Accession No. NM_030915); Calmin (calponin-like, transmembrane) (Genbank Accession No. NM_024734); Chromosome 14 open reading frame 156 (Genbank Accession No. NM_031210); Guanine nucleotide binding protein (G protein) alpha 12 (Genbank Accession No. NM_007353); and SRY (sex determining region Y)-box 18 (Genbank Accession No. NR_003287) (corresponding to biomarkers listed in Table 9).

[0074] In a preferred embodiment, the one or more biomarkers is selected from the group consisting of Guanine nucleotide binding protein (G protein), beta polypeptide 1; Prothymosin, alpha (gene sequence 28); Early growth response 1; *Homo sapiens* leptin receptor gene-related protein (HS0BRGRP); Wiskott-Aldrich syndrome protein interacting protein; CD97 antigen; Crystallin, zeta (quinone reductase); Adaptor-related protein complex 1, sigma 2 subunit; Desmocollin 2; Chemokine (C—C motif) ligand 3; Interleukin 8 receptor, beta; ATP-binding cassette, sub-family C (CFTR/MRP), member 3; Actinin, alpha 1; NAD kinase; Platelet/endothelial cell adhesion molecule (CD31 antigen); Esterase D/formylglutathione hydrolase; Chromosome 20 open reading frame 111; Cathepsin Z; Integrin alpha-X (antigen CD11c); Lectin, galactoside-binding, soluble, 8 (galectin 8); CD86 antigen (CD28 antigen ligand 2, B7-2 antigen); Interleukin 8; Actin, gamma 1; Glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID); Cell division cycle 2-like 6 (CDK8-like); Major histocompatibility complex, class II, DQ beta 1; Coagulation factor II (thrombin) receptor-like 1; Splicing factor 3b, subunit 1, 155 kDa; mRNA; cDNA DKEZp56400862; Amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer disease); Cold autoinflammatory syndrome 1; Kruppel-like factor 11; Nuclear prelamin A recognition factor; Calmin (calponin-like, transmembrane); and SRY (sex determining region Y)-box 18 (corresponding to biomarkers listed in Table 9 that are increased in $\geq 80\%$ of responders vs. non-responders). More preferably, the one or more biomarkers is selected from the group consisting of Interleukin 8 receptor, beta; Platelet/endothelial cell adhesion molecule (CD31 antigen); Integrin alpha-X (antigen CD11c); Interleukin 8; Amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer disease); and Kruppel-like factor 11 (corresponding to biomarkers listed in Table 9 that are increased in $\geq 90\%$ of responders vs. non-responders). Even more preferably, at least one of the biomarkers is Integrin alpha-X (antigen CD11c) (corresponding to a biomarker listed in Table 9 that is increased in 100% of responders vs. non-responders). In each of the embodiments, increased expression of the one or more biomarkers is predictive of responsiveness of the subject to a TNF α inhibitor.

[0075] In another preferred embodiment, the one or more biomarkers is selected from the group consisting of Aquaporin 3; Similar to ribosomal protein S24, clone MGC:8595;

Transmembrane emp24 domain trafficking protein 2; Superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1; Calmodulin 1 (phosphorylase kinase, delta); *Homo sapiens* isocitrate dehydrogenase 1 (NADP+) soluble (IDH1); Tumor protein D52; *Homo sapiens* predicted osteoblast protein (GS3786); Cytochrome c oxidase subunit VIIb; CUG triplet repeat, RNA binding protein 2; Ubiquinol-cytochrome c reductase hinge protein; Glutamate-cysteine ligase, catalytic subunit; Rap guanine nucleotide exchange factor (GEF) 2; Ataxin 1; Ectonucleotide pyrophosphatase/phosphodiesterase 4; MAL, T-cell differentiation protein; Glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase; Carboxypeptidase A3; Charcot-Leyden crystal protein; NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7 kDa; Platelet factor 4 variant 1; Poly(A) binding protein interacting protein 1; Sterol-C4-methyl oxidase-like; PIM-1 oncogene; GATA binding protein 2; Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide; KIAA0746 protein; Transcription factor 4; Major histocompatibility complex, class II, DQ alpha 1; Phospholipase C-like 2; TM2 domain containing 1; SUB1 homolog (*S. cerevisiae*); Cytochrome b-5; Neugrin, neurite outgrowth associated; Ribosomal protein S26, 40S ribosomal protein; CCR4-NOT transcription complex, subunit 6; Ubiquinol-cytochrome c reductase complex (7.2 kD); Hepatocellular carcinoma-associated antigen 112; GGA binding partner; Cornichon homolog 4 (*Drosophila*); Hypothetical protein FLJ21616; *Homo sapiens* hypothetical protein FLJ10134; Erythroblast membrane-associated protein; LR8 protein; Likely ortholog of mouse limb-bud and heart gene (LBH); Chromosome 14 open reading frame 156; and Guanine nucleotide binding protein (G protein) alpha 12 (corresponding to biomarkers listed in Table 9 that are decreased in $\geq 80\%$ of responders vs. non-responders). More preferably, the one or more biomarkers is selected from the group consisting of *Homo sapiens* predicted osteoblast protein (GS3786); Charcot-Leyden crystal protein; Neugrin, neurite outgrowth associated; Hypothetical protein FLJ21616; and *Homo sapiens* hypothetical protein FLJ10134 (corresponding to biomarkers listed in Table 9 that are decreased in $\geq 90\%$ of responders vs. non-responders). Even more preferably, the one or more biomarkers is *Homo sapiens* predicted osteoblast protein (GS3786) or *Homo sapiens* hypothetical protein FLJ10134 (corresponding to biomarkers listed in Table 9 that are decreased in 100% of responders vs. non-responders). In each of these embodiments, decreased expression of the one or more biomarkers is predictive of responsiveness of the subject to a TNF α inhibitor.

[0076] In a particularly preferred aspect, the invention provides a method for predicting responsiveness to a TNF α inhibitor in a subject having an autoimmune disorder the method comprising: (i) assaying the subject for increased expression of a biomarker, which biomarker is CD11c, and (ii) predicting responsiveness of the subject to the TNF α inhibitor based on increased expression of CD11c in the subject.

[0077] In yet another particularly preferred embodiment, the invention provides a method for predicting responsiveness to a TNF α inhibitor, which TNF α inhibitor is adalimumab, in a subject having an autoimmune disorder the method comprising: (i) assaying the subject for expression of one or more biomarkers predictive of responsiveness to adalimumab in the autoimmune disorder, and (ii) predicting responsiveness of the subject to adalimumab based on expression of the one or more biomarkers in the subject. Preferably,

the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-82 (or selected from the group consisting of the biomarkers set forth in Table 9). In more preferred embodiments, the subsets of sequences within SEQ ID NO: 1-82 that are either increased or decreased, as set forth in detail above, can be assayed.

[0078] In the methods of the invention for predicting responsiveness to a TNF α inhibitor in a subject having an autoimmune disorder, the expression of one or more biomarkers predictive of responsiveness to a TNF α inhibitor in the autoimmune disorder can be assayed in the subject using techniques well-established in the art. In a preferred embodiment, the expression of the one or more biomarkers in the subject is assayed by obtaining an mRNA sample from the subject (e.g., isolated from peripheral blood mononuclear cells, by standard methods) and detecting the expression of mRNA(s) encoding the one or more biomarkers in the mRNA sample using standard molecular biology techniques, such as PCR analysis. A preferred method of PCR analysis is reverse transcriptase-polymerase chain reaction (RT-PCR). Other suitable systems for mRNA sample analysis include microarray analysis (e.g., using Affymetrix's microarray system or Illumina's BeadArray Technology).

[0079] Additionally or alternatively, in certain situations it may be possible to assay for the expression of one or more biomarkers at the protein level, using a detection reagent that detects the protein product encoded by the mRNA of the biomarker(s). For example, if an antibody reagent is available that binds specifically to the biomarker protein product to be detected, and not to other proteins, then such an antibody reagent can be used to detect the expression of the biomarker of interest in a cellular sample from the subject, or a preparation derived from the cellular sample, using standard antibody-based techniques known in the art, such as FACS analysis, ELISA and the like.

[0080] It will be readily understood by the ordinarily skilled artisan that essentially any technical means established in the art for detecting biomarkers, at either the nucleic acid or protein level, can be adapted to detection of the biomarkers discussed herein and applied in the methods of the current invention for predicting responsiveness to a TNF α inhibitor in a subject having an autoimmune disorder.

[0081] The biomarkers described herein were originally identified in patients having rheumatoid arthritis (see the Examples) and thus a particularly preferred autoimmune disorder in which to apply the methods of the invention is rheumatoid arthritis. The mechanism of action of the TNF α pathway, however, is thought to be common to a large number of autoimmune disorders and TNF α inhibitors have been shown to be effective therapy in a variety of different autoimmune disorders. Accordingly, the method of the invention for predicting responsiveness to a TNF α inhibitor can be applied to essentially any autoimmune disorder in which TNF α inhibitor therapy is applied. Other preferred autoimmune disorders include Crohn's disease, ulcerative colitis, psoriasis, psoriatic arthritis, juvenile arthritis and ankylosing spondylitis. Other non-limiting examples of autoimmune disorders include autoimmune diabetes, multiple sclerosis, systemic lupus erythematosus, rheumatoid spondylitis, gouty arthritis, allergy, autoimmune uveitis, nephrotic syndrome, multisystem autoimmune diseases, autoimmune hearing loss, adult respiratory distress syndrome, shock lung, chronic pulmonary inflammatory disease, pulmonary sarcoidosis, pulmo-

nary fibrosis, silicosis, idiopathic interstitial lung disease, chronic obstructive pulmonary disease, asthma, restenosis, spondyloarthropathies, Reiter's syndrome, autoimmune hepatitis, inflammatory skin disorders, vasculitis of large vessels, medium vessels or small vessels, endometriosis, prostatitis and Sjogren's syndrome.

Biomarkers for Monitoring an Autoimmune Disorder in a Subject

[0082] In another aspect, the invention provides methods of monitoring an autoimmune disorder in a subject having the autoimmune disorder based on biomarker expression patterns established using microarray analysis of, for example, RA subjects vs. normal donors, RA subjects vs. RA subjects treated with a TNF α inhibitor and/or RA subjects treated with a TNF α inhibitor vs. RA responders to TNF α inhibitors. In these monitoring methods, the subject is assayed for expression of one or more biomarkers (using techniques, for example, as described in the previous section), thereby monitoring the autoimmune disorder in the subject.

[0083] In one embodiment of the monitoring method, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 83-133 (or the biomarkers set forth by name in Table 3, namely v-maf musculoaponeurotic fibrosarcoma oncogene homolog F; Diphtheria toxin receptor (DTR); DEAH (Asp-Glu-Ala-His) box polypeptide 15; Ribonucleotide reductase M2 polypeptide; Solute carrier family 6, member 8; 6-phosphofructo-2-kinase/fructose-2,6-bisphosphate 3; Ferrochelatase (protoporphyrin); Nuclear factor, interleukin 3 regulated; Thrombomodulin; Major histocompatibility complex, class II, DM beta; Forkhead box O3A; Hemoglobin, gamma A, gamma G; Synuclein, alpha (non A4 component of amyloid precursor); Hemoglobin, gamma A; Amphiregulin (schwannoma-derived growth factor); Lipoyltransferase 1; Solute carrier family 4, anion exchanger, member 1; S100 calcium binding protein A12 (calgranulin C); Keratin 1 (epidermolytic hyperkeratosis); Carbonic anhydrase I; CD1C antigen, c polypeptide; Tumor necrosis factor, alpha-induced protein 6; Ribonuclease, RNase A family, 2; Hemoglobin, delta; Transferrin receptor (p90, CD71); Ring finger protein 10; Chromosome 1 open reading frame 63; Hemoglobin, alpha 1, alpha 2; CD69 antigen (p60, early T-cell activation antigen); APEX nuclease (multifunctional DNA repair enzyme) 1; Membrane-spanning 4-domains, subfamily A, member 3; Heat shock 70 kDa protein 8; Hypothetical protein MGC12760; GABA(A) receptor-associated protein like 1, like 3; Aminolevulinate, delta-, synthase 2; Major histocompatibility complex, class II, DP alpha 1; Morf4 family associated protein 1-like 1; Aldehyde dehydrogenase 1 family, member A1; Formin binding protein 4; Zinc finger protein 24 (KOX 17); Hypothetical protein L0054103; Selenium binding protein 1; Hematopoietically expressed homeobox; Major histocompatibility complex, class II, DM alpha; Eukaryotic translation initiation factor 2-alpha kinase 1; Ankyrin repeat domain 49; Hypothetical protein FLJ20701; Zinc finger protein 331; Membrane-spanning 4-domains, subfamily A, member 4; Tensin 1; and Family with sequence similarity 46, member A, respectively).

[0084] In another embodiment of the monitoring method, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 134-177, 110, 112, 118, 123

and 131 (or the biomarkers set forth by name in Table 4, namely Uncharacterized hypothalamus protein HT007; Dual specificity phosphatase 22; Proteasome (prosome, macropain) subunit, beta type, 7; Membrane-spanning 4-domains, subfamily A, member 4; DKFZP434C171 protein; Protein phosphatase 1, catalytic subunit, beta isoform; Splicing factor, arginine/serine-rich 5; Sorting nexin 11; Farnesyltransferase, CAAX box, alpha; Peroxisomal D3,D2-enoyl-CoA isomerase; Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide; UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransferase 1; Hypothetical protein FLJ11259; APEX nuclease (multifunctional DNA repair enzyme) 1; Geranylgeranyl diphosphate synthase 1; Down syndrome critical region gene 5; Calpain 7; Major histocompatibility complex, class II, DP alpha 1; Brix domain containing 5; Chromosome 21 open reading frame 59; Tumor necrosis factor (ligand) superfamily, member 10; Chromosome 10 open reading frame 86; CD1D antigen, d polypeptide; Ewing sarcoma breakpoint region 1; Ribonuclease P 40 kDa subunit; PHD finger protein 20; Thioredoxin interacting protein; Ubiquinol-cytochrome c reductase core protein II; Hypothetical protein FLJ22662; Preimplantation protein 3; DKFZP564G2022 protein; Dipeptidase 2; Hemoglobin, alpha 1, alpha 2; Frequently rearranged in advanced T-cell lymphomas; DEAD (Asp-Glu-Ala-Asp) box polypeptide 48; Tumor necrosis factor, alpha-induced protein 2; Nucleophosmin (nucleolar phosphoprotein B23, numatrin); Interleukin 13 receptor, alpha 1; Leukocyte specific transcript 1, LST1; CGI-121 protein; RAS p21 protein activator 4/hypothetical protein FLJ21767; Cathepsin S; CD63 antigen (melanoma 1 antigen); JTV1 gene; KIAA0174; Thrombospondin 1; Hypothetical protein L0054103; Interferon regulatory factor 1; and SEC11-like 1 (*S. cerevisiae*)).

[0085] More preferably, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 134-150, 112, 118 (or the biomarkers set forth by name in Table 4 as being upregulated, namely Uncharacterized hypothalamus protein HT007; Dual specificity phosphatase 22; Proteasome (prosome, macropain) subunit, beta type, 7; Membrane-spanning 4-domains, subfamily A, member 4; DKFZP434C171 protein; Protein phosphatase 1, catalytic subunit, beta isoform; Splicing factor, arginine/serine-rich 5; Sorting nexin 11; Farnesyltransferase, CAAX box, alpha; Peroxisomal D3,D2-enoyl-CoA isomerase; Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide; UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransferase 1; Hypothetical protein FLJ11259; APEX nuclease (multifunctional DNA repair enzyme) 1; Geranylgeranyl diphosphate synthase 1; Down syndrome critical region gene 5; Calpain 7; Major histocompatibility complex, class II, DP alpha 1; Brix domain containing 5; and Chromosome 21 open reading frame 59), wherein expression of the one or more biomarkers is increased in the subject.

[0086] Additionally or alternatively, more preferably the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 151-177, 110 and 123 (or the biomarkers set forth by name in Table 4 as being downregulated, namely Tumor necrosis factor (ligand) superfamily, member 10; Chromosome 10 open reading frame 86; CD1D antigen, d polypeptide; Ewing sarcoma breakpoint region 1; Ribonuclease P 40 kDa subunit; PHD finger protein 20; Thioredoxin interacting protein; Ubiquinol-cytochrome c

reductase core protein II; Hypothetical protein FLJ22662; Preimplantation protein 3; DKFZP564G2022 protein; Dipeptidase 2; Hemoglobin, alpha 1, alpha 2; Frequently rearranged in advanced T-cell lymphomas; DEAD (Asp-Glu-Ala-Asp) box polypeptide 48; Tumor necrosis factor, alpha-induced protein 2; Nucleophosmin (nucleolar phosphoprotein B23, numatrin); Interleukin 13 receptor, alpha 1; Leukocyte specific transcript 1, LST1; CGI-121 protein; RAS p21 protein activator 4/hypothetical protein FLJ21767; Cathepsin S; CD63 antigen (melanoma 1 antigen); JTV1 gene; KIAA0174; Thrombospondin 1; Hypothetical protein L0054103; Interferon regulatory factor 1; and SEC11-like 1 (*S. cerevisiae*), wherein expression of the one or more biomarkers is decreased in the subject.

[0087] In yet another embodiment of the monitoring method, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 178-292, 91 and 97 (or the biomarkers set forth by name in Table 5, namely HLA-B associated transcript-1 (D6S81E); Interleukin enhancer binding factor 2, 45 kD (ILF2); Isolate Liv chaperone protein HSP90 beta (HSP90BETA) mRNA; Lysyl-tRNA synthetase mRNA, complete cds; nuclear gene for mitochondrial product; alternatively spliced; Tryptophanyl-tRNA synthetase (WARS); Profilin 1 (PFN1), mRNA; Seryl-tRNA synthetase (SARS); Similar to KIAA1007 protein, clone MGC: 692, mRNA, complete cds; CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344); *Homo sapiens* KIAA0064 gene product (KIAA0064), mRNA; Chromosome segregation 1 (yeast homolog)-like (CSE1L), mRNA; Protein phosphatase 1, regulatory subunit 7 (PPP1R7), mRNA; DEADH (Asp-Glu-Ala-AspHis) box polypeptide 1 (DDX1), mRNA; Threonyl-tRNA synthetase (TARS), mRNA; Dead box protein 15 mRNA, complete cds; SRY (sex determining region Y)-box 4/DEF=Human DNA sequence from clone RP3-322L4 on chromosome 6; Galactosidase, beta 1 (GLB1), mRNA; ATP-binding cassette, sub-family E (OABP), member 1; NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (14 kD, B14) (NDUFA6), mRNA; Pericentriolar material 1 (PCM1), mRNA; Excision repair cross-complementing rodent repair deficiency, complementation group 3 (ERCC3), mRNA; KIAA0907 protein (KIAA0907), mRNA; v-crk avian sarcoma virus CT10 oncogene homolog; 6-phosphofructo-2-kinasefructose-2,6-biphosphatase 3 (PFKFB3), mRNA./PROD=6-phosphofructo-2-kinase-fructose-2,6-biphosphatase 3; KIAA0766 gene product (KIAA0766), mRNA; N-acetylgalactosaminidase, alpha- (NAGA), mRNA; Protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1), mRNA; Crystallin, zeta (quinone reductase) (CRYZ), mRNA; KIAA0429 gene product (KIAA0429), mRNA; SET domain, bifurcated 1 (SETDB1), mRNA; NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3 (12 kD, B12) (NDUFB3), mRNA; Diphtheria toxin receptor (DTR); Thrombomodulin (THBD), mRNA; Protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform (PPM1A), mRNA; CD37 antigen (CD37), mRNA; Hemoglobin, gamma G (HBG2), mRNA; Protein phosphatase 1D magnesium-dependent, delta isoform (PPM1D), mRNA; Hematopoietically expressed homeobox (HHEX), mRNA; Amphiregulin (schwannoma-derived growth factor) (AREG), mRNA; Early growth response 2 (Krox-20 (*Drosophila*) homolog) (EGR2), mRNA; 2,5-oligoadenylate synthetase 1 (40-46 kD) (OAS1), transcript variant E16, mRNA;

Early growth response 3 (EGR3), mRNA./PROD=early growth response 3; *Homo sapiens* MD-2 protein (MD-2), mRNA; *Homo sapiens* MAX dimerization protein (MAD), mRNA; DKEZP586A011 protein (DKEZP586A011), mRNA; 78 kDa gastrin-binding protein mRNA, complete cds; Transferrin receptor (p90, CD71), clone MGC:3151, mRNA, complete cds; *Homo sapiens* mRNA; cDNA DKFZp564N1272 (from clone DKFZp564N1272); complete cds; GABA-A receptor-associated protein like 1 (GABARAPL1) mRNA, complete cds; Translocation protein 1; *Homo sapiens* clone 016b03 My027 protein mRNA, complete cds; Protein kinase-related oncogene (PIM1) mRNA, complete cds; MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C); eIF-2-associated p67 homolog mRNA, complete cds; Human mRNA for hCREM (cyclic AMP-responsive element modulator) type 2 protein, complete cds; Apurinic endonuclease (APE) mRNA, complete cds./PROD=apurinic endonuclease; TATA box binding protein (TBP)-associated factor, RNA polymerase II, D, 100 kD; Human mRNA for ZFM1 protein alternatively spliced product, complete cds./PROD=ZFM1 protein, alternatively spliced product; Trachea cellular apoptosis susceptibility protein (CSE1) mRNA, complete cds; Similar to eukaryotic translation initiation factor 3, subunit 8 (110 kD), clone MGC:8693, mRNA, complete cds; GABA-A receptor-associated protein mRNA, complete cds./PROD=GABA-A receptor-associated protein; Human (clone 2-5) synuclein (NACP) mRNA, complete cds; Human putative ribosomal protein 51 mRNA; Aldehyde dehydrogenase 1, soluble (ALDH1), mRNA./PROD=aldehyde dehydrogenase 1, soluble; *Homo sapiens* mRNA for KIAA1057 protein, partial cds; RBP1-like protein; Ring finger protein 4; KIAA0197 protein; *Homo sapiens* mRNA; cDNA DKFZp586F1323 (from clone DKFZp586F1323); *Homo sapiens* mRNA; cDNA DKFZp5641052 (from clone DKFZp5641052); *Homo sapiens* mRNA for Hmob33 protein, 3 untranslated region; *Homo sapiens* mRNA; cDNA DKFZp586F1019 (from clone DKFZp586F1019); partial cds; Myosin, light polypeptide 4, alkali; atrial, embryonic; *H. sapiens* novel gene from PAC 117P20, chromosome 1; *Homo sapiens* clone 24582 mRNA sequence; Heterogeneous nuclear ribonucleoprotein H1 (H); Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide; Cyclin T2; cDNA: FLJ23227 fis, clone CAE00645, highly similar to AF052138; Hypothetical protein FLJ12619; C-terminal binding protein 1; SEC22, vesicle trafficking protein (*S. cerevisiae*)-like 1; Hemoglobin, alpha 1; *Homo sapiens* clone 24659 mRNA sequence/DEF=*Homo sapiens* clone 24659 mRNA sequence; Calcium channel, voltage-dependent, PQ type, alpha 1A subunit; *H. sapiens* SMAS mRNA; *H. sapiens* HEX gene encoding homeobox related protein; Mitogen-activated protein kinase kinase kinase 4; Serine palmitoyltransferase (LCB2) mRNA, partial cds; KIAA0971 protein/DEF=*Homo sapiens* cDNA FLJ11495 fis, clone HEMBA1001950, highly similar to *Homo sapiens* mRNA for KIAA0971 protein; ESTs, Hs.97109; ESTs, Weakly similar to ALU7_HUMAN ALU; DEAD-box protein abstrakt (ABS), mRNA; KIAA1513 protein (KIAA1513), mRNA; Cell division protein FtsJ (FJH1), mRNA; F-box only protein 3 (FBXO3), mRNA; Purinergic receptor (family A group 5) (P2Y5), mRNA; Integral inner nuclear membrane protein (MAN1), mRNA; Fanconi anemia, complementation group F (FANCF), mRNA; Hypothetical protein FLJ12820 (FLJ12820), mRNA; Hypothetical protein FLJ13119

(FLJ13119), mRNA; Hypothetical protein FLJ20189 (FLJ20189), mRNA; Hypothetical protein FLJ20701 (FLJ20701), mRNA; *Homo sapiens* chromosome 12 open reading frame 5 (C12ORF5), mRNA; Hypothetical protein FLJ22555 (FLJ22555), mRNA; Hypothetical protein FLJ11110 (FLJ11110), mRNA; CGI-12 protein (LOC51001), mRNA; Triggering receptor expressed on myeloid cells 1 (TREM1), mRNA; betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5; PNAS-25 mRNA, complete cds.; *Homo sapiens* mRNA for FLJ00043 protein, partial cds; *Homo sapiens* cDNA: FLJ21737 fis, clone COLF3396; *Homo sapiens* cDNA FLJ13399 fis, clone PLACE1001395/DEF=*Homo sapiens* cDNA FLJ13399 fis, clone PLACE1001395; Novel MAFF (v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein F) LIKE protein; Heparin-binding EGF-like growth factor mRNA, complete cds; *E. coli* 7,8-diamino-pelargonic acid (bioA), biotin synthetase (bioB), 7-keto-8-amino-pelargonic acid synthetase (bioF), bioC protein, and dethiobiotin synthetase (bioD), complete cds; *Escherichia coli*/REF=J04423/DEF=*E. coli* bioC protein corresponding to nucleotides 4609-4883 of J04423/LEN=777 (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)).

[0088] More preferably, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 178-185; 187-200, 202, 203, 205-207; 211, 213, 214, 216, 220, 221, 226, 228, 229, 231, 232, 234, 235, 238-247, 249, 250, 253, 262-265, 268-282 and 285-288 (or the biomarkers set forth by name in Table 5 as being upregulated, namely HLA-B associated transcript-1 (D6S81E); Interleukin enhancer binding factor 2, 45 kD (ILF2); Isolate Liv chaperone protein HSP90 beta (HSP90BETA) mRNA; Lysyl-tRNA synthetase mRNA, complete cds; nuclear gene for mitochondrial product; alternatively spliced; Tryptophanyl-tRNA synthetase (WARS); Profilin 1 (PFN1), mRNA; Seryl-tRNA synthetase (SARS); Similar to KIAA1007 protein, clone MGC: 692, mRNA, complete cds; *Homo sapiens* KIAA0064 gene product (KIAA0064), mRNA; Chromosome segregation 1 (yeast homolog)-like (CSE1L), mRNA; Protein phosphatase 1, regulatory subunit 7 (PPP1R7), mRNA; DEADH (Asp-Glu-Ala-AspHis) box polypeptide 1 (DDX1), mRNA; Threonyl-tRNA synthetase (TARS), mRNA; Dead box protein 15 mRNA, complete cds; SRY (sex determining region Y)-box 4/DEF=Human DNA sequence from clone RP3-322L4 on chromosome 6; Galactosidase, beta 1 (GLB1), mRNA; ATP-binding cassette, sub-family E (OABP), member 1; NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (14 kD, B14) (NDUFA6), mRNA; Pericentriolar material 1 (PCM1), mRNA; Excision repair cross-complementing rodent repair deficiency, complementation group 3 (ERCC3), mRNA; KIAA0907 protein (KIAA0907), mRNA; v-crk avian sarcoma virus CT10 oncogene homolog; KIAA0766 gene product (KIAA0766), mRNA; N-acetylglucosaminidase, alpha (NAGA), mRNA; Crystallin, zeta (quinone reductase) (CRYZ), mRNA; KIAA0429 gene product (KIAA0429), mRNA; SET domain, bifurcated 1 (SETDB1), mRNA; CD37 antigen (CD37), mRNA; Protein phosphatase 1D magnesium-dependent, delta isoform (PPM1D), mRNA; Hematopoietically expressed homeobox (HHEX), mRNA; 2,5-oligoadenylate synthetase 1 (40-46 kD) (OAS1), transcript variant E16, mRNA; DKFZP586A011 protein (DKFZP586A011), mRNA; 78 kDa gastrin-binding protein mRNA, complete cds; *Homo sapiens* clone 016b03 My027

protein mRNA, complete cds; MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C); eIF-2-associated p67 homolog mRNA, complete cds; Apurinic endonuclease (APE) mRNA, complete cds./PROD=apurinic endonuclease; TATA box binding protein (TBP)-associated factor, RNA polymerase II, D, 100 kD; Trachea cellular apoptosis susceptibility protein (CSE1) mRNA, complete cds; Similar to eukaryotic translation initiation factor 3, subunit 8 (110 kD), clone MGC:8693, mRNA, complete cds; Human putative ribosomal protein 51 mRNA; Aldehyde dehydrogenase 1, soluble (ALDH1), mRNA./PROD=aldehyde dehydrogenase 1, soluble; *Homo sapiens* mRNA for KIAA1057 protein, partial cds; RBP1-like protein; Ring finger protein 4; KIAA0197 protein; *Homo sapiens* mRNA; cDNA DKFZp586F1323 (from clone DKFZp586F1323); *Homo sapiens* mRNA; cDNA DKFZp5641052 (from clone DKFZp5641052); *Homo sapiens* mRNA for Hmob33 protein, 3 untranslated region; *Homo sapiens* mRNA; cDNA DKFZp586F1019 (from clone DKFZp586F1019); partial cds; *H. sapiens* novel gene from PAC 117P20, chromosome 1; *Homo sapiens* clone 24582 mRNA sequence; Cyclin T2; *H. sapiens* HEX gene encoding homeobox related protein; Mitogen-activated protein kinase kinase 4; Serine palmitoyltransferase (LCB2) mRNA, partial cds; KIAA0971 protein/DEF=*Homo sapiens* cDNA FLJ11495 fis, clone HEMBA1001950, highly similar to *Homo sapiens* mRNA for KIAA0971 protein; DEAD-box protein abstract (ABS), mRNA; KIAA1513 protein (KIAA1513), mRNA; Cell division protein FtsJ (FJH1), mRNA; F-box only protein 3 (FBXO3), mRNA; Purinergic receptor (family A group 5) (P2Y5), mRNA; Integral inner nuclear membrane protein (MAN1), mRNA; Fanconi anemia, complementation group F (FANCF), mRNA; Hypothetical protein FLJ12820 (FLJ12820), mRNA; Hypothetical protein FLJ13119 (FLJ13119), mRNA; Hypothetical protein FLJ20189 (FLJ20189), mRNA; Hypothetical protein FLJ20701 (FLJ20701), mRNA; *Homo sapiens* chromosome 12 open reading frame 5 (C12ORF5), mRNA; Hypothetical protein FLJ22555 (FLJ22555), mRNA; Hypothetical protein FLJ11110 (FLJ11110), mRNA; CGI-12 protein (LOC51001), mRNA; PNAS-25 mRNA, complete cds.; *Homo sapiens* mRNA for FLJ00043 protein, partial cds; *Homo sapiens* cDNA: FLJ21737 fis, clone COLF3396; *Homo sapiens* cDNA FLJ13399 fis, clone PLACE1001395/DEF=*Homo sapiens* cDNA FLJ13399 fis, clone PLACE1001395), wherein expression of the one or more biomarkers is increased in the subject.

[0089] Additionally or alternatively, more preferably the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 186, 201, 204, 208, 209, 91, 210, 212, 97, 215, 217-219, 222-225, 227, 230, 233, 236, 237, 248, 251, 252, 254-261, 266, 267, 283, 284 and 289-292 (or the biomarkers set forth by name in Table 5 as being down-regulated, namely CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344); 6-phosphofructo-2-kinasefructose-2,6-biphosphatase 3 (PFKFB3), mRNA./PROD=6-phosphofructo-2-kinase-fructose-2,6-biphosphatase 3; Protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1), mRNA; NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3 (12 kD, B12) (NDUFB3), mRNA; Diphtheria toxin receptor (DTR); Thrombomodulin (THBD), mRNA; Protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha iso-

form (PPM1A), mRNA; Hemoglobin, gamma G (HBG2), mRNA; Amphiregulin (schwannoma-derived growth factor) (AREG), mRNA; Early growth response 2 (Krox-20 (Drosophila) homolog) (EGR2), mRNA; Early growth response 3 (EGR3), mRNA./PROD=early growth response 3; *Homo sapiens* MD-2 protein (MD-2), mRNA; *Homo sapiens* MAX dimerization protein (MAD), mRNA; Transferrin receptor (p90, CD71), clone MGC:3151, mRNA, complete cds; *Homo sapiens* mRNA; cDNA DKFZp564N1272 (from clone DKFZp564N1272); complete cds; GABA-A receptor-associated protein like 1 (GABARAPL1) mRNA, complete cds; Translocation protein 1; Protein kinase-related oncogene (PIM1) mRNA, complete cds; Human mRNA for hCREM (cyclic AMP-responsive element modulator) type 2 protein, complete cds; Human mRNA for ZFM1 protein alternatively spliced product, complete cds./PROD=ZFM1 protein, alternatively spliced product; GABA-A receptor-associated protein mRNA, complete cds./PROD=GABA-A receptor-associated protein; Human (clone 2-5) synuclein (NACP) mRNA, complete cds; Myosin, light polypeptide 4, alkali; atrial, embryonic; Heterogeneous nuclear ribonucleoprotein H1 (H); Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide; cDNA: FLJ23227 fis, clone CAE00645, highly similar to AF052138; Hypothetical protein FLJ12619; C-terminal binding protein 1; SEC22, vesicle trafficking protein (*S. cerevisiae*)-like 1; Hemoglobin, alpha 1; *Homo sapiens* clone 24659 mRNA sequence/DEF=*Homo sapiens* clone 24659 mRNA sequence; Calcium channel, voltage-dependent, PQ type, alpha 1A subunit; *H. sapiens* SMA5 mRNA; ESTs, Hs.97109; ESTs, Weakly similar to ALU7_HUMAN ALU; Triggering receptor expressed on myeloid cells 1 (TREM1), mRNA; betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5; Novel MAFF (v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein F) LIKE protein; Heparin-binding EGF-like growth factor mRNA, complete cds; *E. coli* 7,8-diamino-pelargonic acid (bioA), biotin synthetase (bioB), 7-keto-8-amino-pelargonic acid synthetase (bioF), bioC protein, and dethiobiotin synthetase (bioD), complete cds; *Escherichia coli*/REF=J04423/DEF=*E. coli* bioC protein corresponding to nucleotides 4609-4883 of J04423/LEN=777 (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)), wherein expression of the one or more biomarkers is decreased in the subject.

[0090] In yet another embodiment of the monitoring method, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 87, 97, 101, 293, 92, 272, 93, 107, 108, 121 and 123 (or the biomarkers set forth by name in Table 6 as pre-treatment biomarkers, namely Solute carrier family 6; Amphiregulin; Keratin 1; Hemoglobin, alpha 1; MHC-II, DM beta; Purinergic receptor P2Y, G-protein coupled 5; Forkhead box O3A; Transferrin receptor (p90, CD71); Ring finger protein 10; Formin binding protein 4; and Hypothetical protein LOC54103), wherein the subject is monitored prior to treatment with a TNF α inhibitor.

[0091] In yet another embodiment of the monitoring method, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 290, 209, 98, 112, 116, 121, 130, 155, 92, 289, 216 and 131 (or the biomarkers set forth by name in Table 6 as post-treatment biomarkers, namely Diphtheria toxin receptor; Heparin-binding EGF-like growth factor; Lipoyltransferase 1; APEX nuclease (multi-

funct. DNA repair enzyme) 1; GABA(A) receptor-associated protein like 1/3; Formin binding protein 4; Zinc finger protein 331; Ribonuclease P 40 kDa subunit; MHC class II, DM beta; v-maf fibrosarc. oncogene homolog F (avian); 2',5'-oligoadenylate synthetase 1, 40/46 kDa; and Membrane-spanning 4-domains, subfam. A, memb. 4), wherein the subject is monitored after treatment with a TNF α inhibitor.

[0092] In yet another embodiment of the monitoring method, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 97, 102, 29, 294, 295, 91, 131, 290, 100, 134, 296, 297, 298, 299, 136, 174 and 300 (or the biomarkers set forth by name in Table 7, namely Amphiregulin; Carbonic anhydrase 1; Charcot-Leyden crystal protein; Clusterin C; Tumor necrosis factor alpha induced protein 6; Thrombomodulin; Membrane-spanning 4-domains, subfamily A, member 4; Diptheria toxin receptor; S100 calcium binding protein A1; Uncharacterized hypothalamus protein HT007; MHC-class-II; HLA-DR alpha; Hypothetical protein L0054103; Tumor necrosis factor alpha; Interleukin 1 beta; Proteasome subunit beta type 7 precursor; and Protein KIAA0174; Microsomal signal peptidase 18 kDa subunit).

[0093] A preferred autoimmune disorder in which to apply the methods of the invention for monitoring an autoimmune disorder is rheumatoid arthritis. However, the monitoring methods can be applied to essentially any autoimmune disorder in which TNF α inhibitor therapy is applied, including the autoimmune disorders listed in the previous section. Selection and Use of Treatment Regimens with TNF α Inhibitors

[0094] Given the observation that the expression pattern of particular biomarkers in an autoimmune disorder subject influences the responsiveness of the subject to a TNF α inhibitor, one can select an appropriate treatment regimen for the subject based on the expression of one or more biomarkers in the subject. Accordingly, in one embodiment, the above-described method for predicting the responsiveness to a TNF α inhibitor in a subject having an autoimmune disorder further comprises selecting a treatment regimen with the TNF α inhibitor based upon expression of the one or more biomarkers in the subject. In another aspect, the method still further comprises administering the TNF α inhibitor to the subject according to the treatment regimen such that the autoimmune disorder is inhibited in the subject.

[0095] In another embodiment, the invention provides a method for selecting a treatment regimen for therapy with a TNF α inhibitor in a subject having an autoimmune disorder, the method comprising:

[0096] assaying the subject for expression of one or more biomarkers predictive of responsiveness to a TNF α inhibitor for treatment of the autoimmune disorder; and

[0097] selecting a treatment regimen with a TNF α inhibitor based upon expression of the one or more biomarkers in the subject.

[0098] In yet another embodiment, the invention provides a method of treating a subject having an autoimmune disorder with a TNF α inhibitor, the method comprising:

[0099] assaying the subject for expression of one or more biomarkers predictive of responsiveness to a TNF α inhibitor for treatment of the autoimmune disorder;

[0100] selecting a treatment regimen with a TNF α inhibitor based upon expression of the one or more biomarkers in the subject; and

[0101] administering the TNF α inhibitor according to the treatment regimen such that the subject is treated for the autoimmune disorder.

[0102] The treatment regimen that is selected typically includes at least one of the following parameters and more typically includes many or all of the following parameters: the type of agent chosen for administration, the dosage, the formulation, the route of administration and/or the frequency of administration.

[0103] Particularly preferred TNF α inhibitors are biologic agents that have been approved by the FDA for use in humans in the treatment of rheumatoid arthritis, which agents include adalimumab (HUMIRATM), infliximab (REMICADETM) and etanercept (ENBRELTM), most preferably adalimumab (HUMIRATM).

[0104] In one embodiment, the TNF α inhibitor is an anti-tumor necrosis factor-alpha (TNF α) antibody, or antigen-binding portion thereof. For example, the anti-TNF α antibody, or antigen-binding portion thereof, can be a humanized antibody, a chimeric antibody or a multivalent antibody.

[0105] In another embodiment, the anti-TNF α antibody, or antigen-binding portion thereof, is a human antibody, preferably a human antibody, or antigen-binding portion thereof, that binds to human TNF α with high affinity and a low off rate, and has a high neutralizing capacity. Preferably, the human antibodies are recombinant, neutralizing human anti-hTNF α antibodies. The most preferred recombinant, neutralizing antibody used in the method of the invention is referred to herein as adalimumab, also referred to as HUMIRA[®] or D2E7 (the amino acid sequence of the adalimumab VL region is shown in SEQ ID NO: 303; the amino acid sequence of the adalimumab VH region is shown in SEQ ID NO: 304). The properties of D2E7 (adalimumab; Humira[®]) have been described in Salfeld et al., U.S. Pat. Nos. 6,090,382, 6,258, 562, and 6,509,015, which are each incorporated by reference herein.

[0106] Other examples of TNF α antibodies include chimeric and humanized murine anti-hTNF α antibodies which have undergone clinical testing for treatment of rheumatoid arthritis (see e.g., Elliott et al. (1994) *Lancet* 344:1125-1127; Elliot et al. (1994) *Lancet* 344:1105-1110; Rankin et al. (1995) *Br. J. Rheumatol.* 34:334-342). In another embodiment, the TNF α antibody used in the invention is infliximab (Remicade[®], Johnson and Johnson; described in U.S. Pat. No. 5,656,272, incorporated by reference herein), CDP571 (a humanized monoclonal anti-TNF-alpha IgG4 antibody), CDP 870 (a humanized monoclonal anti-TNF-alpha antibody fragment), an anti-TNF dAb (Peptech), and CNTO 148 (golimumab; Medarex and Centocor, see also WO 02/12502).

[0107] In one embodiment, the TNF α inhibitors used in the methods of the invention include adalimumab antibodies and antibody portions, adalimumab-related antibodies and antibody portions, adalimumab-related DVD-Ig or dual specific antibodies, and other human antibodies and antibody portions with equivalent properties to adalimumab, such as high affinity binding to hTNF α with low dissociation kinetics and high neutralizing capacity. In one embodiment, a treatment regimen of the invention provides treatment with an isolated human antibody, or an antigen-binding portion thereof, that dissociates from human TNF α with a K_d of 1×10^{-8} M or less and a K_{off} rate constant of 1×10^{-3} s⁻¹ or less, both determined by surface plasmon resonance, and neutralizes human TNF α cytotoxicity in a standard in vitro L929 assay with an IC₅₀ of 1×10^{-7} M or less. More preferably, the isolated human anti-

body, or antigen-binding portion thereof, dissociates from human TNF α with a K_{off} of $5 \times 10^{-4} \text{ s}^{-1}$ or less, or even more preferably, with a K_{off} of $1 \times 10^{-4} \text{ s}^{-1}$ or less. More preferably, the isolated human antibody, or antigen-binding portion thereof, neutralizes human TNF α cytotoxicity in a standard in vitro L929 assay with an IC_{50} of $1 \times 10^{-8} \text{ M}$ or less, even more preferably with an IC_{50} of $1 \times 10^{-9} \text{ M}$ or less and still more preferably with an IC_{50} of $1 \times 10^{-10} \text{ M}$ or less. In a preferred embodiment, the antibody is an isolated human recombinant antibody, or an antigen-binding portion thereof.

[0108] It is well known in the art that antibody heavy and light chain CDR3 domains play an important role in the binding specificity/affinity of an antibody for an antigen. Accordingly, in another aspect, the TNF α inhibitor used in the treatment method of the invention is a human anti-TNF α antibody that has slow dissociation kinetics for association with hTNF α and that has light and heavy chain CDR3 domains that structurally are identical to or related to those of adalimumab. Position 9 of the adalimumab VL CDR3 can be occupied by Ala or Thr without substantially affecting the K_{off} . Accordingly, a consensus motif for the adalimumab VL CDR3 comprises the amino acid sequence: Q-R-Y-N-R-A-P-Y-(T/A) (SEQ ID NO: 305). Additionally, position 12 of the adalimumab VH CDR3 can be occupied by Tyr or Asn, without substantially affecting the K_{off} . Accordingly, a consensus motif for the adalimumab VH CDR3 comprises the amino acid sequence: V-S-Y-L-S-T-A-S-S-L-D-(Y/N) (SEQ ID NO: 306). Moreover, as demonstrated in Example 2 of U.S. Pat. No. 6,090,382, the CDR3 domain of the adalimumab heavy and light chains is amenable to substitution with a single alanine residue (at position 1, 4, 5, 7 or 8 within the VL CDR3 or at position 2, 3, 4, 5, 6, 8, 9, 10 or 11 within the VH CDR3) without substantially affecting the K_{off} . Still further, the skilled artisan will appreciate that, given the amenability of the adalimumab VL and VH CDR3 domains to substitutions by alanine, substitution of other amino acids within the CDR3 domains may be possible while still retaining the low off rate constant of the antibody, in particular substitutions with conservative amino acids. Preferably, no more than one to five conservative amino acid substitutions are made within the adalimumab VL and/or VH CDR3 domains. More preferably, no more than one to three conservative amino acid substitutions are made within the adalimumab VL and/or VH CDR3 domains. Additionally, conservative amino acid substitutions should not be made at amino acid positions critical for binding to hTNF α . Positions 2 and 5 of the adalimumab VL CDR3 and positions 1 and 7 of the adalimumab VH CDR3 appear to be critical for interaction with hTNF α and thus, conservative amino acid substitutions preferably are not made at these positions (although an alanine substitution at position 5 of the adalimumab VL CDR3 is acceptable, as described above) (see U.S. Pat. No. 6,090,382).

[0109] Accordingly, in another embodiment, the antibody or antigen-binding portion thereof preferably contains the following characteristics:

[0110] a) dissociates from human TNF α with a K_{off} rate constant of $1 \times 10^{-3} \text{ s}^{-1}$ or less, as determined by surface plasmon resonance;

[0111] b) has a light chain CDR3 domain comprising the amino acid sequence of SEQ ID NO: 305, or modified from SEQ ID NO: 305 by a single alanine substitution at position 1, 4, 5, 7 or 8 or by one to five conservative amino acid substitutions at positions 1, 3, 4, 6, 7, 8 and/or 9;

[0112] c) has a heavy chain CDR3 domain comprising the amino acid sequence of SEQ ID NO: 306, or modified from SEQ ID NO: 306 by a single alanine substitution at position 2, 3, 4, 5, 6, 8, 9, 10 or 11 or by one to five conservative amino acid substitutions at positions 2, 3, 4, 5, 6, 8, 9, 10, 11 and/or 12.

[0113] More preferably, the antibody, or antigen-binding portion thereof, dissociates from human TNF α with a K_{off} of $5 \times 10^{-4} \text{ s}^{-1}$ or less. Even more preferably, the antibody, or antigen-binding portion thereof, dissociates from human TNF α with a K_{off} of $1 \times 10^{-4} \text{ s}^{-1}$ or less.

[0114] In yet another embodiment, the antibody or antigen-binding portion thereof preferably contains a light chain variable region (LCVR) having a CDR3 domain comprising the amino acid sequence of SEQ ID NO: 305, or modified from SEQ ID NO: 305 by a single alanine substitution at position 1, 4, 5, 7 or 8, and with a heavy chain variable region (HCVR) having a CDR3 domain comprising the amino acid sequence of SEQ ID NO: 306, or modified from SEQ ID NO: 306 by a single alanine substitution at position 2, 3, 4, 5, 6, 8, 9, 10 or 11. Preferably, the LCVR further has a CDR2 domain comprising the amino acid sequence of SEQ ID NO: 307 (i.e., the adalimumab VL CDR2) and the HCVR further has a CDR2 domain comprising the amino acid sequence of SEQ ID NO: 308 (i.e., the adalimumab VH CDR2). Even more preferably, the LCVR further has CDR1 domain comprising the amino acid sequence of SEQ ID NO: 309 (i.e., the adalimumab VL CDR1) and the HCVR has a CDR1 domain comprising the amino acid sequence of SEQ ID NO: 310 (i.e., the adalimumab VH CDR1). The framework regions for VL preferably are from the V κ I human germline family, more preferably from the A20 human germline V κ gene and most preferably from the adalimumab VL framework sequences shown in FIGS. 1A and 1B of U.S. Pat. No. 6,090,382. The framework regions for VH preferably are from the V μ 3 human germline family, more preferably from the DP-31 human germline VH gene and most preferably from the adalimumab VH framework sequences shown in FIGS. 2A and 2B of U.S. Pat. No. 6,090,382.

[0115] Accordingly, in another embodiment, the antibody or antigen-binding portion thereof preferably contains a light chain variable region (LCVR) comprising the amino acid sequence of SEQ ID NO: 303 (i.e., the adalimumab VL) and a heavy chain variable region (HCVR) comprising the amino acid sequence of SEQ ID NO: 304 (i.e., the adalimumab VH). In certain embodiments, the antibody comprises a heavy chain constant region, such as an IgG1, IgG2, IgG3, IgG4, IgA, IgE, IgM or IgD constant region. Preferably, the heavy chain constant region is an IgG1 heavy chain constant region or an IgG4 heavy chain constant region. Furthermore, the antibody can comprise a light chain constant region, either a kappa light chain constant region or a lambda light chain constant region. Preferably, the antibody comprises a kappa light chain constant region. Alternatively, the antibody portion can be, for example, a Fab fragment or a single chain Fv fragment.

[0116] In other embodiments, the TNF α inhibitor of the invention is etanercept (described in WO 91/03553 and WO 09/406,476), infliximab (described in U.S. Pat. No. 5,656,272), CDP571 (a humanized monoclonal anti-TNF-alpha IgG4 antibody), CDP 870 (a humanized monoclonal anti-TNF-alpha antibody fragment), D2E7 (a human anti-TNF mAb), soluble TNF receptor Type I, or a pegylated soluble TNF receptor Type I (PEGs TNF-R1).

[0117] The TNF α antibody of the invention can be modified. In some embodiments, the TNF α antibody or antigen binding fragments thereof, is chemically modified to provide a desired effect. For example, pegylation of antibodies and antibody fragments of the invention may be carried out by any of the pegylation reactions known in the art, as described, for example, in the following references: *Focus on Growth Factors* 3:4-10 (1992); EP 0 154 316; and EP 0 401 384 (each of which is incorporated by reference herein in its entirety). Preferably, the pegylation is carried out via an acylation reaction or an alkylation reaction with a reactive polyethylene glycol molecule (or an analogous reactive water-soluble polymer). A preferred water-soluble polymer for pegylation of the antibodies and antibody fragments of the invention is polyethylene glycol (PEG). As used herein, "polyethylene glycol" is meant to encompass any of the forms of PEG that have been used to derivatize other proteins, such as mono (C1-C10) alkoxy- or aryloxy-polyethylene glycol.

[0118] Methods for preparing pegylated antibodies and antibody fragments of the invention will generally comprise the steps of (a) reacting the antibody or antibody fragment with polyethylene glycol, such as a reactive ester or aldehyde derivative of PEG, under conditions whereby the antibody or antibody fragment becomes attached to one or more PEG groups, and (b) obtaining the reaction products. It will be apparent to one of ordinary skill in the art to select the optimal reaction conditions or the acylation reactions based on known parameters and the desired result.

[0119] In yet another embodiment of the invention, TNF α antibodies or fragments thereof can be altered wherein the constant region of the antibody is modified to reduce at least one constant region-mediated biological effector function relative to an unmodified antibody. To modify an antibody of the invention such that it exhibits reduced binding to the Fc receptor, the immunoglobulin constant region segment of the antibody can be mutated at particular regions necessary for Fc receptor (FcR) interactions (see e.g., Canfield, S. M. and S. L. Morrison (1991) *J. Exp. Med.* 173:1483-1491; and Lund, J. et al. (1991) *J. Immunol.* 147:2657-2662). Reduction in FcR binding ability of the antibody may also reduce other effector functions which rely on FcR interactions, such as opsonization and phagocytosis and antigen-dependent cellular cytotoxicity.

[0120] An antibody or antibody portion of the invention can be derivatized or linked to another functional molecule (e.g., another peptide or protein). Accordingly, the antibodies and antibody portions of the invention are intended to include derivatized and otherwise modified forms of the anti-TNF α antibodies described herein, including immunoadhesion molecules. For example, an antibody or antibody portion of the invention can be functionally linked (by chemical coupling, genetic fusion, noncovalent association or otherwise) to one or more other molecular entities, such as another antibody (e.g., a bispecific antibody or a diabody), a detectable agent, a cytotoxic agent, a pharmaceutical agent, and/or a protein or peptide that can mediate association of the antibody or antibody portion with another molecule (such as a streptavidin core region or a polyhistidine tag).

[0121] One type of derivatized antibody is produced by crosslinking two or more antibodies (of the same type or of different types, e.g., to create bispecific antibodies). Suitable crosslinkers include those that are heterobifunctional, having two distinctly reactive groups separated by an appropriate spacer (e.g., m-maleimidobenzoyl-N-hydroxysuccinimide

ester) or homobifunctional (e.g., disuccinimidyl suberate). Such linkers are available from Pierce Chemical Company, Rockford, Ill.

[0122] Useful detectable agents with which an antibody or antibody portion of the invention may be derivatized include fluorescent compounds. Exemplary fluorescent detectable agents include fluorescein, fluorescein isothiocyanate, rhodamine, 5-dimethylamine-1-naphthalenesulfonyl chloride, phycoerythrin and the like. An antibody may also be derivatized with detectable enzymes, such as alkaline phosphatase, horseradish peroxidase, glucose oxidase and the like. When an antibody is derivatized with a detectable enzyme, it is detected by adding additional reagents that the enzyme uses to produce a detectable reaction product. For example, when the detectable agent horseradish peroxidase is present, the addition of hydrogen peroxide and diaminobenzidine leads to a colored reaction product, which is detectable. An antibody may also be derivatized with biotin, and detected through indirect measurement of avidin or streptavidin binding.

[0123] Selection of the particular parameters of the treatment regimen can be based on known treatment parameters for the TNF α inhibitor previously established in the art. For example, a non-limiting example of a treatment regimen for adalimumab (HUMIRATM) is 40 mg every other week by subcutaneous injection. A non-limiting example of a treatment regimen for etanercept (ENBRELTM) is 50 mg/week by subcutaneous injection. A non-limiting example of a treatment regimen for infliximab (REMICADETM) is 3 mg/kg by intravenous infusion at weeks 0, 2 and 6, then every 8 weeks. A treatment regimen can include administration of the TNF α inhibitor alone or can include combination of the TNF α inhibitor with other therapeutic agents, such as methotrexate (e.g., 10-20 mg/week) or prednisolone (e.g., 10 mg/week). Other suitable treatment regimens for the TNF α inhibitors discussed herein will be readily apparent to the ordinarily skilled artisan based on prior studies of preferred administration parameters for the TNF α inhibitor.

[0124] For administration to a subject, a TNF α inhibitor typically is formulated into a pharmaceutical composition containing the TNF α inhibitor and a pharmaceutically acceptable carrier. Therapeutic compositions typically must be sterile and stable under the conditions of manufacture and storage. Pharmaceutical compositions also can be administered in combination therapy, i.e., combined with other agents, such as other TNF α inhibitors and/or other therapeutic agents, such as traditional therapeutic agents for the treatment of autoimmune disorders, such as rheumatoid arthritis.

[0125] As used herein, "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like that are physiologically compatible. Preferably, the carrier is suitable for intravenous, intramuscular, subcutaneous, parenteral, spinal or epidermal administration (e.g., by injection or infusion). Depending on the route of administration, the active compound may be coated in a material to protect the compound from the action of acids and other natural conditions that may inactivate the compound.

[0126] The pharmaceutical compositions may include one or more pharmaceutically acceptable salts. A "pharmaceutically acceptable salt" refers to a salt that retains the desired biological activity of the parent compound and does not impart any undesired toxicological effects (see e.g., Berge, S. M., et al. (1977) *J. Pharm. Sci.* 66:1-19). Examples of such

salts include acid addition salts and base addition salts. Acid addition salts include those derived from nontoxic inorganic acids, such as hydrochloric, nitric, phosphoric, sulfuric, hydrobromic, hydroiodic, phosphorous and the like, as well as from nontoxic organic acids such as aliphatic mono- and dicarboxylic acids, phenyl-substituted alkanolic acids, hydroxy alkanolic acids, aromatic acids, aliphatic and aromatic sulfonic acids and the like. Base addition salts include those derived from alkaline earth metals, such as sodium, potassium, magnesium, calcium and the like, as well as from nontoxic organic amines, such as N,N'-dibenzylethylenediamine, N-methylglucamine, chlorprocaine, choline, diethanolamine, ethylenediamine, procaine and the like.

[0127] A pharmaceutical composition also may include a pharmaceutically acceptable anti-oxidant. Examples of pharmaceutically acceptable antioxidants include: (1) water soluble antioxidants, such as ascorbic acid, cysteine hydrochloride, sodium bisulfate, sodium metabisulfite, sodium sulfite and the like; (2) oil-soluble antioxidants, such as ascorbyl palmitate, butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), lecithin, propyl gallate, alpha-tocopherol, and the like; and (3) metal chelating agents, such as citric acid, ethylenediamine tetraacetic acid (EDTA), sorbitol, tartaric acid, phosphoric acid, and the like.

[0128] Examples of suitable aqueous and nonaqueous carriers that may be employed in the pharmaceutical compositions include water, ethanol, polyols (such as glycerol, propylene glycol, polyethylene glycol, and the like), and suitable mixtures thereof, vegetable oils, such as olive oil, and injectable organic esters, such as ethyl oleate. Proper fluidity can be maintained, for example, by the use of coating materials, such as lecithin, by the maintenance of the required particle size in the case of dispersions, and by the use of surfactants.

[0129] These compositions may also contain adjuvants such as preservatives, wetting agents, emulsifying agents and dispersing agents. Prevention of presence of microorganisms may be ensured both by sterilization procedures and by the inclusion of various antibacterial and antifungal agents, for example, paraben, chlorobutanol, phenol sorbic acid, and the like. It may also be desirable to include isotonic agents, such as sugars, sodium chloride, and the like into the compositions. In addition, prolonged absorption of the injectable pharmaceutical form may be brought about by the inclusion of agents which delay absorption such as aluminum monostearate and gelatin.

[0130] Pharmaceutically acceptable carriers include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. The use of such media and agents for pharmaceutically active substances is known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the pharmaceutical compositions of the invention is contemplated. Supplementary active compounds can also be incorporated into the compositions.

[0131] A TNF α inhibitor of the present invention can be administered via one or more routes of administration using one or more of a variety of methods known in the art. As will be appreciated by the skilled artisan, the route and/or mode of administration will vary depending upon the desired results. A preferred route of administration, particularly for antibody agents, is by intravenous injection or infusion. Other preferred routes of administration include intramuscular, intradermal, intraperitoneal, subcutaneous, spinal or other

parenteral routes of administration, for example by injection or infusion. The phrase "parenteral administration" as used herein means modes of administration other than enteral and topical administration, usually by injection, and includes, without limitation, intravenous, intramuscular, intraarterial, intrathecal, intracapsular, intraorbital, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous, subcuticular, intraarticular, subcapsular, subarachnoid, intraspinal, epidural and intrasternal injection and infusion. Alternatively, a TNF α inhibitor of the invention can be administered via a non-parenteral route, such as a topical, epidermal or mucosal route of administration, for example, intranasally, orally, vaginally, rectally, sublingually or topically.

[0132] In a preferred embodiment, the subject to be treated with the TNF α inhibitor is a human subject.

[0133] A preferred autoimmune disorder in which to apply the methods of the invention for selecting and using a treatment regimen is rheumatoid arthritis. However, these methods can be applied to essentially any autoimmune disorder in which TNF α inhibitor therapy is applied, including the autoimmune disorders listed in the previous sections

Kits of the Invention

[0134] In another aspect, the invention pertains to kits for carrying out the methods of the invention. For example, in one embodiment, the invention provides a kit for predicting responsiveness to a TNF α inhibitor in a subject having an autoimmune disorder. In one embodiment, the kit comprises:

[0135] a) means for isolating monocytes;

[0136] b) means for measuring expression in the subject of one or more biomarkers predictive of responsiveness to a TNF α inhibitor in an autoimmune disorder;

[0137] c) means for measuring expression of at least one housekeeping gene; and

[0138] d) instructions for use of the kit to predicting responsiveness to a TNF α inhibitor in a subject having an autoimmune disorder, wherein the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-82 (or the biomarkers set forth by name in Table 9, as described above)

[0139] In one embodiment of the kit, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 6, 7, 10, 15-17, 19, 22, 24, 27, 31, 34-39, 43-47, 49, 51, 54, 55, 57, 59, 61, 62, 64, 70, 75, 79 and 82 (or the biomarkers set forth by name in Table 9 as being increased in $\geq 80\%$ of responders vs. non-responders, as described above), more preferably the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 31, 37, 44, 47, 62 and 70 (or the biomarkers set forth by name in Table 9 as being increased in $\geq 90\%$ of responders vs. non-responders, as described above), and even more preferably at least one of the biomarkers is encoded by a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 44 (or the CD11c biomarkers set forth by name in Table 9 as being increased in 100% of responders vs. non-responders). In each of these embodiments, preferably the instructions for use of the kit instruct that increased expression of the one or more biomarkers is predictive of responsiveness of the subject to a TNF α inhibitor.

[0140] In another embodiment of the kit, the one or more biomarkers is encoded by a nucleic acid molecule comprising

a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-5, 8, 9, 11-14, 18, 20, 21, 23, 25, 26, 28-30, 32, 33, 40-42, 48, 50, 52, 53, 56, 58, 60, 63, 65-69, 71-74, 76-78, 80 and 81 (or the biomarkers set forth by name in Table 9 as being decreased in $\geq 80\%$ of responders vs. non-responders, as described above), more preferably the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 11, 29, 65, 73 and 74 (or the biomarkers set forth by name in Table 9 as being decreased in $\geq 90\%$ of responders vs. non-responders, as described above), and even more preferably the one or more biomarkers is encoded by a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 11 or SEQ ID NO: 74 (or the biomarkers set forth by name in Table 9 as being decreased in 100% of responders vs. non-responders, as described above). In each of these embodiments, preferably the instructions for use of the kit instruct that decreased expression of the one or more biomarkers is predictive of responsiveness of the subject to a TNF α inhibitor.

[0141] In another embodiment of the kit, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 83-133 (or the biomarkers set forth by name in Table 3, as described above).

[0142] In yet another embodiment of the kit, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 134-177, 110, 112, 118, 123 and 131 (or the biomarkers set forth by name in Table 4, as described above), more preferably SEQ ID NO: 134-150, 112, 118 (or the biomarkers set forth by name in Table 4 as being upregulated, as described above), wherein the instructions instruct that expression of the one or more biomarkers is increased in the subject, and/or more preferably SEQ ID NO: 151-177, 110 and 123 (or the biomarkers set forth by name in Table 4 as being downregulated, as described above), wherein the instructions instruct that expression of the one or more biomarkers is decreased in the subject.

[0143] In yet another embodiment of the kit, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 178-292, 91 and 97 (or the biomarkers set forth by name in Table 5, as described above), more preferably SEQ ID NO: 178-185; 187-200, 202, 203, 205-207; 211, 213, 214, 216, 220, 221, 226, 228, 229, 231, 232, 234, 235, 238-247, 249, 250, 253, 262-265, 268-282 and 285-288 (or the biomarkers set forth by name in Table 5 as being upregulated, as described above), wherein the instructions instruct that expression of the one or more biomarkers is increased in the subject, and/or more preferably SEQ ID NO: 186, 201, 204, 208, 209, 91, 210, 212, 97, 215, 217-219, 222-225, 227, 230, 233, 236, 237, 248, 251, 252, 254-261, 266, 267, 283, 284 and 289-292 (or the biomarkers set forth by name in Table 5 as being downregulated, as described above), wherein the instructions instruct that expression of the one or more biomarkers is decreased in the subject.

[0144] In yet another embodiment of the kit, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 87, 97, 101, 293, 92, 272, 93, 107, 108, 121 and 123 (or the biomarkers set forth by name in Table 6 as pre-treatment biomarkers, as described above), wherein the instructions instruct that the subject is monitored prior to

treatment with a TNF α inhibitor. In yet another embodiment of the kit, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 290, 209, 98, 112, 116, 121, 130, 155, 92, 289, 216 and 131 (or the biomarkers set forth by name in Table 6 as post-treatment biomarkers, as described above), wherein the instructions instruct that the subject is monitored after treatment with a TNF α inhibitor.

[0145] In yet another embodiment of the kit, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 97, 102, 29, 294, 295, 91, 131, 290, 100, 134, 296, 297, 298, 299, 136, 174 and 300 (or the biomarkers set forth by name in Table 7, as described above).

[0146] In a preferred embodiment, the means for measuring expression in the subject of the one or more biomarkers predictive of responsiveness to a TNF α inhibitor in an autoimmune disorder comprises a nucleic acid preparation sufficient to detect expression of mRNA encoding the one or more biomarkers in a sample from the subject, such as a peripheral blood mononuclear cell sample from which mRNA is obtained by standard methods. This nucleic acid preparation includes at least one, and may include more than one, nucleic acid probe or primer, the sequence(s) of which is designed such that the nucleic acid preparation can detect the expression of mRNA encoding the biomarker(s) of interest in the sample from the subject. A preferred nucleic acid preparation includes two or more PCR primers that allow for PCR amplification of a segment of the mRNA encoding the biomarker(s) of interest. In a particularly preferred embodiment, the kit comprises a nucleic acid preparation sufficient to detect expression of CD11c mRNA in a sample from the subject.

[0147] Alternatively, the means for detecting expression in the subject of one or more biomarkers predictive of responsiveness to a TNF α inhibitor in an autoimmune disorder can comprise a reagent that detects the gene product of the mRNA encoding the biomarker(s) of interest sufficient to distinguish it from other gene products in a sample from the subject. A non-limiting example of such a reagent is a monoclonal antibody preparation (comprising one or more monoclonal antibodies) sufficient to detect protein expression of the biomarker(s) of interest in a sample from the subject, such as a peripheral blood mononuclear cell sample. In a particularly preferred embodiment, the kit comprises a monoclonal antibody preparation sufficient to detect expression of CD11c protein in a sample from the subject.

[0148] The means for measuring expression of the one or more biomarkers can also include, for example, buffers or other reagents for use in an assay for evaluating biomarker expression (e.g., at either the mRNA or protein level). The instructions can be, for example, printed instructions for performing the assay for evaluating the expression of the one or more biomarkers.

[0149] In a preferred embodiment, the means for measuring expression of at least one housekeeping gene comprises a nucleic acid preparation sufficient to detect expression of mRNA of the housekeeping gene (e.g., GAPDH) in a sample from the subject, such as a peripheral blood mononuclear cell sample from which mRNA is obtained by standard methods. This nucleic acid preparation includes at least one, and may include more than one, nucleic acid probe or primer, the sequence(s) of which is designed such that the nucleic acid preparation can detect the expression of mRNA of the house-

keeping gene(s) in the sample from the subject. A preferred nucleic acid preparation includes two or more PCR primers that allow for PCR amplification of a segment of the mRNA of the housekeeping gene(s). Alternatively, the means for detecting expression in the subject of at least one housekeeping gene can comprise a reagent that detects the gene product of housekeeping gene sufficient to distinguish it from other gene products in a sample from the subject. A non-limiting example of such a reagent is a monoclonal antibody preparation (comprising one or more monoclonal antibodies) sufficient to detect protein expression of housekeeping gene product in a sample from the subject, such as a peripheral blood mononuclear cell sample.

[0150] The means for isolating monocytes can comprise one or more reagents that can be used to separate monocytes from other cell types in a sample of peripheral blood mononuclear cells, for example by positive selection of the monocytes or by negative selection in which all other cell types other than monocytes are removed. In one embodiment, a reagent that binds CD14 on monocytes (e.g., an anti-CD14 antibody) is included in the kit as means to isolate monocytes via positive selection. Alternatively, in another embodiment, reagents such as those commercially available in the Monocyte Isolation Kit II (Miltenyi Biotec, Auburn, Calif.) can be used for negative selection, in which non-monocytes (T cells, B cells, NK cells, dendritic cells, basophils) are indirectly magnetically labeled using a cocktail of biotin-conjugated antibodies against CD3, CD7, CD16, CD19, CD56, CD123 and CD235a (Glycophorin A), as well as anti-biotin MicroBeads, and then highly pure unlabeled monocytes are obtained by depletion of the magnetically labeled cells.

[0151] In another embodiment, the kit can further comprise a TNF α inhibitor for treating an autoimmune disorder in the subject. Preferred TNF α inhibitors for use in the kit include the TNF α inhibitors described in detail above with respect to treatment regimens, in particular anti-TNF α antibodies such as adalimumab, infliximab and/or golimumab, and/or Ig fusion proteins such as etanercept.

[0152] Preferably, the kit is designed for use with a human subject.

Databases and Computer Programs

[0153] In another aspect, the invention pertains to methods of building a database for use in selecting an autoimmune disorder subject for treatment with a TNF α inhibitor, or for use in selecting or monitoring a treatment regimen in an autoimmune disorder subject. The method can comprise receiving, in a computer system, biomarker expression patterns from a plurality of subjects having an autoimmune disorder; and storing the biomarker expression pattern from each subject such that the biomarker expression pattern is associated with an identifier of the subject, wherein the biomarker expression pattern reports expression in the subject of one or more biomarkers encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-82 (or the biomarkers set forth by name in Table 9, as described above). The identifier of the subject can be, for example, the name of the subject or a numerical or symbolic identifier coded to the identity of the subject. The method can further comprise receiving, in the computer system, one or more treatment regimens for treatment of an autoimmune disorder in a subject such that the treatment regimen is associated with the biomarker expression pattern of the subject and the identifier of the subject. A

user can enter the subject's biomarker expression pattern, and optionally the subject's treatment regimen(s), into the computer system. Alternatively, the subject's biomarker expression pattern can be received directly from equipment used in determining the expression of one or more biomarkers in a sample from the subject.

[0154] In another aspect, the invention provides a computer program product useful for building a database for use in selecting or monitoring an autoimmune disorder subject for treatment with a TNF α inhibitor. The computer program can contain executable instructions that when executed cause a processor to perform operations comprising: receiving, in a computer system, a biomarker expression pattern of a subject at one or more biomarkers predictive of responsiveness to a TNF α inhibitor in an autoimmune disorder; and storing the biomarker expression pattern such that the biomarker expression pattern is associated with an identifier of the subject, wherein the biomarker expression pattern reports expression in the subject of one or more biomarkers encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-82 (or the biomarkers set forth by name in Table 9, as described above). Optionally, the computer program can further cause the processor to perform an operation comprising: receiving, in the computer system, a treatment regimen for treatment of an autoimmune disorder in the subject such that the treatment regimen is associated with the biomarker expression pattern of the subject and the identifier of the subject.

[0155] In another aspect, the invention provides a method of selecting an autoimmune disorder subject for a treatment with a TNF α inhibitor. The method can comprise: (i) identifying, in a database comprising a plurality of autoimmune disorder subjects, a subject whose database entry is associated with a biomarker expression pattern that is predictive of responsiveness to treatment with a TNF α inhibitor, and (ii) selecting the subject for treatment with a TNF α inhibitor, wherein the biomarker expression pattern reports expression in the subject of one or more biomarkers encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-82 (or the biomarkers set forth by name in Table 9, as described above). The method can further comprise selecting a treatment regimen by identifying, in the database, a treatment regimen that has been associated with the biomarker expression pattern of the subject and with an identifier of the subject.

[0156] In yet another aspect, the invention provides a computer program product useful for identifying and/or selecting a subject for treatment with a TNF α inhibitor. The computer program can contain executable instructions that when executed cause a processor to perform operations comprising: (i) identifying, in a database including a plurality of autoimmune disorder subjects associated with biomarker expression patterns, a subject that is associated with a biomarker expression pattern that is predictive of responsiveness to treatment with a TNF α inhibitor; and (ii) outputting the identified subject as a subject to be treated with a TNF α inhibitor; wherein the biomarker expression pattern reports expression in the subject of one or more biomarkers encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-82 (or the biomarkers set forth by name in Table 9, as described above). The computer program can further cause the processor to perform

an operation comprising outputting a treatment regimen that is associated with the subject to be treated with the TNF α inhibitor.

[0157] In one embodiment of the above-described methods and computer program, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 6, 7, 10, 15-17, 19, 22, 24, 27, 31, 34-39, 43-47, 49, 51, 54, 55, 57, 59, 61, 62, 64, 70, 75, 79 and 82 (or the biomarkers set forth by name in Table 9 as being increased in $\geq 80\%$ of responders vs. non-responders, as described above), more preferably the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 31, 37, 44, 47, 62 and 70 (or the biomarkers set forth by name in Table 9 as being increased in $\geq 90\%$ of responders vs. non-responders, as described above), and even more preferably at least one of the biomarkers is encoded by a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 44 (or the biomarker, CD11c antigen, set forth by name in Table 9 as being increased in 100% of responders vs. non-responders, as described above). In each of these embodiments, increased expression of the one or more biomarkers is predictive of responsiveness of the subject to a TNF α inhibitor.

[0158] In another embodiment of the above-described methods and computer programs, the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-5, 8, 9, 11-14, 18, 20, 21, 23, 25, 26, 28-30, 32, 33, 40-42, 48, 50, 52, 53, 56, 58, 60, 63, 65-69, 71-74, 76-78, 80 and 81 (or the biomarkers set forth by name in Table 9 as being decreased in $\geq 80\%$ of responders vs. non-responders, as described above), more preferably the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 11, 29, 65, 73 and 74 (or the biomarkers set forth by name in Table 9 as being decreased in $\geq 90\%$ of responders vs. non-responders, as described above), and even more preferably the one or more biomarkers is encoded by a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 11 or SEQ ID NO: 74 (or the biomarkers set forth by name in Table 9 as being decreased in 100% of responders vs. non-responders, as described above). In each of these embodiments, decreased expression of the one or more biomarkers is predictive of responsiveness of the subject to a TNF α inhibitor.

[0159] In another embodiment of the above-described methods and/or computer programs, the biomarker expression pattern(s) can be for one or more biomarkers selected from the group consisting of SEQ ID NO: 83-133 (or the biomarkers set forth by name in Table 3, as described above).

[0160] In yet another embodiment of the above-described methods and/or computer programs, the biomarker expression pattern(s) can be for one or more biomarkers selected from the group consisting of SEQ ID NO: 134-177, 110, 112, 118, 123 and 131 (or the biomarkers set forth by name in Table 4, as described above), more preferably SEQ ID NO: 134-150, 112, 118 (or the biomarkers set forth by name in Table 4 as having increased expression, as described above), wherein expression of the one or more biomarkers is increased in the subject, and/or more preferably SEQ ID NO: 151-177, 110 and 123 (or the biomarkers set forth by name in

Table 4 as having decreased expression, as described above), wherein expression of the one or more biomarkers is decreased in the subject.

[0161] In yet another embodiment of the above-described methods and/or computer programs, the biomarker expression pattern(s) can be for one or more biomarkers selected from the group consisting of SEQ ID NO: 178-292, 91 and 97 (or the biomarkers set forth by name in Table 5, as described above), more preferably SEQ ID NO: 178-185; 187-200, 202, 203, 205-207; 211, 213, 214, 216, 220, 221, 226, 228, 229, 231, 232, 234, 235, 238-247, 249, 250, 253, 262-265, 268-282 and 285-288 (or the biomarkers set forth by name in Table 5 as having increased expression, as described above), wherein expression of the one or more biomarkers is increased in the subject, and/or more preferably SEQ ID NO: 186, 201, 204, 208, 209, 91, 210, 212, 97, 215, 217-219, 222-225, 227, 230, 233, 236, 237, 248, 251, 252, 254-261, 266, 267, 283, 284 and 289-292 (or the biomarkers set forth by name in Table 5 as having decreased expression, as described above), wherein expression of the one or more biomarkers is decreased in the subject.

[0162] In yet another embodiment of the above-described methods and/or computer programs, the biomarker expression pattern(s) can be for one or more biomarkers selected from the group consisting of SEQ ID NO: 87, 97, 101, 293, 92, 272, 93, 107, 108, 121 and 123 (or the biomarkers set forth by name in Table 6 as pre-treatment biomarkers, as described above), wherein the subject is monitored prior to treatment with a TNF α inhibitor. In yet another embodiment of the above-described methods and/or computer programs, the biomarker expression pattern(s) can be for one or more biomarkers selected from the group consisting of SEQ ID NO: 290, 209, 98, 112, 116, 121, 130, 155, 92, 289, 216 and 131 (or the biomarkers set forth by name in Table 6 as post-treatment biomarkers, as described above), wherein the subject is monitored after treatment with a TNF α inhibitor.

[0163] In yet another embodiment of the above-described methods and/or computer programs, the biomarker expression pattern(s) can be for one or more biomarkers selected from the group consisting of SEQ ID NO: 97, 102, 29, 294, 295, 91, 131, 290, 100, 134, 296, 297, 298, 299, 136, 174 and 300 (or the biomarkers set forth by name in Table 7, as described above).

[0164] Computer systems and database software well established in the art can be adapted for use in the methods and computer program products of the invention for building and searching a database for use in selecting or monitoring a treatment regimen for a subject having an autoimmune disorder or for selecting a particular autoimmune disorder subject for treatment with a TNF α inhibitor.

[0165] The present invention is further illustrated by the following examples which should not be construed as further limiting. The contents of all references, patents and published patent applications cited throughout this application are expressly incorporated herein by reference in their entirety.

EXAMPLES

Example 1

Materials and Methodologies

[0166] In this example, the materials and methodologies used in the subsequent Examples are described.

Patients

[0167] Purified monocytes (MO) derived from a total of 84 RA patients were used. The clinical data for the RA patients,

pre- and post-anti-TNF α treatment, is summarized in Table 1. All patients fulfilled the revised American College of Rheumatology (ACR) criteria (Arnett, F. C. et al. (1988) *Arthritis Rheum.* 31:315-324). Patients were defined as responders ($\geq$ continuous ACR score 40) or non-responders ($\leq$ continuous ACR score 30) to anti-TNF α monotherapy, MTX monotherapy or combination therapy. In order to account for a gradual transition from clinical responders to non-responders to therapy, a continuous ACR response evaluation was performed by applying the ACR criteria, but by defining 10% response steps instead of the usual 20, 50, and 70% steps. This was also done to allow more detailed analyses of the correlation between the ACR response and the mRNA expression levels of the predictive marker CD11c.

[0168] For Affymetrix $\text{\textregistered}$ microarray analysis, MO samples from 7 RA patients (RA1-RA7; all females) undergoing the Abbott DE011 trial were used (ReACT; monoclonal antibody Adalimumab $\text{\textregistered}$). In this multicenter, double-blinded study patients received Adalimumab $\text{\textregistered}$ (20 mg weekly or 40 mg biweekly) in the outpatient Rheumatology Clinic of the Charité University Hospital in Berlin, Germany, for a total of 2 years. Non-steroidal anti-inflammatory drugs and 10 mg prednisolone-equivalent per week were allowed in addition to the anti-TNF α therapy. For TaqMan $\text{\textregistered}$ real-time PCR, 26 patients (RA8-RA84 from the Abbott DE013 trial) were used (ATTRACT). In this study Adalimumab $\text{\textregistered}$, methotrexate (MTX; 10-20 mg/week) or a combination of both therapeutics was applied.

[0169] The mean time interval between the two MO samples (blood sampling before and during therapy) was 9.4 ± 1.8 months (mean $\pm$ SEM; range 4-13.5 months), the mean age 50.3 ± 3.9 years (range 39-70), and the mean disease duration 18.6 ± 5.3 years (range 4-38). As controls, healthy individuals were recruited (n=7; 6 females, 1 male; mean age 36.1 ± 7.4 years). RA patients RA1-RA84 were recruited from the Rheumatology Clinic of the Charité University Clinic, the Rheumaklinik of the Charité in Berlin-Buch, and from the Schlossparklinik in Berlin.

Separation of Peripheral Blood Mononuclear Cells, Purification of Monocytes, RNA Isolation

[0170] Peripheral blood (30 to 35 ml) was obtained by venopuncture, immediately stored in heparin-containing vacutainers (Beckton-Dickinson, Rutherford, N.J., USA), and cooled to 4 $^{\circ}$ C. Blood samples were subjected to a Ficoll-Hypaque gradient (d=1.077 g/ml; Biochrom, Berlin, Germany). To enrich MO, negative selection magnetic cell sorting (MACS; Miltenyi; Bergisch Gladbach, Germany) was subsequently applied. Successful purification of MO (purity of 83-90%; $1.3\text{--}3.2 \times 10^6$ MO/patient) was validated by FACS analysis using CD14 and CD45 antibodies (Beckman-Coulter, Krefeld, Germany). In all cases, purified MO showed >98% vitality using propidium iodide staining (Pharmingen, San-Diego, Calif., USA). MO preparation was performed at 4 $^{\circ}$ C. After purification, MO were lysed in RLT lysis buffer and total RNA was isolated using the RNeasy mini elute kit (Qiagen, Düsseldorf, Germany; yield 1.5-3.2 μ g/sample). Quantification and quality control of RNA was performed at 260/280 nm using a Bioanalyzer 2100 unit (Agilent, Palo Alto, Calif., USA).

RNA Amplification and Labeling

[0171] For target synthesis, 500 ng of total RNA were amplified using the standard protocol of the manufacturer

(Affymetrix $\text{\textregistered}$, Palo Alto, Calif., USA) and the Megascript kit (Ambion, Cambridgeshire, UK).

Biotin-Labeling of cRNA and Gene-Chip Hybridization

[0172] Biotinylated cRNA target was generated from amplified cRNAs using the Bioarray high-yield transcription kit (Enzo, New York, N.Y., USA). Samples were hybridized to Affymetrix $\text{\textregistered}$ test and HG-U133A GeneChip arrays.

[0173] Following washing and staining, arrays were scanned twice at 3 μ m resolution using a confocal scanner with an argon laser instrument (Agilent $\text{\textregistered}$ G2500A GeneArray Scanner; Agilent, CA, USA).

Bioinformatic Analysis of Differentially Expressed Genes in ND and RA Patients Pre- and Post Anti-TNF α Treatment

[0174] All GeneChips were analyzed for signal calculation and pairwise comparisons using the GCOS 1.4 software package with standard settings provided by Affymetrix $\text{\textregistered}$. Scaling was performed to a target value of 150 and normalization was set to "1". Pairwise comparison data were grouped to generate a percentage level of increased and decreased comparisons. Fold-changes were calculated from the mean of the SLR values in pairwise comparisons. Filtering was performed on the basis of "increased/decreased" comparisons with a percentage cutoff as indicated in the results. For hierarchical clustering, the software tool "Gene Expression Similarity Investigation Suite" (Genesis; Sturn, A. et al. (2002) *Bioinformatics* 18:207-208; <http://genome.tugraz.at/Software/GenesisCenter.html>) was applied using normalized signal intensities, Pearson distance correlation, and complete linkage clustering. Prediction analysis was performed using the PAM software (<http://www.bioconductor.org>; Khan, J. et al. (2001) *Nat. Med.* 7:673-679).

Data Sets of Publication

[0175] The complete ASCII-file datasets have been deposited in the microarray GEO database (<http://www.ncbi.nlm.nih.gov/geo/>).

TaqMan $\text{\textregistered}$ Real Time PCR

[0176] Real-time PCR (RT-PC) was performed using a TaqMan $\text{\textregistered}$ 7500 system and pre-designed TaqMan $\text{\textregistered}$ low density gene expression primers (Applied Biosystems; Foster City, Calif., USA) or, in the case of CD11c, the primer Hs01015072_g1 (commercially available from Applied Biosystems) in a Bio-Rad iQ real time PCR system (iCycler; Bio-Rad; München, Germany). The housekeeping gene GAPDH was used for normalization of the cDNA content. Quantification was performed using the SDS 2.2.0 software (Applied Biosystems); results were expressed as relative quantities of the logarithm of the $\Delta\Delta$ CT values (log RQ), as the relative quantity of expression (RQ; fold-change in comparison to normal donor expression), or as the % expression as normalized to GAPDH.

Literature-Associated Pathway Analysis Using Ingenuity

[0177] Gene ontology and gene interaction analyses were executed using the Ingenuity $\text{\textregistered}$ Pathway analysis tool v.4.0 (Ingenuity, Redwood City, Calif., USA; Jenssen, T. K. et al. (2001) *Nat. Genet.* 28:21-28; <http://www.ingenuity.com>). Highest scoring neighborhood analysis of literature-based gene connections was performed by comparing up- and downregulated genes in anti-TNF α responders and non-responders (pre- and post-treatment). Significantly regulated

genes in both comparisons were merged from the networks 1 to 5, complemented by transcription factors and finally overlaid with their relative expression values.

Expression-Based Pathway Analysis Using Kyoto Encyclopedia of Genes and Genomes (KEGG)

[0178] The KEGG pathway analysis (Kanehisa, M. and Bork, P. (2003) *Nat. Genet.* 33:305-310) was performed using selected genes from the comparison of microarray data in responders and non-responders either pre- or post-treatment with anti-TNF α . Upregulated genes and downregulated genes within the illustrated pathways were color-coded in a gradient fashion (SLR 0.5 to ≥ 1.5). A total of 4 pathways out of the 8 most highly ranked pathways were selected for illustration.

Statistical Analysis

[0179] The non-parametric Mann-Whitney U test was applied to analyze differences between data from RA patients and normal donors, from untreated and anti-TNF α -treated RA patients, and from responders and non-responders to anti-TNF α -therapy. Correlation analyses between experimental and clinical/laboratory parameters of the patients were performed using the Pearson test and the software SPSS 13.0™ (SPSS Inc., Chicago, Ill., USA). For the U test, statistically significant differences were accepted for $P \leq 0.05$; for correlation analyses, the acceptance level was reduced to $P \leq 0.01$ to account for multiple comparisons.

Example 2

Clinical and Laboratory Assessments for RA Patients and Normal Donors

[0180] Two of the seven anti-TNF α -treated RA patients used for microarray analysis, i.e., patients RA4 and RA6, were non-responders to therapy according to the ACR improvement criteria ($\leq$ continuous ACR 30 score). In general, this was also reflected in the respective percent-reduction of other clinical parameters of local or systemic inflammation. The group of seven RA patients employed for microarray analysis in the present study constituted a representative RA cohort, as demonstrated by well-known correlations among clinical parameters pre- and post-anti-TNF α treatment, as summarized in Table 2.

[0181] The identification of patients RA4 and RA6 as non-responders was also confirmed by hierarchical clustering of clinical parameters.

Example 3

Gene Expression Profiling and Analysis

Differential Gene Expression in Responders Versus Non-Responders to Anti-TNF α -Therapy

[0182] A total of 119 differentially-expressed genes was identified by comparing RA and normal donors (ND; $n=7$ each; total of 49 comparisons). Hierarchical clustering of ND, as well as RA patients pre- and post-treatment with these genes also identified 5 responders and 2 non-responders (RAantiTNF4 and RAantiTNF6).

[0183] In order to select therapeutically relevant genes, a subpopulation of 51 differentially-expressed genes was then identified by the simultaneous comparison between RA versus normal donors (ND; total of 49 comparisons) and RA

responders ($n=5$) pre- versus post-anti-TNF α therapy (25 comparisons). These genes showed an increase or decrease of the signal log ratio (SLR; between -4.36 and 4.61) in $>70\%$ of the pair-wise comparisons between RA and ND. These genes are summarized in Table 3.

[0184] Hierarchical clustering with these genes resulted in precise (100%) classification of ND, RA patients pre-treatment, and clinically-defined responders ($\geq$ continuous ACR score 40; clustered as ND) or non-responders ($\leq$ continuous ACR score 30; clustered as RA; note RAantiTNF4 and RAantiTNF6). This was confirmed by supervised pattern discovery using prediction analysis of microarrays (PAM analysis) at a threshold value of 4.3 in order to minimize the misclassification error. Table 4 summarizes the results of the PAM analysis, showing 49 selected genes, five of them overlapping with genes listed in Table 3. In this case, both non-responders (RAantiTNF4 and RAantiTNF6) were classified as RA patients, whereas the responders, RAantiTNF1-3, RAantiTNF5, and RAantiTNF7, were classified either as normals or as anti-TNF α -treated RA patients. Notably, ND showed the lowest misclassification error at the threshold value (0.00; i.e., the highest similarity among individuals), followed by pre-treatment RA patients (0.14), and anti-TNF α -treated RA patients (0.42).

[0185] Identification of responders/non-responders was also confirmed by hierarchical clustering of RA patients post-treatment. A total of 117 genes differentially expressed in RA responders versus RA non-responders was identified in post-anti-TNF α therapy samples, which showed an increase or decrease in 100% of the respective pair-wise comparisons (total of 10 comparisons). The 117 genes identified in this analysis are summarized in Table 5, three of which genes overlap with the genes summarized in Table 3. Hierarchical clustering with these genes resulted in precise (100%) classification of responders and non-responders to therapy.

[0186] A number of the differentially-expressed genes showed highly significant correlations with clinical or laboratory parameters pre- and/or post-anti-TNF α treatment, indicating a potential clinical relevance of the genes and contributing to the selection of genes for validation with TaqMan® real-time RT-PCR. These genes are summarized in Table 6.

Example 4

Real-Time RT-PCR Validation of Genes Differentiating Responders and Non-Responders

[0187] Sixteen genes with a likely pathogenetic importance in RA (and 6 control genes) from Affymetrix® gene expression profiling were selected for validation by TaqMan® real-time RT-PCR ($n=10$ anti-TNF α -treated RA patients prior to therapy; $n=14$ ND). The RT-PCR results confirmed the results of Affymetrix® gene expression profiling for 17 of 22 genes (approx. 77%), summarized in Table 7. This applied to genes regarded as differentially expressed in RA versus ND by Affymetrix® analysis (decreased: $<-70\%$; increased: $>70\%$) and to equally expressed control genes. By real-time RT-PCR, 18 genes showed significantly differential expression ($p \leq 0.000$ for 7 genes; $p \leq 0.041$ for the remaining) in MO from RA patients responding to anti-TNF α therapy versus ND, including genes 10 upregulated in RA (Amphiregulin, Charcot-Leyden crystal protein, TNF α -induced protein 6, thrombomodulin, membrane-spanning 4-domains, subfamily A—member 4, S100 calcium binding protein A1, TNF α ,

IL-1 β , lipoyltransferase 1, and interferon regulatory protein 1), as well as 8 genes downregulated in RA (Uncharacterized hypothalamus protein HT007, MHC class II HLA-DR-alpha, hypothetical protein L0054103, proteasome subunit beta type 7 precursor, protein KIAA0174, microsomal signal peptidase 18 kDa subunit, ring zinc finger protein 361, and protein phosphatase 1, catalytic subunit, beta isoform). However, the expression for these genes showed no significant differences for the direct comparison between RA responders and non-responders to anti-TNF α therapy.

[0188] The potential clinical relevance of some of the differentially expressed genes is underlined by a significant correlation with the ACR response at different time points during anti-TNF α therapy, as summarized in Table 8.

[0189] Validation of the 22 selected genes by TaqMan® real-time RT-PCR confirmed the results of Affymetrix® gene expression profiling for 17 of 22 genes (approx. 77% true positives or negatives), in accordance with the rates reported in other gene expression studies and therefore underlining the validity of the present data. The 18 genes showing significantly differential expression in MO from RA patients responding to anti-TNF α therapy versus ND included several genes with a likely pathogenetic importance in RA (e.g., amphiregulin, TNF α -induced protein 6, thrombomodulin, membrane-spanning 4-domains, subfamily A—member 4, S100 calcium binding protein A1, TNF α , IL-1 β , lipoyltransferase 1, interferon regulatory protein 1, MHC class II HLA-DR-alpha).

Example 5

Gene Expression Profiling and Analysis

Differential Gene Expression in Responders Versus Non-Responders Prior to Anti-TNF α -Therapy (Predictive Genes)

[0190] Using a threshold of $\geq 80\%$ for the pairwise comparisons between future RA responders and future RA non-responders prior to anti-TNF α therapy, a total of 82 predictive genes was identified (11 genes for a threshold of $\geq 90\%$; 3 genes for 100%). These genes are summarized in Table 9. The latter group (100%) consisted of 2 known proteins (*Homo sapiens* predicted osteoblast protein (GS3786); integrin alpha-X (antigen CD11c) and an unknown protein (*Homo sapiens* hypothetical protein FLJ10134). In particular the antigen CD11c appears highly interesting, since it is a surface molecule on human MO (and other cells of the myelomonocytic lineage), and since it has known inflammatory functions. Hierarchical clustering with the selected genes resulted again in precise (100%) predictive classification of future responders and non-responders to therapy. Marginal co-clustering of the patient RA5 with the non-responders RA4 and RA6 at the threshold values 80% and 100% possibly identified RA5 as a 'weak' responder, as also indicated by a marginal position in the hierarchical clustering of clinical parameters.

[0191] Interestingly, future responders to anti-TNF α -therapy (when directly compared to non-responders) showed a pattern shift from the recently described 'inflammatory' MO to 'resident' MO subsets (Gordon, S. et al. (2005) *Nat. Immunol.* 5:953-963) both prior to therapy and post-treatment. Although most of the individual molecules showed an identical pattern shift in both pre-treatment and post-treatment comparisons, in particular the activating (CD16a,b) and inhibiting Fc γ -receptors (CD32) displayed an opposite

behavior. This pattern shift was observed despite the fact that all pre-treatment or post-treatment comparisons between RA patients (all, future responders, future non-responders) and ND indicated a dominance of 'inflammatory' MO in the respective RA groups. Post-treatment, strikingly, responders to anti-TNF α -therapy became barely distinguishable from ND in contrast to non-responders, which still showed a clear 'inflammatory' predominance. These results indicate that successful anti-TNF α -therapy acts by blocking TNF α signaling via TNF α -receptors 1 and 2 and by subsequent induction of a major change in the composition of pro-inflammatory and other MO subsets.

Example 6

Real-Time RT-PCR Validation of Predictive CD11c

[0192] TaqMan® real-time RT-PCR confirmed the discrimination of future RA responders (n=15) from future non-responders (n=12) to anti-TNF monotherapy (at the level of continuous ACR score 30) on the basis of their CD11c mRNA expression in monocytes.

[0193] TaqMan® real-time RT-PCR confirmed the separation of future RA responders n=55 from future non-responders n=12 to anti-TNF α monotherapy on the basis of their CD11c mRNA expression in MO. The results are summarized in the bar graph of FIG. 1. This clear separation was lost in the case of combination therapy with anti-TNF α /MTX, possibly due to a differential importance of the CD11c mRNA expression for the anti-TNF α and MTX components.

[0194] Of the 3 genes identified by pairwise comparison between RA responders and RA non-responders prior to treatment at the level of 100% (and confirmed by TaqMan® real-time RT-PCR), the antigen CD11c appears of particular interest, since it is expressed on the surface of human MO (and other cells of the myelomonocytic lineage, e.g. dendritic cells), and since it has known functions in inflammatory reactions (e.g., as the complement receptor 4) and cell adhesion.

[0195] The validity of CD11c as a predictive biomarker is further underlined by a significant correlation ($r=0.651$, $P<0.0001$, $n=27$) between the CD11c expression prior to therapy and the future percentage of the ACR response, illustrated in the graph of FIG. 2.

[0196] Except for 1 RA patient with a borderline ACR response of 30 and a CD11c mRNA level directly at the distinction threshold (who was therefore classified as a false negative), the threshold level (40%) almost fully distinguished future responders from nonresponders (100% specificity, 94% sensitivity, and 96% power). This clear separation was lost in the case of combination therapy with anti-TNF/ methotrexate (MTX), possibly owing to a differential importance of the CD11c mRNA expression for the anti-TNF and MTX treatment components. This was further underlined by the fact that: i) future responders to MTX monotherapy did not significantly differ in their CD11c mRNA expression level from future nonresponders to MTX monotherapy; and ii) there was no significant correlation between the future ACR response of RA patients treated with MTX monotherapy and their CD11c mRNA expression (data not shown).

[0197] Strikingly, this was true not only for the continuous ACR score, but also for the clinically applied, discrete ACR criteria.

[0198] A significant correlation ($r=0.656$, $P<0.0001$, $n=27$) was observed between CD11c expression and the future percentage of strict ACR response, illustrated in the

graph in FIG. 3. This finding complements and expands previous reports on the identification of molecules capable of predicting a future response to anti-TNF α therapy (Lequerre, T. et al. (2006) *Arthritis Res. Ther.* 8:R105; Toh, M. L. et al. (2006) *Arthritis Rheum.* 54:2109-2118).

Example 7

Ingenuity® Pathway Analysis

[0199] Ingenuity® pathway analysis of the genes in Tables 3 and 5 indicated a direct or indirect influence of anti-TNF α therapy on several molecules thought to be relevant for the pathogenesis and/or severity of RA, e.g., HLA-DMA/B (Morel, J. et al. (2004) *Ann. Rheum. Dis.* 63:1581-1586), CD69 (Marzio, R. et al. (1999) *Immunopharmacol. Immunotoxicol.* 2:565-582) thrombomodulin (Cobankara, V. et al. (2004) *Clin. Rheumatol.* 23:430-434), membrane-spanning 4-domains, subfamily A—member 4 (Fujikado, N. et al. (2006) *Arthritis Res. Ther.* 8:1-13), and forkhead box 03a (Jonsson, H. et al. (2005) *Nat. Med.* 11:666-671). The present approach, therefore, represents a powerful tool to identify gene regulation patterns applicable for diagnosis, as well as for therapy stratification and monitoring in rheumatic diseases, in particular in view of the fact that blood MO are much more easily available than synovial tissue samples. This is further supported by the fact that a high number of individual genes show significant correlations with clinical parameters in RA patients pre- and/or post-anti-TNF α treatment (see Table 6).

[0200] Pairwise comparison between RA responders and RA non-responders prior to treatment yielded a number of genes suitable for the prediction of a future response to anti-TNF α therapy (82 genes for a threshold of $\geq 80\%$; 11 genes for $\geq 90\%$; 3 genes for 100%; summarized in Table 9), resulting in exact classification of future responders and non-responders upon hierarchical clustering. Using all genes differentially expressed in the above comparison at a threshold level of 70% (256 pre-treatment; 1295 post-treatment) for Ingenuity® pathway analysis, the differences between responders and non-responders either pre-treatment or post-treatment were concentrated in the functional gene ontology terms cellular movement, haematological system development, immune response, cell-to-cell signaling and interaction, as well as immunological disease.

[0201] In particular, numerous relevant mediators were identified: i) pro-inflammatory cytokines (e.g., interleukin-8 [IL8], chemokine (C—C motif) ligand 5 [CCL5], chemokine

(C—X—C motif) ligand 5 [CXCL5], and chemokine (C—X—C motif) ligand 10 [CXCL10]); ii) pro-destructive enzymes (e.g., matrix metalloproteinase 9 [MMP9]); iii) adhesion molecules and Fc γ -receptors (galectin-8 [LGALS8], integrin alpha-X [ITGAX] or CD11c, Fc-gamma receptor IIb [FCGR2B] or CD32, CD86 [CD86] and platelet/endothelial cell adhesion molecule 1 [PECAM1] or CD31); iv) signal transduction molecules (e.g., protein kinase B [AKT1], apoptosis regulator Bel-2 [BCL2], p21-activated protein kinase 1 [PAK1]); and v) transcription factors (e.g., Mad-related protein 2 [SMAD2], interferon regulatory factor 1 [IRF1], c-myc [MYB], early growth response protein 1 [EGR1], signal transducer and activator of transcription 1 [STAT1], and nuclear factor NF- κ B 1 [NFKB1]; for the remaining abbreviations see the respective gene cards [http://www.genecards.org/index.shtml]). These molecules were differentially expressed between RA responders and RA non-responders either pre-treatment or post-treatment and in some cases even inverted their expression upon anti-TNF α -therapy (see interleukin-8 receptor beta [IL8RB], Amyloid-beta A4 precursor [APP]; overexpressed in RA responders pre-treatment and underexpressed post-treatment). Similar opposite variations in transcript levels between RA responders and RA non-responders have recently been reported when comparing baseline to 3-month results (Lequerre, T. et al. (2006) *Arthritis Res. Ther.* 8:R105).

[0202] Most strikingly, the transcription of TNF α itself, as well the transcription of members of the subsequent NFKB-pathway (NFKB1 and inhibitor of NF- κ B [IKKB]), was upregulated in RA responders post-treatment. This previously unreported finding at first sight questions the central pro-inflammatory role of TNF α in RA. However, several caveats should be considered: i) The mRNA expression levels of TNF α measured in the present study may not be proportional to the levels of circulating TNF α protein and/or bioactivity, the latter apparently predictive of the clinical response to TNF α inhibition (Marotte, H. et al. (2005) *Arthritis Res. Ther.* 7:R149-155); ii) TNF α , in addition to its well-established pro-inflammatory properties, may also exhibit phase-dependent immunosuppressive properties (Kassiotis, G. et al. (2001) *J. Exp. Med.* 193:427-434).

[0203] Several interesting pathways with potential importance for the mechanisms underlying susceptibility to anti-TNF α -therapy were identified by KEGG pathway analysis; including Apoptosis and the MAPK pathways.

TABLE 1

Clinical parameters of patients before and after anti-TNF treatment									
Patient	Methods Affymetrix (A) real-time (R/P)	Duration of treatment, mo	Disease duration, y	Age, y	Gender	RF	Morning stiffness, min (% reduction)	Swollen joint count 68 (% reduction)	Painful joint count 68 (% reduction)
RA1-1110006211	A/P	0	4	52	F	+	320	10	19
RA1-aTNF	A	13.5					15 (95)	3 (70)	8 (58)
RA2-1110005181	A/P	0	9	53	F	+	180	16	50
RA2-aTNF	A	6					0 (100)	1 (94)	19 (62)
RA3-1110005291	A/P	0	18	39	F	+	0	10	28
RA3-aTNF	A	5.5					0 (0)	2 (80)	8 (29)
RA4-1110005031	A/P	0	12	47	F	+	720	20	43
RA4-aTNF	A	17					60 (92)	19 (5)	35 (19)
RA5-1110004141	A/P	0	38	70	F	+	120	11	56
RA5-aTNF	A	15					120 (0)	2 (82)	61 (0)
RA6-1110004131	A/P	0	38	51	F	+	60	12	27

TABLE 1-continued

Clinical parameters of patients before and after anti-TNF treatment									
RA6-aTNF	A	4					60 (0)	4 (67)	28 (0)
RA7-1110006221	A/P	0	11	40	F	+	150	18	44
RA7-aTNF	A	4.5					10 (93)	5 (72)	25 (43)
RA8-06507	R	0	<1	28	F	-	120	14	17
RA8-aTNF/MTX	R	6					0 (100)	0 (100)	3 (82)
RA9-06513	R	0	1	53	F	-	120	16	20
RA9-aTNF/MTX	R	4.5					15 (87)	12 (25)	16 (20)
RA10-05602	R	0	1	48	F	+	180	8	40
RA10-MTX	R	3.5					240 (0)	10 (0)	29 (27)
RA11-05610	R/P	0	<1	38	F	-	360	14	22
RA11-aTNF	R	6					30 (92)	3 (79)	9 (59)
RA12-05609	R/P	0	1	63	F	+	60	17	29
RA12-aTNF	R	6					10 (83)	5 (71)	9 (69)
RA13-05608	R	0	2	44	F	+	45	12	24
RA13-aTNF/MTX	R	6					0 (100)	0 (100)	1 (96)
RA14-05612	R/P	0	1	29	F	+	60	8	11
RA14-aTNF/MTX	R	6					0 (100)	0 (100)	0 (100)
RA15-06504	R/P	0	2	47	F	+	60	10	23
RA15-aTNF	R	6					20 (67)	2 (80)	3 (87)
RA16-06308	R/P	0	<1	60	F	+	120	17	29
RA16-aTNF/MTX	R	6					15 (87)	1 (94)	16 (45)
RA17-06516	R	0	1	36	F	+	30	17	17
RA11-aTNF	R/P	6					15 (50)	11 (35)	0 (100)
RA18-06309	R	0	1	83	F	-	30	11	27
RA18-aTNF/MTX	R	6					0 (100)	0 (100)	0 (100)
RA19-05613	R/P	0	2	63	F	+	120	25	43
RA19-aTNF	R	6					15 (87)	9 (64)	17 (60)
RA20-06304	R/P	0	<1	50	F	-	60	12	29
RA20-aTNF	R	6					0 (100)	2 (83)	5 (83)
RA21-06514	R/P	0	2	56	F	-	30	21	52
RA21-aTNF/MTX	R	6					30 (0)	15 (29)	16 (69)
RA22-05606	R/P	0	<1	36	F	+	60	12	22
RA22-aTNF/MTX	R	6					0 (100)	2 (83)	9 (83)
RA23-06306	R/P	0	1	34	F	+	30	13	27
RA23-aTNF	R	3					30 (0)	18 (0)	27 (0)
RA24-06305	R	0	n.d.	18	F	+	30	14	20
RA24-MTX	R	6					60 (0)	2 (86)	8 (60)
RA25-06515	R/P	0	<1	54	M	-	45	22	43
RA25-aTNF	R	6					20 (66)	7 (68)	28 (35)
RA26-06506	R/P	0	1	50	F	-	60	9	23
RA26-aTNF	R	6					120 (0)	20 (0)	45 (0)
RA27-05601	R/P	0	1	42	F	+	60	8	24
RA27-aTNF	R	6.5					60 (0)	7 (12)	30 (0)
RA28-1110004171	P	0	n.d.	34	F	+	60	20	47
RA28-aTNF		3.5					0 (100)	4 (80)	4 (91)
RA29-1110011271	P	0	11	62	F	+	120	8	35
RA29-aTNF/MTX		0.5					120 (0)	9 (0)	44 (0)
RA30-1110010101	P	0	7	35	F	+	120	8	12
RA30-aTNF/MTX		10					0 (100)	2 (75)	7 (42)
RA31-1110004121	P	0	13	33	F	+	30	11	27
RA31-aTNF		6					20 (67)	2 (82)	7 (74)
RA32-1110008092	P	0	20	43	F	+	60	14	38
RA32-aTNF		6.5					0 (100)	6 (57)	7 (72)
RA33-1110005121	P	0	8	61	F	-	180	19	59
RA33-aTNF		17.5					120 (66)	2 (89)	12 (81)
RA34-1110111281	P	0	12	66	F	+	90	10	5
RA34-MTX		12					120 (0)	8 (20)	9 (0)
RA35-1110112121	P	0	6	63	F	+	180	8	20
RA35-MTX		9					0	3 (63)	4 (80)
RA36-1110201231	P	0	10	36	F	0	60	30	19
RA36-MTX		4					30 (50)	0 (100)	0 (100)
RA37-1110211051	P	0	1	59	F	+	180	2	21
RA37-MTX		3					15 (92)	0 (100)	4 (81)
RA38-1110309012	P	0	<1	32	F	+	180	7	29
RA38-MTX		3					0 (100)	1 (85)	3 (90)
RA39-1110309122	P	0	1	26	F	+	180	6	23
RA39-MTX		3					15 (92)	1 (83)	9 (41)
RA40-1110310302	P	0	1	45	F	+	10	10	17
RA40-MTX		4					0 (100)	0 (100)	2 (88)
RA41-1110411251	P	0	<1	58	F	0	180	6	16
RA41-MTX		3					0 (100)	0 (100)	2 (88)
RA42-1110409071	P	0	1	52	F	0	0	9	4
RA42-MTX		3					0 (0)	0 (100)	0 (100)
RA43-1110409141	P	0	<1	58	M	+	10	8	22

TABLE 1-continued

Clinical parameters of patients before and after anti-TNF treatment									
RA43-MTX		3					10 (0)	0 (100)	5 (77)
RA44-1110409223	P	0	1	67	F	0	60	12	20
RA44-MTX		3					0 (100)	0 (100)	4 (80)
RA45-1110411291	P	0	<1	44	F	0	30	25	43
RA45-MTX		3					0 (100)	9 (64)	17 (60)
RA46-1110602212	P	0	10	45	F	+	120	3	13
RA46-aTNF/MTX		6					120 (0)	0 (100)	21 (0)
RA47-1110503081	P	0	21	57	F	+	360	8	10
RA47-TNF		6					180 (50)	7 (14)	11 (0)
RA48-1110703082	P	0	7	60	F	+	240	0	10
RA48-TNF		6					120 (50)	0 (0)	5 (50)
RA49-1110309122	P	0	1	26	F	+	180	6	24
RA49-MTX		9					15 (92)	1 (83)	9 (62)
RA50-1100308202	P	0	6	63	F	+	0	0	18
RA50-MTX		3					0 (0)	1 (0)	2 (89)
RA51-1110309111	P	0	2	45	M	+	180	16	30
RA51-MTX		3					120 (33)	9 (44)	24 (20)
RA52-1110401081	P	0	1	62	F	+	0	0	18
RA52-MTX		5.5					0 (0)	0 (0)	0 (100)
RA53-1110406011	P	0	1	61	F	+	30	10	33
RA53-MTX		3					5 (83)	0 (100)	1 (97)
RA54-1110406112	P	0	3	61	M	+	10	6	22
RA54-MTX		3					0 (100)	0 (100)	5 (77)
RA55-1110406111	P	0	<1	57	F	+	60	2	12
RA55-MTX		3					0 (100)	0 (100)	2 (83)
RA56-1110407131	P	0	1	63	F	+	30	9	30
RA56-MTX		3					0 (100)	0 (100)	6 (80)
RA57-1110407281	P	0	2	56	F	+	0	7	19
RA57-MTX		3					0 (0)	0 (100)	2 (89)
RA58-1110409201	P	0	1	61	F	+	10	5	16
RA58-MTX		3					0 (100)	0 (100)	4 (75)
RA59-1110410271	P	0	6	35	M	+	15	0	5
RA59-MTX		3					0 (100)	0 (0)	2 (60)
RA60-1110503231	P	0	1	71	F	+	30	6	23
RA60-MTX		3					0 (100)	0 (100)	5 (78)
RA61-1110504061	P	0	1	51	F	+	45	12	27
RA61-MTX		3					0 (100)	0 (100)	0 (100)
RA62-1110505301	P	0	1	59	F	0	120	2	9
RA62-MTX		3					0 (100)	0 (100)	12 (0)
RA63-1110507281	P	0	2	43	F	+	30	10	17
RA63-MTX		3					0 (100)	6 (40)	15 (12)
RA64-1110511281	P	0	<1	69	F	+	90	7	21
RA64-MTX		3					0 (100)	1 (86)	2 (90)
RA65-1110405273	P	0	5	55	F	+	0	0	2
RA65-aTNF/MTX		4					10 (0)	6 (0)	16 (0)
RA66-1110502091	P	0	36	62	F	+	30	13	14
RA66-aTNF/MTX		30					15 (50)	2 (85)	14 (0)
RA67-1110507261	P	0	25	43	F	+	0	4	5
RA67-aTNF/MTX		25					0 (0)	0 (100)	1 (80)
RA68-1110603141	P	0	12	72	F	+	30	7	7
RA68-aTNF		12					60 (0)	0 (100)	0 (100)
RA69-1110510181	P	0	2	33	F	+	50	6	6
RA69-aTNF/MTX		12					0 (100)	0 (100)	0 (100)
RA70-06303	P	0	1	53	F	+	30	14	17
RA70-aTNF/MTX		6					10 (66)	0 (100)	0 (100)
RA71-06516	P	0	3	79	F	+	30	17	17
RA71-TNF		6					15 (50)	0 (100)	11 (35)
RA72-06510	P	0	3	68	F	+	10	25	34
RA72-TNF		6					10 (0)	2 (92)	0 (100)
RA73-06309	P	0	1	36	F	0	45	11	27
RA73-TNF/MTX		6					0 (100)	0 (100)	0 (100)
RA74-06310	P	0	3	48	F	0	360	14	22
RA74-TNF		12					15	6 (57)	14 (36)
RA75-06307	P	0	2	51	F	+	360	16	22
RA75-MTX		6					0 (100)	2 (87)	3 (86)
RA76-06311	P	0	3	43	F	+	120	14	36
RA76-TNF		3					0 (100)	0 (100)	0 (100)
RA77-06513	P	0	1	53	F	0	120	16	20
RA77-TNF/MTX		4.5					15 (87)	12 (25)	16 (20)
RA78-06512	P	0	1	83	F	0	30	15	53
RA78-MTX		5.5					15 (50)	27 (0)	63 (0)
RA79-06514	P	0	2	56	F	0	30	21	52
RA79-TNF/MTX		6					30 (0)	15 (29)	16 (69)
RA80-1110505241	P	0	4	47	F	+	24	5	9

TABLE 1-continued

Clinical parameters of patients before and after anti-TNF treatment									
RA80-TNF/MTX		3.5					36 (0)	4 (20)	4 (56)
RA81-06305	P	0	1	18	F	+	30	8	20
RA81-MTX		6					60 (0)	2 (75)	14 (70)
RA82-05602	P	0	1	48	F	+	180	29	40
RA82-MTX		3.5					240 (0)	10 (66)	8 (20)
RA83-05607	P	0	3	61	M	+	120	25	40
RA83-MTX		8					0 (100)	3 (88)	3 (92)
RA84-06302	P	0	3	42	F	+	60	16	39
RA84-MTX		6					10 (83)	6 (62)	18 (51)
	Patient	ESR, mm/hr (% reduction)	CRP, mg/L (% reduction)	HAQ score (% reduction)	DAS28 (% reduction)	ACR improvement (% continuous score)			
	RA1-1110006211	69	57.5	2.0	6.0				
	RA1-aTNF	8 (88)	2.0 (97)	1.3 (35)	3.1 (48)	50			
	RA2-1110005181	46	52.2	1.6	6.3				
	RA2-aTNF	12 (74)	2.8 (94)	1.0 (37)	2.9 (54)	60			
	RA3-1110005291	72	61.1	1.5	6.1				
	RA3-aTNF	16 (78)	3.9 (93)	1.0 (33)	4.1 (33)	60			
	RA4-1110005031	58	85.3	2.1	6.9				
	RA4-aTNF	40 (31)	20.0 (77)	1.3 (38)	6.5 (6)	0			
	RA5-1110004141	80	41.5	2.1	6.3				
	RA5-aTNF	11 (86)	4.5 (88)	1.4 (33)	4.0 (37)	50			
	RA6-1110004131	46	36.0	1.6	5.9				
	RA6-aTNF	32 (30)	22.3 (39)	1.6 (0)	5.1 (14)	10			
	RA7-1110006221	30	17.3	1.9	6.0				
	RA1-aTNF	14 (53)	11.3 (35)	1.3 (32)	4.1 (32)	40			
	RA8-06507	30	<3.5	1.6	6.1				
	RA8-aTNF/MTX	4 (87)	<3.5 (0)	0.0 (100)	2.4 (61)	70			
	RA9-06513	34	<3.5	1.3	6.2				
	RA9-aTNF/MTX	14 (59)	<3.5 (0)	1.4 (0)	5.2 (26)	20			
	RA10-05602	31	<3.5	2.2	7.1				
	RA10-MTX	39 (0)	<3.5 (0)	2.3 (0)	6.8 (4)	0			
	RA11-05610	40	39.2	1.4	6.5				
	RA11-aTNF	45 (0)	36.4 (7)	0.3 (79)	4.3 (34)	50			
	RA12-05609	22	14.3	0.5	6.6				
	RA12-aTNF	30 (0)	<3.5 (100)	0.3 (40)	4.3 (35)	50			
	RA13-05608	32	5.1	0.8	6.1				
	RA13-aTNF/MTX	28 (12)	<3.5 (100)	0.0 (100)	2.7 (56)	90			
	RA14-05612	35	13.1	1.0	5.0				
	RA14-aTNF/MTX	8 (77)	<3.5 (100)	0.0 (100)	1.7 (66)	100			
	RA15-06504	28	<3.5	1.8	6.3				
	RA15-aTNF	24 (14)	4.1 (0)	1.3 (28)	3.5 (44)	50			
	RA16-06308	56	<3.5	1.8	7.3				
	RA16-aTNF/MTX	28 (50)	<3.5 (0)	1.3 (28)	4.8 (44)	40			
	RA17-06516	80	22.8	1.8	6.5				
	RA17-aTNF	24 (30)	27.5 (0)	0.6 (67)	3.2 (51)	30			
	RA18-06309	24	39.4	1.3	6.5				
	RA18-aTNF/MTX	8 (67)	8.5 (78)	0.6 (54)	1.9 (71)	70			
	RA19-05613	53	31.5	2.3	8.5				
	RA19-aTNF	85 (0)	40.0 (0)	1.3 (43)	5.6 (34)	60			
	RA20-06304	24	10.0	1.0	6.6				
	RA20-aTNF	16 (33)	10.0 (0)	1.0 (0)	3.8 (42)	30			
	RA21-06514	34	<3.5	1.4	8.3				
	RA21-aTNF/MTX	6 (82)	<3.5 (0)	0.9 (36)	5.4 (35)	20			
	RA22-05606	40	23.1	2.4	6.2				
	RA22-aTNF/MTX	30 (25)	7.3 (68)	0.8 (67)	4.2 (32)	50			
	RA23-06306	90	61.1	2.1	7.1				
	RA23-aTNF	62 (33)	53.4 (23)	2.0 (5)	7.2 (0)	0			
	RA24-06305	22	29.1	0.3	4.7				
	RA24-MTX	20 (10)	31.3 (0)	0.1 (33)	4.1 (13)	20			
	RA25-06515	34	<3.5	1.0	8.0				
	RA25-aTNF	9 (74)	<3.5 (0)	1.6 (0)	5.8 (27)	0			
	RA26-06506	16	<3.5	1.5	5.9				
	RA26-aTNF	50 (0)	<3.5 (0)	1.9 (0)	8.3 (0)	0			
	RA27-05601	30	6.8	1.1	5.8				
	RA27-aTNF	58 (0)	16.9 (0)	1.5 (0)	6.7 (0)	0			
	RA28-1110004171	30	7.0	1.8	6.2				
	RA28-aTNF	16 (47)	6.9 (1)	0.4 (78)	3.6 (42)	80			
	RA29-1110011271	19	16.5	n.d.	4.3				
	RA29-aTNF/MTX	9 (53)	3.0 (72)	n.d.	4.1 (13)	0			
	RA30-1110010101	52	42.6	n.d.	5.3				

TABLE 1-continued

Clinical parameters of patients before and after anti-TNF treatment					
RA30-aTNF/MTX	17 (63)	10.1 (76)	n.d.	2.6 (51)	50
RA31-1110004121	33	7.8	1.3	5.2	
RA31-aTNF	18 (45)	5.9 (24)	0.9 (31)	3.4 (35)	40
RA32-1110008092	29	18.4	n.d.	6.8	
RA32-aTNF	28 (3)	21.0 (0)	n.d.	3.4 (50)	50
RA33-1110005121	28	22.4	1.8	6.3	
RA33-aTNF	26 (7)	14.0 (36)	1.9 (0)	4.1 (35)	20
RA34-1110111281	18	9.0	1.43	4.29	
RA34-MTX	13 (28)	12.0 (0)	0.74 (49)	5.10 (0)	0
RA35-1110112121	17	66.0	2.67	6.3	
RA35-MTX	12 (29)	<3.5 (100)	0.67 (76)	3.5 (45)	60
RA36-1110201231	38	45.0	2.33	6.3	
RA36-MTX	17 (55)	5.0 (89)	0.33 (86)	2.1 (67)	80
RA37-1110211051	27	11.0	2.44	5.5	
RA37-MTX	8 (70)	5.0 (55)	1.44 (41)	2.9 (47)	40
RA38-1110309012	20	8.1	1.11	5.4	
RA38-MTX	10 (50)	1.2 (85)	0.44 (60)	2.5 (54)	70
RA39-1110309122	101	33.0	2.67	6.5	
RA39-MTX	81 (20)	44.5 (0)	2.10 (21)	5.6 (14)	20
RA40-1110310302	72	77.6	2.1	6.8	
RA40-MTX	18 (75)	6.9 (91)	1.1 (49)	3.4 (50)	50
RA41-1110411251	17	<3.5	2.4	5.4	
RA41-MTX	12 (29)	<3.5 (0)	0 (100)	3.1 (43)	80
RA42-1110409071	37	22.0	2.1	5.7	
RA42-MTX	5 (87)	6.6 (70)	0.4 (81)	1.1 (81)	80
RA43-1110409141	27	32.0	2.3	5.9	
RA43-MTX	3 (89)	4.6 (86)	2.0 (13)	1.7 (71)	70
RA44-1110409223	55	62.6	1.33	3.13	
RA44-MTX	12 (78)	3.80 (94)	1.40 (0)	4.93 (0)	70
RA45-1110411291	34	18.0	1.4	4.9	
RA45-MTX	20 (41)	12.6 (30)	0 (100)	2.2 (65)	60
RA46-1110602212	74	17.8	1.7	5.8	
RA46-aTNF/MTX	20 (63)	2.7 (85)	1.1 (35)	4.4 (24)	30
RA47-1110503081	74	<3.5	2.0	6.5	
RA47-TNF	20 (0)	<3.5 (0)	2.8 (0)	6.7 (0)	0
RA48-1110703082	28	106.0	1.1	6.2	
RA48-TNF	120 (12)	83.6 (21)	1.0 (9)	4.1 (34)	0
RA49-1110309122	40	33.0	0.9	6.6	
RA49-MTX	40 (0)	34.5 (0)	0.7 (22)	5.7 (14)	10
RA50-11100308202	28	9.8	1.4	4.6	
RA50-MTX	21 (25)	9.9 (0)	1.7 (0)	4.0 (13)	0
RA51-1110309111	10	4.0	2.2	6.1	
RA51-MTX	5 (50)	1.3 (77)	2.1 (5)	5.1 (16)	0
RA52-1110401081	30	6.5	1.1	4.4	
RA52-MTX	25 (17)	4.8 (26)	0.1 (91)	2.3 (48)	90
RA53-1110406011	10	23.0	1.78	6.4	
RA53-MTX	0 (100)	3.1 (87)	0.3 (83)	2.4 (62)	80
RA54-1110406112	10	9.0	0.7	5.2	
RA54-MTX	20 (0)	16.7 (0)	1.9 (0)	3.3 (37)	40
RA55-1110406111	25	24.8	1.9	5.4	
RA55-MTX	12 (52)	6.7 (73)	0.3 (84)	2.4 (56)	80
RA56-1110407131	55	37.8	1.67	8.8	
RA56-MTX	14 (75)	1.0 (97)	1.10 (34)	3.7 (58)	30
RA57-1110407281	21	3.9	1.6	5.5	
RA57-MTX	10 (52)	<3.5 (100)	0.2 (87)	2.5 (55)	70
RA58-1110409201	20	<3.5	2.2	4.3	
RA58-MTX	14 (30)	<3.5 (0)	0.4 (82)	2.0 (53)	70
RA59-1110410271	12	<3.5	0.8	2.6	
RA59-MTX	25 (0)	7.9 (0)	0.8 (0)	2.7 (0)	30
RA60-1110503231	14	5.6	2	5.9	
RA60-MTX	8 (43)	4.9 (12)	0.9 (55)	3.1 (47)	40
RA61-1110504061	16	<3.5	2.5	7.0	
RA61-MTX	4 (75)	<3.5 (0)	0.4 (84)	1.0 (86)	70
RA62-1110505301	10	<3.5	2.1	4.7	
RA62-MTX	6 (40)	<3.5 (0)	1.1 (48)	3.2 (26)	40
RA63-1110507281	68	42.0	1.8	6.0	
RA63-MTX	20 (71)	33.0 (21)	1.1 (39)	4.0 (33)	30
RA64-1110511281	25	14.5	1.2	5.8	
RA64-MTX	10 (60)	27.0 (0)	0.9 (25)	3.0 (48)	20
RA65-1110405273	6	<3.5	1.2	3.0	

TABLE 1-continued

Clinical parameters of patients before and after anti-TNF treatment						
RA65-aTNF/MTX	12 (0)	<3.5 (0)	0.8 (33)	4.7 (0)		0
RA66-1110502091	10	<3.5	1.9	4.2		
RA66-aTNF/MTX	12 (0)	4.2 (0)	0 (100)	4.1 (2)		40
RA67-1110507261	32	11.4	1.7	4.4		
RA67-aTNF/MTX	16 (50)	7.7 (32)	1.1 (35)	2.8 (36)		30
RA68-1110603141	72	4.8	1.3	4.7		
RA68-aTNF	4 (94)	<3.5 (100)	0.0 (100)	2.4 (49)		30
RA69-1110510181	12	9.0	3.0	4.7		
RA69-aTNF/MTX	26 (0)	<3.5 (100)	1.1 (63)	2.4 (49)		80
RA70-06303	26	31.9	1.3	5.8		
RA70-aTNF/MTX	6 (77)	0 (100)	0.1 (92)	1.6 (73)		70
RA71-06516	80	22.8	1.8	6.5		
RA71-TNF	24 (70)	7.5 (67)	0.6 (67)	3.2 (49)		30
RA72-06510	80	41.6	2.1	8.2		
RA72-TNF	58 (27)	21.4 (49)	1.5 (29)	2.6 (68)		70
RA73-06309	24	39.4	1.3	6.5		
RA73-TNF/MTX	8 (75)	8.5 (78)	0.6 (54)	1.9 (71)		70
RA74-06310	30	21.9	3.0	8.1		
RA74-TNF	13 (57)	14.3 (35)	2.3 (23)	2.9 (64)		50
RA75-06307	64	83.4	2.6	7.0		
RA75-MTX	22 (66)	11.5 (86)	0.8 (69)	2.2 (69)		70
RA76-06311	32	53.1	0.8	7.0		
RA76-TNF	8 (75)	4.9 (91)	0.1 (87)	1.7 (75)		80
RA77-06513	34	<3.5	1.3	6.2		
RA77-TNF/MTX	14 (59)	<3.5 (0)	1.4 (0)	5.3 (15)		20
RA78-06512	33	7.4	2.4	6.7		
RA78-MTX	8 (76)	4.9 (34)	3.0 (0)	8.3 (0)		0
RA79-06514	34	<3.5	1.3	8.3		
RA79-TNF/MTX	6 (82)	<3.5 (0)	0.9 (31)	5.4 (35)		20
RA80-1110505241	24	10.2	1.3	4.4		
RA80-TNF/MTX	36 (0)	<3.5 (100)	1.1 (15)	4.1 (7)		20
RA81-06305	22	29.1	0.3	6.0		
RA81-MTX	20 (9)	31.3 (0)	0.1 (33)	4.1 (32)		20
RA82-05602	31	<3.5	2.1	4.0		
RA82-MTX	39 (0)	<3.5 (0)	2.3 (0)	6.5 (0)		0
RA83-05607	29	4.6	2.5	7.8		
RA83-MTX	12 (59)	0 (100)	1.3 (52)	3.1 (60)		60
RA84-06302	30	9.6	2.5	7.4		
RA84-MTX	24 ()	<3.5 (100)	0.8 (68)	5.3 (28)		60

A = Affymetrix; R = real-time RT-PCR (validation of gene expression); P = real-time RT-PCR (validation of predictive gene); RF = rheumatoid factor; ESR = erythrocyte sedimentation rate; CRP = C-reactive protein concentration; HAQ = Health Assessment Questionnaire; DAS28 = disease activity score (28 joints); + = positive; - = negative; n.d. = not determined; aTNF = anti-TNF monoclonal antibody therapy; MTX = methotrexate therapy

TABLE 2

Correlations among clinical parameters (Pearson correlation test; pre- and post-anti-TNF α treatment)		
	r-value	p-value
Morning stiffness/Swollen joint count 28	0.718	0.004
Morning stiffness/Swollen joint count 68	0.664	0.010
Swollen joint count 28/Swollen joint count 68	0.990	0.000
Painful joint count 28/Painful joint count 68	0.794	0.001
ESR/CRP	0.854	0.000
ESR/VAS (physician)	0.764	0.001
ESR/DAS 28	0.813	0.000
CRP/Morning stiffness	0.733	0.003
CRP/Swollen joint count 28	0.762	0.002
CRP/Swollen joint count 68	0.728	0.003
CRP/DAS 28	0.786	0.001
DAS 28/Swollen joint count 28	0.891	0.000

TABLE 2-continued

Correlations among clinical parameters (Pearson correlation test; pre- and post-anti-TNF α treatment)		
	r-value	p-value
DAS 28/Swollen joint count 68	0.878	0.000
DAS 28/Painful joint count 28	0.660	0.010
VAS (physician)/Swollen joint count 68	0.672	0.008
VAS (physician)/Painful joint count 28	0.697	0.006
VAS (physician)/DAS 28	0.790	0.001
Different clinical parameters showed correlations in RA patients pre- and post anti-TNF α treatment (n = 14 in all cases).		
ESR = erythrocyte sedimentation rate;		
CRP = C-reactive protein;		
DAS 28 = disease activity score (28 joints); and		
VAS (physician) = visual analogue score (physician's global assessment)		

TABLE 3

Genes differentially regulated in peripheral blood monocytes of both RA patients versus normal donors and RA patients pre-versus post-anti-TNF α					
Affymetrix ID	Gene name	Increased (%)	Decreased (%) RA vs. ND	Fold change	SLR
36711_at	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F	71.43	14.29	3.44	1.78
38037_at	Diphtheria toxin receptor (DTR)	71.43	10.20	2.87	1.52
201386_s_at	DEAH (Asp-Glu-Ala-His) box polypeptide 15	2.04	73.47	-1.66	-0.73
201890_at	Ribonucleotide reductase M2 polypeptide	81.63	8.16	4.39	2.13
202219_at	Solute carrier family 6, member 8	71.43	8.16	8.44	3.08
202464_s_at	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	81.63	—	2.74	1.46
203115_at	Ferrochelatase (protoporphyrin)	83.67	8.16	3.87	1.95
203574_at	Nuclear factor, interleukin 3 regulated	77.55	—	2.16	1.11
203887_s_at	Thrombomodulin	71.43	16.33	2.49	1.32
203932_at	Major histocompatibility complex, class II, DM beta	2.04	75.51	-1.82	-0.87
204131_s_at	Forkhead box O3A	77.55	4.08	2.21	1.14
204419_x_at	Hemoglobin, gamma A, gamma G	75.51	6.12	2.88	1.52
204467_s_at	Synuclein, alpha (non A4 component of amyloid precursor)	71.43	4.08	3.60	1.85
204848_x_at	Hemoglobin, gamma A	75.51	6.12	3.83	1.94
205239_at	Amphiregulin (schwannoma-derived growth factor)	81.63	4.08	6.13	2.62
205571_at	Lipoyltransferase 1	—	79.59	-1.90	-0.93
205592_at	Solute carrier family 4, anion exchanger, member 1	77.55	10.20	4.83	2.27
205863_at	S100 calcium binding protein A12 (calgranulin C)	71.43	4.08	1.69	0.76
205900_at	Keratin 1 (epidermolytic hyperkeratosis)	75.51	6.12	4.03	2.01
205950_s_at	Carbonic anhydrase I	81.63	4.08	5.88	2.56
205987_at	CD1C antigen, c polypeptide	—	87.76	-2.93	-1.55
206025_s_at	Tumor necrosis factor, alpha-induced protein 6	71.43	—	3.85	1.94
206111_at	Ribonuclease, RNase A family, 2	73.47	—	1.95	0.97
206834_at	Hemoglobin, delta	83.67	10.20	4.08	2.03
207332_s_at	Transferrin receptor (p90, CD71)	81.63	2.04	2.35	1.23
208632_at	Ring finger protein 10	71.43	6.12	2.06	1.04
209007_s_at	Chromosome 1 open reading frame 63	4.08	73.47	-2.14	-1.10
209458_x_at	Hemoglobin, alpha 1, alpha 2	85.71	2.04	3.00	1.59
209795_at	CD69 antigen (p60, early T-cell activation antigen)	71.43	12.24	2.95	1.56
210027_s_at	APEX nuclease (multifunctional DNA repair enzyme) 1	—	75.51	-1.93	-0.94
210254_at	Membrane-spanning 4-domains, subfamily A, member 3	73.47	16.33	3.41	1.77
210338_s_at	Heat shock 70 kDa protein 8	6.12	71.43	-2.09	-1.06
211038_s_at	Hypothetical protein MGC12760	—	71.43	-2.07	-1.05
211458_s_at	GABA(A) receptor-associated protein like 1, like 3	71.43	—	1.95	0.96
211560_s_at	Aminolevulinate, delta-, synthase 2	87.76	4.08	24.35	4.61
211991_s_at	Major histocompatibility complex, class II, DP alpha 1	4.08	79.59	-3.01	-1.59
212199_at	Morf4 family associated protein 1-like 1	2.04	75.51	-1.94	-0.96
212224_at	Aldehyde dehydrogenase 1 family, member A1	4.08	75.51	-2.56	-1.36
212232_at	Formin binding protein 4	—	77.55	-1.83	-0.87
212534_at	Zinc finger protein 24 (KOX 17)	6.12	71.43	-1.49	-0.58
213142_x_at	Hypothetical protein LOC54103	4.08	73.47	-1.77	-0.82
214433_s_at	Selenium binding protein 1	71.43	10.20	4.59	2.20
215933_s_at	Hematopoietically expressed homeobox	—	75.51	-1.83	-0.87
217478_s_at	Major histocompatibility complex, class II, DM alpha	4.08	73.47	-2.02	-1.01
217736_s_at	Eukaryotic translation initiation factor 2-alpha kinase 1	75.51	—	1.97	0.98
219069_at	Ankyrin repeat domain 49	—	73.47	-1.59	-0.67
219093_at	Hypothetical protein FLJ20701	—	85.71	-3.32	-1.73
219228_at	Zinc finger protein 331	77.55	8.16	3.94	1.98
219607_s_at	Membrane-spanning 4-domains, subfamily A, member 4	91.84	—	2.96	1.57
221748_s_at	Tensin 1	81.63	4.08	4.29	2.10
221766_s_at	Family with sequence similarity 46, member A	—	71.43	-1.71	-0.77

TABLE 3-continued

Genes differentially regulated in peripheral blood monocytes of both RA patients versus normal donors and RA patients pre-versus post-anti-TNF α								
Affymetrix ID	Increased (%)	Decreased (%)	Fold change	SLR	Increased (%)	Decreased (%)	Fold change	SLR
	RA-aTNF vs. RA (all)				RA-aTNF vs. RA (responder)			
36711_at	28.57	61.22	-2.78	-1.48	12.00	80.00	-5.88	-2.56
38037_at	12.24	73.47	-2.59	-1.37	—	84.00	-3.70	-1.89
201386_s_at	44.90	14.29	1.43	0.51	60.00	—	1.81	0.85
201890_at	2.04	69.39	-3.86	-1.95	4.00	64.00	-3.88	-1.96
202219_at	12.24	59.18	-5.17	-2.37	4.00	72.00	-6.96	-2.80
202464_s_at	12.24	69.39	-2.18	-1.12	—	84.00	-3.01	-1.59
203115_at	20.41	63.27	-2.18	-1.12	16.00	72.00	-2.25	-1.17
203574_at	10.20	53.06	-1.54	-0.62	—	76.00	-2.06	-1.04
203887_s_at	12.24	65.31	-2.34	-1.23	—	76.00	-3.14	-1.65
203932_at	63.27	4.08	1.64	0.71	84.00	—	1.68	0.75
204131_s_at	18.37	55.10	-1.42	-0.50	4.00	64.00	-1.41	-0.50
204419_x_at	14.29	75.51	-3.18	-1.67	8.00	92.00	-4.16	-2.04
204467_s_at	24.49	65.31	-2.26	-1.18	16.00	80.00	-2.93	-1.55
204848_x_at	16.33	65.31	-3.22	-1.69	4.00	80.00	-4.63	-2.21
205239_at	20.41	71.43	-3.36	-1.75	—	96.00	-5.91	-2.56
205571_at	51.02	12.24	1.35	0.44	72.00	—	1.61	0.69
205592_at	16.33	65.31	-3.81	-1.93	8.00	76.00	-5.63	-2.49
205863_at	14.29	55.10	-1.49	-0.58	8.00	56.00	-1.56	-0.64
205900_at	20.41	67.35	-2.31	-1.21	16.00	84.00	-3.18	-1.67
205950_s_at	22.45	67.35	-2.87	-1.52	16.00	84.00	-4.14	-2.05
205987_at	63.27	2.04	1.72	0.79	68.00	—	1.72	0.78
206025_s_at	12.24	59.18	-1.97	-0.98	4.00	72.00	-2.74	-1.46
206111_at	8.16	67.35	-1.59	-0.67	—	72.00	-1.68	-0.75
206834_at	20.41	65.31	-3.13	-1.64	16.00	80.00	-4.59	-2.20
207332_s_at	2.04	79.59	-2.45	-1.29	—	84.00	-2.57	-1.36
208632_at	12.24	59.18	-1.71	-0.78	4.00	68.00	-1.69	-0.76
209007_s_at	57.14	14.29	1.54	0.62	76.00	4.00	1.87	0.90
209458_x_at	8.16	63.27	-2.09	-1.06	4.00	76.00	-2.60	-1.38
209795_at	14.29	75.51	-3.18	-1.67	16.00	76.00	-3.77	-1.92
210027_s_at	67.35	10.20	1.64	0.72	84.00	—	2.02	1.02
210254_at	14.29	79.59	-4.56	-2.19	20.00	76.00	-3.69	-1.88
210338_s_at	55.10	18.37	1.57	0.66	68.00	4.00	2.04	1.03
211038_s_at	42.86	16.33	1.29	0.37	56.00	4.00	1.46	0.55
211458_s_at	16.33	65.31	-1.92	-0.94	—	84.00	-2.75	-1.46
211560_s_at	16.33	75.51	-10.81	-3.43	8.00	80.00	-20.53	-4.36
211991_s_at	75.51	8.16	2.37	1.24	80.00	4.00	2.54	1.34
212199_at	59.18	10.20	1.56	0.64	80.00	—	2.11	1.08
212224_at	71.43	12.24	2.28	1.19	92.00	—	2.74	1.45
212232_at	48.98	14.29	1.27	0.35	72.00	—	1.57	0.65
212534_at	53.06	4.08	1.35	0.43	76.00	—	1.45	0.53
213142_x_at	51.02	12.24	1.25	0.32	72.00	—	1.51	0.60
214433_s_at	18.37	65.31	-3.08	-1.62	12.00	68.00	-3.55	-1.83
215933_s_at	55.10	6.12	1.51	0.59	76.00	0.00	1.85	0.88
217478_s_at	61.22	12.24	1.68	0.75	64.00	8.00	1.85	0.88
217736_s_at	14.29	51.02	-1.46	-0.54	8.00	60.00	-1.41	-0.50
219069_at	57.14	12.24	1.30	0.38	84.00	—	1.58	0.66
219093_at	71.43	8.16	2.43	1.28	84.00	—	2.59	1.37
219228_at	10.20	71.43	-3.26	-1.70	12.00	80.00	-4.62	-2.21
219607_s_at	6.12	73.47	-1.95	-0.96	—	80.00	-2.06	-1.04
221748_s_at	24.49	65.31	-2.12	-1.08	16.00	80.00	-2.42	-1.28
221766_s_at	53.06	10.20	1.30	0.38	80.00	—	1.66	0.73

The table presents the percentage of pairwise comparisons between the respective groups showing an increase or decrease for the fold-change/Signal Log Ratio (SLR; 51 candidate genes were selected); n = 7 each for the comparisons RA vs. ND and RA- α TNF vs. RA (all); n = 5 for the comparison RA- α TNF vs. RA (responder).

The pairwise comparison RA- α TNF vs. RA (all) is shown in the central 4 columns to assess the effect of treatment on differential gene expression in all TNF α -treated RA patients.

RA = rheumatoid arthritis (pre-anti-TNF α treatment); ND = normal donor; RA- α TNF = rheumatoid arthritis (post-anti-TNF α treatment)

TABLE 4

Genes differentially regulated in peripheral blood monocytes of both RA patients versus normal donors and RA patients pre-versus post-anti-TNF α therapy (PAM analysis)		
Affymetrix ID	Gene title	RA score
221622_s_at	Uncharacterized hypothalamus protein HT007	0.7405
218845_at	Dual specificity phosphatase 22	0.6694
200786_at	Proteasome (prosome, macropain) subunit, beta type, 7	0.5297
219607_s_at	Membrane-spanning 4-domains, subfamily A, member 4	0.4449
212886_at	DKFZP434C171 protein	0.2690
201407_s_at	Protein phosphatase 1, catalytic subunit, beta isoform	0.2653
212266_s_at	Splicing factor, arginine/serine-rich 5	0.1771
53912_at	Sorting nexin 11	0.1277
200090_at	Farnesyltransferase, CAAX box, alpha	0.1167
218025_s_at	Peroxisomal D3,D2-enoyl-CoA isomerase	0.1032
204232_at	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	0.0993
201722_s_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1	0.0942
218627_at	Hypothetical protein FLJ11259	0.0841
210027_s_at	APEX nuclease (multifunctional DNA repair enzyme) 1	0.0817
202322_s_at	Geranylgeranyl diphosphate synthase 1	0.0646
221689_s_at	Down syndrome critical region gene 5	0.0549
203356_at	Calpain 7	0.0535
211991_s_at	Major histocompatibility complex, class II, DP alpha 1	0.0515
218462_at	Brix domain containing 5	0.0378
218123_at	Chromosome 21 open reading frame 59	0.0173
214329_x_at	Tumor necrosis factor (ligand) superfamily, member 10	-0.0025
219067_s_at	Chromosome 10 open reading frame 86	-0.0046
205789_at	CD1D antigen, d polypeptide	-0.0104
209214_s_at	Ewing sarcoma breakpoint region 1	-0.0111
213427_at	Ribonuclease P 40 kDa subunit	-0.0471
209422_at/206567_s_at	PHD finger protein 20	-0.0480/-0.0698
201010_s_at	Thioredoxin interacting protein	-0.0520
200883_at	Ubiquinol-cytochrome c reductase core protein II	-0.0521
218454_at	Hypothetical protein FLJ22662	-0.0544
202918_s_at	Preimplantation protein 3	-0.0574
212204_at	DKFZP564G2022 protein	-0.0698
219452_at	Dipeptidase 2	-0.0800
209458_x_at	Hemoglobin, alpha 1, alpha 2	-0.0809
219889_at	Frequently rearranged in advanced T-cell lymphomas	-0.0832
201303_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 48	-0.0836
202510_s_at	Tumor necrosis factor, alpha-induced protein 2	-0.0872
221923_s_at	Nucleophosmin (nucleolar phosphoprotein B23, numatrin)	-0.0902
201887_at	Interleukin 13 receptor, alpha 1	-0.1075
211582_x_at	Leukocyte specific transcript 1, LST1	-0.1193
219030_at	CGI-121 protein	-0.1259
212706_at	RAS p21 protein activator 4/hypothetical protein FLJ21767	-0.1393
202902_s_at	Cathepsin S	-0.1644
200663_at	CD63 antigen (melanoma 1 antigen)	-0.1764
202138_x_at/209971_x_at	JTV1 gene	-0.1950/-0.2868
200851_s_at	KIAA0174	-0.2019
201109_s_at	Thrombospondin 1	-0.2079
213142_x_at	Hypothetical protein LOC54103	-0.2285
202531_at	Interferon regulatory factor 1	-0.2904
216274_s_at	SEC11-like 1 (<i>S. cerevisiae</i>)	-0.6951

Positive RA scores indicate genes overexpressed in RA,
negative RA scores indicate those underexpressed in RA.

PAM = Prediction analysis of microarrays;

bold and underlined letters indicate genes overlapping with the 51 genes identified by Affymetrix® gene expression profiling and analysis (see Table 3).

TABLE 5

Genes differentially regulated in RA-anti-TNF α responders versus RA-anti-TNF α non-responders (post anti-TNF α therapy)					
Affymetrix ID	In-creased (%)	De-creased (%)	Gene title	Fold change	SLR
200041_s_at	100	0	HLA-B associated transcript-1 (D6S81E)	2.53	1.34
200052_s_at	100	0	Interleukin enhancer binding factor 2, 45 kD (ILF2)	3.73	1.90
200064_at	100	0	Isolate Liv chaperone protein HSP90 beta (HSP90BETA) mRNA	2.66	1.41
200079_s_at	100	0	Lysyl-tRNA synthetase mRNA, complete cds; nuclear gene for mitochondrial product; alternatively spliced	2.16	1.11

TABLE 5-continued

Genes differentially regulated in RA-anti-TNF α responders versus RA-anti-TNF α non-responders (post anti-TNF α therapy)					
Affymetrix ID	In-creased (%)	De-creased (%)	Gene title	Fold change	SLR
200629_at	100	0	Tryptophanyl-tRNA synthetase (WARS)	2.14	1.10
200634_at	100	0	Profilin 1 (PFN1), mRNA	2.16	1.11
200802_at	100	0	Seryl-tRNA synthetase (SARS)	2.20	1.14
200860_s_at	100	0	Similar to KIAA1007 protein, clone MGC: 692, mRNA, complete cds	2.11	1.08
200983_x_at	0	100	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344)	-2.43	-1.28
200991_s_at	100	0	<i>Homo sapiens</i> KIAA0064 gene product (KIAA0064), mRNA	2.71	1.44
201112_s_at	100	0	Chromosome segregation 1 (yeast homolog)-like (CSE1L), mRNA	2.01	1.01
201214_s_at	100	0	Protein phosphatase 1, regulatory subunit 7 (PPP1R7), mRNA	2.17	1.12
201241_at	100	0	DEADH (Asp-Glu-Ala-AspHis) box polypeptide 1 (DDX1), mRNA	2.30	1.20
201263_at	100	0	Threonyl-tRNA synthetase (TARS), mRNA	2.14	1.10
201386_s_at	100	0	Dead box protein 15 mRNA, complete cds	2.22	1.15
201417_at	100	0	SRY (sex determining region Y)-box 4 /DEF = Human DNA sequence from clone RP3-322L4 on chromosome 6	3.18	1.67
201576_s_at	100	0	Galactosidase, beta 1 (GLB1), mRNA	2.00	1.00
201872_s_at	100	0	ATP-binding cassette, sub-family E (OABP), member 1	2.28	1.19
201892_s_at	100	0	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (14 kD, B14) (NDUFA6), mRNA	2.19	1.13
202174_s_at	100	0	Pericentriolar material 1 (PCM1), mRNA	2.08	1.06
202176_at	100	0	Excision repair cross-complementing rodent repair deficiency, complementation group 3 (ERCC3), mRNA	2.93	1.55
202220_at	100	0	KIAA0907 protein (KIAA0907), mRNA	2.39	1.26
202225_at	100	0	v-crk avian sarcoma virus CT10 oncogene homolog	2.10	1.07
202464_s_at	0	100	6-phosphofructo-2-kinasefructose-2,6-bisphosphatase 3 (PFKFB3), mRNA. /PROD = 6-phosphofructo-2-kinase-fructose-2,6-bisphosphatase 3	-3.25	-1.70
202545_at	100	0	KIAA0766 gene product (KIAA0766), mRNA	1.38	0.46
202838_at	100	0	N-acetylgalactosaminidase, alpha-(NAGA), mRNA	1.82	0.86
202896_s_at	0	100	Protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1), mRNA	-2.00	-1.00
202950_at	100	0	Crystallin, zeta (quinone reductase) (CRYZ), mRNA	2.51	1.33
203037_s_at	100	0	KIAA0429 gene product (KIAA0429), mRNA	2.41	1.27
203155_at	100	0	SET domain, bifurcated 1 (SETDB1), mRNA	4.23	2.08
203371_s_at	0	100	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3 (12 kD, B12) (NDUFB3), mRNA	-2.13	-1.09
203821_at	0	100	Diphtheria toxin receptor (DTX)	-3.63	-1.86
203887_s_at	0	100	Thrombomodulin (THBD), mRNA	-2.75	-1.46
203966_s_at	0	100	Protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform (PPM1A), mRNA	-2.73	-1.45
204192_at	100	0	CD37 antigen (CD37), mRNA	3.66	1.87
204419_x_at	0	100	Hemoglobin, gamma G (HBG2), mRNA	-5.50	-2.46
204566_at	100	0	Protein phosphatase 1D magnesium-dependent, delta isoform (PPM1D), mRNA	2.00	1.00
204689_at	100	0	Hematopoietically expressed homeobox (HHEX), mRNA	2.04	1.03
205239_at	0	100	Amphiregulin (schwannoma-derived growth factor) (AREG), mRNA	-3.38	-1.04
205249_at	0	100	Early growth response 2 (Krox-20 (<i>Drosophila</i>) homolog) (EGR2), mRNA	-2.55	-1.35
205552_s_at	100	0	2,5-oligoadenylate synthetase 1 (40-46 kD) (OAS1), transcript variant E16, mRNA	2.08	1.06
206115_at	0	100	Early growth response 3 (EGR3), mRNA. /PROD = early growth response 3	-6.54	-2.71
206584_at	0	100	<i>Homo sapiens</i> MD-2 protein (MD-2), mRNA	-2.16	-1.11
206877_at	0	100	<i>Homo sapiens</i> MAX dimerization protein (MAD), mRNA	-3.92	-1.97
207170_s_at	100	0	DKFZP586A011 protein (DKFZP586A011), mRNA	2.20	1.14
208631_s_at	100	0	78 kDa gastrin-binding protein mRNA, complete cds	2.04	1.03
208691_at	0	100	Transferrin receptor (p90, CD71), clone MGC: 3151, mRNA, complete cds	-2.30	-1.20
208868_s_at	0	100	<i>Homo sapiens</i> mRNA; cDNA DKFZp564N1272 (from clone DKFZp564N1272); complete cds	-3.18	-1.67
208869_s_at	0	100	GABA-A receptor-associated protein like 1 (GABARAPL1) mRNA, complete cds	-3.29	-1.72
208942_s_at	0	100	Translocation protein 1	-2.93	-1.55
209092_s_at	100	0	<i>Homo sapiens</i> clone 016b03 My027 protein mRNA, complete cds	2.07	1.05
209193_at	0	100	Protein kinase-related oncogene (PIM1) mRNA, complete cds	-2.51	-1.33
209200_at	100	0	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	2.48	1.31
209861_s_at	100	0	eIF-2-associated p67 homolog mRNA, complete cds	2.55	1.35
209967_s_at	0	100	Human mRNA for hCREM (cyclic AMP-responsive element modulator) type 2 protein, complete cds	-3.07	-1.62
210027_s_at	100	0	Apurinic endonuclease (APE) mRNA, complete cds. /PROD = apurinic endonuclease	2.23	1.16
210053_at	100	0	TATA box binding protein (TBP)-associated factor, RNA polymerase II, D, 100 kD	2.23	1.16
210172_at	0	100	Human mRNA for ZFM1 protein alternatively spliced product, complete cds. /PROD = ZFM1 protein, alternatively spliced product	-2.16	-1.11
210766_s_at	100	0	Trachea cellular apoptosis susceptibility protein (CSE1) mRNA, complete cds	2.28	1.19
210949_s_at	100	0	Similar to eukaryotic translation initiation factor 3, subunit 8 (110 kD), clone MGC: 8693, mRNA, complete cds	2.53	1.34
211458_s_at	0	100	GABA-A receptor-associated protein mRNA, complete cds. /PROD = GABA-A receptor-associated protein	-3.18	-1.67
211546_x_at	0	100	Human (clone 2-5) synuclein (NACP) mRNA, complete cds	-4.92	-2.30
212199_at	100	0	Human putative ribosomal protein S1 mRNA	2.22	1.15
212224_at	100	0	Aldehyde dehydrogenase 1, soluble (ALDH1), mRNA. /PROD = aldehyde dehydrogenase	3.18	1.67

TABLE 5-continued

Genes differentially regulated in RA-anti-TNF α responders versus RA-anti-TNF α non-responders (post anti-TNF α therapy)					
Affymetrix ID	In-creased (%)	De-creased (%)	Gene title	Fold change	SLR
			1, soluble		
212388_at	100	0	<i>Homo sapiens</i> mRNA for KIAA1057 protein, partial cds	3.10	1.63
212591_at	100	0	RBP1-like protein	2.03	1.02
212696_s_at	100	0	Ring finger protein 4	3.05	1.61
212709_at	100	0	KIAA0197 protein	2.10	1.07
212714_at	100	0	<i>Homo sapiens</i> mRNA; cDNA DKFZp586F1323 (from clone DKFZp586F1323)	2.13	1.09
212893_at	100	0	<i>Homo sapiens</i> mRNA; cDNA DKFZp564I052 (from clone DKFZp564I052)	2.01	1.01
212989_at	100	0	<i>Homo sapiens</i> mRNA for Hmob33 protein, 3 untranslated region	2.25	1.17
213410_at	100	0	<i>Homo sapiens</i> mRNA; cDNA DKFZp586F1019 (from clone DKFZp586F1019); partial cds	2.53	1.34
213515_x_at	0	100	Myosin, light polypeptide 4, alkali; atrial, embryonic	-4.69	-2.23
213528_at	100	0	<i>H. sapiens</i> novel gene from PAC 117P20, chromosome 1	2.87	1.52
213604_at	100	0	<i>Homo sapiens</i> clone 24582 mRNA sequence	2.07	1.05
213619_at	0	100	Heterogeneous nuclear ribonucleoprotein H1 (H)	-2.48	-1.31
213655_at	0	100	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	-3.03	-1.60
213743_at	100	0	Cyclin T2	2.08	1.06
213788_s_at	0	100	cDNA: FLJ23227 fis, clone CAE00645, highly similar to AF052138	-2.20	-1.14
213872_at	0	100	Hypothetical protein FLJ12619	-4.29	-2.1
213979_s_at	0	100	C-terminal binding protein 1	-4.41	-2.14
214257_s_at	0	100	SEC22, vesicle trafficking protein (<i>S. cerevisiae</i>)-like 1	-2.97	-1.57
214414_x_at	0	100	Hemoglobin, alpha 1	-2.04	-1.03
214696_at	0	100	<i>Homo sapiens</i> clone 24659 mRNA sequence /DEF = <i>Homo sapiens</i> clone 24659 mRNA sequence	-2.93	-1.55
214933_at	0	100	Calcium channel, voltage-dependent, PQ type, alpha 1A subunit	-2.17	-1.12
215043_s_at	0	100	<i>H. sapiens</i> SMA5 mRNA	-4.08	-2.03
215933_s_at	100	0	<i>H. sapiens</i> HEX gene encoding homeobox related protein	2.17	1.12
216199_s_at	100	0	Mitogen-activated protein kinase kinase kinase 4	2.77	1.47
216202_s_at	100	0	Serine palmitoyltransferase (LCB2) mRNA, partial cds	2.75	1.46
216996_s_at	100	0	KIAA0971 protein /DEF = <i>Homo sapiens</i> cDNA FLJ11495 fis, clone HEMBA1001950, highly similar to <i>Homo sapiens</i> mRNA for KIAA0971 protein	2.20	1.14
217554_at	0	100	ESTs, Hs.97109	-3.63	-1.86
217682_at	0	100	ESTs, Weakly similar to ALU7_HUMAN ALU	-3.01	-1.59
217840_at	100	0	DEAD-box protein abstrakt (ABS), mRNA	2.39	1.26
218229_s_at	100	0	KIAA1513 protein (KIAA1513), mRNA	2.07	1.05
218356_at	100	0	Cell division protein FtsJ (FJH1), mRNA	2.20	1.14
218432_at	100	0	F-box only protein 3 (FBXO3), mRNA	2.16	1.11
218589_at	100	0	Purinergic receptor (family A group 5) (P2Y5), mRNA	2.68	1.42
218604_at	100	0	Integral inner nuclear membrane protein (MAN1), mRNA	2.04	1.03
218689_at	100	0	Fanconi anemia, complementation group F (FANCF), mRNA	8.94	3.16
218889_at	100	0	Hypothetical protein FLJ12820 (FLJ12820), mRNA	2.01	1.01
218973_at	100	0	Hypothetical protein FLJ13119 (FLJ13119), mRNA	2.07	1.05
219069_at	100	0	Hypothetical protein FLJ20189 (FLJ20189), mRNA	2.23	1.16
219093_at	100	0	Hypothetical protein FLJ20701 (FLJ20701), mRNA	3.32	1.73
219099_at	100	0	<i>Homo sapiens</i> chromosome 12 open reading frame 5 (C12ORF5), mRNA	2.13	1.09
219176_at	100	0	Hypothetical protein FLJ22555 (FLJ22555), mRNA	2.13	1.09
219243_at	100	0	Hypothetical protein FLJ11110 (FLJ11110), mRNA	2.07	1.05
219363_s_at	100	0	CGI-12 protein (LOC51001), mRNA	2.31	1.21
219434_at	0	100	Triggering receptor expressed on myeloid cells 1 (TREM1), mRNA	-4.35	-2.12
221485_at	0	100	betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	-2.71	-1.44
221652_s_at	100	0	PNAS-25 mRNA, complete cds.	2.55	1.35
221755_at	100	0	<i>Homo sapiens</i> mRNA for FLJ00043 protein, partial cds	3.44	1.09
221970_s_at	100	0	<i>Homo sapiens</i> cDNA: FLJ21737 fis, clone COLF3396	2.41	1.27
222127_s_at	0.1	0	<i>Homo sapiens</i> cDNA FLJ13399 fis, clone PLACE1001395 /DEF = <i>Homo sapiens</i> cDNA FLJ13399 fis, clone PLACE1001395	2.31	1.21
36711_at	0	100	Novel MAFF (v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein F) LIKE protein	-3.54	-1.16
38037_at	0	100	Heparin-binding EGF-like growth factor mRNA, complete cds	-3.63	-1.86
AFFX-BioB-M_at	0	100	<i>E. coli</i> 7,8-diamino-pelargonic acid (bioA), biotin synthetase (bioB), 7-keto-8-amino-pelargonic acid synthetase (bioF), bioC protein, and dethiobiotin synthetase (bioD), complete cds	-4.69	-2.58
AFFX-r2-Ec-bioC-3_at	0	100	<i>Escherichia coli</i> /REF = J04423 /DEF = <i>E coli</i> bioC protein corresponding to nucleotides 4609-4883 of J04423 /LEN = 777 (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)	-4.22	-1.86

The listed genes (n = 117) show differential expression in 100% of the pairwise comparisons;

bold and underlined letters indicate genes overlapping with the 51 genes identified by Affymetrix® gene expression profiling and analysis (see Table 3)

TABLE 6

Correlations between clinical parameters and differentially expressed genes (Pearson correlation test; pre- and post-anti-TNF α treatment; n = 7 for all; bold letters identify genes occurring twice, bold and italics letters identify genes occurring ≥ 3 times)				
	Affymetrix_ID	Gene title	r-value	p-value
Pre-anti-TNF α treatment				
Leuko/	202219_at	Solute carrier family 6	0.901	0.006**
	205239_at	Amphiregulin	0.879	0.009**
Thromb/	205900_at	Keratin 1	0.923	0.003**
Mono/	204018_x_at	Hemoglobin, alpha 1	-0.908	0.005**
GPT/	203932_at	MHC-II, DM beta	-0.912	0.004**
	218589_s_at	Purinergic receptor P2Y, G-protein coupled 5	-0.919	0.003**
Hb/	205900_at	Keratin 1	-0.944	0.001**
MoStiff/	202219_at	Solute carrier family 6	0.893	0.007**
	203932_at	MHC-II, DM beta	-0.898	0.006**
	204131_s_at	Forkhead box O3A	0.917	0.004**
	205239_at	Amphiregulin	0.954	0.001**
	207332_s_at	Transferrin receptor (p90, CD71)	0.926	0.003**
	208632_at	Ring finger protein 10	0.913	0.004**
DisDur/	212232_at	Formin binding protein 4	0.955	0.001**
	213142_x_at	Hypothetical protein LOC54103	0.877	0.009**
Post-anti-TNF α treatment				
ESR/	38037_at	Diphtheria toxin receptor	0.928	0.003 **
	203821_at	Heparin-binding EGF-like growth factor	0.928	0.003 **
	205571_at	Lipoyltransferase 1	-0.898	0.006 **
	210027_s_at	APEX nuclease (multifunct. DNA repair enzyme) 1	-0.944	0.001 **
	211458_s_at	GABA(A) receptor-associated protein like 1 / 3	0.947	0.001 **
	212232_at	Formin binding protein 4	-0.890	0.007 **
	219228_at	Zinc finger protein 331	0.894	0.007**
CRP/	38037_at	Diphtheria toxin receptor	0.968	0.000 **
	203821_at	Heparin-binding EGF-like growth factor	0.963	0.001 **
	205571_at	Lipoyltransferase 1	-0.946	0.001 **
	210027_s_at	APEX nuclease (multifunct. DNA repair enzyme) 1	-0.950	0.001 **
	211458_s_at	GABA(A) receptor-associated protein like 1 / 3	0.948	0.001 **
	212232_at	Formin binding protein 4	-0.908	0.005 **
Thromb/	205571_at	Lipoyltransferase 1	-0.934	0.002 **
	212232_at	Formin binding protein 4	-0.921	0.003 **
Granulo/	213427_at	Ribonuclease P 40 kDa subunit	-0.875	0.010**
Hb/	38037_at	Diphtheria toxin receptor	-0.930	0.002 **
	203821_at	Heparin-binding EGF-like growth factor	-0.948	0.001 **
	203932_at	MHC class II, DM beta	0.885	0.008**
	210027_s_at	APEX nuclease (multifunct. DNA repair enzyme) 1	0.971	0.000 **
	211458_s_at	GABA(A) receptor-associated protein like 1 / 3	-0.951	0.001 **
Dis_act/	36711_at	v-maf fibrosarc. oncogene homolog F (avian)	0.932	0.002**
	205552_s_at	2',5'-oligoadenylate synthetase 1, 40/46 kDa	-0.951	0.001**
	211458_s_at	GABA(A) receptor-associated protein like 1 / 3	0.896	0.006 **
	212232_at	Formin binding protein 4	-0.898	0.006 **
DAS28/	36711	v-maf fibrosarc. oncogene homolog F (avian)	0.940	0.002**
	205552_s_at	2',5'-oligoadenylate synthetase 1, 40/46 kDa	-0.898	0.006**
	205571_at	Lipoyltransferase 1	-0.937	0.002 **
	211458_s_at	GABA(A) receptor-associated protein like 1 / 3	0.897	0.006 **
	212232_at	Formin binding protein 4	-0.973	0.000 **
Sw28/	219607_s_at	Membrane-spanning 4-domains, subfam. A, memb. 4	0.931	0.002**

GPT = glutamate pyruvic transferase;

Hb = haemoglobin;

MoStiff = Morning stiffness (minutes);

DisDur = Disease duration (years);

ESR = erythrocyte sedimentation rate;

CRP = C-reactive protein;

DAS 28 = disease activity score (28 joints);

Sw = number of swollen joints (28 joints)

TABLE 7

TaqMan PCR validation in anti-TNF α -treated RA patients and normal donors						
Time point	Gene Description	Gene title	Applera ID	PCR		
				RA- α TNF (responder) versus ND (RQ; Means $\pm$ SEM)	Max - Δ RQ (Therapy)	p value (U-Test)
Validated genes						
BL	AREG	Amphiregulin	Hs00155832_m1	10.23 $\pm$ 2.93	-7.60	0.000
BL	CA-1	Carbonic anhydrase 1	Hs00266139_m1	6.83 $\pm$ 3.49	-5.93	n.s.
BL	CLC	Charcot-Leyden crystal protein	Hs00171342_m1	5.36 $\pm$ 4.82	-3.26	0.041
BL	CLU	Clusterin C	Hs00156548_m1	3.94 $\pm$ 2.87	-2.77	n.s.
BL	TNFAIP6	Tumor necrosis factor alpha induced protein 6	Hs00218482_m1	1.71 $\pm$ 0.40	0.82	0.000
BL	THBD	Thrombomodulin	Hs00264920_s1	1.58 $\pm$ 1.08	-0.53	0.041
BL	MS4A4A	Membrane-spanning 4-domains, subfamily A, member 4	Hs00254770_m1	1.54 $\pm$ 0.42	0.71	0.041
BL	DTR	Diphtheria toxin receptor	Hs00181813_m1	1.21 $\pm$ 0.44	-1.10	n.s.
BL	S100A12	S100 calcium binding protein A1	Hs00194525_m1	1.07 $\pm$ 0.21	0.11	0.041
BL	HT007	Uncharacterized hypothalamus protein HT007	Hs00218482_m1	0.51 $\pm$ -0.09	0.01	0.000
BL	HLA-DR	MHC-class-II; HLA-DR alpha	Hs00219578_m1	0.59 $\pm$ -0.15	0.09	0.000
BL	LOC54103	Hypothetical protein LOC54103	Hs00367929_m1	0.90 $\pm$ -0.21	-0.24	0.041
BL	TNF	Tumor necrosis factor alpha	Hs00174128_m1	1.22 $\pm$ 0.53	-0.84	0.041
BL	IL1B	Interleukin 1 beta	Hs00174097_m1	1.14 $\pm$ 0.42	-0.28	0.041
BL	PSMB7	Proteasome subunit beta type 7 precursor	Hs00160607_m1	0.72 $\pm$ -0.19	0.16	0.041
BL	KIAA0174	Protein KIAA0174	Hs00796085_sh	0.89 $\pm$ 0.30	0.08	0.041
BL	SPC18	Microsomal signal peptidase 18 kDa subunit	Hs00819308_m1	0.96 $\pm$ 0.11	-0.25	0.041
Discrepancies between Affymetrix and TaqMan PCR						
BL	LIPT1	Lipoyltransferase 1	Hs00376962_m1	2.17 $\pm$ 0.54	-0.68	0.000
BL	ZNF361	Ring zinc finger protein 361	Hs00367929_m1	0.55 $\pm$ -0.11	-0.14	0.000
BL	THBS1	Thrombospondin-1	Hs00170236_m1	0.88 $\pm$ 0.25	-0.34	n.s.
BL	IRF1	Interferon regulatory protein 1	Hs00233698_m1	4.95 $\pm$ 0.18	3.37	0.000
BL	PPP1CB	Protein phosphatase 1, catalytic subunit, beta isoform	Hs00160349_m1	0.93 $\pm$ 0.09	-0.28	0.041
Affymetrix						
	Time point	Affymetrix ID	RA- α TNF (responder) versus ND (% of comp.)	FC RA- α TNF (responder) versus ND (Means)	RA- α TNF all versus ND (% of comp.)	FC RA- α TNF all versus ND (Means)
Validated genes						
	BL	205239_at	82.86	5.48	81.63	6.13
	BL	205950_s_at	88.57	4.92	81.63	5.88
	BL	206207_at	62.86	2.46	73.47	3.97
	BL	222043_at	68.57	2.57	75.51	2.68
	BL	206026_s_at	62.86	2.07	73.27	2.24
	BL	203887_s_at	74.29	2.64	71.43	2.49
	BL	219607_s_at	88.57	2.66	91.84	2.96
	BL	38037_at	68.57	2.91	71.43	2.87
	BL	205863_at	62.86	1.50	71.43	1.69
	BL	221622_s_at	-88.57	-1.74	-85.71	-1.66
	BL	208894_at	-65.71	-1.77	-75.51	-2.15
	BL	222150_s_at	-80.00	-1.84	-73.47	-1.71
	BL	207113_s_at	34.29	1.03	-46.94	-1.28
	BL	205067_at	57.14	1.62	57.02	1.44
	BL	200786_at	-54.29	-1.27	-57.74	-1.27
	BL	200851_s_at	-42.86	-1.17	-46.94	-1.23
	BL	201290_at	-17.14	-1.04	-72.24	-1.03
Discrepancies between Affymetrix and TaqMan PCR						
	BL	205571_at	-74.29	-1.74	-79.59	-1.90
	BL	219228_at	77.14	4.19	77.55	3.94
	BL	201110_s_at	85.71	16.35	77.55	12.60

TABLE 7-continued

TaqMan PCR validation in anti-TNF α -treated RA patients and normal donors					
BL	202531_at	-40.00	-1.30	-55.70	-1.44
BL	201409_s_at	60.00	1.63	57.14	1.69

Validation of 22 selected genes from Affymetrix ® gene expression profiling by Taqman real-time RT-PCR (10 anti-TNF α -treated RA patients prior to therapy; 14 normal donors – ND); genes differentially expressed (decreased: <–70%; increased: >70%) in RA versus ND according to the Affymetrix ® analysis are shown in normal type, equally-expressed genes are displayed in italics; RQ = relative quantity; FC = fold-change; BL = baseline (pre-antiTNF α therapy)

TABLE 8

Correlations between TaqMan PCR results and the ACR response in anti-TNF α -treated RA patients						
Gene description	Time point	Gene title	Applera ID	r-value	p	n
CA1	w 12	Carbonic anhydrase 1	Hs00266139_m1	0.642	0.045	10
CA1	w 26			0.962	0.000	9
CLC	w 4	Charcot-Leyden crystal protein	Hs00171342_m1	0.766	0.027	8
THBD	w 4	Thrombomodulin	Hs00264920_s1	0.766	0.027	8
THBS1	w 26	Thrombospondin 1	Hs00170236_m1	–0.710	0.032	9
IRF1	w 4	Interferon regulatory factor 1	Hs00233698_m1	0.778	0.023	8

TABLE 9

Genes differentially regulated in RA-anti-TNF α responders versus RA-anti-TNF α non-responders (pre-anti-TNF α therapy; predictive genes)					
Affymetrix ID	Gene title	Increased (%)	Decreased (%)	Fold-Change	SLR
39248_at	Aquaporin 3	10	80	–4.6	–2.19
200061_s_at	Similar to ribosomal protein S24, clone MGC: 8595	0	80	–1.39	–0.47
200087_s_at	Transmembrane emp24 domain trafficking protein 2	0	80	–1.6	–0.63
200642_at	Superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1)	0	80	–1.8	–0.84
200655_s_at	Calmodulin 1 (phosphorylase kinase, delta)	0	80	–1.5	–0.59
200745_s_at	Guanine nucleotide binding protein (G protein), beta polypeptide 1	80	0	1.6	0.66
200772_x_at	Prothymosin, alpha (gene sequence 28)	80	0	1.7	0.75
201193_at	<i>Homo sapiens</i> isocitrate dehydrogenase 1 (NADP+) soluble (IDH1)	0	80	–1.4	–0.49
201690_s_at	Tumor protein D52	0	80	–3.3	–1.73
201693_s_at	Early growth response 1	80	0	3.1	1.61
201889_at	<i>Homo sapiens predicted osteoblast protein (GS3786)</i>	0	100	–1.7	–0.74
202110_at	Cytochrome c oxidase subunit VIIb	0	80	–1.6	–0.64
202157_s_at	CUG triplet repeat, RNA binding protein 2	0	80	–1.6	–0.64
202233_s_at	Ubiquinol-cytochrome c reductase hinge protein	0	80	–1.7	–0.74
202378_s_at	Homos sapiens leptin receptor gene-related protein (HS0BRGRP)	80	20	1.15	0.20
202664_at	Wiskott-Aldrich syndrome protein interacting protein	80	0	1.9	0.91
202910_s_at	CD97 antigen	80	10	1.6	0.70
202922_at	Glutamate-cysteine ligase, catalytic subunit	0	80	–2.3	–1.17
202950_at	Crystallin, zeta (quinone reductase)	80	0	2.2	1.16
203097_s_at	Rap guanine nucleotide exchange factor (GEF) 2	20	80	–1.3	–0.38
203231_s_at	Ataxin 1	0	80	–8.2	–3.03
203300_x_at	Adaptor-related protein complex 1, sigma 2 subunit	80	20	1.9	0.89
204160_s_at	Ectonucleotide pyrophosphatase/phosphodiesterase 4	10	80	–2.4	–1.27
204750_s_at	Desmocollin 2	80	0	12.9	3.69
204777_s_at	MAL, T-cell differentiation protein	10	80	–2.6	–1.39
205042_at	Glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase	0	80	–1.9	–0.95
205114_s_at	Chemokine (C—C motif) ligand 3	80	0	2.0	0.96
205624_at	Carboxypeptidase A3	0	80	–4.0	–2.00
206207_at	Charcot-Leyden crystal protein	0	90	–4.9	–2.29
206790_s_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7 kDa	0	80	–1.5	–0.61
207008_at	Interleukin 8 receptor, beta	90	0	4.0	2.00
207815_at	Platelet factor 4 variant 1	20	80	–2.4	–1.28
208051_s_at	Poly(A) binding protein interacting protein 1	0	80	–1.6	–0.68
208161_s_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	80	0	4.3	2.10
208637_x_at	Actinin, alpha 1	80	0	2.4	1.24
208918_s_at	NAD kinase	80	0	1.5	0.59
208982_at	Platelet/endothelial cell adhesion molecule (CD31 antigen)	90	0	1.6	0.71
209009_at	Esterase D/fornylglutathione hydrolase	80	20	1.5	0.54
209020_at	Chromosome 20 open reading frame 111	80	20	1.5	0.54
209146_at	Sterol-C4-methyl oxidase-like	0	80	–1.9	–0.89
209193_at	PIM-1 oncogene	10	80	–2.3	–1.19

TABLE 9-continued

Genes differentially regulated in RA-anti-TNF α responders versus RA-anti-TNF α non-responders (pre-anti-TNF α therapy; predictive genes)					
Affymetrix ID	Gene title	Increased (%)	Decreased (%)	Fold-Change	SLR
209710_at	GATA binding protein 2	20	80	-3.5	-1.81
210042_s_at	Cathepsin Z	80	20	1.9	0.94
210184_at	<i>Integrin alpha-X (antigen CD11c)</i>	<u>100</u>	0	2.3	1.22
210732_s_at	Lectin, galactoside-binding, soluble, 8 (galectin 8)	80	0	2.4	1.23
210895_s_at	CD86 antigen (CD28 antigen ligand 2, B7-2 antigen)	80	10	1.9	0.92
211506_s_at	Interleukin 8	90	0	3.2	1.67
211734_s_at	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide	0	80	-5.0	-2.31
211995_x_at	Actin, gamma 1	80	0	1.4	0.46
212314_at	KIAA0746 protein	10	80	-1.7	-0.73
212335_at	Glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)	80	0	1.5	0.54
212386_at	Transcription factor 4	0	80	-2.5	-1.29
212671_s_at	Major histocompatibility complex, class II, DQ alpha 1	10	80	-3.3	-1.72
212897_at	Cell division cycle 2-like 6 (CDK8-like)	80	0	1.8	0.83
212999_x_at	Major histocompatibility complex, class II, DQ beta 1	80	20	1.8	0.88
213309_at	Phospholipase C-like 2	0	80	-1.9	-0.9
213506_at	Coagulation factor II (thrombin) receptor-like 1	80	0	2.4	1.23
213883_s_at	TM2 domain containing 1	10	80	-1.4	-0.46
214305_s_at	Splicing factor 3b, subunit 1, 155 kDa	80	20	1.5	0.62
214512_s_at	SUB1 homolog (<i>S. cerevisiae</i>)	0	80	-1.7	-0.76
214807_at	MRNA; cDNA DKFZp564O0862	80	10	1.7	0.79
214953_s_at	Amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer disease)	90	0	1.9	0.93
215726_s_at	Cytochrome b-5	0	80	-2.1	-1.08
216016_at	Cold autoinflammatory syndrome 1	80	0	6.1	2.60
217722_s_at	Neugrin, neurite outgrowth associated	0	90	-1.9	-0.91
217753_s_at	Ribosomal protein S26, 40S ribosomal protein	10	80	-2.9	-1.51
217970_s_at	CCR4-NOT transcription complex, subunit 6	0	80	-1.9	-0.91
218190_s_at	Ubiquinol-cytochrome c reductase complex (7.2 kD)	0	80	-2.0	-1.03
218345_at	Hepatocellular carcinoma-associated antigen 112	10	80	-3.9	-1.95
218486_at	Kruppel-like factor 11	90	0	2.1	1.06
218545_at	GGA binding partner	0	80	-1.6	-0.67
218728_s_at	Cornichon homolog 4 (<i>Drosophila</i>)	0	80	-1.8	-0.84
219269_at	Hypothetical protein FLJ21616	0	90	-2.1	-1.06
219410_at	<i>Homo sapiens hypothetical protein FLJ10134</i>	0	<u>100</u>	-4.7	-2.33
219862_s_at	Nuclear prelamin A recognition factor	80	0	1.5	0.62
219905_at	Erythroblast membrane-associated protein	0	80	-1.8	-0.85
220532_s_at	LR8 protein	10	80	-5.2	-2.39
221011_s_at	Likely ortholog of mouse limb-bud and heart gene (LBH)	0	80	-2.8	-1.47
221042_s_at	Calmin (calponin-like, transmembrane)	80	0	1.9	0.89
221434_s_at	Chromosome 14 open reading frame 156	0	80	-1.7	-0.72
221737_at	Guanine nucleotide binding protein (G protein) alpha 12	10	80	-2.0	-1.96
AFFX-M27830_5_at	SRY (sex determining region Y)-box 18	80	0	4.3	2.09

The criterion for gene selection (total of 82) was the percentage of pairwise comparisons between future RA responders and future RA non-responders to anti-TNF α therapy showing an increase or decrease for the fold-change/Signal Log Ratio prior to therapy; bold letters indicate a percentage of 80% for the pairwise comparisons (total of 10), bold and italic letters ***90%***, bold, italic, and underlined letters ***100%*** in the latter case, also the gene names are shown in bold, italic, and underlined letters.

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SUMMARY OF SEQUENCE LISTING

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SUMMARY OF SEQUENCE LISTING

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full-length n.t.		

SUMMARY OF SEQUENCE LISTING

SEQ ID NO:	AffymetrixID	Sequence
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302	CD11c	mttrraalllftalatslgfnldteeltafrvds agfgdsvvgyanswvvvgapqkitaanqtgglyq cgystgacepigliqvpeavnmslglslasttsp sqllacgptvhhcgrnmyltglcflfgptqltq rlpvsrqecprqeqdivflidgsgsisrnfatm mnfvravisqfqrpstqfslmqfsnkgfthftfe efrrssnpllslasvhlqgftytataignvvhr lfhasygarrdaakilivitdgkkgdsldykdv ipmadaagiiryaigvglafqnrnswnkelndias kpsqehifkvedfdalkdiqnqlkekifaiegte tsssssfelemaqegfsavftpdgvpvgavgsft wsggaflyppnmsptfmrnsqenvdmrdsylgys telalwkvgqslvlgapryghtgkaviftqvsrq wrnkkaevtqtqigsyfgaslcsvdvdsgstdlv ligaphyieqtrggqsvcpplrgrwrrwcdavl ygeqghpwgrfgaaltvlgdvngdkltdvviqap geeenrgavylfhgvlgpsispsghsqriagsqls srlqyfgqalsggqdltqdgldvavgargqvll lrrpvlwvgvsmqfipaeiprsafecreqvvse qtlvqsniclyidkrsknllqsrldlqssvtdldla

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SUMMARY OF SEQUENCE LISTING

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303	Adalimumab V _L	Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
304	Adalimumab V _H	Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
305	Adalimumab V _L CDR3	Gln Arg Tyr Asn Arg Ala Pro Tyr Xaa Xaa = Thr or Ala
306	Adalimumab V _H CDR3	Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Xaa Xaa = Tyr or Asn
307	Adalimumab V _L CDR2	Ala Ala Ser Thr Leu Gln Ser
308	Adalimumab V _H CDR2	Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu Gly
309	Adalimumab V _L CDR1	Arg Ala Ser Gln Gly Ile Arg Asn Tyr Leu Ala
310	Adalimumab V _H CDR1	Asp Tyr Ala Met His

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 310

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 <213> ORGANISM: Homo sapiens
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 <223> OTHER INFORMATION: AffymetrixID: 39248_at

<400> SEQUENCE: 1

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cataatgcag gcatgaaggg tggagtgaag tcaggtcata agtttcatgt ttgcttttgt    180
tttgttttgt ttttaatgta tgtagcagat gttacagtct tagggatccg ggatgggaga    240
ccccacttta gaaagggtcg tcactccttt aatcctcta                               279
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<210> SEQ ID NO 2
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 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(483)
 <223> OTHER INFORMATION: AffymetrixID: 200061_s_at

<400> SEQUENCE: 2

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agacagaaat tcgggaaaaa ctagccaaaa tgtacaagac cacaccggat gtcattcttg    180
tatttggatt cagaactcat tttggtggtg gcaagacaac tggctttggc atgatttatg    240
attccctgga ttatgcaaag aaaaatgaac ccaaacatag acttgcaaga catggcctgt    300
atgagaagaa aaagacctca agaaagcaac gaaaggaacg caagaacaga atgaagaaag    360
tcagggggac tgcaaaggcc aatgttggtg ctggcaaaaa gtgagctgga gattggatca    420
cagccgaagg agtaaagggt ctgcaatgat gttagctgtg gccactgtgg atttttcgca    480
aga                                                    483
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<210> SEQ ID NO 3
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 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
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 <221> NAME/KEY: misc_feature
 <222> LOCATION: (227)..(227)
 <223> OTHER INFORMATION: n is a, c, g, or t
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(474)
 <223> OTHER INFORMATION: AffymetrixID: 200087_s_at

<400> SEQUENCE: 3

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tttttggcac atgtgaatct tgttttgtgt aaaatgaaat tactttctct tgttctctga    120
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tgatgggttt aaaattaaaa gagcatccgg ttttggtatg gggatgatcc aggattatgt	180
tgtgactgat acatattagt tacttggtct tttttttttt ttttttngga tctttgcaag	240
ggcaaaacta caagtaacga gttttatata attaatTTaa atttgttaca ggttttcatg	300
ttcaggataa accatacttc caccttgggt gagaacactt gcaacagttt attaatgagg	360
tgactttcac cttaggacaa ctggtgcatg ccaagttttt tgtgtgtgtg aaacacttca	420
aaactgattt aaaagatgta aattttaaTt tggttgtatc taatatgccc cagg	474

<210> SEQ ID NO 4
 <211> LENGTH: 452
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(452)
 <223> OTHER INFORMATION: AffymetrixID: 200642_at

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catgagtttg gagataatac ggcaggctgt accagtgcag gtccctcactt taatcctcta	180
tccagaaaac acggtgggcc aaaggatgaa gagaggcatg ttggagactt gggcaatgtg	240
actgctgaca aagatggtgt ggccgatgtg tctattgaag attctgtgat ctactctca	300
ggagaccatt gcatcattgg ccgcacactg gtggtccatg aaaaagcaga tgacttgggc	360
aaaggtggaa atgaagaaag tacaaagaca ggaaacgctg gaagtcgttt ggcttgtggt	420
gtaattggga tcgccaata aacattccct tg	452

<210> SEQ ID NO 5
 <211> LENGTH: 457
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
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 <222> LOCATION: (1)..(457)
 <223> OTHER INFORMATION: AffymetrixID: 200655_s_at

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gataaaccgt tgagacgtgg cccactggt aggatggtcc tcttgactt cgtgtgctcc	180
gaccatggt gacgatgaca caccctggtg gcatgccctg gtatgttgggt ttagcgttgt	240
ctgcattgtt ctagagtga acaggtgtca ggctgtcact gttcacacaa atttttaata	300
agaaacattt accaaggag catctttgga ctctctgttt taaaacctt ctgaaccatg	360
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ttcaaagaaa ttacagttta cgtccattcc aagttgt	457

<210> SEQ ID NO 6
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<223> OTHER INFORMATION: AffymetrixID: 200745_s_at

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ttgtgaagtt ggaggggaagt ttataatagc ctaacactac cccaccccca actaggagga      180
acctctgttt tcaagagaga tgcctgtcct gtgcttgat agtcagtaa ttatttgtgt      240
atgaaacaat gtacaaatca atgttttgaa aataatgac tcagactttc taagttaaag      300
ttttaaaaat ttgattgttt tgccatatgt ggtgggttta ctcttagaat cgcagtgtgt      360
agaaaatgct caaaagtgc tatgggactc agtccttagg tgtcttttt cttttaagaa      420
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<223> OTHER INFORMATION: n is a, c, g, or t

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<223> OTHER INFORMATION: n is a, c, g, or t

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<223> OTHER INFORMATION: n is a, c, g, or t

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<223> OTHER INFORMATION: n is a, c, g, or t

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<223> OTHER INFORMATION: n is a, c, g, or t

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<223> OTHER INFORMATION: n is a, c, g, or t

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<223> OTHER INFORMATION: n is a, c, g, or t

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<223> OTHER INFORMATION: n is a, c, g, or t
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<222> LOCATION: (327)..(327)
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<223> OTHER INFORMATION: n is a, c, g, or t
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<223> OTHER INFORMATION: n is a, c, g, or t
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<223> OTHER INFORMATION: n is a, c, g, or t
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<223> OTHER INFORMATION: n is a, c, g, or t
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<223> OTHER INFORMATION: n is a, c, g, or t
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<222> LOCATION: (507)..(507)
<223> OTHER INFORMATION: n is a, c, g, or t
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<221> NAME/KEY: misc_feature
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<223> OTHER INFORMATION: AffymetrixID: 200772_x_at

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ctcgctttct ttttaatccc cntgcatcgg atcaccggcg tgccccacca tgtcagacgc      180
agccgtagac accagctccg aaatcaccac caaggactta aaggagaaga aggaagtgtg      240
ggaagaggca gaaanatgga agaganncgc ccctgctnaa cgggnaatgc tnnananant      300
gaggaanaat ggggnagcag gaggctngac aatngaggta gacgaangaa ganggaagan      360
anggtgggga nggaangagg anggaggana gaangaaggt gantggtgan ggaangagga      420
ntggangant gaangatgag gaagctgagt cagctacggg caagcgggca gctgaangat      480
gatgaggatg acgatgtcga taccaangaa gcagaagacc gacgaggatg actagacagc      540


<210> SEQ ID NO 8
<211> LENGTH: 492
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(492)
<223> OTHER INFORMATION: AffymetrixID: 201193_at

<400> SEQUENCE: 8

tagccacagt attgtccctt aaaatatgca taaagtagaa attcactgcc tccccctcct      60
gtccatgacc ttgggcacag ggaagtcttg gtgtcataga tatcccgttt tgtgaggtag      120
agctgtgcat taaacttgca catgactgga acgaagtatg agtgcaactc aaatgtgttg      180
aagatactgc agtcattttt gtaaagacct tgctgaatgt ttccaataga ctaaatactg      240
tttaggccgc aggagagttt ggaatccgga ataaatacta cctggagtct tgtcctctcc      300
atttttctct ttctcctcct ggccctggcct gaatattata ctactctaaa tagcatattt      360
catccaagtg caataatgta agctgaatct tttttggact tctgctggcc tgttttattt      420
cttttatata aatgtgattt ctcagaaatt gatattaaac actatcttat cttctcctga      480
actgttgatt tt                                     492


<210> SEQ ID NO 9
<211> LENGTH: 391
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(391)
<223> OTHER INFORMATION: AffymetrixID: 201690_s_at

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<400> SEQUENCE: 9

```
atgatactgt agaacctgtc tcctactttg aaaactgaat gtcagggtg agtgaatcaa    60
agtgtctaga catatttgca tagaggccaa ggtattctat tctaataact gcttactcaa    120
cactaccacc ttttccttat actgtatatg attatggcct acaatgttgt atttgttatt    180
tattaaattg tgattgtttt attattgttt atgccaaatg ttaactgcc a gcttggagt    240
gacctaaagc attttttaa agcatggcta gatttacttc agtataaatt atcttatgaa    300
aaccaaaatt taaaagccac aggtgttgat tgttataaaa taacatgctg ccattcttga    360
ttgctagagt ttttgttagt actttggatg c                                391
```

<210> SEQ ID NO 10

<211> LENGTH: 501

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(501)

<223> OTHER INFORMATION: AffymetrixID: 201693_s_at

<400> SEQUENCE: 10

```
gggcttttcg acatgacagc aaccttttct cccaggacaa ttgaaatttg ctaaagggaa    60
aggggaaaga aagggaaaag ggagaaaaag aaacacaaga gacttaaagg acaggaggag    120
gagatggcca taggagagga gggttcctct taggtcagat ggaggttctc agagccaagt    180
cctccctctc tactggagtg gaaggtctat tggccaacaa tcctttctgc ccacttcccc    240
ttccccaatt actattccct ttgacttcag ctgcctgaaa cagccatgtc caagttcttc    300
acctctatcc aaagaacttg atttgcattg attttggata aatcatttca gtatcatctc    360
catcatatgc ctgacccctt gctcccttca atgctagaaa atcgagttgg caaaatgggg    420
tttgggcccc tcagagccct gccctgcacc cttgtacagt gtctgtgcca tggatttcgt    480
ttttcttggg gtactcttga t                                501
```

<210> SEQ ID NO 11

<211> LENGTH: 489

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(489)

<223> OTHER INFORMATION: AffymetrixID: 201889_at

<400> SEQUENCE: 11

```
ttgaccccaa atgactttat acccaattct acataaaaat atagaagatc tatctttttt    60
tgttaccttc agatgttcac taaataactc agtttttaag cagaagtttt cagggcatta    120
aatatatgtt gtgtatgaag tatctcaaac tggaacataa atttagtgat caaactgcc a    180
ttcacagtgt aaggcagcac ttaaatttcg aacctaaagt ttagatgcat tgtataaaaa    240
aacctaaaag cagtatctgt tatttagctg taaaccaagt tggaagctat tcggataatt    300
tcttaaatat tgatgaactt tggagtactg tttcttcctt caaactgaat gtaattaatt    360
catgaataaa tgcaccttat atgtttaaac aatctttgta tacttttggg atttttggtg    420
cttatatgct aaatcacatt cagcatgtgt attttgacat taaaataact tccctcaatt    480
ctgtaaat
```

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<210> SEQ ID NO 12
<211> LENGTH: 409
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(409)
<223> OTHER INFORMATION: AffymetrixID: 202110_at

<400> SEQUENCE: 12

tcagctcact tcaagggtag ctgaagcgaa ttggcaccaa agcagcagct gtattgccgc	60
agttctagct tcaccttcac gatgtttccc ttggtcaaaa gcgcactaaa tcgtctccaa	120
gttcgaagca ttcagcaaac aatggcaagg cagagccacc agaaacgtac acctgatttt	180
catgacaaat acggtaaatgc tgtattagct agtggagcca ctttctgtat tgttacatgg	240
acatatgtag caacacaagt cggaatagaa tggaacctgt cccctgttgg cagagttacc	300
ccaaaggaat ggaggaatca gtaatcatcc cagctggtgt aataatgaat tgtttaaaaa	360
acagctcata attgatgcca aattaaagca ctgtgtaccc attaagata	409

<210> SEQ ID NO 13
<211> LENGTH: 511
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(511)
<223> OTHER INFORMATION: AffymetrixID: 202157_s_at

<400> SEQUENCE: 13

tgtggcaaaa acgtttcttt cttatttttt ttcttttctt aaaacagact tgaaagtatt	60
atacagggat tggcattctt cccggtcact ggtaacaata gcaatatgtg tccagggaca	120
cagaatgttg gtttctaaca gactacttcc aaaaacagtt tgagaaaaaa actgtctgat	180
tttaagtctc tagaggtctg taatagtttt tacatttttc aggcagtgtg aagttttttg	240
ataaggccat tttaggtggc tcactttctc attaagatat atatatagaa ccactttttg	300
tagattagta taagaaaaat atttaccctg ttttggggca aatgctacct atttgtgtca	360
ccctttgctg aactcacagt tagacaatcc atggtttaat gcacatgaaa ttacctatat	420
tttatactgt ttcaatgtac aggagaaaag ttactgtaaa ctgtgttatg ttggtgcttc	480
tgtgaattaa gttgtggttt catcatgagt c	511

<210> SEQ ID NO 14
<211> LENGTH: 480
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(480)
<223> OTHER INFORMATION: AffymetrixID: 202233_s_at

<400> SEQUENCE: 14

gctcgtgttg aatctagaac cgtagccaga catgggactg gaggacgagc aaaagatgct	60
taccgaatcc ggagatccctg aggaggagga agaggaagag gaggaattag tggatccctc	120
aacaacagtg agagagcaat gcgagcagtt ggagaaatgt gtaaaggccc gggagcggct	180
agagctctgt gatgagcgtg attcctctcg atcacataca gaagaggatt gcacggagga	240

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gctctttgac ttcttgcatg cgagggacca ttgcgtggcc cacaaactct ttaacaactt    300
gaaataaatg tgtggactta agttgcaccc cagtcttcat catctgggca tcagaatatt    360
tccttatggt ttggatgta ccatttggtt cttatttggt taactgtaag ttcacatcaa    420
cctcatgggt ttggcttgag gctggtagct tctatgtaat tcgcaatgat tccatctaaa    480

```

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<210> SEQ ID NO 15
<211> LENGTH: 556
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(556)
<223> OTHER INFORMATION: AffymetrixID: 202378_s_at

```

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<400> SEQUENCE: 15

```

```

acatgtgcac atgcggcatt ttactatgaa atttaatatg ctgggttttt taataccttt    60
atatatcatg ttcactttaa gaaagacttc ataagtagga gatgagtttt attctcagca    120
aatagacctg tcaaatttag attatgttac tcaaattatg ttacttggtt ggtgtttcat    180
gtagtcacgg tgctctcaga aaatatatta acgcagtctt gtaggcagct gccaccttat    240
gcagtgcacg gaaacctttt gcttggggat gtgcttgag aggagataa cgctgaagca    300
ggcctctcat gaccaggaa ggccggggtg gatccctctt tgtgtttag tccatgctat    360
taaaagtgtg gccacagac caagagcctc aacatttctt agagccttat tagaaatgca    420
gaatctgaag cccactctg gaccaggac attttgatga gatccaaagg agttgtatgc    480
acatgaaagt ttgagaagca tcatcataga gaagtaaca tcacacccaa ctctcttctc    540
ttccagtggt ctaaac                                     556

```

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<210> SEQ ID NO 16
<211> LENGTH: 529
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (75)..(75)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(529)
<223> OTHER INFORMATION: AffymetrixID: 202664_at

```

```

<400> SEQUENCE: 16

```

```

gaaatcagag cttacatgtg tgttttttta taacattttc agataaatgt attcaacatg    60
taatacagta ttttnacatt cacctcttat tttatattga aatgtattac agtattaaaa    120
ctcagtggtc agtatttatt tcactatgca ttttatttag taaagccag gagaaatgtt    180
taatccaatg gtgccttact ttgtgattta aaagaaatca actttttttt atgtctaagt    240
agtagattat ttgcatattt gtaaaaactg ttaggtcttt atattttaaa gtgtaatacc    300
agttttgtta ttttagtagc agaaatggga tgattgttaa agttcccaa aaatgttggc    360
atgaaattaa tttttccctc cttatagtca aggaccgtag aggaagaaaa actttttttt    420
catatcatgc actatgtaaa cagacacatt ttgctatctg tgcacacagg atagtgttaag    480
tggtagggta gagactaccc tagacatctg catctttgta agtttagcca                529

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<210> SEQ ID NO 17

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<211> LENGTH: 478
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(478)
<223> OTHER INFORMATION: AffymetrixID: 202910_s_at

<400> SEQUENCE: 17

```
ctgtggccac agcagctttg tacacgaaga ccatccatcc tcccttcgtc caccactcta      60
ctccctccac cctccctccc tgatcccgty tgccaccagg agggagtggc agctatagtc      120
tggcaccaaaa gtccaggaca cccagtgggg tggagtcgga gccactggtc ctgctgctgg      180
ctgcctctct gctccacctt gtgacccagg gtggggacag gggctggccc agggctgcaa      240
tgcagcatgt tgccttgcca cctgtggcca gtactcgga cagactaagg gcgcttgctc      300
catcctggac ttttcctctc atgtctttgc tgcagaactg aagagactag gcgctggggc      360
tcagcttccc tcttaagcta agactgatgt cagaggcccc atggcgaggc ccttgggggc      420
cactgcctga ggctcacggt acagaggcct gccctgcctg gccgggcagg aggttctc      478
```

<210> SEQ ID NO 18
<211> LENGTH: 276
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (57)..(57)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(276)
<223> OTHER INFORMATION: AffymetrixID: 202922_at

<400> SEQUENCE: 18

```
aaaaatggcg ttcttctctt gtggcctggt attctgattg ctgctgtata cagtttngtc      60
actctttagt ttttagttaa gcatactgat agactttcct ctaaaagcca ttcactccag      120
attttacctg gggaatatc tacatactgc ttactttctc tataaaactc atcaataaat      180
catgaaaggc actgagtttt gtaaatcagg accctaaatg ttaattgta aataagtttc      240
agataattat tatagctttg cgttgaagtt tgttgt      276
```

<210> SEQ ID NO 19
<211> LENGTH: 486
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(486)
<223> OTHER INFORMATION: AffymetrixID: 202950_at

<400> SEQUENCE: 19

```
taacatgtta gttgtcattt ggcattgagtg tgcattccag taattcttaa ttgatatttg      60
attaattcca tacctttgat taaaacatgc tagttcaaaa taagactgct cagtttccaa      120
gggttttcaa gcctacttac ctttataaag gttctctagt ctctgattag ccatgactgt      180
attggacttt gaacattttc tgaactaaaa acctctatc taaactaatc tcatttggat      240
gtgtaagtct tttgtaaagg caagaataaa taatatccag gacaatttat tagttttctc      300
agtattttcc caaatattag aatatattact tcattattgg ttggctgccg atgaccccat      360
```


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atgttctgtg agaatagtag ctttatcttt gatataatac atagtctcca aataggtaat	420
acttcgcaat tgattagatt ttcagagtag atttagagtt atctgttttt ctggtgaggg	480
tcaaatt	486

<210> SEQ ID NO 20
 <211> LENGTH: 539
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(539)
 <223> OTHER INFORMATION: AffymetrixID: 203097_s_at

<400> SEQUENCE: 20

tttccattaa attcagctga tcatattgat cagtagataa acgtaaatag cttcaaattt	60
taaaagtgga attgcagtggt ttttctcactg tatcaaacia tgctcagtgct ttattttaata	120
attctcttct gtatcatggc atttgtctac ttgcttatta cattgtcaat tatgcatttg	180
taattttaca tgtaatatgc attatttgcc agttttatta tataggctat ggacctcatg	240
tgcatataga aagacagaaa tctagctcta ccacaagttg cacaatggtt atctaagcat	300
taagtaattg tagaacatag gactgctaatt ctcagttcgc tctgtgatgt caagtgcaga	360
atgtacaatt aactggtgat ttcctcatac ttttgatact actgtacct gtatgtcttt	420
tagaaagaca ttggtggagt ctgtatccct tttgtatttt taatacaata attgtacata	480
ttggttatat tttgttgtaa gatggtagaa atgtactatg tttatgcttc tacatccag	539

<210> SEQ ID NO 21
 <211> LENGTH: 444
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(444)
 <223> OTHER INFORMATION: AffymetrixID: 203231_s_at

<400> SEQUENCE: 21

tgcaccaggt gaaaacaggg ccagcagact ccatggccca attcggtttc ttcggtggtg	60
atgtgaaagg agagaattac actttttttt tttttaagtg gcgtggaggc ctttgcttcc	120
acatttggtt ttaaccaga atttctgaaa tagagaattt aagaacacat caagtaataa	180
atatacagag aatatacttt tttataaagc acatgcattc gctatttgtt tgggttggtt	240
tcctctcttt tccacggaca gtgttgtgtt tctggcatag ggaaactcca aacaacttgc	300
acacctctac tccggagctg agatttcttt tacatagatg acctcgcttc aaatacgtaa	360
ccttactgat gataggatct tttctgttag cactatacct tgtgggaatt tttttttaa	420
tgtacacctg atttgagaag ctga	444

<210> SEQ ID NO 22
 <211> LENGTH: 526
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(526)
 <223> OTHER INFORMATION: AffymetrixID: 203300_x_at

<400> SEQUENCE: 22

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gaacttggtc agaccgtttt agcacggaaa cctaaaatgt gcagcttcct tgagtggcga	60
gatctgaaga ttgtttacaa aagatatgct agtctgtatt tttgctgtgc tattgaggat	120
caggacaatg aactaattac cctggaaata attcatcggt atgtggaatt acttgacaag	180
tatttcggca gtgtctgtga actagatatc atctttaatt ttgagaaggc ttattttatt	240
ttggatgagt ttcttttggg aggggaagtt caggaaacat ccaagaaaaa tgccttaaa	300
gcaattgagc aggctgatct actgcaggag gaagctgaaa cccacgtag tgttcttgaa	360
gaaattggac tgacataact ctccctccctt gttgatgact tcttgaggca ttccacacac	420
tgtataggtt cactcccttc atgtccatgt tagctcatgg tgtaagatga tgtcttgta	480
gtattactgt tttgctaagc cgcttcattc atgcctacac aatttt	526

<210> SEQ ID NO 23
 <211> LENGTH: 502
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (112)..(112)
 <223> OTHER INFORMATION: n is a, c, g, or t
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (200)..(200)
 <223> OTHER INFORMATION: n is a, c, g, or t
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(502)
 <223> OTHER INFORMATION: AffymetrixID: 204160_s_at

<400> SEQUENCE: 23

ttgtggtgtg tgagaggcat tttcaaaccc tgtataaata atccatgctg ttggtcataa	60
gttaactgta ttaagaacag taaaataaat aaaaaccaat agtactaatt tngctttaa	120
aaaatttcta atttttttca cataaaacaa ttatcctaaa ggtaaatagt tgatcgaaac	180
agaataatag aaaaattctn ctttaatttc cattaaaaag caaatagcat tgacacattt	240
aaagcttttc atttaaaagta gtggatgttt ttgaagtatc taaaatagta gcagaatatt	300
ttatacttgg tccttgcaat ggtgtgagtt ttaatgattg cattatcgtg attggtggtt	360
atgagtttca gaaatctata cttggcatcc aactcatgag tggattttat ataggatgga	420
acaggaaggt atgtcctgtc agtatcttaa ccttttcaac aagacattta cctatttgtc	480
ttctcttacg ttctcaaaat at	502

<210> SEQ ID NO 24
 <211> LENGTH: 244
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(244)
 <223> OTHER INFORMATION: AffymetrixID: 204750_s_at

<400> SEQUENCE: 24

gaccctcgcg atcttaatat ttgccagtga tgccctgcaa aatgtgacat tacatgttcc	60
ctccaaacta gatgccgaga aacttggttg tagagttaac ctgaaagagt gctttacagc	120
tgcaaatcta attcattcaa gtgacatcga cttccaaatt ttggaggatg gtacagtcta	180
tacaacaaat actattctat tgtcctcgga gaagagaagt tttacatat tactttccaa	240

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cact	244
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<210> SEQ ID NO 25
 <211> LENGTH: 504
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(504)
 <223> OTHER INFORMATION: AffymetrixID: 204777_s_at

<400> SEQUENCE: 25

ggaagtcttc ataaagccgc agtagaactt gagctgaaaa cccagatggg gttaactggc	60
cgccccactt tccggcataa ctttttagaa aacagaaatg cccttgatgg tggaaaaaag	120
aaaacaacca cccccccact gcccaaaaaa aaaagccctg ccctgttgct cgtgggtgct	180
gtgtttactc tcccgtgtgc cttcgcgtcc ggggtgggag cttgctgtgt ctaacctcca	240
actgctgtgc tgtctgctag ggtcacctcc tgtttgtgaa aggggacctt cttgttcggg	300
ggtgggaagt ggcgaccgtg acctgagaag gaaagaaaga tcctctgtctg acccctggag	360
cagctctcga gaactacctg ttggtattgt ccacaagctc tcccgagcgc cccatcttgt	420
gccatgtttt aagtcttcat ggatgttctg catgtcatgg ggactaaaac tcaccaaca	480
gatctttcca gaggtccatg gtgg	504

<210> SEQ ID NO 26
 <211> LENGTH: 268
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(268)
 <223> OTHER INFORMATION: AffymetrixID: 205042_at

<400> SEQUENCE: 26

ttacatttga actatattct tcctagtggg ttagtgtgaa aaagagtttg gctgattcct	60
aaaactctgc cagccctgca gtaatctcca ggcttggtta ttgttcagac attccatggg	120
gattcctggg aaggaagctt ggctgctcag tttctgagtc tggggtgaga taatgttctg	180
gaaggacatc tgttcttttg tgtaattctc catggtgaaa tctgctctgt acatcagaca	240
attgcattgc taccaagttt cataccaa	268

<210> SEQ ID NO 27
 <211> LENGTH: 507
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(507)
 <223> OTHER INFORMATION: AffymetrixID: 205114_s_at

<400> SEQUENCE: 27

gattccacag aatttcatag ctgactactt tgagacgagc agccagtgt ccaagcccgg	60
tgctactctc ctaaccaagc gaagccggca ggtctgtgct gacccagtg aggagtgggt	120
ccagaaatat gtcagcgacc tagagctgag tgccctgagg gtccagaagc ttcgaggccc	180
agcgacctcg gtgggccagt ggggaggagc aggagcctga gccttgggaa acatgcgtgt	240
gacctccaca gctacctctt ctatggactg gttgttgcca aacagccaca ctgtgggact	300

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cttcttaact taaattttta tttatttata ctatttagtt tttgtaattt attttcgatt 360
tcacagtgtg tttgtgattg tttgctctga gagttccctt gtcctctccc ccttccctca 420
caccgcgtct ggtgacaacc gagtgggtgt catcagcctg tgtaggcagt catggcacca 480
aagccaccag actgacaaat gtgtatc 507

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<210> SEQ ID NO 28
<211> LENGTH: 565
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(565)
<223> OTHER INFORMATION: AffymetrixID: 205624_at

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<400> SEQUENCE: 28
tatgaaaccc gctacatcta tggccaata gaatcaacaa tttacccgat atcaggttct 60
tcttttagact gggcttatga cctgggcac aaacacacat ttgcctttga gctccgagat 120
aaaggcaaat ttggttttct ccttccagaa tcccgataa agccaacgtg cagagagacc 180
atgctagctg tcaaatttat tgccaagtat atcctcaagc atacttccta aagaactgcc 240
ctctgtttgg aataagccaa ttaatccttt tttgtgcctt tcatcagaaa gtcaatcttc 300
agttatcccc aaatgcagct tctatttcac ctgaatcctt ctcttgcctc ttaagtccc 360
atgttactgc tgtttgcttt tacttacttt cagtagcacc ataacgaagt agctttaagt 420
gaaacctttt aactaccttt ctttgctcca agtgaagttt ggaccagca gaaagcatta 480
ttttgaaagg tgatatacag tggggcacag aaaacaaatg aaaaccctca gtttctcaca 540
gattttcacc atgtggcttc atcaa 565

```

```

<210> SEQ ID NO 29
<211> LENGTH: 493
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(493)
<223> OTHER INFORMATION: AffymetrixID: 206207_at

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<400> SEQUENCE: 29
aggagacaac aatgtccctg ctaccogtgc catacacaga ggctgcctct ttgtctactg 60
gttctactgt gacaatcaaa gggcgaccac ttgtctgttt cttgaatgaa ccatatctgc 120
agggtggattt ccacactgag atgaaggagg aatcagacat tgtcttccat ttccaagtgt 180
gctttggctg tcgtgtgtgc atgaacagcc gtgagtatgg ggctggaag cagcaggtgg 240
aatccaagaa catgcccttt caggatggcc aagaatttga actgagcctc tcagtgtctg 300
cagataagta ccaggtaatg gtcaatggcc aatcctctta cacctttgac catagaatca 360
agcctgaggc tgtgaagatg gtgcaagtgt ggagagatat ctccctgacc aaatttaatg 420
tcagctatct aaagagataa ccagacttca tgttgccaag gaatccctgt ctctacgtga 480
acttgggatt cca 493

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<210> SEQ ID NO 30
<211> LENGTH: 218
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(218)
<223> OTHER INFORMATION: AffymetrixID: 206790_s_at

<400> SEQUENCE: 30
gaacttactt cagattgtgc gggaccactg ggttcattgt cttgtcccta tgggatttgt      60
cattggatgt tatttagaca gaaagagtga tgaacggcta actgccttcc ggaacaagag      120
tatgttatatt aaaaggggat tgcaaccag tgaagaagtt acctggaagt aaagactggc      180
tagattatcg aatgttcaca ttttaaagtt ctgagaga                               218

<210> SEQ ID NO 31
<211> LENGTH: 453
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(453)
<223> OTHER INFORMATION: AffymetrixID: 207008_at

<400> SEQUENCE: 31
acctaacgaa gtatccttca gcctgaaaga ggaatgaagt actcatacat gttacaacac      60
ggacgaacct tgaaaacttt atgctaagtg aaataagcca gacatcaaca gataaatagt      120
ttatgattcc acctacatga ggtactgaga gtgaacaaat ttacagagac agaaagcaga      180
acagtgatta ccagggactg aggggagggg agcatgggaa gtgacggttt aatgggcaca      240
gggtttatgt ttaggatgtt gaaaaagttc tgcagataaa cagtagtgat agttgtaccg      300
caatgtgact taatgccact aaattgacac ttaaaaatgg tttaaatggt caattttgtt      360
atgtatatatt tatatcaatt taaaaaaaaa cctgagcccc aaaaggtatt ttaatcacca      420
aggctgatta aaccaaggct agaaccacct gcc                               453

<210> SEQ ID NO 32
<211> LENGTH: 385
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(385)
<223> OTHER INFORMATION: AffymetrixID: 207815_at

<400> SEQUENCE: 32
caagccctgc tgtacaagaa aatcattaag gaacatttgg agagttagct actagctgcc      60
taagtgtgca ctttcaatct aactgtgaaa gaattctctg atgtttgtat tacccttctt      120
atatttatatt aacaaaataa atcaagttgt ggtatagtca atctatttct taataatact      180
gcaaaaaataa tgctgacaca tcacaatttc atattttaaa attccagaa ttttaagcaa      240
aaagcattat gaaggaaggc ttggtttaat aaagactgat tttgttcagt gttatatgtt      300
agctgataca tatttgttca tttatgtgat tgcagtactt tatagctaca tatttacctt      360
gaatgttaca attagcttgc caata                               385

<210> SEQ ID NO 33
<211> LENGTH: 491
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(491)

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<223> OTHER INFORMATION: AffymetrixID: 208051_s_at

<400> SEQUENCE: 33

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gaactccag ctaaacaacc aagacttcac tgaagattta ttccaattct agaattgttc    60
tttttttatt ttttttttt tcaactgact aacttcatta ccttaaagcc tagaacatta    120
ttctgcttta tttatatggc tttctcaatt ttattttgta gcatgggttg aatcgaactt    180
tttactagag aattttacta gatatttgtc attcaagttt tcactctgctt tataaattgat    240
acaccttgag ggctactttt ctaatacttt tacctataat gtggtaccca cctcagcccc    300
taataaataa tatttttacc ctaatgtcaa atctttttcc caggctaact aaaaactgtg    360
tacaaaagga ttgcttgtaa atatgcatgt aaatagttct gttaataacc cactgtttta    420
catttggtac atctgtgtct gctaatacag ttagctttct cacttttctg cttgtttgtt    480
cagtcgaat t                                                    491
```

<210> SEQ ID NO 34

<211> LENGTH: 382

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(382)

<223> OTHER INFORMATION: AffymetrixID: 208161_s_at

<400> SEQUENCE: 34

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gatagcaaac actgggggca ccttaagatt ttgcacctgt aaagtgcctt acagggtaac    60
tgtgctgaat gcttttagatg aggaaatgat cccaagtgg tgaatgacac gcctaaggtc    120
acagctagtt tgagccagtt agactagtcc cccggtctcc cgattcccaa ctgagtgtta    180
tttgacact gcaactgttt caaataacga ttttatgaaa tgacctctgt cctccctctg    240
atttttcata ttttcctaaa gtttcgttcc tgttttttaa taaaaagctt tttcctctg    300
gaacagaaga cagctgctgg gtcaggccac cctaggaac tcagtcctgt actctggggg    360
gctgctgaa tccattaaaa at                                                    382
```

<210> SEQ ID NO 35

<211> LENGTH: 543

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(543)

<223> OTHER INFORMATION: AffymetrixID: 208637_x_at

<400> SEQUENCE: 35

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ggccccgagg agttcaaagc ctgcctcatc agcttgggtt atgatattgg caacgacccc    60
caggggagaag cagaatttgc ccgcatcatg agcattgtgg accccaaccg cctgggggta    120
gtgacattcc aggccttcat tgacttcacg tcccgcgaga cagccgacac agatacagca    180
gaccaagtca tggtcttcct caagatcctg gctggggaca agaactacat taccatggac    240
gagctgcgcc gcgagctgcc acccgaccag gctgagtact gcatcgcgcg gatggcccc    300
tacaccggcc ccgactccgt gccaggtgct ctggactaca tgtecttctc caggcgctg    360
tacggcgaga gtgacctcta atccaccccg cccggccgcc ctctgtctgt gcgcctgcc    420
ctgccttgca cctccgcctg cgcccatctc ctgcctgggt tcggtttcag ctcccagcct    480
```

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ccacccgggt gagctggggc ccacgtggca tcgatacctcc ctgcccgcca agtgacagtt 540

tac 543

<210> SEQ ID NO 36
 <211> LENGTH: 165
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(165)
 <223> OTHER INFORMATION: AffymetrixID: 208918_s_at
 <400> SEQUENCE: 36

gaaatgggct gggagtgtt ctgtctgtct gacaccccgcc ggtgggtccc tggagcgccg 60

cctccagctg ccgcaatttc catgccagga tatttttccg caaatcagtc ggttgaaatt 120

cagaggagtc agaatgactc gacctgtcct tcaatgttga taata 165

<210> SEQ ID NO 37
 <211> LENGTH: 189
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (75)..(189)
 <223> OTHER INFORMATION: n is a, c, g, or t
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(189)
 <223> OTHER INFORMATION: AffymetrixID: 208982_at

<400> SEQUENCE: 37

attgctgtct aaagaagtgg tctcctgagg tcttaagaca ttcttgacag tgtcttgagt 60

gggtgggaga gagngtctg tcattgcgct gtggaatttc acagatgaga accacgccta 120

gccaaaaatca cttttcctgt ttgcctcagt gacacagctg cagggaccct cgtggatgtt 180

gtattaaat 189

<210> SEQ ID NO 38
 <211> LENGTH: 355
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(355)
 <223> OTHER INFORMATION: AffymetrixID: 209009_at

<400> SEQUENCE: 38

gagcttcccc aactcataaa tgccaatttt ccagtggatc cccaaaggat gtctattttt 60

ggccactcca tgggaggtca tggagctctg atctgtgtct tgaataatcc tggaaatac 120

aaatctgtgt cagcattttgc tccaatttgc aacctgtac tctgtccctg gggcaaaaaa 180

gcctttagtgt gatatttggg aacagatcaa agtaaatgga aggettatga tgctaccac 240

cttgtgaaat cctatccagg atctcagctg gacatactaa ttgatcaagg gaaagatgac 300

cagtttcttt tagatggaca gttactccct gataacttca tagctgcctg tacag 355

<210> SEQ ID NO 39
 <211> LENGTH: 564
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(564)
<223> OTHER INFORMATION: AffymetrixID: 209020_at

<400> SEQUENCE: 39
caggggcagt cgttgagcct ttgagaactt ctgttccaag gctcccatca gagagtaaga      60
aggaagactc ctctgacgct acccaagtcc cccaagcaag tctcaaagcc agtgatctct      120
ctgactttca atcagtttcc aagctaaacc aggggcaagc catgcacatg cataggcaag      180
gaatgccagt gtaagagatg gcatgatatg gaagtgtatt ccttttcagg cctgcagagt      240
gtccctccct tggctccaga acgaagatcc acacttgagg actactctca gtcgctgcac      300
gccagaactc tgtctggctc tccccgatcc tgtcttgagc aagctcgagt cttcgtggat      360
gatgtgacca ttgaggacct gtcaggctac atggagtatt acttgatat tcccaagaaa      420
atgtcccaca tgggcagaaa tgatgtacac ctgatatcaa gaagctaatt catatgcttt      480
aaaccaatga aggcttgtca aagagattta gttaatggca gaccttgtgg ccactttgtg      540
tgagaagaca tctctttctg ctca                                         564

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<210> SEQ ID NO 40
<211> LENGTH: 339
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(339)
<223> OTHER INFORMATION: AffymetrixID: 209146_at

<400> SEQUENCE: 40
gaacctcatc aattgatagc agtgagtgac tgaagcttcc aaatcaagaa aagccggcac      60
caagaacttc cattctaacc tagagctgac cagtttgagc tgattctctc tttgaagagt      120
ccttcttgat tgcagtgacg tactggcatt tctgaatgga tgtaagtgga gtattttagt      180
ctaaaggcct ttcaaattac ttgaattttt ttaaaaattg aggagcttta tttctattta      240
cccttcattt tttgtatata aaatttccat tgtcattaaa aactgtatct tgaaactttg      300
tgaactgact tgctgtattt gcactttgag ctcttgaaa                               339

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<210> SEQ ID NO 41
<211> LENGTH: 465
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(465)
<223> OTHER INFORMATION: AffymetrixID: 209193_at

<400> SEQUENCE: 41
gattgtagtg gatctaattt ttcagaaatt ttgcctttaa gttattttac ctgtttttgt      60
ttcttgtttt gaaagatgcg cattctaacc tggagggtcaa tgttatgtat ttatttatTT      120
atttatTTtg ttcccttctc attccaagct tccatagctg ctgccctagt tttctttcct      180
cctttctctc tctgacttgg ggaccttttg ggggagggct gcgacgcttg ctctgtttgt      240
ggggtgacgg gactcaggcg ggacagtgcg gcagctccct ggcttctgtg gggccctca      300
cctacttacc caggtgggtc cgggctctgt ggggtgatggg gaggggcatt gctgactgtg      360
tatataggat aattatgaaa agcagttctg gatgggtgtgc cttccagatc ctctctgggg      420

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ctgtgttttg agcagcaggt agcctggctg gttttatctg agtga 465

<210> SEQ ID NO 42
<211> LENGTH: 535
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(535)
<223> OTHER INFORMATION: AffymetrixID: 209710_at

<400> SEQUENCE: 42

gatccacag ccctagtatg aaagctgggg gtggggaggg gcctttgctg cccttggttt 60
ctgggggctg gttggcattt gctggcctgg cagggggtga aggcaggagt tgggggcagg 120
tcaggaccag gaccacaggga gaggtgtgt ccctgctggg gtctcaggtc cagctttact 180
gtggctgtct ggatccttcc caaggtacag ctgtatataa acgtgtcccg agcttagatt 240
ctgtatgcgg tgacggcggg gtgtggtggc ctgtgagggg cccttgggcc aggaggagga 300
ttgtgctgat gtagtgacca agtgcaatat gggcgggcag tcgtgcagg gagcaccacg 360
gccagaagta acttattttg tactagtgtc cgcataagaa aaagaatcgg cagtattttc 420
tgtttttatg ttttattttg cttgttttat tttggattag tgaactaagt tattgttaat 480
tatgtacaac atttatatat tgtctgtaaa aaatgtatgc tatcctctta ttcct 535

<210> SEQ ID NO 43
<211> LENGTH: 527
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(527)
<223> OTHER INFORMATION: AffymetrixID: 210042_s_at

<400> SEQUENCE: 43

gaaatctacg caaatggtcc catcagctgt ggaataatgg caacagaaag actggcaaac 60
tacaccggag gcatctatgc cgaataccag gacaccacat atataaacca tgtcgtttcc 120
gtggctgggt ggggcatcag tgatgggact gactactgga ttgtccgga ttcattgggt 180
gaaccatggg gcgagagagg ctggctgagg atcgtgacca gcaacctataa ggatgggaag 240
ggcgccagat acaaccttgc catcgaggag cactgtacat ttggggaccc catcgtttaa 300
ggccatgtca ctagaagcgc agtttaagaa aaggcatggt gacctatgac cagaggggat 360
cctatggtta tgtgtgccag gctggctggc aggaactggg gtggctatca atattggatg 420
gcgaggacag cgtggtactg gctgcgagtg ttcctgagag ttgaaagtgg gatgacttat 480
gacacttgca cagcatggct ctgcctcaca atgatgcagt cagccac 527

<210> SEQ ID NO 44
<211> LENGTH: 536
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(536)
<223> OTHER INFORMATION: AffymetrixID: 210184_at

<400> SEQUENCE: 44

cagttctgaa tatgctgctc atccccacct gtcttcaaca gctcccatc accctcagga 60

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caatgtctga actctccagc ttcgctgag aagtcctt ccatcccaga ggggtgggtt	120
cagggcgac agcatgagag cctctgtgcc cccatcacc tcgtttccag tgaattagt	180
tcattgtcag atcagctcag ggcttcatcg tggggctctc agttccgatt cccaggtc	240
aattgggagt gagatgcctg catgtgggt tctgcacagc tggcctccg cggttgggtc	300
aacattgctg gcctggaagg gaggagcgc ctctaggag ggacatggc ccggtgcggc	360
tgcagctcac cagccccagg ggcagaagag acccaaccac ttcctatatt ttgaggtat	420
gaatatagta cctgaaaaa tgccaagcac tagattattt ttttaaaaag cgtactttaa	480
atgtttgtgt taatacacat taaaacatcg cacaaaaacg atgcattctac cgctcc	536

<210> SEQ ID NO 45
 <211> LENGTH: 132
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(132)
 <223> OTHER INFORMATION: AffymetrixID: 210732_s_at

<400> SEQUENCE: 45

cccagcttc tagtaataga ggaggagaca tttctaaat cgcaccaga actgtctaca	60
ccaagagcaa agattcgact gtcaatcaca ctttgacttg caccaaaata ccacctatga	120
actatgtgtc aa	132

<210> SEQ ID NO 46
 <211> LENGTH: 398
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(398)
 <223> OTHER INFORMATION: AffymetrixID: 210895_s_at

<400> SEQUENCE: 46

gtgtacataa atttgacctg ctcatctata cacggttacc cagaacctaa gaagatgagt	60
gttttgctaa gaaccaagaa ttcaactatc gagtatgatg gtattatgca gaaatctcaa	120
gataatgtca cagaactgta cgacgtttcc atcagcttgt ctgtttcatt cctgatgtt	180
acgagcaata tgacctctt ctgtattctg gaaactgaca agacggcgtt tttatcttca	240
cctttctcta tagagcttga ggaccctcag cctccccag accacattcc ttggattaca	300
gctgtacttc caacagttat tatatgtgtg atggttttct gtctaattct atggaaatgg	360
aagaagaaga agcggcctcg caactcttat aaatgtgg	398

<210> SEQ ID NO 47
 <211> LENGTH: 216
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(216)
 <223> OTHER INFORMATION: AffymetrixID: 211506_s_at

<400> SEQUENCE: 47

gtgtgaaggt gcagttttgc caaggagtgc taaagaactt agatgtcagt gcataaagac	60
atactccaaa cctttccacc ccaaatttat caaagaactg agagtgtatt agatgggacc	120

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acactgcgcc aacacagaaa ttattgtaaa gctttctgat ggaagagagc tctgtctgga 180

ccccaggaa aactgggtgc agagggtgt ggagaa 216

<210> SEQ ID NO 48
 <211> LENGTH: 378
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(378)
 <223> OTHER INFORMATION: AffymetrixID: 211734_s_at

<400> SEQUENCE: 48

acatctccat tacaaatgcc acagttgaag acagtgaac ctactactgt acgggcaaag 60

tgtggcagct ggactatgag tctgagcccc tcaacattac tgtaataaaa gctccgcgtg 120

agaagtactg gctacaattt tttatcccat tgttggtggt gattctgttt gctgtggaca 180

caggattatt tatctcaact cagcagcagg tcacatttct cttgaagatt aagagaacca 240

ggaaaggctt cagacttctg aaccacatc ctaagccaaa ccccaaaaac aactgatata 300

attactcaag aaatatattgc aacattagtt tttttccagc atcagcaatt gctactcaat 360

tgtcaaacac agcttgca 378

<210> SEQ ID NO 49
 <211> LENGTH: 529
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(529)
 <223> OTHER INFORMATION: AffymetrixID: 211995_x_at

<400> SEQUENCE: 49

agtactcggg gtggatcggg ggctccatcc tggcctcact gtccaccttc cagcagatgt 60

ggattagcaa gcaggagtac gacgagtcgg gccctccat cgtccaccgc aaatgcttct 120

aaacggactc agcagatgag tagcatttgc tgcattgggt aattgagaat agaaatttgc 180

ccctggcaaa tgcacacacc tcattgtagc ctcacgaaac tggaataagc cttcgaaaag 240

aaattgtcct tgaagcttgc atctgatatc agcactggat tgtagaactt gttgctgatt 300

ttgaccttgc attgaagtta actgttcccc ttggtatttg ttttaataccc tgtacatata 360

tttgagtcca acctttagta cgtgtggctt ggtcacttcg tggctaaggt aagaacgtgc 420

ttgtggaaga caagtctgtg gcttggtgag tctgtgtggc cagcagctc tgatctgtgc 480

agggatttaa cgtgtcaggc ctgagtgctc tgggatttct ctagaggct 529

<210> SEQ ID NO 50
 <211> LENGTH: 535
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (327)..(327)
 <223> OTHER INFORMATION: n is a, c, g, or t
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(535)
 <223> OTHER INFORMATION: AffymetrixID: 212314_at

<400> SEQUENCE: 50

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tatttttggtta cctgtgcttg ccacagccct gttcctcaaa gctgaattga tagatttctc	60
tttgacttcc aagacctagc agttataagg caccttgaaa taaattgttt gtgcctggaa	120
atgcagggag ggcaatagct ttgtaaattg gtttacattt ttctccttga atttttctag	180
ggctcctagt ctccgaatc atttaattgc attgtcggat atcttttaca tttcaattgc	240
aatccatgaa attacattta gaagattctt agtacttaac tgtagtcttc tccatgaatt	300
acacgttaga atagactggc agcaacngaa tatgcagcaa gtaagcctct agcttatagt	360
ttcatcccta cccctcatgc ctgcgtgagt ctgtacaggg atatgtgtgt gtgtgtgtgt	420
gtgtgtgtgt tagagaggaa gaggaagagc agaatgtctg tatactacat gctgctaagg	480
tagtgaataa atcagtaatg caatatgttg ggtccaaact actctttgca ctact	535

<210> SEQ ID NO 51
 <211> LENGTH: 475
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(475)
 <223> OTHER INFORMATION: AffymetrixID: 212335_at

<400> SEQUENCE: 51

accacgcttg gctaagaaca cctaaatttt tatgtttctt ggctcaaaaa ccagttccat	60
ttctaattgtt gtctcaciaa gaaggctaata tgggtggtgag acagcagggg aggaggaaga	120
gctgtgggttt gtaactgttt caactcaggc aataagcgat tttagcttta tttaaagtct	180
tctgtccagc ttttaagcact ttgtaagaca tggctgaaag tagcttttct atcagaattg	240
cagatagtca tgttgggcta acagtcaatt ggatatattc ctttacctca catgacccca	300
gcaactgtgg tggatatctag aggtgaaaca ggcaagtcaa atggacacct ctgctgtgaa	360
tgttttagag aaggaaatc aaaaaatgtt gtaactgaaa gcaactgttg atatgggtat	420
cggctttctt tttcactttg actcttaaca ttatcagtea acttccacat taatg	475

<210> SEQ ID NO 52
 <211> LENGTH: 179
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(179)
 <223> OTHER INFORMATION: AffymetrixID: 212386_at

<400> SEQUENCE: 52

gagatttacc atgtatcagt gcctggcttt ttgttataaa gctttgtttg tctagtgtc	60
ttttgtata aaatagactg tagtacccc tagtaggaaa aaaaaaaaaac taaattttaa	120
aataaaaaat atatttggct tatttttcgc aggagcaatc cttttatacc atgaatatt	179

<210> SEQ ID NO 53
 <211> LENGTH: 295
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (114)..(114)
 <223> OTHER INFORMATION: n is a, c, g, or t
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (224)..(224)

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<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(295)
<223> OTHER INFORMATION: AffymetrixID: 212671_s_at

<400> SEQUENCE: 53

```
accaatgagg ttcctgaggt cacagtgttt tccaagtctc ccgtgacact gggtcagccc      60
aacacccctca tctgtcttgt ggacaacatc tttcctcctg tggteaacat cacntggctg    120
agcaatgggg actcagtcac agaagggtgtt tctgagacca gcttcctctc caagagtgat    180
cattccttct tcaagatcag ttacctcacc ttcctccctt ctgntgatga gatttatgac    240
tgcaagggtgg agcactgggg cctggatgag cctcttctga aacactggga gcctg         295
```

<210> SEQ ID NO 54
<211> LENGTH: 565
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (134)..(134)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(565)
<223> OTHER INFORMATION: AffymetrixID: 212897_at

<400> SEQUENCE: 54

```
aaggagacct ttgaagcttt ttgagggcaa actttacctt tgtgggtccc aaatgatggc      60
atttctcttt gaaatttatt agatactgtt atgtcccccagggttacagg aggggcatcc     120
ctcagcctat gggnacacc caaactagga ggggttattg acaggaagga atgaatccaa     180
gtgaaggctt tctgctcttc gtgttacaaa ccagtttcag agttagcttt ctggggagggt    240
gtgtgtttgt gaaaggaatt caagtgttgc aggacagatg agctcaaggt aaggtagctt    300
tggcagcagg gctgatacta tgaggctgaa acaatccttg tgatgaagta gatcatgcag    360
tgacatacaa agaccaagga ttatgtatat ttttatatct ctgtggtttt gaaactttag    420
tacttagaat ttggccttc tgcactactc ttttgcctt acgaacataa tggactctta     480
agaatggaaa gggatgacat ttacctatgt gtgctgcctc attcctggtg aagcaactgc    540
tacttgctct ctatgcctct aaaat                                           565
```

<210> SEQ ID NO 55
<211> LENGTH: 358
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (61)..(61)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (95)..(95)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (100)..(100)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (182)..(182)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (189)..(189)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (218)..(218)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (227)..(227)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (229)..(229)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (244)..(244)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (258)..(258)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (261)..(261)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (271)..(271)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (302)..(302)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (313)..(313)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (324)..(324)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (331)..(331)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(358)
<223> OTHER INFORMATION: AffymetrixID: 212999_x_at

<400> SEQUENCE: 55

cactgcagaa tgaaggaaca tcccttgagg tgaccagcc aacctgtggc cagaaggagg      60
ntgtacctt gaaaagacac tgaaagcatt ttgngtgtn aagtaagggt gggcagagga      120
ggtagaaaat caattcaatt gtcgcatcat tcatggttct ttaatattga tgctcagtgc      180
antggcctna gaatatccca gcctctcttc tggtttgntg agtgctntnt aagtaagcat      240
ggtngaattg ttgggggnc natatagtga nccttggtca ctggtgtttc aaacattctg      300
gnaagtcaca tcnatcaaga atanttttta ntttaagaa agcataacca gcaataaa      358

<210> SEQ ID NO 56
<211> LENGTH: 441
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(441)
<223> OTHER INFORMATION: AffymetrixID: 213309_at

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<400> SEQUENCE: 56

```

gtatgtagca atcctgcgtg tgaaggcaaa taaactcttt aacaggcaat tatattgctg    60
gccaaaatat gctatatattg tatacaaaga cattctaact cagttccagt atgaagaaag    120
attattcact ctagctccac tgagaaacat tttcctaagt gaaaacaatt tcttaagatg    180
gaaatggatt ggattgtcaa attattattht attggagaaa aaaacctgat ctacacattt    240
ttacttatat ggggttgcca gagtctctgg gttctagatg attttggtgg catgcttgct    300
gagccataat tactaaagag aatgtaagtg gacgggttcc ctgaatcccc ggggtccttg    360
gagagccatc gaggagaatg tgcaattgga ctgaagctcc ctggctgaag atacatgccg    420
agtcagcaca tgggtagaga t                                         441

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<210> SEQ ID NO 57

<211> LENGTH: 431

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (178)..(178)

<223> OTHER INFORMATION: n is a, c, g, or t

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(431)

<223> OTHER INFORMATION: AffymetrixID: 213506_at

<400> SEQUENCE: 57

```

gcacacagag atttgagaac cattgttctg aatgctgctt ccatttgaca aagtgccgtg    60
ataatttttg aaaagagaag caaacaatgg tgtctctttt atgttcagct tataatgaaa    120
tctgtttgtt gacttattag gactttgaat tatttcttta ttaaccctct gagttttngt    180
atgtattatt attaaagaaa aatgcaatca ggatttttaa catgtaaata caaattttgt    240
ataacttttg atgacttcag tgaaatttcc aggtagtctg agtaatagat tgttttgcca    300
cttagaatag catttgccac ttagtatttt aaaaaataat tgttgagta tttattgtca    360
gttttgttca ctgtttatct aatacaaaat tataaagcct tcagaggggt tggaccacat    420
ctctttggaa a                                         431

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<210> SEQ ID NO 58

<211> LENGTH: 251

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(251)

<223> OTHER INFORMATION: AffymetrixID: 213883_s_at

<400> SEQUENCE: 58

```

agagaacttc tagtgtatgg atttaaagat ttctcttttt cattcatata ccattttatg    60
agttctgtat aattttttgt ggtttttgtt ttgttgagtt aaagtatatt attgtgagat    120
ttatttaata ggacttcctt tgaaagctgt ataatagtgt ttctcgggct tctgtctcta    180
tgagagatag cttattactc tgatactctt taatctttta caaaggcaag ttgccacttg    240
tcatttttgt t                                         251

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<210> SEQ ID NO 59

<211> LENGTH: 332

<212> TYPE: DNA

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<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(332)
<223> OTHER INFORMATION: AffymetrixID: 214305_s_at

<400> SEQUENCE: 59

gttctgaccc ctggaaagac accaattggc acaccagcca tgaacatggc taccctact 60
ccaggtcaca taatgagtat gactcctgaa cagcttcagg cttggcggtg ggaaagagaa 120
attgatgaga gaaatcgccc actttctgat gaggaattag atgctatggt ccagagaagga 180
tataaggtag ttctctctcc agctgggtat gttcctattc gaactccagc tcgaaagctg 240
acagctactc caacaccttt ggggtggtatg actgggtttcc acatgcaaac tgaagatcga 300
actatgaaaa gtgttaatga ccagccatct gg 332

<210> SEQ ID NO 60
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (32)..(32)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(241)
<223> OTHER INFORMATION: AffymetrixID: 214512_s_at

<400> SEQUENCE: 60

gaccaagagg gtgttcgact gctagagccg ancgaagcga tgcctaaatc aaaggaactt 60
gtttcttcaa gctcttctgg cagtgtattc gacagtgagg ttgacaaaaa gttaaagagg 120
aaaaagcaag ttgctccaga aaaacctgta aagaacaaaa agacaggtga gacttcgaga 180
gccctgtcat cttctaaaca gagcagcagc agcagagatg ataacatggt tcagattggg 240
a 241

<210> SEQ ID NO 61
<211> LENGTH: 436
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (156)..(156)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (244)..(244)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (250)..(252)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (254)..(254)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (264)..(264)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (304)..(304)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (306)..(306)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (321)..(321)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (338)..(338)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (356)..(356)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(436)
<223> OTHER INFORMATION: AffymetrixID: 214807_at

<400> SEQUENCE: 61

tcttcattcc acgagaattt tgatttttaa cagcagtcctc tctttttctc agcattgcaa      60
atatatatgt atatatatat tcatgaccaa agtatcgctt actgaccatg cagctgtataa      120
ccttctgtgc ctatcaaaca aatacatagc atgaanctaa ttttagaagt ttcattggggg      180
aatttttaggg gaaagtataa acctaagagt gagtgaatgg agatgattca tggaaaaaaaa      240
aaanaaaaaa nnanatgtgc tatnaggcag agttattaac ttcttttagt tgtgttttga      300
gatngngttc tgctcttggt ncccaggctg gagtgcantg gcgtgatctc gtctcnctgc      360
aacctccgcc tcccagggtc aagcgattct cctgccccag ctactttgga ggctgaagtg      420
taagagttgc ttgagc                                         436

<210> SEQ ID NO 62
<211> LENGTH: 448
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(448)
<223> OTHER INFORMATION: AffymetrixID: 214953_s_at

<400> SEQUENCE: 62

atagattctc tcctgattat ttatcacata gccccttagc cagttgtata ttattcttgt      60
ggtttgtgac ccaattaagt cctactttac atatgcttta agaatcgatg ggggatgctt      120
catgtgaacg tgggagtcca gctgcttctc ttgcctaagt attcctttcc tgatcactat      180
gcattttaaa gttaaacatt tttaagtatt tcagatgctt tagagagatt ttttttccat      240
gactgcattt tactgtacag attgctgctt ctgctatatt tgtgatatag gaattaagag      300
gatacacacg tttgtttctt cgtgcctggt ttatgtgcac acattaggca ttgagacttc      360
aagcttttct tttttgttcc acgtatcttt gggctcttga taaagaaaag aatccctggt      420
cattgtaagc acttttacgg ggcggggtg                                         448

<210> SEQ ID NO 63
<211> LENGTH: 383
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (319)..(319)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(383)
<223> OTHER INFORMATION: AffymetrixID: 215726_s_at

<400> SEQUENCE: 63
gacagaccaa agttaacaa gcctccggaa actcttatca ctactattga ttctagtccc      60
agttggtgga ccaactgggt gatccctgcc atctctgcag tggccgtcgc cttgatgtat      120
cgctatata tggcagagga ctgaacacct cctcagaagt cagcgcagga agagcctgct      180
ttggacacgg gagaaaagaa gccattgcta actacttcaa ctgacagaaa ccttcacttg      240
aaaacaatga ttttaataata tctcttttct tttcttccga cattagaaac aaaacaaaaa      300
gaactgtcct ttctgcgcnc aaatttttcg agtgtgcctt tttattcatt tactttattt      360
tgatgtttcc ttaatgtgta att                                     383

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<210> SEQ ID NO 64
<211> LENGTH: 492
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(492)
<223> OTHER INFORMATION: AffymetrixID: 216016_at

<400> SEQUENCE: 64
gccaatgcta aaaagctgca gatccagccc agccagctgg aattgttcta ctgtttgtac      60
gagatgcagg aggaggactt cgtgcaaagg gccatggact atttcccaa gattgagatc      120
aatctctcca ccagaatgga ccacatggtt tcttctttt gcattgagaa ctgtcatcgg      180
gtggagtcac tgtccctggg gtttctccat aacatgccc aggaggaaga ggaggaggaa      240
aagggaaggcc gacaccttga tatggtgcag tgtgtcctcc caagctctc tcattgctgc      300
tgttctcatg ggtaaggaaa ctgcgcttcc aggtgcttcc tctgcttcc tcgccagctt      360
cttcttggca cctgcctcct ctcattctt ttcaactatc ttccaaatac tgttgccaca      420
gtcatatcat aatgccacca ctgtctgtt gagactcctt catgagcaaa gattgatgta      480
tggtaggtgg at                                               492

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<210> SEQ ID NO 65
<211> LENGTH: 275
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(275)
<223> OTHER INFORMATION: AffymetrixID: 217722_s_at

<400> SEQUENCE: 65
ggagatgcct cgtgaaacac agctgggcaa gtattaatgt atatggaaca gcctggattt      60
ctgcatatgg ataagccacc ttggaatagg aagaggtggt gagcctggac tgtgggagga      120
aagagctgcg tggatagatt caaacttctc gtggtagtgc tcccagctcg acctctgtag      180
accttcagta ctactcttc ttgcttaggc tctctgtgtg ttgaaagcca tcccggtgtg      240
catgtgttgt tacaatttct tgtgatactt gcaat                                     275

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<210> SEQ ID NO 66
<211> LENGTH: 339
<212> TYPE: DNA

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<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(339)
<223> OTHER INFORMATION: AffymetrixID: 217753_s_at

<400> SEQUENCE: 66

tggtcgtgcc aaaaagggcc gcggccacgt gcagcctatt cgctgcacta actgtgccc	60
atgcgtgccc aaggacaagg ccattaagaa attcgtcatt cgaaacatag tggaggccgc	120
agcagtcagg gacatttctg aagcgagcgt cttcgatgcc tatgtgcttc ccaagctgta	180
tgtgaagcta cattactgtg tgagttgtgc aattcacagc aaagtagtca ggaatcgatc	240
tcgtgaagcc cgcaaggacc gaacaccccc accccgattt agacctgcgg gtgctgcccc	300
agctccccc ccaaagccca tgtaaggagc tgagttctt	339

<210> SEQ ID NO 67
<211> LENGTH: 532
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(532)
<223> OTHER INFORMATION: AffymetrixID: 217970_s_at

<400> SEQUENCE: 67

tgagctggag ctggttggac taatgagact gaggaagcag cttttcctac gatctgcatt	60
atgtaatcac aggtccagag agctttatgg aagcgggaga ggaggagcac ttactcatgt	120
tgtatttgtt aatggaggat gtcactcttt catagatgct agaactagag tgcacttggt	180
agatgctaaa ggtttagact ttacacaaaa tgtcttcac tgtatttgtt attgtctaca	240
atatatttga atttggggca gcatattaag atgtaatggc ctgttatgtc ttgaaaatac	300
ttgttttgcc tcttccagc atactgcatt ctgtggatca gtttgaacag cttctccacc	360
ttatttggac agtgataaat tgaaccaaga gtgtagattt acaagtgtaa ccttcaaaag	420
aggaagaact atttggggtc tgtaggtaac gaacagtcac accaaaatag actatgatgc	480
ttttgttaag aaaggtttca tgttttagat attttccgtg tcctaataaa tt	532

<210> SEQ ID NO 68
<211> LENGTH: 379
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(379)
<223> OTHER INFORMATION: AffymetrixID: 218190_s_at

<400> SEQUENCE: 68

tgaagaaaca tggcgccgcg gacgttgact tcgaaattgt actccctgct gttccgcagg	60
acctccacct tcgccctcac catcatcgtg ggcgtcatgt tcttcgagcg cgccttcgat	120
caaggcgccg acgctatcta cgaccacatc aacgagggga agctgtggaa acacatcaag	180
cacaagtatg agaacaagta gttccttgga ggcccccatc caggccagaa ggaccaggtc	240
caccagcag ctgtttgccc agagctggag cctcagcttg aagatgatgc tcaaggctact	300
cttcattggc caccattcgc tgttggcaag aaacggcttt acttacaaaa cagactcttt	360
acctctctgct gtgtttgaa	379

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<210> SEQ ID NO 69
<211> LENGTH: 545
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(545)
<223> OTHER INFORMATION: AffymetrixID: 218345_at

<400> SEQUENCE: 69

gatttccgat atggctactc ttattacaac agtgccctgcc gcattctccag ctcgagtgc 60
tggaacactc cagccccac tcagagtcca gaagaagtca gaaggctaca cctatgtacc 120
tccttcattg acatgctgaa ggccttggtc agaacccttc aggccatgct cttgggtggt 180
tggattctgc tgcttctggc atctctggcc cctctgtggc tgtactgtcg gagaatgttc 240
ccaaccaaag ggaaaagaga ccagaaggaa atgttggaag tgagtggaaat ctagccatgc 300
ctctctgat tattagtgc tggtgcttct gcaccgggcg tcctgtcatc tgactgctgg 360
aagaagaacc agactgagga aaagaggctt ttcaacagcc ccagttatcc tggccccatg 420
accgtggcca cagccctgct ccagcagcac ttgcccattc cttacacccc ttccccatcc 480
tgctccgctt catgtccct cctgagtgt catgtgataa taaactctca tgttattgtt 540
cccag 545

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<210> SEQ ID NO 70
<211> LENGTH: 557
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (101)..(101)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(557)
<223> OTHER INFORMATION: AffymetrixID: 218486_at

<400> SEQUENCE: 70

gactgtacac actataaatg gcatacaatt tggatatttt tcttaattat gacatgcaaa 60
gtaatgtgag tcctgccagt attctgggtg ataaggtctt ntgagtattt ggttgcttgt 120
cacaacattc tccaagcagt gatatttcta aagaggagat acatgttgaa aacggtttta 180
atttacattt ccatttctgt attacatttg gaaatacttt gtgtaaacca tcccccttcc 240
acctccattt gtctgttgaa agattttaag ttggaacag ttctgtctg aaaactcttc 300
tgagaaccac aaacctgtgt tatggattcg gcattggagcc ctgagctggc ggctctgggt 360
gtcgacggcc gctggagagg tgggctcccc tcgtgcactt tattgcctgg gcagttttgc 420
ttgatctttt gtgactttga gccttttaag tagtttgaat gataagactt aaaatgtttc 480
ataattatgt tttatgtaac agactttgac attattttaa cgagcatgtg taatgtaact 540
ttctcttttg aatcata 557

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<210> SEQ ID NO 71
<211> LENGTH: 541
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(541)

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<223> OTHER INFORMATION: AffymetrixID: 218545_at

<400> SEQUENCE: 71

```

agcatggatt tcaacatcac ttatttatct gtataattgg aaataaaaca ccgatatgat      60
agagaatcat tccggcatta cctaacctct tctgcagttg gatctatgta ttttcattgg    120
tctactgaaa acgaacaata caattaaaag cactaaagat tattatatta attcaacttt    180
gatctgatat atcacttaaa cttaaaggggt gtgtgtgggt tatgcttggt tcctatttct    240
gctctttaa gatactttga atcaataaaa ccattagtct acaaatcaaa ttgtgaactt    300
aatctctaga aagagaatat aactcagcca tttataggaa tttagggtca agtacaggat    360
atatgaaatc ttttcccagt atttcagaat gtacttaatt cacaggcagg atgcttcaat    420
gcaaaatcat gaatatTTTT aattcaaaac taaaatgtca ttaatatgta tgtatgcaaa    480
tgttttatct tattttctga aatgcatcta ctttcatggg ctttgtacgt ttctgagatt    540
t                                                                    541

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<210> SEQ ID NO 72

<211> LENGTH: 160

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(160)

<223> OTHER INFORMATION: AffymetrixID: 218728_s_at

<400> SEQUENCE: 72

```

atatcgatac attatgggtgc cgagtggtaa catgggagtg tttgatccaa cagaaataca      60
caatcgaggg gagctgaagt cacacatgaa agaagccatg atcaagcttg gtttccactt    120
gctctgcttc ttcattgtatc tttatagtat gatcttagct                          160

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<210> SEQ ID NO 73

<211> LENGTH: 461

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

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

<223> OTHER INFORMATION: AffymetrixID: 219269_at

<400> SEQUENCE: 73

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aggetagaaa atcttgctgc tccgtcttag cattccaaga gagtgcctcc aggtatttag      60
atagccctca gttctcaaat attagactac gtgtaaaatc ttgggtacct ttagattcct    120
gtaacactag tctgtactcc cttttccttc cccaagactg ataggatgca agctgaggtc    180
gtggcacagg aatgacagac accatttggg gagtatccac agagtcaaag gaacactaga    240
atccccacct cagcgtgagg ataattgatt tccagctgca ataagccgtg cctcattata    300
gccacactgt ggctagatta tacttccttg ggtgctgtgc taagaatgac aatggaaaaa    360
gccgatctca gattttgttt gaagttaaca tgctgacac agacatcctt tcctctcaca    420
agctgtgtga cttagtagat aaaatactgc cttctgcctt t                                                                    461

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<210> SEQ ID NO 74

<211> LENGTH: 563

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(563)
<223> OTHER INFORMATION: AffymetrixID: 219410_at

<400> SEQUENCE: 74
tgtttctcac catatgcttt tgttggcatt atgcagtaac cattgtcatc gttggaatga      60
attatgcttt cattacctgg ttggttaaat ctagacttaa gaggctctgc tcctcagaag      120
ttggacttct gaaaaatgct gaacgagaac aagaatcaga agaagaaatg tgactttgat      180
gagcttccag tttttctaga taaacctttt cttttttaca ttgttcttgg ttttgtttct      240
cgatcttttg ttgggagaac agctggctaa ggatgactct aagtgtactg tttgcatttc      300
caatttggtt aaagtatttg aatttaaata ttttcttttt agctttgaaa atattttggg      360
tgatactttc attttgcaca tcatgcacat catggtattc aggggctaga gtgatttttt      420
tccagattat ctaaagttag atgccacac tatgaaagaa atatttgttt tatttgcctt      480
atagatatgc tcaaggttac tgggcttgct actatttgta actccttgac catggaatta      540
tacttgttta tcttgttgct gca                                              563

<210> SEQ ID NO 75
<211> LENGTH: 472
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(472)
<223> OTHER INFORMATION: AffymetrixID: 219862_s_at

<400> SEQUENCE: 75
cggccaagga gctgttcaac gaggatgtgg aggaggtcac ttaccgagcc ctgagaaaca      60
aagacttcca agaggtcacc cttgagaaga acggagaggt ggtgttacgc tttgctgcag      120
cctatggctt tcgaaacatc cagaacatga tcttgaagct taagaagggc aagttcccat      180
tccactttgt ggaggtcctc gcctgtgctg gaggatgctt aaatggcaga ggccaagccc      240
agactccaga cggacatgcg gataaggccc tgctgcggca gatggaaggc atttacgctg      300
acatccctgt gcggcgtccg gagtccagtg cacacgtgca ggagctgtac caggagtggc      360
tggaggggat caactcccc aaggcccag aggtgctgca taccacgtac cagagccagg      420
agcgtggcac acacagcctg gacatcaagt ggtgaagtca ggccagggcc tt              472

<210> SEQ ID NO 76
<211> LENGTH: 396
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(396)
<223> OTHER INFORMATION: AffymetrixID: 219905_at

<400> SEQUENCE: 76
ggctcacgtg attatggagg cggttaaatc ccaagatctg caggataagt cagcaagatg      60
gagtccecatg agagctgatg gtttagttcc agtctgatgg cagcaggctt gacgccaagg      120
aagagatgat gtttaattca agtccgaagg caaggaaaaa gctgatggtc ctgtccaaag      180
gctattaggc aggaagaatt ctcttagggc agagttagct cttttgttct attcaggcct      240
tcaactgatt cagcaaggcc cgccacatt tgggaggaca gtctgcatta ctcagtctac      300

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tgatttgaat gttaatgtca ttgcgaaaca cctcacagg aacactcaga ataatgtttg 360
accaaatagc tgggcatctt gtgaccagc taagtg 396

<210> SEQ ID NO 77
<211> LENGTH: 533
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(533)
<223> OTHER INFORMATION: AffymetrixID: 220532_s_at

<400> SEQUENCE: 77

atctggcaaa ctgaaccctt tttatacatc gacactgtgt gtgatcgctc agaccctgtc 60
ttccctacca ctgggtacag atggatgcgg cgaagtcaag agaaccaatg gcagaaggag 120
gagtgtagag cttacatgca gatgctgagg aagttgttca cagcaatccg tgcctgttcc 180
ctggctgtct gtgtcttgaa ggtcattgtg tccttggttt ccttgggagt aggtcttcga 240
aacttgtgtg gccagagctc ccagccctg aatgaggaag gatcagagaa gaggtactgt 300
ggggagaatt cagtgcctcc ttcgacctc agggagcaga cctccactgc cattgtctctg 360
tgagccgcca aagacccac ggggtgccc catgtcctg tctagggcag cccagggccc 420
ccactctgg ctctcacac ttgcctccc tatggcctc ctccagacc tctctcttc 480
ttctccccac atccgcacct gctgttcca ctctggggtt ctcaagtcca tga 533

<210> SEQ ID NO 78
<211> LENGTH: 488
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(488)
<223> OTHER INFORMATION: AffymetrixID: 221011_s_at

<400> SEQUENCE: 78

gagtgttca tccatactc cattccctc cctcccttg tggacgggg tcttgccttt 60
tcaattcctg tgttttggtg tcttccctta tctgtaccc tgaatcacct gtcctggtct 120
tgctgtgtga tgggaacatg cttgtaaact gcgtaacaaa tctactttgt gtatgtgtct 180
gtttatgggg gtggtttatt atttttctg gtccctagac cactttgtat gaccgtttgc 240
agtctgagca ggccaggggc tgacagctaa tgtcaggacc ctacagcgtg gagectgtctg 300
gggggaccca gctgctcttg gacaagtggc tgagctccta tctggcctcc tctttttttt 360
ttttttcaag taatttgtgt gtatttctaa ctgattgtat tgaaaaaatt ctagtatttt 420
cagtaaaaat gcctgttgtg agatgaacct cctgtaactt ctatctgttc ttttttgagg 480
ctcagggg 488

<210> SEQ ID NO 79
<211> LENGTH: 526
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(526)
<223> OTHER INFORMATION: AffymetrixID: 221042_s_at

<400> SEQUENCE: 79

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tgaccccatg gacagccatc agtcccagga atccccaac ctggaaaaca tagcaaacc	60
cctagaagaa aatgtaacga aagaatcaat cagtagtaaa aaaaaggaaa aaaggaaaca	120
tgtggaccac gtagaaagt cactatttgt agcaccagga agtggtcaat cctcagatga	180
cctagaagaa gacagtagcg actacagcat tccttccagg actagtcaca gtgactccag	240
catttacctt cgacgacata ctcataggtc ttcggaatcg gatcatttta gctatgttca	300
gttgaggaac gcagcagatc tggatgacag aagaaaccga atattaacca ggaaggccaa	360
cagctcagga gaagccatgt cactggggag ccacagcccg cagagtgact cctgacaca	420
gcttgctccag cagccggata tgatgtattt tattctcttc ctgtggtcc tgggtgactg	480
cttgctgctc ttcccacaac tggatgtag caggctctga tacgtg	526

<210> SEQ ID NO 80
 <211> LENGTH: 230
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(230)
 <223> OTHER INFORMATION: AffymetrixID: 221434_s_at

<400> SEQUENCE: 80

cctcagcagc gcgaggtgct gcggcgctgc gtagaagtat caatcagccg gttgcttttg	60
tgagaagaat tccttggtgact gcggcgctga gtcagctgaa agaacacttt gcacagtctg	120
gccatgtcag aaggtgcatt ttaccttttg acaaggagac tggctttcac agaggttttg	180
gttgggttca gttttcttca gaagaaggac ttcggaatgc actacaacag	230

<210> SEQ ID NO 81
 <211> LENGTH: 350
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(350)
 <223> OTHER INFORMATION: AffymetrixID: 221737_at

<400> SEQUENCE: 81

gaaatctatt tttaactctt atgttcgtag agaaattggt tcaaggattt tgagtcatag	60
gtctgtaatt tatagagatc tctagaattc ttattgtaat ttctactt ctttgataaa	120
agaaaaataa gtcagattgt taactccaag attgaaaaaa aaaactcttg aaagaagatt	180
attagttgta actaatttgg gggttctggg cacagacatc taacctggta ttgtaaggca	240
gaggtccca ttggaatggt agtgggccg gtcagttggt catggtgtaa gctttgcaca	300
gtgtattaac attgggaggg tctggcttga aaatttgcc accctcagcc	350

<210> SEQ ID NO 82
 <211> LENGTH: 97
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(97)
 <223> OTHER INFORMATION: AffymetrixID: AFFX-M27830_5_at

<400> SEQUENCE: 82

tagttttacc ctactgatga tgtgtgttg ccatggtaat cctgctcagt acgagaggaa	60
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ccgcagggttc agacatttgg tgtatgtgct tggctga

97

<210> SEQ ID NO 83
<211> LENGTH: 535
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (39)..(39)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (43)..(44)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (53)..(53)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (62)..(62)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (70)..(70)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (74)..(74)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (86)..(86)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (113)..(113)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (124)..(124)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (127)..(127)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (142)..(142)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (148)..(148)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (171)..(465)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(535)
<223> OTHER INFORMATION: AffymetrixID: 36711_at

<400> SEQUENCE: 83

ttgcacggat ctaagttatt ctccccagcc agagcccgng cttnctgctc ccngggaaaa	60
gntggcggtan tggncctgag ctgggnttta tattttatat ctgcaataa atnacatttt	120
atcttanatt tagggaaagc cngagagnaa caacaaaaaa tgtttaagcc nnnnnnnnnn	180
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn	240
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn	300

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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 360
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 420
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnntattg cccggctcct 480
agaatttatt tatttctctga cttacagcaa gcgagttatc gtcttctgta ttttg 535

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<210> SEQ ID NO 84
<211> LENGTH: 494
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (124)..(124)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (184)..(184)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (237)..(262)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (447)..(464)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(494)
<223> OTHER INFORMATION: AffymetrixID: 38037_at

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<400> SEQUENCE: 84
ccactctatg agttggactt cagtcttgcc taggcgattt tgtctacat ttgtgttttg 60
aaagcccaag gtgctgatgt caaagtgtaa cagatatcag tgtctccccg tgctctctcc 120
ctgncagatc tcagaagagg ttgggcttcc atgcctgtag ctttctcggg cctcaccccc 180
catngcccca ggcccacagc gtgggaactc actttccctt gtgtcaagac atttctnnnn 240
nnnnnnnnnn nnnnnnnnnn nnaactccatg caggggtcag tgcagcagag gacagctctg 300
agaaggtatt agcaaagcaa aaggctgaga aggaacaggg aacattggag ctgactgttc 360
ttggttaactg attacctgcc aattgctacc gagaaggttg gaggtgggga aggctttgta 420
taatccccac cacctcacca aaacgannnn nnnnnnnnnn nnnngtcctt tctggaagtt 480
tctggtgccca ttcc 494

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<210> SEQ ID NO 85
<211> LENGTH: 492
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(492)
<223> OTHER INFORMATION: AffymetrixID: 201386_s_at

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<400> SEQUENCE: 85
ggagatcatc tgacactgct gaacgtctac catgctttta aacaaaatca tgaatcggtt 60
cagtgggtgt atgacaactt cattaactac aggtccctga tgtccgcaga caatgtacgc 120
cagcagctat ctogaattat ggacagattt aatttgctc gtcgaagtac tgactttaca 180
agcagggact attatattaa tataagaaaa gctttgggta ctgggtatct tatgcagggt 240
gcacatttag aacgaacagg gcattactta actgtgaaag ataaccaggt gggttcagttg 300

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catccctcta ctgttcttga ccacaaacct gaatgggtgc tttataatga gtttgttcta 360
acaacaaaga attacatccg gacatgtaca gatatcaagc cagaatgggt ggtgaaaatt 420
gccccccaat attatgacat gagcaatttc ccacagtgtg aagcaaagag acagttggac 480
cgcatcattg cc 492

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<210> SEQ ID NO 86
<211> LENGTH: 378
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(378)
<223> OTHER INFORMATION: AffymetrixID: 201890_at

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<400> SEQUENCE: 86
gctactttga attaatctgc ctttatgttt gggagaagaa agctgagaca ttgcatgaaa 60
gatgatgaga gataaatgtt gatcttttgg ccccatattgt taattgtatt cagtatttga 120
acgtcgtcct gtttattgtt agttttcttc atcatttatt gtatagacaa tttttaaatc 180
tctgtaatat gatacathtt cctatctttt aagttattgt tacctaaagt taatccagat 240
tatatgggtc ttatatgtgt acaacattaa aatgaaaggc tttgtcttgc attgtgaggt 300
acaggcggaa gttggaatca ggttttagga ttctgtctct cattagctga ataattgtgag 360
gattaacttc tgccagct 378

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<210> SEQ ID NO 87
<211> LENGTH: 448
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(448)
<223> OTHER INFORMATION: AffymetrixID: 202219_at

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<400> SEQUENCE: 87
aagcttcgag ctgttgctg tgtgagtctg ttgtgtggat gtgcgtgtgt ggtccccagc 60
cccagactgg attggaagg tgcatggtgg gggcctcggg gctgtcccca cgctgtccct 120
ttgccacaag tctgtggggc aagaggctgc aatattccgt cctgggtgtc tgggctgcta 180
acctggcctg ctcaggcttc ccaccctgtg cggggcacac cccaggaag ggaccctgga 240
cacggctccc acgtccagc ttaagggtga tgcacttccc gcacctccag tcttctgtgt 300
agcagcttta acccagcttt gtctgtcacg tccagtcccg agacggctga gtgaccccaa 360
gaaaggcttc cccgacaccc agacagaggc tgcagggctg gggctgggtg aggggtggcg 420
gcctgcgggg acattctact gtgctaaa 448

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<210> SEQ ID NO 88
<211> LENGTH: 371
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(371)
<223> OTHER INFORMATION: AffymetrixID: 202464_s_at

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<400> SEQUENCE: 88
tattctgtcc tgagaccacg ggcaaagctc ttccattttg agagagaaga aaaactgttt 60

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ggaaccacac caatgatatt tttctttgta atacttgaaa tttatttttt tattattttg 120
atagcagatg tgctatttat ttatttaata tatgtataag gagtcctaaa caatagaaaag 180
ctgtagaagc thtagagata ggcttcagtt gttaattggt ttggagcctc ctatgtgtga 240
cttatgactc tctgtgttct gtgtatttgt ctgaattaat gacctgggat ataaagctat 300
gctagctttc aaacaggaga tgccttcaga aagctttgta tattttgcag ttgccagacc 360
aataaaaatac c 371

```

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<210> SEQ ID NO 89
<211> LENGTH: 530
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (69)..(69)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(530)
<223> OTHER INFORMATION: AffymetrixID: 203115_at

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<400> SEQUENCE: 89

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aactccaatt caggagccct tgcgagtata tctgaagcac ttatttgcta aggaaacctg 60
aattgatanc agtactgtgc tgtctggaat aatgtccttg atactgagtt gggaccagac 120
tggtctttat agtgacaggc aaagaggaat ttattgagat cactgctcat ggcatttggt 180
gctgtaagaa gtgttgccct tgattgttac taaccacgga tgggtaacgg tcatacatta 240
ggctagtgtt tggtaggaca aaatcttttt agagctttga gaattgtcat cctgttggtc 300
aactttgaaa tacaaatggt tgccttggtta attagcaatg aactgctggc agtttcttca 360
gctgtgtata tacggatctg gcttttaatt gatgaatcaa cttctacaga aacttttgca 420
gggacagtgt tgatgaggca gtttagcttg ccagggtgat gataaagccc aggtccctgc 480
atgtatagtg ctcttctaaa gaatatgcat tcttgaacta cttaactttt 530

```

```

<210> SEQ ID NO 90
<211> LENGTH: 497
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(497)
<223> OTHER INFORMATION: AffymetrixID: 203574_at

```

```

<400> SEQUENCE: 90

```

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gtatggtaca ttcttctctt actcctttct cagtgcaggt gactaacatt caagattggt 60
ctctcaaate ggagcactgg catcaaaaag aactgagtgg caaaactcag aatagtttca 120
aaactggagt tgttgaaatg aaagacagtg gctacaaagt ttctgaccca gagaacttgt 180
atttgaagca ggggatagca aacttatctg cagagggtgt ctcactcaag agacttatag 240
ccacacaacc aatctctgct tcagactctg ggtaaattac tactgagtaa gagctgggca 300
tttagaaaga tgtcatttgc aatagagcag tccattttgt attatgctga attttcactg 360
gacctgtgat gtcatttcac tgtgatgtgc acatgttgte tgtttggtgt ctttttgtgc 420
acagattatg atgaagatta gattgtgtta tcaactctgcc tgtgtatagt cagatagtc 480
atgcgaaggc tgtatat 497

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<210> SEQ ID NO 91
<211> LENGTH: 326
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(326)
<223> OTHER INFORMATION: AffymetrixID: 203887_s_at

<400> SEQUENCE: 91

cagggggtgt gtctgtctcag taatttgagg acaaccattc cagactgctt ccaattttct	60
ggaatacatg aaatatagat cagttataag tagcaggcca agtcaggccc ttattttcaa	120
gaaactgagg aattttcttt gtgtagcttt gctctttggt agaaaaggct aggtacacag	180
ctctagacac tgccacacag ggtctgcaag gtctttggtt cagctaagct aggaatgaaa	240
tcttgcttca gtgtatggaa ataaatgtat catagaaatg taacttttgt aagacaaagg	300
ttttctctct ctattttgta aactca	326

<210> SEQ ID NO 92
<211> LENGTH: 533
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(533)
<223> OTHER INFORMATION: AffymetrixID: 203932_at

<400> SEQUENCE: 92

tcttacgggg acacttacac ctgtgtggta gagcacattg gggctcctga gcccatcctt	60
cgggactgga cacctgggct gtcccccattg cagaccctga aggtttctgt gtctgcagt	120
actctgggcc tgggcctcat catcttctct cttggtgtga tcagctggcg gagagctggc	180
cactctagtt acactcctct tcctgggtcc aattattcag aaggatggca catttcctag	240
aggcagaatc ctacaacttc cactccaagt gagaaggaga ttcaaactca atgatgctac	300
catgcctctc caacatcttc aaccccctga cattatcttg gatcctatgg tttctccatc	360
caattctttg aatttcccag tctcccctat gtaaaactta gcaacttggg ggacctcatt	420
cctgggacta tgctgtaacc aaattattgt ccaaggctat attctggga tgaatataat	480
ctgaggaagg gagttaaga ccctcctggg gctctcagtg tgccatagag gac	533

<210> SEQ ID NO 93
<211> LENGTH: 419
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(419)
<223> OTHER INFORMATION: AffymetrixID: 204131_s_at

<400> SEQUENCE: 93

ttaccattcc gggttcagac atcacaagct tttgagcgca tggaactcca taaactaaca	60
aattacataa actaaagggg gattttcttt cttcttttgt ttggtagaaa attatccttt	120
tctaaaaact gaacaatggc acaattgttt gctatgtgca cccgtccagg acagaaccgt	180
gcataggcaa aaggagtgga gcacagcgtc cggcccagtg tgtttccggt tctgagtcag	240
ggtgatctgt ggacgggacc ccagcaccaa gtctacgggt gccagatcag tagggcctgt	300

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gatttcctgt cagtgtcctc agctaattgtg aacagtgttg gtctgctggt tagaaactag 360

aatattgata ttttcaggaa agaaatcagc tcagctctcc actcattgcc aaatgtcac 419

<210> SEQ ID NO 94

<211> LENGTH: 507

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(507)

<223> OTHER INFORMATION: AffymetrixID: 204419_x_at

<400> SEQUENCE: 94

acactcgctt ctggaacgtc tgaggttata aataagctcc tagtccagac gccatgggtc 60

atttcacaga ggaggacaag gctactatca caagcctgtg gggcaagggtg aatgtggaag 120

atgctggagg agaaaccctg ggaaggctcc tgggtgtcta cccatggacc cagaggttct 180

ttgacagctt tggcaacctg tcctctgctc ctgccatcat gggcaacccc aaagtcaagg 240

cacatggcaa gaaggtgctg acttccttgg gagatgccat aaagcacctg gatgatctca 300

agggcacctt tgcccagctg agtgaactgc actgtgacaa gctgcatgtg gatcctgaga 360

acttcaagct cctgggaaat gtgctggtga ccgttttggc aatccatttc ggcaaagaat 420

tcacccctga ggtgcaggct tcctggcaga agatggtgac tggagtggcc agtgcctgt 480

cctccagata ccactgagct cactgcc 507

<210> SEQ ID NO 95

<211> LENGTH: 309

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(309)

<223> OTHER INFORMATION: AffymetrixID: 204467_s_at

<400> SEQUENCE: 95

ctcggaattc cctgaagcaa cactgccaga agtgtgtttt ggtatgcact ggttccttaa 60

gtggctgtga ttaattattg aaagtgggtt gttgaagacc ccaactacta ttgtagagtg 120

gtctatttct cccttcaatc ctgtcaatgt ttgctttatg tattttgggg aactgttgtt 180

tgatgtgtat gtgtttataa ttgttatata tttttaattg agccttttat taacatatat 240

tgttattttt gtctcgaaat aatttttttag ttaaaatcta ttttgtctga tattggtgtg 300

aatgctgta 309

<210> SEQ ID NO 96

<211> LENGTH: 521

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

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

<223> OTHER INFORMATION: AffymetrixID: 204848_x_at

<400> SEQUENCE: 96

acactcgctt ctggaacgtc tgagattata aataagctcc tagtccagac gccatgggtc 60

atttcacaga ggaggacaag gctactatca caagcctgtg gggcaagggtg aatgtggaag 120

atgctggagg agaaaccctg ggaaggctcc tgggtgtcta cccatggacc cagaggttct 180

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ttgacagctt tggcaacctg tcctctgcct ctgccatcat gggcaacccc aaagtcaagg    240
cacatggcaa gaaggtgctg acttccttgg gagatgccat aaagcacctg gatgatctca    300
agggcacctt tggccagctg agtgaactgc actgtgacaa gctgcagtgtg gatcctgaga    360
acttcaagct cctgggaaat gtgctggtga ccgttttggc aatccatttc ggcaaagaat    420
tcacccctga ggtgcaggct tcctggcaga agatggtgac tgcagtggcc agtgccctgt    480
cctccagata ccactgagcc tcttgcccat gattcagagc t                            521

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<210> SEQ ID NO 97
<211> LENGTH: 472
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(472)
<223> OTHER INFORMATION: AffymetrixID: 205239_at

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<400> SEQUENCE: 97

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atttcaaaat ttctgcattc acggagaatg caaatatata gagcacctgg aagcagtaac    60
atgcaaatgt cagcaagaat atttcggtga acggtgtggg gaaaagtcca tgaaaactca    120
cagcatgatt gacagtagtt tatcaaaaat tgcattagca gccatagctg cctttatgtc    180
tgctgtgata ctcacagctg ttgctgttat tacagtccag cttagaagac aatacgtcag    240
gaaatatgaa ggagaagctg aggaacgaaa gaaacttcga caagagaatg gaaatgtaca    300
tgctatagca taactgaaga taaaattaca ggatatcaca ttggagtcac tgccaagtca    360
tagccataaa tgatgagtcg gtccctcttc cagtggatca taagacaatg gacccttttt    420
gttatgatgg ttttaaaact tcaattgtca ctttttatgc tatttctgta ta          472

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<210> SEQ ID NO 98
<211> LENGTH: 477
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(477)
<223> OTHER INFORMATION: AffymetrixID: 205571_at

```

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<400> SEQUENCE: 98

```

```

gatcaggagc aatgccactg ctagcatacc ttccttagtg aaaaatcttt tggaaaagga    60
tcccactctg acctgtgaag tactaatgaa tgctgttget acagagtatg ctgcctatca    120
tcaaattgat aatcacattc acctaaataa cccaacggat gagacactgt ttcttggaaat    180
aaatagcaaa gccaaagaac tgcaaaactg ggagtggata tatggcaaaa ctccaaagtt    240
tagtataaat acttcctttc atgtgttata tgaacagtca cacttggaat ttaaagtatt    300
catagacata aagaatggaa gaattgaaat ttgtaatat gaagcacctg atcattgggt    360
gccattggaa atacgtgaca aattaaattc aagtottatt ggcagtaagt tttgccaac    420
tgaaactacc atgctaacaa atatattact tagaacatgt ccacaagacc acaaact    477

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<210> SEQ ID NO 99
<211> LENGTH: 422
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(422)

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<223> OTHER INFORMATION: AffymetrixID: 205592_at

<400> SEQUENCE: 99

```

tggggggccac agactcaaca tgtgtgtgtg gtgggggtcc agcccaacat agagtaacat      60
tatttgtacc tcccaggcta gctcagtcca tgggaggctc tctgtccct gaaagctgac      120
accacacctt caccacttcg cccatgctac agttcagttt cctcgtctgt aaaatgggga      180
tgataatggt acctaccttg cagtgttgtt ataaggatta aaggagacag tgcaagaaaa      240
ggccttggtt ggtgaagagc ccaacctcgg aggggagctg ctgggatcct ccttatcttg      300
actgggatgt cctgtctccc ccctcccctt gctccttgaa catggccaag gaaagtgaaa      360
aacaaaaatt attcactctg ctagcacctt tccccttgat gcctgggaat aggttttgcc      420
aa                                                                    422

```

<210> SEQ ID NO 100

<211> LENGTH: 362

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(362)

<223> OTHER INFORMATION: AffymetrixID: 205863_at

<400> SEQUENCE: 100

```

tagctccaca ttctgtgca ttgaggggtt aacattaggc tgggaagatg aaaaaacttg      60
aagagcatct ggaggaatt gtcaatatct tccaccaata ctgagttcgg aaggggcatt      120
ttgacacctt ctctaagggt gagctgaagc agctgcttac aaaggagctt gcaaacacca      180
tcaagaatat caaagataaa gctgtcattg atgaaatatt ccaaggcctg gatgctaadc      240
aagatgaaca ggtcgacttt caagaattca tatccctggt agccattgcg ctgaaggctg      300
cccattacca caccacaaaa gagtaggtag ctctctgaag gctttttacc cagcaatgtc      360
ct                                                                    362

```

<210> SEQ ID NO 101

<211> LENGTH: 416

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(416)

<223> OTHER INFORMATION: AffymetrixID: 205900_at

<400> SEQUENCE: 101

```

tcaagtccct tgggtggcagt tccagcgtga ggtttgtttc taccacttat tccggagtaa      60
ccagataaa agatgccctc tgtttcatta gctctagttc tccccagca tcaactaaca      120
atatgcttgg caagaccgag gtcgatttgt cccagcctta cgggagaaaa gagctatggt      180
tagttacact agtcatect attccccag ctctttcttt tctgctgttt cccaatgaag      240
ttttcagatc agtggcaatc tcagttccct tgctatgacc ctgctttgtt ctttcccag      300
aaacagtcca gcagtgaaca ccaccacat gacatttcaa gcaccacctt aagccagcca      360
gagtaggacc agttagacct aggggtgtgga cagctccttg catettaaca ctgtgc      416

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<210> SEQ ID NO 102

<211> LENGTH: 560

<212> TYPE: DNA

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```

<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(560)
<223> OTHER INFORMATION: AffymetrixID: 205950_s_at

<400> SEQUENCE: 102
gagccccatt cacaaathtt gaccctctta ctctccttcc ttcacccctg gattttctgga    60
cctacccttg ctctctgact catcctctcc tttatgagag tgtaacttgg atcatctgta    120
aggagagcat cagtgtcagc tcagagcagc tggcacaatt ccgcagcctt ctatcaaagt    180
ttgaaggtga taacgctgtc cccatgcagc acaacaaccg cccaacccaa cctctgaagg    240
gcagaacagt gagagcttca ttttgatgat tctgagaaga aacttgctct tcctcaagaa    300
cacagccctg cttctgacat aatccagtta aaataataat ttttaagaaa taaatattatt    360
tcaatattag caagacagca tgccttcaaa tcaatctgta aaactaagaa acttaaattt    420
tagttcttac tgcttaattc aaataataat tagtaagcta gcaaatagta atctgtaagc    480
ataagcttat cttaaattca agtttagttt gaggaattct ttaaaattac aactaagtga    540
tttgtatgtc tatttttttc                                     560

```

```

<210> SEQ ID NO 103
<211> LENGTH: 447
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(447)
<223> OTHER INFORMATION: AffymetrixID: 205987_at

<400> SEQUENCE: 103
ccagctgttg ctggtttgtc atgcctccgg cttctacca aagcctgttt gggtgacatg    60
gatgcggaat gaacaggagc aactggggcac taaacatggt gatattcttc ctaatgctga    120
tgggacatgg tatcttcagg tgatcctgga ggtggcatct gaggagcctg ctggcctgtc    180
ttgtcgagtg agacacagca gtctaggagg ccaggacatc atcctctact ggggacacca    240
ctcttccatg aattggattg ccttggtagt gatagtgcc ttggtgattc taatagtcct    300
tgtgttatgg tttaagaagc actgctcata tcaggacatc ctgtgagact ctcccccctg    360
actcccccat tgtgttaaga acccagcaac ccaggagcct agtacaatat agtgatgcca    420
tcccgtcgac tctccattta aattggtt                                     447

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```

<210> SEQ ID NO 104
<211> LENGTH: 490
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(490)
<223> OTHER INFORMATION: AffymetrixID: 206025_s_at

<400> SEQUENCE: 104
ggatacccca ttgtgaagcc agggcccaac tgtggatttg gaaaaactgg cattattgat    60
tatggaatcc gtctcaatag gagtgaaaga tgggatgcct attgctacaa cccacacgca    120
aaggagtgtg gtggcgtctt tacagatcca aagcaaattt ttaaatctcc aggtctccca    180
aatgagtacg aagataacca aatctgtctc tggcacatta gactcaagta tggtcagcgt    240

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attcacctga gttttttaga ttttgacctt gaagatgacc caggttgctt ggttgattat 300
gttgaaatat atgacagtta cgatgatgtc catggctttg tgggaagata ctgtggagat 360
gagcttccag atgacatcat cagtacagga aatgtcatga ccttgaagtt tctaagtgat 420
gcttcagtga cagctggagg tttccaaatc aaatatgttg caatggatcc tgtatccaaa 480
tccagtcaag 490

```

```

<210> SEQ ID NO 105
<211> LENGTH: 479
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(479)
<223> OTHER INFORMATION: AffymetrixID: 206111_at

```

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<400> SEQUENCE: 105

```

```

gtttacctgg gctcaatggt ttgaaacca gcacatcaat atgacctccc agcaatgcac 60
caatgcaatg caggtcatta acaattatca acggcgatgc aaaaacccaa atactttcct 120
tcttacaact tttgctaacg tagttaatgt ttgtggtaac ccaaatatga cctgtcctag 180
taacaaaact cgcaaaaatt gtcaccacag tggaagccag gtgcctttaa tccactgtaa 240
cctcacaact ccaagtccac agaatatctc aaactgcagg tatgcgcaga caccagcaaa 300
catgttctat atagttgcat gtgacaacag agatcaacga cgagaccctc cacagtatcc 360
ggtggttcca gttcacctgg atagaatcat ctaagctcct gtatcagcac tctcatcat 420
cactcatctg ccaagctcct caatcatagc caagatccca tctctccata tactttggg 479

```

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<210> SEQ ID NO 106
<211> LENGTH: 524
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(524)
<223> OTHER INFORMATION: AffymetrixID: 206834_at

```

```

<400> SEQUENCE: 106

```

```

ggagaagact gctgtcaatg ccctgtgggg caaagtgaac gtggatgcag ttggtggtga 60
ggccctgggc agattactgg tggctacccc ttggaccagc aggttctttg agtcctttgg 120
ggatctgtcc tctcctgatg ctgttatggg caaccctaag gtgaaggctc atggcaagaa 180
ggtgctaggt gccttttagt atggcctggc tcacctggac aacctcaagg gcactttttc 240
tcagctgagt gagctgcact gtgacaagct gcacgtggat cctgagaact tcaggctctt 300
gggcaatgtg ctggtgtgtg tgctggcccg caactttggc aaggaattca cccacaaat 360
gcaggctgcc tatcagaagg tgggtgctgg tgtggctaata gccctggctc acaagtacca 420
ttgagatcct ggactgtttc ctgataacca taagaagacc ctatttcctt agattctatt 480
ttctgaactt gggaacacaa tgcctacttc aagggtatgg ctcc 524

```

```

<210> SEQ ID NO 107
<211> LENGTH: 560
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(560)

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<223> OTHER INFORMATION: AffymetrixID: 207332_s_at

<400> SEQUENCE: 107

```

aaggagagtc ccctgaaggt ctgacacgtc tgcctaccca ttcgtggtga tcaattaaat    60
gtaggtatga ataagttcga agctccgtga gtgaaccatc atataaacgt gtagtacagc    120
tgtttgtcat agggcagttg gaaacggcct cctagggaaa agttcatagg gtctcttcag    180
gttcttagtg tcacttacct agatttacag cctcacttga atgtgtcact actcacagtc    240
tctttaatct tcagttttat ctttaatctc ctcttttata ttggactgac atttagcgta    300
gctaagtga aaggatcatg ctgagattcc tgggtcgggt gttacgcaca cgtacttaaa    360
tgaaagcatg tggcatgttc atcgataaac acaatatgaa tacagggcac gcattttgca    420
gcagtgaagtc tcttcagaaa acccttttct acagttaggg ttgagttact tctatcaag    480
ccagtacgtg ctaacaggct caatatctct gaatgaaata tcagactagt gacaagctcc    540
tggctcttgag atgtcttctc                                     560

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<210> SEQ ID NO 108

<211> LENGTH: 482

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (159)..(159)

<223> OTHER INFORMATION: n is a, c, g, or t

<220> FEATURE:

<221> NAME/KEY: misc_feature

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

<223> OTHER INFORMATION: AffymetrixID: 208632_at

<400> SEQUENCE: 108

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aaccacagaat ggcacacact gctctgctgt agcatcatgt cagggtctcc tggactcagt    60
acacctctca gtttgtcttt taaaaaacag ctgaatcttt actacctatt tagttctctt    120
tgtaaaagaa acagggggtg gaataaaatg gatttaggna caccagttt gaattgcagt    180
tttttttttt ctgacacatg gccaggctgt ggtgccagct taatggagta ggctgtcctt    240
ggcacttgca tgtgtgaaag gaggggtttg cctctctctg agcatggctt gagttggtaa    300
ggaaagctgt aactcacgaa gccctgagac ctgctacccc taagatcgag cttgttttca    360
gtgactggct tgagtcatag gaggaggagt ctggtacagc tgcaggagag caggggccatc    420
tgaagcggta gcattgccac catctccctc tcacttagag cagttttctt atgccttggt    480
tt                                     482

```

<210> SEQ ID NO 109

<211> LENGTH: 494

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(494)

<223> OTHER INFORMATION: AffymetrixID: 209007_s_at

<400> SEQUENCE: 109

```

gaagatggaa ctcgaaatcc caatgaaaaa cctacccagc aaagaagcat agcttttagc    60
tctaataatt ctgtagcaaa gccaatataa aaatcagcta aagctgccac agaagaggca    120
tcttcaagat caccaaaaat agatcagaaa aaaagtccat atggactgtg gataacctatc    180

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taaaagaaga aaactgatgg ctaagtttgc atgaaaactg cactttattg caagtttagt	240
tttctagcat tatcccatcc ctttgagcca ttcaggggta cttgtgcatt taaaaaccaa	300
cacaaaaaga tgtaaatact taacactcaa atattaacat tttagggttc tcttgagat	360
atgagagata gcacagatgg accaaagggt atgcacaggt gggagtcttt tgtatatagt	420
tgtaaatatt gtcttggtta tgtaaaaatg aaatttttta gacacagtaa ttgaactgta	480
ttcctgtttt gtat	494

<210> SEQ ID NO 110
 <211> LENGTH: 445
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(445)
 <223> OTHER INFORMATION: AffymetrixID: 209458_x_at

<400> SEQUENCE: 110

agagaaccca ccattgtgct gtctcctgcc gacaagacca acgtcaaggc cgcttggggt	60
aaggteggcg cgcacgctgg cgagtatggt gcggaggccc tggagaggat gttcctgtcc	120
ttccccacca ccaagaccta ctcccgccac ttgcacctga gccacggctc tgcccagggt	180
aagggccacg gcaagaaggt ggccgacgcy ctgaccaacg ccgtggcgca cgtggacgac	240
atgccccacg cgctgtccgc cctgagcgac ctgcacgcgc acaagcttcg ggtggaccgc	300
gtcaacttca agctcctaag ccaactgcctg ctggtgaccc tggccgcccc cctccccgcc	360
gagttcaccg ctgcggtgca cgctccctg gacaagtcc tggcttctgt gageaccgtg	420
ctgacctcca aataccgtta agctg	445

<210> SEQ ID NO 111
 <211> LENGTH: 432
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(432)
 <223> OTHER INFORMATION: AffymetrixID: 209795_at

<400> SEQUENCE: 111

tagtctaatt gaatccctta aactcaggga gcatttataa atggcaaatg cttatgaaac	60
taagatttgt aatatttctc tctttttaga gaaatttgcc aatttacttt gttatttttc	120
cccaaaaaga atgggatgat cgtgtattta tttttttact tcctcagctg tagacaggtc	180
cttttcgatg gtacatattt ctttgctttt ataacttttt atacagtgtc ttacagagaa	240
aagacataag caaagactat gaggaatatt tgcaagacat agaatagtgt tggaaaatgt	300
gcaatatgtg atgtggcaaa tctctattag gaaatattct gtaactttca gacctagaat	360
aatactagtc ttataatagg tttgtgactt tcctaaatca attctattac gtgcaatact	420
tcaatacttc at	432

<210> SEQ ID NO 112
 <211> LENGTH: 535
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(535)

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<223> OTHER INFORMATION: AffymetrixID: 210027_s_at

<400> SEQUENCE: 112

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tgggatgaag cctttcgcaa gttcctgaag ggcttggtt cccgaaagcc ccttgtgtg      60
tgtggagacc tcaatgtggc acatgaagaa attgaccttc gcaaccccaa gggaacaaaa    120
aagaatgctg gcttcacgcc acaagagcgc caaggcttcg gggaattact gcaggctgtg    180
ccactggctg acagcttttag gcacctctac cccaacacac cctatgccta caccttttgg    240
acttatatga tgaatgctcg atccaagaat gttgggtggc gccttgatta ctttttgttg    300
tcccactctc tgttacctgc attgtgtgac agcaagatcc gttccaaggc cctcgcgagt    360
gatcactgtc ctatcacctc ataccatgca ctgtgacacc acccctaaat cacttttgagc    420
ctgggaaata agccccctca actaccattc cttctttaaa cactcttcag agaaatctgc    480
attctatttc tcatgtataa aacgaggaat cctccaacca ggctcctgtg ataga        535

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<210> SEQ ID NO 113

<211> LENGTH: 368

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (220)..(220)

<223> OTHER INFORMATION: n is a, c, g, or t

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(368)

<223> OTHER INFORMATION: AffymetrixID: 210254_at

<400> SEQUENCE: 113

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atacaccagc agggcaatta gcagcttggg gaagttggaa gtctcgatgt tgtgatagta      60
gaccacggag gtgacagcag ccatgaacgc catcccggtt ggcatgtaca ggtgcagatg    120
gtgggattcg gtcaccccat cagacaggat gccctctgca atctcacaca ccaggacgaa    180
gagcagcatg aaggtcagga tccaccgcag gttgtgccc n gggaaatgaa gccatgtgct    240
gtggtggatg tgcaccttgg agctctgact tccccatcca atgaagagga tggggaaggt    300
gatgaagagt aggaagacgt gcggcaccac gttgagcgcg tccacaaagc agccgttgtt    360
gaggaccc

```

<210> SEQ ID NO 114

<211> LENGTH: 414

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(414)

<223> OTHER INFORMATION: AffymetrixID: 210338_s_at

<400> SEQUENCE: 114

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gaactgaatg ctgacctgtt ccgtggcacc ctggaccag tagagaaagc ccttcgagat      60
gccaaactag acaagtcaca gattcatgat attgtcctgg ttggtggttc tactcgtatc    120
cccaagattc agaagcttct ccaagacttc ttcaatggaa aagaactgaa taagagcatc    180
aaccctgatg aagctgttgc ttatggtgca gctgtccagg cagecatctt gtetggagac    240
aagtctgaga atgttcaaga tttgtctgct ttggatgtca ctctctttc ccttggtatt    300
gaaactgctg gtggagtcat gactgtcttc atcaagcgta ataccacat tcctaccaag    360

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cagacacaga ctttcactac ctattctgac aaccagcctg gtgtgcttat tcag 414

<210> SEQ ID NO 115
<211> LENGTH: 557
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(557)
<223> OTHER INFORMATION: AffymetrixID: 211038_s_at

<400> SEQUENCE: 115

tggtgttctt tgaatgccta tcttcctttt gtgcctcgga acctctcacg cctgccacaa 60
gttactcttt tcttggtag ttctgaactt taaataaggt aatgcctgta agaatgccat 120
aaatgctcaa taattgtcat ctgttattat tttcatcagt aacatcatct gaatcatcag 180
tattgtctgc ttttaacagc tgcatttttc attgtccaaa tatagtcaca tacatttgac 240
cattttataa ttattgaata ataaattcgt tctgctattt tacaatgaaa aataatgctg 300
cagagagcat ttttgcacat gtatcgtggc agatgtaggc cagaggctct tctttatcca 360
tcctatggcc aacctatgaa tgtatacacg tttaatgaga ttttgccagc aatcaaagcc 420
ttcagggaaa atgtccctag ctctttacta catcagatca aggactctgg ataattggca 480
taacatcctg gaatagctga aacagagata ttattctctg ctgtcctctg ttgtctttgt 540
cttttcacgt cttaata 557

<210> SEQ ID NO 116
<211> LENGTH: 545
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(545)
<223> OTHER INFORMATION: AffymetrixID: 211458_s_at

<400> SEQUENCE: 116

aaatagcatt aaactggaat tgacagagtg agttgagcat ctctgtctaa cctgctcttt 60
ctctctggtg ctctctcatc caccctacc ttggaattta ataagcttca ggcatttcca 120
attgcagact aaaaccatt ctaccatctc ctctagtatt ttccatgtat caggacagag 180
atgtcttatg tagggaaggg gcaggatga agtgaggtag attatctata cctctcactc 240
attcaggatt ctctctccca tgctgctgtc ccttcattct cactctcaca ggaatgctat 300
gtgatggcca gctgcttccc ttcttggtta tccactgcag ctgctagtta gaaaggtttg 360
cagggatgac ttttagtaaa tcatggggat tttattgatt tattatcact tataggattt 420
tgtgggggtg gagtggggag caggaattgc actcagacat gacatttcaa ttcattctctg 480
caaatgaaaa gggttcttcc tcttggggga aatctgtgtg tcagttctgt cagctgcaag 540
ttctt 545

<210> SEQ ID NO 117
<211> LENGTH: 441
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(441)
<223> OTHER INFORMATION: AffymetrixID: 211560_s_at

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<400> SEQUENCE: 117

```

tccccatccg ggtgggcaat gcagcactca acagcaagct ctgtgatctc ctgctctcca    60
agcatggcat ctatgtgcag gccatcaact acccaactgt ccccgggggt gaagagctcc    120
tgcgcttggc accctcccc caccacagcc ctcagatgat ggaagatttt gtggagaagc    180
tgctgtggc ttggactgcg gtggggctgc ccctccagga tgtgtctgtg gctgcctgca    240
atttctgtcg cgtctctgta cactttgagc tcattgagtga gtgggaacgt tcctacttcg    300
ggaacatggg gccccagtat gtcaccacct atgcctgaga agccagctgc ctaggattca    360
caccaccact gcgcttcaact tgggtccagg cctactcctg tcttctgctt tgttgtgtgc    420
ctctagctga attgagccta a                                         441

```

<210> SEQ ID NO 118

<211> LENGTH: 131

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (85)..(85)

<223> OTHER INFORMATION: n is a, c, g, or t

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(131)

<223> OTHER INFORMATION: AffymetrixID: 211991_s_at

<400> SEQUENCE: 118

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gcactgggag gcccaagagc caatccagat gcctgagaca acggagactg tgctctgtgc    60
cctgggcctg gtgtctgggc tagtnggcac catcgtgggc accgtcctca tcataaagtc    120
tctgcgttct g                                         131

```

<210> SEQ ID NO 119

<211> LENGTH: 482

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (377)..(377)

<223> OTHER INFORMATION: n is a, c, g, or t

<220> FEATURE:

<221> NAME/KEY: misc_feature

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

<223> OTHER INFORMATION: AffymetrixID: 212199_at

<400> SEQUENCE: 119

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attttgctgt tacctttgtg acctgattgt tttttggaac acgtcaagac gtgggatcag    60
aatcttccaa ctttagaggt gcaatggaag aactacgct acttggttga gctgggtgaa    120
gaatgtatta atgagactgc ttgcataaa actgggaaga aagagaagac agttggagat    180
ggaagatggt tttgtatata ttttggaaact ttagttcctc tgtgagacga aagaggagag    240
ctatgttttg tgacacattg tctgatatat attgtgtaac ctgtcagggt agttgattta    300
gacaacatag ctgacctttt atgacaaggc agtttgaata gggactattg taataccctc    360
acacattata ggggcancag agaatggcat ggaagagaca gtctacagag agctttaaga    420
ggccggagaa aggaaaagac attatcaggg cctggaaagt ctcttcaggt tcatcagggt    480
ag                                         482

```

<210> SEQ ID NO 120

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<211> LENGTH: 419
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (249)..(249)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(419)
<223> OTHER INFORMATION: AffymetrixID: 212224_at

<400> SEQUENCE: 120
acagtgttct ctaatgttac agatgagatg cgcattgcc aagaggagat ttttggacca      60
gtgcagcaaa tcatgaagt taaatcttta gatgacgtga tcaaaagagc aaacaatact      120
ttctatggct tatcagcagg agtgtttacc aaagacattg ataaagccat aacaatctcc      180
tctgctctgc aggcaggaac agtgtgggtg aattgctatg gcgtggtaag tgcccagtgc      240
ccctttggnt gggattcaag atgtctggaa atggaagaga actgggagag tacggtttcc      300
atgaatatac agagggtcaa acagtcacag tgaaaatctc tcagaagaac tcataaagaa      360
aatacaagag tggagagaag ctcttcaata gctaagcatc tccttacagt cactaatat      419

<210> SEQ ID NO 121
<211> LENGTH: 343
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(343)
<223> OTHER INFORMATION: AffymetrixID: 212232_at

<400> SEQUENCE: 121
agaaggcagc tctgcattct accttgcttg actggaattg tctgaagctt tttctggcct      60
cttttctcta gtcggccacc cctgaagtgc tgaggctctaa gtggtttacc tctgtctgat      120
agatggccac actctttaga gtagttctca taagttctag aactggtagc tcggtcgttt      180
cgcacactag gtggcataca ggcagcagca ggtgttcata tccttgattt tgagaatttc      240
ccctcaagta tgtggcagta aatacaacaa gacactctat gtattaatgt ctccattgtc      300
ttaacctgtg tccaaaacaa aattcacctc ctttctttat gtg                        343

<210> SEQ ID NO 122
<211> LENGTH: 427
<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, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(427)
<223> OTHER INFORMATION: AffymetrixID: 212534_at

<400> SEQUENCE: 122
gtggattgtt tgtatccctt acctgcttcc tattgggtta tgtgtggata tattgttttt      60
attgtttcag catctecttc cccatcttct ggtaacacaa cctttattta tttgtgggga      120
acctattccc tgtggcttag gtgagcatgt gaccaggcct ggcctcctga gtcccacagc      180
ttcctagcca cagtataaaa agaattggnt atataactta agccaggcta aggaaagccc      240

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ttaacagaac ttctgtgga actactggaa agaaggcttt atggagatcc caggaaccaa	300
ggaccatgta agcctgaatt tgtgccatgt ggagagagtc tgtctgagga gaaactcgga	360
tgctagcaga aatggaaaga gaactaagtt ctgatgtcat tttctggag gccctagatc	420
cagctgt	427

<210> SEQ ID NO 123
 <211> LENGTH: 497
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(497)
 <223> OTHER INFORMATION: AffymetrixID: 213142_x_at

<400> SEQUENCE: 123

ctgctgccat tttaatcttg ctcattaacc ttactccttt gagaattctt taacaatatt	60
taaaattggt aacaaaaata gtttagccat aattgttttag ccatgtgagt ttcaggttgg	120
tacacgttca gacagaactg ctgtatcaca ttccaatttt gaatagccag tgagcaatca	180
agtgtagaga aatgataaat ggcctaagaa ggcatacagt ggcataaacg atgctcttcc	240
tagtagctta ataggccaca agctagtctt tgttgctctc tgaataaaaa tatgctttaa	300
aaatgtaggg aacagtgtct agaaaagcaa aaactagggtg tgtcattgaa ataataggca	360
taaaaattaa atgttacata agaacactat ttggaaagag ggtcctttta aaaactgaat	420
ttgtactaaa tcagatttgc catgtccagt acagaataat ttgtacttag tatttgcagc	480
agggtttgtc tttgtga	497

<210> SEQ ID NO 124
 <211> LENGTH: 543
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (324)..(324)
 <223> OTHER INFORMATION: n is a, c, g, or t
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(543)
 <223> OTHER INFORMATION: AffymetrixID: 214433_s_at

<400> SEQUENCE: 124

cttctcggga ggcagcattg ttaagggagg cctgtgcaa gtgctggagg acgaggaact	60
aaagtcccag ccagagcccc tagtggtcaa gggaaaacgg gtggctggag gccctcagat	120
gatccagctc agcctggatg ggaagcgcct ctacatcacc acgtcgtgt acagtgcctg	180
ggacaagcag ttttaccctg atctcatcag ggaaggctct gtgatgctgc aggttgatgt	240
agacacagta aaaggagggc tgaagttgaa ccccaacttc ctggtggact tcgggaagga	300
gccccttggc ccagcccttg cccnatgagc tccgtaccc tggggcgat tgtagctctg	360
acatctggat ttgaaggctc caccctcatc acccacactc cctatcttgg gccctcactt	420
ccttggggac ctggcttcat tctgtctctc cttggcacc gaccttggc agcatgtacc	480
acacagccaa gctgagactg tggcaatgtg ttgagtcata tacatttact gaccactgtt	540
gct	543

<210> SEQ ID NO 125

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<211> LENGTH: 501
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (37)..(37)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (437)..(437)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (452)..(452)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(501)
<223> OTHER INFORMATION: AffymetrixID: 215933_s_at

<400> SEQUENCE: 125
ggacagttcc tgtgatcaga ggcaagattt gcccagngaa cagaataaag gtgcttcttt      60
ggatagctct caatgttcgc cctccctgc ctcaggagaa gaccttgaat cagagatttc      120
agaggattct gatcaggaag tggacattga gggcgataaa agctatttta atgctggatg      180
atgaccactg gcattggcat gttcagaaaa ctggatttag gaataatgtt ttgctacaga      240
aaatcttcat agaagaactg gaaggctata taagaaaggg aatcaattct ctggtattct      300
ggaaacctaa aaatatattg tgcaactgctc aattaacaaa cctacatgga gaccttaatt      360
ttgacttaac aaatagttta tgtactgctc ttaggttggt ttgataaagt gacattatag      420
tgattaaatt ctttcnctt taaaaaaca gntagtgggt ttcactattt ataaatagga      480
ccttcttgaa cgacttttct g                                     501

<210> SEQ ID NO 126
<211> LENGTH: 424
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(424)
<223> OTHER INFORMATION: AffymetrixID: 217478_s_at

<400> SEQUENCE: 126
ctgttttgtc agtaatctct tcccacccat gctgacagtg aactggcagc atcattccgt      60
ccctgtggaa ggatttgggc ctacttttgt ctcagctgct gatggactca gcttcaggc      120
cttttcttac ttaaacttca caccagaacc ttctgacatt ttctoctgca ttgtgactca      180
cgaaattgac cgctacacag caattgccta ttgggtaccc cggaacgcac tgccctcaga      240
tctgctggag aatgtgctgt gtggcggtgc ctttggcctg ggtgtgctgg gcatcatcgt      300
gggcattggt ctcacatct acttcggaa gccttgctca ggtgactgat tcttcagac      360
cagagtttga tgccagcagc ttcggccatc caaacagagg atgetcagat ttctcacatc      420
ctgc                                     424

<210> SEQ ID NO 127
<211> LENGTH: 530
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(530)
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<223> OTHER INFORMATION: AffymetrixID: 217736_s_at

<400> SEQUENCE: 127

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tctgtctggt ctctctctag aagggtctac cgcagaaatt gatgtgtgct cctgcacctc    60
gtcactgccc aagcccgggc ctgcacatac tcaactggact gttccagttt tgacagctgc    120
cagtcttcct gcccctttca cactgcagct gaagttcatt acctgaagga cgctcatca    180
tttcattcct tggtccaaa ccttctgctg cctctaagat aaaagctcaa cttcttaaca    240
gtgtacagtg tgcaacttcc aaccttttta tctgttctct ccaccttcag tttagcgtea    300
ttccaaaacc acacccttgc aaagctttgt actccgcacc ccagatgac tccaggcagc    360
tcagatctct ttcctgcctt tgccctgcac tgttccccgg tacttctctc tttattgtag    420
cactcagctc ccagccaat ctgtacatcc ctgagaggca gcgatctgat gaattggttt    480
ttgaatccca gaaagggctc gccatggagt tggcagtcac cagggtagat    530

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<210> SEQ ID NO 128

<211> LENGTH: 262

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

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

<223> OTHER INFORMATION: AffymetrixID: 219069_at

<400> SEQUENCE: 128

```

gaatattgta tactgcaccc cctaccacaa tttacacaat cctgtggata gtctacctc    60
accttggtca acctacatga tccttaagct aatggcgaat cagcatgacc tttagacat    120
gcacacaact atacctttgt ccaacagatc ataatatatc tgctatccaa ctgggttttac    180
ctgcctaate ctactgattt gggcactgct tgtatagtct ctcaagttca caggaaatgt    240
tgattttcta aggtctcat tt    262

```

<210> SEQ ID NO 129

<211> LENGTH: 490

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(490)

<223> OTHER INFORMATION: AffymetrixID: 219093_at

<400> SEQUENCE: 129

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tagagaccca tgcatctta acctaaaggg aaatcttatt gcgttatcat aaaattgatg    60
atatcttagg gtcagaattg cctttttttt tattttgaat gggagctct cactaaaaca    120
atcctgagat ttcttaattt catggttctt taaatattat aaacacagag tcaacataga    180
atgaaattgt atttgtaaaa atacacacat tggaggacaa gagcagatga ctacttttcg    240
aagtaatgct gctccttctt aaaagtctgt tttcaatcct ggtaatatga ggggcactgc    300
ggcacctaag aagccttaaa tgagagctaa tccaatttag agagcgatgg tgcagcatt    360
tcgggtctga tatctgtgtg tccgtatctg cgtttgtgtg cgtgtacgtg tgcccctgtg    420
tgtgggcccc gttttcaggc atgtagaata agcatggagt catattgagg aggactcact    480
tcttgaagat    490

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<210> SEQ ID NO 130

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<211> LENGTH: 446
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(446)
<223> OTHER INFORMATION: AffymetrixID: 219228_at

<400> SEQUENCE: 130

gggggttcgag cctcgttaag cacgagagga tacatacggg cgagaagccg tacaagtgca	60
cagaatgtgg gaaggccttc aattgtggct atcacctcac tcagcacgag agaatccaca	120
caggcgaaac cccgtataaa tgtaaggagt gtgggaaggc tttcatttat ggatcgagcc	180
tcgtgaaaca tgagagaatt cataccgggg tgaacccta tgggtgtaca gaatgtggga	240
agagctttag tcacggccat cagcttacac aacatcagaa aacgcacagt ggggcgaaat	300
cctacgaatg taaggagtgc gggaaggcat gtaaccacct aaaccatctc cgagaacatc	360
agaggatcca caacagttga agagcctttt gaacgcagta gcccgctcgt atctatggtt	420
tcgctttcca cagtttggtta cctgca	446

<210> SEQ ID NO 131
<211> LENGTH: 331
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(331)
<223> OTHER INFORMATION: AffymetrixID: 219607_s_at

<400> SEQUENCE: 131

atcaacacat ttagcttggc gttttattca ttccatcacc cttactgtaa ctactatggc	60
aactcaaata attgtcatgg gactatgtcc atcttaatgg gtctggatgg catggtgctc	120
ctcttaagtg tgctggaatt ctgcattgct gtgtccctct ctgcccttgg atgtaaagtg	180
ctctgttgta cccctggtgg ggttggtgta attctgccat cacattctca catggcagaa	240
acagcatctc ccacaccact taatgaggtt tgaggccacc caaagatcaa cagacaaatg	300
ctccagaaat ctatgctgac tgtgacacaa g	331

<210> SEQ ID NO 132
<211> LENGTH: 149
<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, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(149)
<223> OTHER INFORMATION: AffymetrixID: 221748_s_at

<400> SEQUENCE: 132

atattttgta tcatcgtgcc tatagccgct gccaccgtgt ataaatcctg gtgntgctc	60
cttatcctgg acatgaatgt attgtacact gacgcgtccc cactcctgta cagctgcttt	120
gtttctttgc aatgcattgt atggcttta	149

<210> SEQ ID NO 133
<211> LENGTH: 534
<212> TYPE: DNA

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```
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (120)..(120)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (308)..(308)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(534)
<223> OTHER INFORMATION: AffymetrixID: 221766_s_at

<400> SEQUENCE: 133

gattttccagg aagcctttga tcacctttgt aacaagatca ttgccaccag gaacccagag      60
gaaatccgag ggggaggcct gcttaagtac tgcaacctct tggtgagggg ctttaggccn      120
gcctctgatg aaatcaagac ctttcaaagg tatatgtggt ccagggtttt catcgacttc      180
tcagacattg gagagcagca gagaaaactg gagtcctatt tgcagaacca ctttgtggga      240
ttggaagacc gcaagtatga gtatctcatg acccttcatg gagtggtaaa tgagagcaca      300
gtgtgccttg atgggacatg aaagaagaca gactttaaac cttatcacca tgctggctat      360
ccgggtgtta gctgacaaa atgtcattcc taatgtggct aatgtcactt gctattacca      420
gccagcccc tatgtagcag atgccaactt tagcaattac tacattgcac aggttcagcc      480
agtattcacg tgccagcaac agacctactc cacttggeta ccttgcaatt aaga          534

<210> SEQ ID NO 134
<211> LENGTH: 503
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(503)
<223> OTHER INFORMATION: AffymetrixID: 221622_s_at

<400> SEQUENCE: 134

atgcatcatt ggctacactt ccatttttgt ctactgttgt tactgacaag ctttttgtaa      60
ttgatgcttt gtattcagat aatataagca aggaaaactg tgttttcaga agctcactga      120
ttggcatagt ttgtggtggt ttctatccca gttctttggc ttttactaaa aatggacgcc      180
tggaaccaa gtatcatacc gttccactgc caccaaaaagg aagggtttta atccattgga      240
tgacgctttg tcaaacacaa atgaaattaa ttgcgattcc tctagtcttt cagattatgt      300
ttggaatatt aaatggctat accattatgc aagtatttga aagagacact tgagaaaaact      360
atacatgaag agtaacaaa aaaatgaatg gttgctaact tagcaaaatg aagtttctat      420
aaagaggact caggcattgc tgaaagagtt aaaagtaact gtgaacaaat aatttgttct      480
gtgccttttg cctggtatat agc          503

<210> SEQ ID NO 135
<211> LENGTH: 515
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(515)
<223> OTHER INFORMATION: AffymetrixID: 218845_at

<400> SEQUENCE: 135
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aaaacattct ggccgctcca ggaattctga agttctgggc ctttctcaga agactgtaat    60
gtacctgaag ttcttgaaat attgcaaacc cacagagttt aggctggtgc tgccaaaaag    120
aaaagcaaca tagagtttaa gtatccagta gtgatttgta aacttgtttt tcatttgaag    180
ctgaatatat acgtagtcac gtttatgttg agaactaagg atattcttta gcaagagaaa    240
atattttccc cttatcccca ctgctgtgga ggtttctgta cctcgcttgg atgctgttaa    300
ggatcccggg agccttgccg cactgccttg tgggtggcct ggcgctcgtg attgcttcct    360
gtgaacgcct cccaaggacg agcccagtg agttgtgtgg gcgtgaactc tgcccgtgtg    420
ttctcaaatt ccccagcttg ggaaatagcc cttggtgtgg gttttatctc tggtttgtgt    480
tctccgtggt ggaattgacc gaaagctcta tgttt                                515

```

```

<210> SEQ ID NO 136
<211> LENGTH: 504
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(504)
<223> OTHER INFORMATION: AffymetrixID: 200786_at

```

```

<400> SEQUENCE: 136
gttacattgg tgcagcccta gttttagggg gagtagatgt tactggacct cacctctaca    60
gcatctatcc tcatggatca actgataagt tgccttatgt caccatgggt tctggctcct    120
tggcagcaat ggctgtatct gaagataagt ttaggccaga catggaggag gaggaagcca    180
agaatctggt gagcgaagcc atgcgagctg gcactctcaa cgacctgggc tccggaagca    240
acattgacct ctgcgtcatc agcaagaaca agctggattt tctccgcca tacacagtgc    300
ccaacaagaa ggggaccagg cttggccggt acaggtgtga gaaagggact actgcagtcc    360
tactgagaaa aatcactcct ctggagattg aggtgctgga agaaacagtc caaacaatgg    420
acacttcctg aatggcatca gtgggtggct ggccgcggtt ctggaagggt gtgagcattg    480
aggcccagta agacactcat gtgg                                504

```

```

<210> SEQ ID NO 137
<211> LENGTH: 492
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(492)
<223> OTHER INFORMATION: AffymetrixID: 212886_at

```

```

<400> SEQUENCE: 137
acaggcacat caggctgcag aatgcgcttt agaaagcatt gttttagtcc aggcacagtg    60
gctcacgcct gtaatccag cactttggga ggccgagggt ggtggatcac aaggttggga    120
gattgagacc atcctggcta acacagtga accctgtctc tactaaaaaa atacaaaaaa    180
ttagcttggc gtggtggtgg gcgcctgtag tcccagcagc ttgggagggt gaggtggag    240
aatggtgtga acccaggagg cggagcttgc agtgagccaa gatcgcgcca ctgcaactcca    300
gcccgggtga cagagcaaga ctccgtctca aaaaaaagaa aagaaaaaag aaagcattgt    360
tttaattgag aggggcaggg ctggagaagg agcaagttgt ggggagccag gcttcctca    420
cgcagcctgt ggtggatgtg ggaaggagat caacttctcc tactctggg acagacgatg    480

```

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tatggaaact aa 492

<210> SEQ ID NO 138
<211> LENGTH: 316
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (173)..(173)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(316)
<223> OTHER INFORMATION: AffymetrixID: 201407_s_at

<400> SEQUENCE: 138

ggatgtgatt ctaaaagctt ttattgagca ttgtcaaatt tgtaagcttc atagggatgg 60
acatcatatc tataatgccc ttctatatgt gctaccatag atgtgacatt ttgacctta 120
atatcgtctt tgaaaatgtt aaattgagaa acctgttaac ttacatttta tgnattggca 180
cattgtatta cttactgcaa gagatatttc attttcagca cagtgcacaaa gttctttaa 240
atgcatatgt ctttttttct aattccgttt tgttttaaag cacattttaa atgtagtttt 300
ctcatttagt aaaagt 316

<210> SEQ ID NO 139
<211> LENGTH: 525
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(525)
<223> OTHER INFORMATION: AffymetrixID: 212266_s_at

<400> SEQUENCE: 139

gttgagtttg cctcttatgg tgacttaaag aatgctattg aaaaactttc tggaaaggaa 60
ataaatggga gaaaaataaa attaatgaa ggcagcaaaa ggcacagtag gtcaagaagc 120
aggctctcgat cccggaccag aagttcctct aggtctcgta gccgatcccg ttcccgtagt 180
cgcaaatctt acagccggtc aagaagcagg agcaggagcc ggagccggag caagtccgt 240
tctgttagta ggtctcccg gcttgagaag agccagaaac gtggttcttc aagtagatct 300
aagtctccag catctgtgga tcgccagagg tcccggtecc gatcaaggtc cagatcagtt 360
gacagtgga attaaactgt aaataacttg ccctgggggc ctttttttaa aaaacaaaaa 420
ccacaaaaat tcccaaacca tacttgctaa aaattctggt aagtatgtgc ttttctgtgg 480
gggtgggatt tggaaggggg gttgggttgg gctggatata tttgt 525

<210> SEQ ID NO 140
<211> LENGTH: 581
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (72)..(74)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (239)..(253)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (268)..(268)

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<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (270)..(305)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (308)..(308)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (446)..(526)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(581)
<223> OTHER INFORMATION: AffymetrixID: 53912_at

<400> SEQUENCE: 140

```
acaatgaggc attctgtcct cctgttgcca ttcttcacat ccaactgagag ccagagctgg      60
taggagccga gnnnccacag gcattctgca ttgctctact cttagggttg tgtgtgtgat      120
ccttccccct cctgtgcgcc actcctccct cctctggcta tctaccctg tctgtgggct      180
cttttactac cagcctatgc tgtgggactg tcatggcatt tagttcagag tggagggggn      240
nnnnnnnnnn nnnaaatgca agtattttnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      300
nnnnnaanat tgttgttgca atttgtgtct aacaagctgt agcagagaag gagggagtga      360
gcgtgggcag tatttccttt cataaatcat gaatttatca gtgtggaaat aatgcttcag      420
aactgtgctc tgtagccctc ctgcannnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      480
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnngcgt gaaccttgtt      540
aggtatactt tacctgatgc tgcttcacgc ctcgcagtct g                          581
```

<210> SEQ ID NO 141
<211> LENGTH: 377
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(377)
<223> OTHER INFORMATION: AffymetrixID: 200090_at

<400> SEQUENCE: 141

```
tccctttgcc tgtggtgtaa aagtgcacac cacaggtatt gctttttaac aagaactgat      60
gtcctctggg tgctgtgtct actcagacta gctctaagta atgtgattct tctaaagcaa      120
agtcattgga tgggaggagg aagaaaaagt ccataaagg aacttttgta gtcttatcaa      180
catataatct aatcccttag catcagctcc tccctcagtg gtacatgcgt caagatttgt      240
agcagtaata actgcaggtc acttgtatgt aatggatgtg aggtagccga agtttggttc      300
agtaagcagg gaatacagtc gttccatcag agctgggtctg cacactcaca ttatcttgct      360
atcactgtaa ccaacta                          377
```

<210> SEQ ID NO 142
<211> LENGTH: 494
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(494)
<223> OTHER INFORMATION: AffymetrixID: 218025_s_at

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<400> SEQUENCE: 142

```

ctccttgggc tattcgatgc cgtgtatgca tctgacaggg caacatttca tacaccattt    60
agtcacctag gccaaagtcc ggaaggatgc tcctcttaca cttttccgaa gataatgagc    120
ccagccaagg caacagagat gcttattttt ggaaagaagt taacagcggg agaggcatgt    180
gctcaaggac ttgttactga agttttccct gatagcactt ttcagaaaga agtctggacc    240
aggctgaagg catttgcaaa gcttccccc aatgccttga gaatttcaaa agaggtaatc    300
aggaaaagag agagagaaaa actacacgct gttaatgctg aagaatgcaa tgtccttcag    360
ggaagatggc tatcagatga atgcacaaat gctgtggtga acttcttacc cagaaaatca    420
aaactgtgat gaccactaca gcagagtaaa gcattgtcaa ggaaggatgt gctgttacct    480
ctgatttcca gtac                                                    494

```

<210> SEQ ID NO 143

<211> LENGTH: 540

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(540)

<223> OTHER INFORMATION: AffymetrixID: 204232_at

<400> SEQUENCE: 143

```

cgatctccag cccaagatga ttccagcagt ggtcttgetc ttactccttt tggttgaaca    60
agcagcggcc ctgggagagc ctcagctctg ctatatctg gatgccatcc tgtttctgta    120
tggaattgtc ctcaccctcc tctactgtcg actgaagatc caagtgcgaa aggcagctat    180
aaccagctat gagaaatcag atggtgttta cacgggcctg agcaccagga accaggagac    240
ttacgagact ctgaagcatg agaaaccacc acagtagctt tagaatagat gcggtcatat    300
tcttctttgg cttctggttc ttccagccct catggttggc atcacatatg cctgcattgc    360
attaacacca gctggcccta cccctataat gatcctgtgt cctaaattaa tatacaccag    420
tggttcctcc tcctgtttaa agactaatgc tcagatgctg ttacggata tttatattct    480
agtcctactc tcttgtccca ccttcttctt cttccccatt cccaactcca gctaaaatat    540

```

<210> SEQ ID NO 144

<211> LENGTH: 559

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(559)

<223> OTHER INFORMATION: AffymetrixID: 201722_s_at

<400> SEQUENCE: 144

```

attttgtttt catctgtgat agtcattgat gcttttattt tccttggggg gctgaaattg    60
agctgaaaaa aaaagcctct ttgaatatag ttttaatttc tctctacagt ttttttgtt    120
tggtttgttg gctgttgtaa ttgtaatttt taattgcctt ctaaaaaatg gaaatttaac    180
aatgtctgat ctcagctgaa caaattagat gtttcagtgt ctcttgggtc aactggctta    240
cagatttaca tgtgcacaca cacacaaatt tcttatcaca ttttcgactt cttcacttga    300
cctaactgat tatgcgaaat acccaagatt catgctactg taccacagat ttgttttcac    360
agcaataaat cttcagttct gttgtttatg attccactta acaaaaggcc tgcagaagtg    420

```

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```

atttattatt tgggtatttg gagataatac atttgatggg tttttggaaa acctttttca    480
ctccatactc agatatgctt cattgtcaaa tgcataattta gattagatta ttgaattgta    540
atgttttatct gctgctttt                                         559

```

```

<210> SEQ ID NO 145
<211> LENGTH: 453
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(453)
<223> OTHER INFORMATION: AffymetrixID: 218627_at

```

```

<400> SEQUENCE: 145

```

```

taatcatttc tgggttcact gcgactcact gtagtgctgg ggatccccct tgtaacactg    60
gaactgaaaag gcagtgatga aagctatgtc aagcattcat tattctgaag aggaggagaa    120
atgccacata cttttcccat gggacctgtg gtggaatgaa tccatacttc tgccctactt    180
cgagcagact tttgttctcg gcgctcctca cgatggagtt tcattgcttca ttttcacatc    240
tctctgcaca attagattgg gagctccttg agggcagagt acgtgcctta atctttatct    300
ttgtaatgcc acaatgaaca gaggcctccc tggtagactg taggagctta agaaatactc    360
actgaatgca tgaatgaatg aatgaacaaa tgaaggaatg actaaggatg tttgtagtgc    420
tataatatag aatgggattt actctgcttt acc                                         453

```

```

<210> SEQ ID NO 146
<211> LENGTH: 553
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(553)
<223> OTHER INFORMATION: AffymetrixID: 202322_s_at

```

```

<400> SEQUENCE: 146

```

```

gtttctcattt cctactattc atgctatttg gtcaaggcct gaaagcaccc aggtgcagaa    60
tatcttgctgc cagagaacag aaaacataga tataaaaaaa tactgtgtac attatcttga    120
ggatgtaggt tcttttgaat acactcgtaa tacccttaa gagcttgaag cttaaagccta    180
taaacagatt gatgcacgtg gtgggaaccc tgagctagta gccttagtaa aacacttaag    240
taagatgttc aaagaagaaa atgaataatg ttaagccatt cttgattgga cctcatagct    300
tatttttagtt aatctttttt ttgtctttta gccttaccac cttttaaaaa atttgttatt    360
ctccagaaac agtaaatagg tgagtagggg tggtgcaagt gaattcgttt tcatttagaa    420
gcccctctgt acagataatc aaaattcaaa gttgaaagaa tcaaaagcag ccacagttat    480
gtaggtctga tttgaatgac ataattgcag tgacaggaca ttgccaccaa ctctatccta    540
ctaccatcaa tgt                                         553

```

```

<210> SEQ ID NO 147
<211> LENGTH: 530
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(530)
<223> OTHER INFORMATION: AffymetrixID: 221689_s_at

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<400> SEQUENCE: 147

```

accgctcgcca ttgccagaaa gagcgattta tggctttgtt cttttcttaa gctcccaatt    60
tggcttcata ctttacctcg tgtgggcctt tttcctgaa tcttggctaa actccttagg    120
tttaacctat tggcctcaaa aatattgggc agttgcatta cctgtctacc tccttattgc    180
tatagtaatt ggctacgtgc tcttgtttgg gattaacatg atgagtacct ctccactcga    240
ctccatccat acaatcacag ataactatgc aaaaaatcaa cagcagaaga aataccaaga    300
ggaggccatt ccagccttaa gagatatttc tattagttaa gtaaaccaaa tgttctttct    360
tgcagccaaa gaactttaca ccaaaaactg aactgtgtgt aaccatagta acaccaagca    420
cgtatttatt tataagtttt tgccattata attttgacca taaattaatt tgaccatctc    480
tcttattaat agagaagtaa aaaatgtaag ttgaccttct cttagattat    530

```

<210> SEQ ID NO 148

<211> LENGTH: 563

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(563)

<223> OTHER INFORMATION: AffymetrixID: 203356_at

<400> SEQUENCE: 148

```

tatacatctt gggcaactag ttaccaaagt aattgtgcca ccataactga ttttaatttt    60
gcattattta tgattttaaa atatttgttg ccaggtgtt atgaaagaat aaagctttta    120
agtagact accttagcat gaagatgtct atgcctaaga atgaaattg ttgaggttat    180
ctccatttca atcatgtacg aagaacttaa agaaattcac tactgcagtt tttattttta    240
aaaaacagta attgagatat tgaagacatt acaatttagt ttgtgtggtc tttttttaa    300
ttgtgtatc gttcagtcct ttgtggcaat agcactttga agaaaataga gaatttaata    360
tatggtgatt gggatatgta gcattcaaaa aaagtgaatt gccagatac tgggtgcatg    420
taaatcccca cttacataaa aaacccatca ggacagaatg atgctcaata ttttaaatt    480
ctaaaaatag ggtgggattt ttcattgtct ctactttata attatcaaaa cttattttgt    540
attgctacta ccttaaattg aaa    563

```

<210> SEQ ID NO 149

<211> LENGTH: 544

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(544)

<223> OTHER INFORMATION: AffymetrixID: 218462_at

<400> SEQUENCE: 149

```

aaatgagcag tgttcgtctt cgtaaagaaa ttaagagaag aggcaaggac cccacagAAC    60
acatactga aataattctg aataatttta caacacggct gggtcattca attggacgta    120
tgtttgcatc tctctttcct cataatcctc aatttatcgg aaggcagggt gccacattcc    180
acaatcaacg ggattacata ttcttcagat ttcacagata catattcagg agtgaaaaga    240
aagtgggaat tcaggaactt ggaccacgtt ttaccttaaa attaaggtct cttcagaaag    300
gaaccttga ttctaaatat ggagagtatg aatgggtcca taagccccgg gaaatggata    360

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caagtagaag aaaattccat ttataaagta ctgagagaaat gatattggat ttgctgaac	420
aggcctatct tgaacttttg taaattattt ttgacagaaat actcttttca aaatggcatt	480
tgctgatttc ataaaccttt cacgtctgga cgaattacca aatgccatga attgccactg	540
tgtg	544

<210> SEQ ID NO 150
 <211> LENGTH: 519
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(519)
 <223> OTHER INFORMATION: AffymetrixID: 218123_at

<400> SEQUENCE: 150

gtggaagccg gtgtctgtgt taccatggag atggtgaaag atgccttga ccagcttcga	60
ggcgcggtga tgattgttta ccccatggg ttgccaccgt atgatcccat ccgcatggag	120
tttgaata aggaagactt gtcgggaaca caggcagggc tcaacgtcat taaagaggca	180
gagcgcgagc tgtggtgggc agccaaggag ctgagaagaa cgaagaagct ttcagactac	240
gtggggaaga atgaaaaaac caaaattatc gccaaagattc agcaaagggg acagggagct	300
ccagcccag agcctattat tagcagttag gagcagaagc agctgatgct gtactatcac	360
agaagacaag aggagctcaa gagattggaa gaaaatgatg atgatgccta tttaaactca	420
ccatggcggtg ataactatgc ttgaaaaga cttttcatg gaggtaaaga cataaagtgg	480
agaccaagat gaagttcacc agctgatgac acttccaaa	519

<210> SEQ ID NO 151
 <211> LENGTH: 272
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (66)..(66)
 <223> OTHER INFORMATION: n is a, c, g, or t
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(272)
 <223> OTHER INFORMATION: AffymetrixID: 214329_x_at

<400> SEQUENCE: 151

aggttgagcgt gtggtgagat catgccacta cactccagcc tggcgacaga gcgagacttg	60
gtttcnaaaa aaaaaaaaaa aaaaacttca gtaagtacgt gttatttttt tcaataaaat	120
tctattacag tatgtcatgt ttgctgtagt gctcatattt attgttgttt ttgttttagt	180
actcacttgt ttcataatat caagattact aaaaatgggg gaaaggactt ctaatctttt	240
tttcataata tctttgacac atattacaga ag	272

<210> SEQ ID NO 152
 <211> LENGTH: 386
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(386)
 <223> OTHER INFORMATION: AffymetrixID: 219067_s_at

<400> SEQUENCE: 152

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cgagaagatc ctgatacccc aatgtccttc tttgactttg tggttgatcc tcattctttc	60
ccccgtacag tggaaaacat ctttcatgtt tccttcatta tacgggatgg ttttgcaaga	120
ataagacttg accaagaccg actgccagta atagagcctg ttagtattaa tgaagaaaat	180
gagggatattg aacataacac acaagttaga aatcaaggaa ttatagcttt gagttaccgt	240
gactgggagg agattgtgaa gacctttgag atttcagagc ctgtgattac tccaagtcag	300
aggcagcaga agccaagtgc ttgatgctag ctgaaggact caaatggata gtgaagtcca	360
aaacggaaaag cggcattgat tgtaca	386

<210> SEQ ID NO 153
 <211> LENGTH: 462
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(462)
 <223> OTHER INFORMATION: AffymetrixID: 205789_at

<400> SEQUENCE: 153

gtcatgaggc agctttcatc acaccctttt aacatttata taaaagaatt taaattcttt	60
ttcaaaaatt acactacaag tttataagcc caaatggctc tgtgaaatca gaagtgcaaa	120
ggtgtgcaaa cttgtatctg aagacctacc agggacaagc aggtaagagc tgatgtgagt	180
gtgtgtgatg ggatctgtaa ggaactggaa cacacatgac ctatccaaag gaatcagctg	240
cagctgcttg ttgtcaagta taaagtcagg acctggcttg gctttaaccg tttttcaaga	300
aaactggaaa tctggatttt cagcgaacat gcttgatttt aaaaggttga ctcaagtttt	360
tacaaaatac tatgtgggac acctcaaata catacctact gactgatgac aaaccagga	420
gtttgtgtgt cttttataaa aagtttgccc tggatgtcat at	462

<210> SEQ ID NO 154
 <211> LENGTH: 546
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(546)
 <223> OTHER INFORMATION: AffymetrixID: 209214_s_at

<400> SEQUENCE: 154

cagtgtccca atccgggttg tggaaaccag aacttcgcct ggagaacaga gtgcaaccag	60
tgtgaaggccc caaagcctga aggcttcctc ccgccacctc ttccgccccg ggggtgtgat	120
cgtggcagag gtggccctgg tggcatgcgg ggaggaagag gtggcctcat ggatcgtggg	180
ggccccgggt gaatgttcag aggtggccgt ggtggagaca gaggtggctt ccgtggtggc	240
cggggcatgg accgaggtgg ctttggtgga ggaagacgag gtggccctgg ggggccccct	300
ggacctttga tggaaacagat gggaggaaga agaggaggac gtggaggacc tggaaaaatg	360
gataaaggcg agcaccgtca ggagcgcaga gatcgccctc actagatgca gagacccgc	420
agagctgcat tgactaccag atttattttt taaaccagaa aatgttttaa atttataatt	480
ccatatttat aatgttggcc acaacattat gattattcct tgtctgtact ttagtatttt	540
tcacca	546

<210> SEQ ID NO 155

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<211> LENGTH: 428
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(428)
<223> OTHER INFORMATION: AffymetrixID: 213427_at

<400> SEQUENCE: 155
cgttgagaga tctccagtgc ccagtgtctc agagcagcga gctggaggga acgccagagg      60
tgtctgtccg ggctctggag ctcttcgact ggctcggcgc cgtcttcagt aatgtcgacc      120
taaataatga gcctaataat ttcatatcaa cctattgctg tcctgagcca agcacagtgg      180
tggcaaaagc ttatttgtgt acaatcactg gcttcatact tccagagaag atctgtctcc      240
tattggaaca tctctgtcac tactttgatg aaccgaagtt agctccatgg gttacactgt      300
ccgttcaagg ctttgagac agccctgttt cttgggaaaa aaatgaacat ggttttcgaa      360
aaggaggaga acatttatat aacttttgta tttttaataa tcaggactat tggcttcaga      420
tggtctgtt                                     428

<210> SEQ ID NO 156
<211> LENGTH: 315
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(315)
<223> OTHER INFORMATION: AffymetrixID: 209422_at

<400> SEQUENCE: 156
cagctcgggc gacaactgca agactccatc tcaaaaaaat aaaaataaaa gaaaagaaag      60
aaatatgtgc actacctaag ttttgtcttt agaaaaacta tccacctata aaaaattacc      120
ttgacaaaaa tagttccggt ttgactaatc attttgtttc ttaagtgggt aagtgtatgc      180
aagggtggatc cttgatgagc caacattgca ctgtggatac atatctatgt ttacgcgcta      240
ttagaacaga aggcgtgtga tatagaaatg ttgctttgaa gcaatatattg caaaacacgc      300
agacttctgt atctg                                     315

<210> SEQ ID NO 157
<211> LENGTH: 543
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(543)
<223> OTHER INFORMATION: AffymetrixID: 201010_s_at

<400> SEQUENCE: 157
gtgttctcct actgcaaata ttttcatatg ggaggatggg tttctcttca tgtaagtcct      60
tggaattgat tctaaggatg tggtcttagc actttaattc ctgtcaaat tttgttctc      120
cccttctgcc atcttaaatg taagctgaaa ctggtctact gtgtctctag ggtaagcca      180
aaagacaaaa aaaattttac tacttttgag attgccccaa tgtacagaat tatataattc      240
taacgcttaa atcatgtgaa agggttgctg ctgtcagcct tgcccactgt gaattcaaac      300
ccaaggagga actcttgatc aagatgccca accctgtgat cagaacctcc aaatactgcc      360
atgagaaact agagggcagg tggtcataaa agccctttga acccccttcc tgccctgtgt      420

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taggagatag ggatattggc cctcactgc agctgccagc acttggtcag tcactctcag	480
ccatagcact ttgttctactg tcctgtgtca gagcactgag ctccaccctt ttctgagagt	540
tat	543

<210> SEQ ID NO 158
 <211> LENGTH: 181
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(181)
 <223> OTHER INFORMATION: AffymetrixID: 200883_at

<400> SEQUENCE: 158

ttgccaaaggc aactcagcag ccatttgatg tttctgcatt taatgccagt tactcagatt	60
ctggactctt tgggatttat actatctccc aggccacagc tgetggagat gttatcaagg	120
ctgcctataa tcaagtaaaa agaatagtctc aaggaaacct ttccaacaca gatgtccaag	180
c	181

<210> SEQ ID NO 159
 <211> LENGTH: 503
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(503)
 <223> OTHER INFORMATION: AffymetrixID: 218454_at

<400> SEQUENCE: 159

gtggctatcc actgttagtt cagaagctgg gcttggacta ctcttatgat ttagctccac	60
gagccaaaat tttccggcgt gaccaaggga aagtgactga tacggcatcc atgaaatata	120
tcatgcgata caacaattat aagaaggatc cttacagtag aggtgacccc tgtaatacca	180
tctgtgtccg tgaggacctg aactcaccta acccaagtcc tggaggttgt tatgacacaa	240
aggtggcaga tatctaccta gcatctcagt acacatccta tgccataagt ggtccacag	300
tacaaggtag cctccctggt ttctgctggg accgtttcaa caaaactcta catcagggca	360
tgccagaggt ctacaacttt gattttatta ccatgaaacc aattttgaaa cttgatataa	420
aatgaaggag ggagatgacg gactagaaga ctgtaaataa gataccaaag gcactatatt	480
agctatgttt ttcccatcag aat	503

<210> SEQ ID NO 160
 <211> LENGTH: 530
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(530)
 <223> OTHER INFORMATION: AffymetrixID: 202918_s_at

<400> SEQUENCE: 160

gagtgtcctg ctatagacta tactagacac acacttgatg gtgctgcatg tcttctgaat	60
agcaataaat attttcccg cagggttagc ataaaggaat catctgtagc gaaactagga	120
tcagtatgcc gtaggattta cagaatattt tcacatgctt attttcatca tcggcagata	180
tttgatgaat atgaaaaatga aacatttttg tgtcatcggt ttactaagtt tgtgatgaaa	240

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tacaatttga tgtccaagga taacctgatt gtaccaatth tagaagagga agtacagaat	300
tcagtttctg gggaaagtga agcatgaagg gaatcatagg aaaaatgtac tgatcatata	360
attaacatta tgtactgtat atatcattht agacacatca atcatgtatc catattatag	420
cttctttgtt tagtataggt ttttgtatgc tgggtttgcc ttttaaaatg ggaataactt	480
tttaagttat tcataagctg tatattcacc agtgtggcac tcatggthtt	530

<210> SEQ ID NO 161
 <211> LENGTH: 403
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(403)
 <223> OTHER INFORMATION: AffymetrixID: 212204_at

<400> SEQUENCE: 161

gcttaactct tttgacatct gctattgtga cacatcccat tgctggcaat gtggtgcaca	60
ctccgaaact tttaactact gttttgtaag cctccaaggg tggcattgca gggtccttag	120
gcaatgttht gtttgcctth atgcagagag gtgctccaag tgcgtgtgatt gagcaccgtg	180
ctagaggaaac tgtaatgctt cagaagttgt agcttatatac aaggaaacag gtctgtctgg	240
cttaatttaa acagttattg catgaagtag cgtggaggcc ctggactgct gctcgttctt	300
taggatggac tgttctggta tctggtattg gtttagagac tgtaataag ggacatcaca	360
aggtgatggg attcatthtga agcactctat ttctgtthta atg	403

<210> SEQ ID NO 162
 <211> LENGTH: 499
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(499)
 <223> OTHER INFORMATION: AffymetrixID: 219452_at

<400> SEQUENCE: 162

atcacttcga ccacatcaag gctgtcattg gatccaagtt catcgggatt ggtggagatt	60
atgatggggc cggcaaatc cctcaggggc tggaagacgt gtccacatac ccggctcctga	120
tagaggagtt gctgagtcgt ggctggagtg aggaagagct tcagggtgtc cttcgtggaa	180
acctgctgcy ggtcttcaga caagtggaaa aggtacagga agaaaacaaa tggcaaagcc	240
ccttggagga caagttcccg gatgagcagc tgagcagttc ctgccactcc gacctctcac	300
gtctgcgtca gagacagagt ctgacttcag gccaggaaact cactgagatt cccatacact	360
ggacagccaa gttaccagcc aagtggctag tctcagagtc cccccccac atggccccag	420
tccttgcaat tgtggccacc ttccagtc ttattctgtg gctctgatga cccagttagt	480
cctgccagat gtcactgta	499

<210> SEQ ID NO 163
 <211> LENGTH: 424
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(424)
 <223> OTHER INFORMATION: AffymetrixID: 219889_at

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<400> SEQUENCE: 163

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tactcaagcg ggtggctctg ggatcctggg ggccctgggtt gggggctagg gagacgccat    60
gtgatggaca ctccaggagc acacagccta gcacagcagc ttataatggg ctctccgggg    120
ccatttgcaa taacagctgc aattccctgg atagacgagt tgatttctc cctctgcccc    180
tccccagcc atgccagctg gcctttgtaa gtgcaggaaa ccgagtagaa aatgtgaccc    240
tccaaatgga gaagctgcca gctttgccat tgtgaacat ggtgaagtgc ttggaacata    300
ctgttcactc actctaaagg cgctgagact gtgctgttgt tctcgttttt atagtcaatg    360
gcttgttcat catccagatg tggctactga catatctaca cttcgacccg gagtgtctgg    420
aatt                                              424

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<210> SEQ ID NO 164

<211> LENGTH: 464

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(464)

<223> OTHER INFORMATION: AffymetrixID: 201303_at

<400> SEQUENCE: 164

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caacttcaact gtatcctcaa tgcattggaga catgccccag aaagagcggg agtccatcat    60
gaaggagttc cggtcgggcg ccagccgagt gcttatttct acagatgtct gggccagggg    120
gttgatgtgc cctcaggtgt ccctcatcat taactatgat ctccctaata acagagaatt    180
gtacatacac agaattggga gatcaggtcg atacggccgg aagggtgtgg ccattaactt    240
tgtaaagaat gacgacatcc gcatcctcag agatctcgag cagtactatt cactcagat    300
tgatgagatg ccgatgaacg ttgctgatct tatctgaagc agcagatcag tgggatgagg    360
gagactgttc acctgctgtg tactcctgtt tggaagtatt tagatccaga ttctacttaa    420
tggggtttat atggacttct ttctcataaa tggcctgccg tctc                      464

```

<210> SEQ ID NO 165

<211> LENGTH: 454

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(454)

<223> OTHER INFORMATION: AffymetrixID: 202510_s_at

<400> SEQUENCE: 165

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gtcgtcttct tatcttcagg tcagctgatt agccacctta gttccatctg caactttagt    60
tcccactggc tgtgtaacct aacatagtca caggctctgg ggactgtcac gtggacatct    120
ttgggaggcc gttattctgc ccaccgcacc ctcggttcat cccctgccct gccgggcacc    180
tcgctctacc ccaggaaaat gtgagctcgt tttcctgtc ggcatgtgct cccctaaagg    240
ctctgtcctt ccttgggcct gaaagtctct tctcagcctg agagggggcc cttecatctc    300
aggcatgact cagccccggt gatgcctctg cagtgtctgag tcaggatttg gggccggctc    360
tcttgggtct gtcccctttt cccaggtact gccttataaa gctgtggcca ggaagtggcc    420
ggtataaagg atgccaagg tctttgtacg tgtg                      454

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<210> SEQ ID NO 166

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<210> SEQ ID NO 167
<211> LENGTH: 477
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(477)
<223> OTHER INFORMATION: AffymetrixID: 201887_at

<400> SEQUENCE: 167

ctgggaagca aaacccatgc ctccccctag ccatttttac tgttatccta tttagatggc      60
catgaagagg atgctgtgaa attcccaaca aacattgatg ctgacagtca tgcagctctgg      120
gagtggggaa gtgactcttt gttcccatcc tcttctttta gcagtaaaat agctgagggga      180
aaaggaggagg aaaaggaagt tatgggaata cctgtggtgg ttgtgatccc taggtcttgg      240
gagctcttgg aggtgtctgt atcagtggat ttcccatccc ctgtgggaaa ttagtaggct      300
catttactgt ttaggtctca gcctatgtgg attttttcct aacataccta agcaaacccta      360
gtgtcaggat ggtaattctt attctttcgt tcagttaagt ttttcccttc atctgggcac      420
tgaagggata tgtgaacaaa tgtaaacatt ttggtagtc ttcaaccagg gattggtt      477
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<210> SEQ ID NO 168
<211> LENGTH: 444
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(444)
<223> OTHER INFORMATION: AffymetrixID: 211582_x_at

<400> SEQUENCE: 168

agccccactg ctggatgagg aacttgaggc aagtcaccag cccctgatca tttcgccctaa      60
aagagcaagg actagagttc ctgacctcca ggccagtcct tgatccctga cctaattgta      120
tcgcggaatg atgatatatg tatctacggg ggccctggggc tgggcgggct cctgcttctg      180
gcagtgtgtc tctgtccgc ctgcctgtgt tggtgcctc gaagagcacc tctgtcctg      240
gtcccaggcc cagggctcct cagagcagga actccactat gcctctctgc agaggtgtgc      300
agtgtcccagc agtgaggggc ctgacctcag gggcagagac aagagaggca ccaaggagga      360
tccaagagct gactatgcct gcattgtcta gaacaacccc acctgagcac ccagacacc      420
ttcctcaacc caggcgggtg gaca                                     444
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<210> SEQ ID NO 169

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<211> LENGTH: 490
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(490)
<223> OTHER INFORMATION: AffymetrixID: 219030_at

<400> SEQUENCE: 169

agttaacaca tcagctggac ctatttcccg aatgcagggt aaccttctg ttatttaaag	60
atgtaaaaaa tgcgggagac ttgagaagaa aggccatgga aggcaccatc gatggatcac	120
tgataaatcc tacagtgatt gttgatccat ttcagatact tgtggcagca aacaaagcag	180
ttcacctcta caaatggga aaaatgaaga caagaactct atctactgaa attattttca	240
acctttcccc aaataacaat atttcagagg ctttgaaaaa atttggatc tcagcaaatg	300
acacttcaat tctaattgtt tacattgaag agggagaaaa acaataaat caagaatacc	360
taatatctca agtagaaggt catcaggttt ctctgaaaaa tcttcctgaa ataatgaata	420
ttacagaagt caaaaagata tataaactct cttcacaaga agaaagtatc gggacattat	480
tggaatgctat	490

<210> SEQ ID NO 170
<211> LENGTH: 412
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (30)..(30)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (37)..(37)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (63)..(63)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (75)..(75)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(412)
<223> OTHER INFORMATION: AffymetrixID: 212706_at

<400> SEQUENCE: 170

agatathtag gtgacttaca gcaaccaatn gcaacanaac aaaatgttaa gaaatgatct	60
ttntatgagg caatnggaaa ttgaaact gatcaactat aggatgattg gaattattaa	120
tttttaaagg tgtgataaga tactgcactt ggctgggcac agtggcacat gcctgtaatc	180
ccagctactt ggcaggctga ggtgggagaa tcgcttgagc tcaggagtgc gagaccagcc	240
tgggcaacgt ggcgaaatcc cgtctttac aaaaacaaac aaacaaacaa aaaagatatt	300
gcagttgtgt tgtaagcgtc cttatctttc agagctacat agtggaatgt ttatggaata	360
tttaggataa atgatatagg catttgggat ttgctgcaaa atgaccacaga gg	412

<210> SEQ ID NO 171
<211> LENGTH: 419
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(419)
<223> OTHER INFORMATION: AffymetrixID: 202902_s_at

<400> SEQUENCE: 171

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caaaatatcg tgctgccaca tgttcaaagt acactgaact tccttatggg agagaagatg    60
tcctgaaaga agctgtggcc aataaaggcc cagtgtctgt tgggttagat gcgcgtcatc   120
cttctttctt cctctacaga agtgggtgtc actatgaacc atcctgtact cagaatgtga   180
atcatgggtg acttgtggtt ggctatgggt atcttaatgg gaaagaatac tggcttgtga   240
aaaacagctg gggccacaac ttggtgaag aaggatatat tcggatggca agaaataaag   300
gaaatcattg tgggattgct agctttccct cttaccaga aatctagagg atctctcctt   360
tttataacaa atcaagaat atgaagcact ttctcttaac ttaatttttc ctgctgtat    419
```

<210> SEQ ID NO 172
<211> LENGTH: 452
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(452)
<223> OTHER INFORMATION: AffymetrixID: 200663_at

<400> SEQUENCE: 172

```
tgtcttatga tcacgtttgc catctttctg tctcttatca tgttggtgga ggtggccgca    60
gccattgctg gctatgtgtt tagagataag gtgatgtcag agtttaataa caacttcagg   120
cagcagatgg agaattaccc gaaaaacaac cacactgctt cgatcctgga caggatgcag   180
gcagatttta agtgctgtgg ggctgctaac tacacagatt gggagaaaat cccttccatg   240
tcgaagaacc gagtccccga ctctgtctgc attaatgtta ctgtgggctg tgggattaat   300
ttcaacgaga aggcgatcca taaggagggc tgtgtggaga agattggggg ctggctgagg   360
aaaaatgtgc tggtggtagc tgcagcagcc cttggaattg cttttgtcga ggttttgga    420
attgtctttg cctgtgcct cgtgaagagt at                                     452
```

<210> SEQ ID NO 173
<211> LENGTH: 517
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(517)
<223> OTHER INFORMATION: AffymetrixID: 202138_x_at

<400> SEQUENCE: 173

```
cagaataaaa aacagccccg ccaagactat cagctgggat tcactttaat ttggaagaat    60
gtgccgaaga cgcagatgaa attcagcatc cagacgatgt gccccatcga aggccaaggg   120
aacattgcac gtttctgtgt ctctctgttt ggccagaagc ataatgctgt caacgcaacc   180
cttagagata gctgggtaga tattgcgatt ttccagttaa aagaggaag cagtaaagaa   240
aaagccgctg ttttccgctc catgaactct gctcttgga agagcccttg gctcgctggg   300
aatgaactca ccgtagcaga cgtggtgctg tggctgttac tccagcagat cggaggtgc    360
agtgtgacag tgccagccaa tgtgcagagg tggatgaggt cttgtgaaaa cctggctcct   420
tttaacacgg ccctcaagct ccttaagtga attgccgtaa ctgattttaa agggtttaga   480
```

-continued

ttttaagaat ggtgctcttt catgcctatt atcagta 517

<210> SEQ ID NO 174
<211> LENGTH: 506
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(506)
<223> OTHER INFORMATION: AffymetrixID: 200851_s_at

<400> SEQUENCE: 174

gttgaaggcc tcgcttagtt gtactggatt ctcagggagc cctctgtggc cttttgcttt 60
gcgtgctggt tcccttgtag cagagggcgg caccgtggaa attctgtttt cctgttagca 120
tattgtgttg gattgcatta ctggcagaga aaggacaagg tgccattcaa gtcctagggt 180
gggcttccag ctgccttaat agaagtactc aagtcttttg ggtagtgagc tggaaagcct 240
acaggaaaag aggggtacct gttttcattt gaaaactttg attcatggaa cctttaaaac 300
taatctcaga aaaatttttg gtgcccagtc agctgtagtt gttcactgct ttcctggatg 360
gatgggactc ttatgtcata acttctgtta ctcctttggc ccatagctaa ggtcactcct 420
ccccacaggg gtggcttttg gattggatga tacagctttt gcttctgtgt agtatacctg 480
tacatacttg ttccagcgag cctttc 506

<210> SEQ ID NO 175
<211> LENGTH: 558
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (124)..(124)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (422)..(422)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(558)
<223> OTHER INFORMATION: AffymetrixID: 201109_s_at

<400> SEQUENCE: 175

tcgatgatgt gactggcggt agctgattaa cccatgtaaa taggcactta aatagaagca 60
ggaaaggagg acaaagactg gcttctggac ttcctccttg atccccccc ttactcatca 120
cctngcagtg gccagaatta gggaatcaga atcaaaccag tgtaaggcag tgctggctgc 180
cattgcctgg tcacattgaa attggtggct tcattctaga tgtagcttgt gcagatgtag 240
caggaaaata ggaaaccta ccatctcagt gagcaccagc tgccctccaa aggaggggca 300
gccgtgctta tttttttatg gttacaatgg cacaaaatta ttatcaacct aactaaaaca 360
ttccttttct cttttttcct gaattatcat ggagttttct aattctctct tttggaatgt 420
angatttttt ttaaatgctt tacgatgtaa aatatattatt ttttacttat tctggaagat 480
ctggctgaag gattattcat ggaacaggaa gaagcgtaaa gactatccat gtcacttttg 540
ttgagagtct tcgtgact 558

<210> SEQ ID NO 176
<211> LENGTH: 502
<212> TYPE: DNA

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```

<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(502)
<223> OTHER INFORMATION: AffymetrixID: 202531_at

<400> SEQUENCE: 176

acaggagtcacgtgtctggctttttcctctgagcccagctgcctggagagggtctcgctgt60
cactggctggctcctaggggaacagaccagtgacccacagaagcataacaccaatccca120
gggctggctctgactaagcgaattgcaataatgaatctcgttccaaagaactaccc180
cttttcagctgagccctgggactgttccaagccagtgaatgtgaaggaactccctc240
cttcggggcattgctccctcagcctcagaggagctctaccctgctccctgctttggctga300
ggggcttgggaaaaaaacttggcacttttctgtgtggatctgcccacattctgatcaga360
ggtgtacactaacatttcccagagctcttggcctttgcaattatttatacagtgccttg420
ctcggggcccaccacccctcaagcccagcagccctcaaaggcccaggagggaagtg480
tgagcgcccttggtatgacttaa502

```

```

<210> SEQ ID NO 177
<211> LENGTH: 513
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (378)..(378)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (413)..(413)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (453)..(453)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(513)
<223> OTHER INFORMATION: AffymetrixID: 216274_s_at

<400> SEQUENCE: 177

ggaatgattgtctcatcgccactaatgactggaaggggttaatggtaat aactggaagt60
gaaagtccgattgtagtgtgctcagtgaggcatggaacctgcatttcatagaggagat120
cttctctttc taacaaatcg agttgaagatcccatacgagtgggagaaattgtgttttc180
aggatagaaggaagagagattcctatagttcaccgagtcttgaagattcatgaaaagcaa240
aatgggcata tcaagtttttgaccaaagga gataataatgcggttgatgacgaggcctc300
tataaacaaggacaacattgctagagaaa aaagatgttg tggggagagcaggggattt360
gttccttata ttggaatngtgacgacccctc atgaatgactatcctaaatt tangtatgca420
gttctctttt tgcgtgggtt attcgtgctg gtnccatcgtg agtaagaagcctgccttget480
gttcctggga agatgccata gttttcgtta ctg513

```

```

<210> SEQ ID NO 178
<211> LENGTH: 338
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(338)

```

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<223> OTHER INFORMATION: AffymetrixID: 200041_s_at

<400> SEQUENCE: 178

```
agaggctttc tcggtatcag cagtttaaag attttcaacg acgaattctt gtggctacca    60
acctattttg ccgaggcatg gacatcgagc gggatgaacat tgcttttaat tatgacatgc    120
ctgaggattc tgacacctac ctgcatcggg tggccagagc aggccggttt ggcaccaagg    180
gcttggtctat cacatttggt tccgatgaga atgatgcaa gatcctcaat gatgtgcagg    240
atcgctttga ggtcaatatt agtgagctgc ctgatgagat agacatctcc tcctacattg    300
aacagacacg gtagaagact cgcccathtt ggaatgtg                                338
```

<210> SEQ ID NO 179

<211> LENGTH: 498

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(498)

<223> OTHER INFORMATION: AffymetrixID: 200052_s_at

<400> SEQUENCE: 179

```
ggacatggtc tgctatacag ctcagactct cgtccgaatc ctctcacatg gtggcttttag    60
gaagatcctt ggccaggagg gtgatgccag ctatcttgct tctgaaatat ctacctggga    120
tggagtgata gtaacacctt cagaaaaggc ttatgagaag ccaccagaga agaaggaagg    180
agaggaagaa gaggagaata cagaaagaac cacctcaagg agaggaagaa gaaagcatgg    240
aaactcagga gtgacattcc cttcactcct tttctacccc aagggaagaa ctggagccta    300
agctgcctgc tactggcttt acatgggtgac agacattccg tggataggaa gatagcagga    360
gaaagtaact ccatagatgt tcattccact gggtgatatt ggcttagctg ccagtctccc    420
atattgtgacc tatgccatcc atctataatg gaggatacca acatttcttc ctaatatctt    480
ataatctcca actcctga                                498
```

<210> SEQ ID NO 180

<211> LENGTH: 478

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(478)

<223> OTHER INFORMATION: AffymetrixID: 200064_at

<400> SEQUENCE: 180

```
aatagacttg tgtcttcacc ttgctgcatt gtgaccagca cctacggctg gacagccaat    60
atggagcgga tcatgaaagc ccaggcactt cgggacaact ccaccatggg ctatatgatg    120
gccaaaaagc acctggagat caaccctgac caccctattg tggagacgct gcggcagaag    180
gctgaggccg acaagaatga taaggcagtt aaggacctgg tgggtgctgct gtttgaacc    240
gccctgctat cttctggctt ttcccttgag gatccccaga cccactccaa ccgcacttat    300
cgcatgatca agctaggtct aggtattgat gaagatgaag tggcagcaga ggaaccaaat    360
gctgcagttc ctgatgagat cccccccttc gagggcgatg aggatgcgtc tcgcatggaa    420
gaagtcgatt aggttaggag ttcatagttg gaaaacttgt gcccttgat agtgtccc    478
```

<210> SEQ ID NO 181

-continued

<211> LENGTH: 508
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(508)
<223> OTHER INFORMATION: AffymetrixID: 200079_s_at

<400> SEQUENCE: 181

```
agctgccaga aacgaacctc ttgaaactg aagaaactcg caaaattctt gatgatattc    60
gtgtggcaaa agctgttgaa tgccctccac ctgggaccac agccaggctc cttgacaagc    120
ttgttgggga gttcctggaa gtgacttgca tcaatcctac attcatctgt gatcaccac    180
agataatgag ccttttggct aaatggcacc gctctaaaga gggctctgact gagcgctttg    240
agctgtttgt catgaagaaa gagatatgca atgcgtatac tgagctgaat gatcccatgc    300
ggcagcggca gctttttgaa gaacaggcca aggccaaggc tgcagggtgat gatgaggcca    360
tgttcataga tgaaaacttc tgtactgccc tggaatatgg gctgcccccc acagctggct    420
ggggcatggg cattgatcga gtcgccatgt ttctcacgga ctccaacaac atcaaggaag    480
tacttctggt tctgccatg aaaccgca                                     508
```

<210> SEQ ID NO 182
<211> LENGTH: 393
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(393)
<223> OTHER INFORMATION: AffymetrixID: 200629_at

<400> SEQUENCE: 182

```
tccagtttac tgaactccag accatgcatg tagtccactc cagaaatcat gtcgcttcc    60
cttggcacac cagtgttctc ctgccaaatg accctagacc ctctgtcctg cagagtcagg    120
gtggcttttc ccctgactgt gtccgatgcc aaggagtctc ggccctccga gatgcttcat    180
tttgaccctt ggctgcagtg gaagtcagca cagagcagtg ccctggctgt gtctggacg    240
ggtggactta gctagggaga aagtcgaggc agcagccctc gaggccctca cagatgtcta    300
ggcaggcctc atttcatcac gcagcatgtg caggcctgga agagcaaagc caaatctcag    360
ggaagtcctt ggttgatgta tctgggtctc etc                               393
```

<210> SEQ ID NO 183
<211> LENGTH: 439
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(439)
<223> OTHER INFORMATION: AffymetrixID: 200634_at

<400> SEQUENCE: 183

```
gaaaacgttc gtcaacatca cgccagctga ggtgggtgtc ctggttgga aagaccggtc    60
aagtttttac gtgaatgggc tgacacttgg gggccagaaa tgttcggtga tccgggactc    120
actgctgcag gatggggaat ttagcatgga tcttcgtacc aagagcaccg gtggggcccc    180
caccttcaat gtcactgtca ccaagactga caagacgcta gtctgtctga tgggcaaaga    240
aggtgtccac ggtggtttga tcaacaagaa atgttatgaa atggcctccc accttcggcg    300
```


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ttcccagtag	tgacctgtgc	tgtcccttcc	ccttcaccgc	tccccacagc	tttgcacccc	360
tttcctcccc	atacacacac	aaaccatttt	attttttggg	ccattacccc	ataccctta	420
ttgctgccaa	aaccacatg					439

<210> SEQ ID NO 184
 <211> LENGTH: 541
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(541)
 <223> OTHER INFORMATION: AffymetrixID: 200802_at

<400> SEQUENCE: 184

taattgcacg	gattaccagg	ctgcgccgct	tcgaatccga	tatgggcaaa	ccaagaagat	60
gatggacaag	gtggagtttg	tccatatgct	caatgctacc	atgtgcgcca	ctacccgtac	120
catctgcgcc	atcctggaga	actaccagac	agagaagggc	atcactgtgc	ctgagaaatt	180
gaaggagttc	atgccgccag	gactgcaaga	actgatcccc	tttgtgaagc	ctgcgcccac	240
tgagcaggag	ccatcaaaga	agcagaagaa	gcaacatgag	ggcagcaaaa	agaaagcagc	300
agcaagagac	gtcacccatg	aaaacaggct	gcagaacatg	gaggtcacccg	atgcttgaac	360
attctgcctt	ccctattttg	caggctttca	tttctgtctg	ctgagatctc	agagcctgcc	420
caacagcagg	gaagccaagc	accattcat	ccccctgccc	ccatctgact	gcgtagctga	480
gaggggaaca	gtgccatgta	ccacacagat	gttctgtctt	cctcgcatgg	gcatagggac	540
c						541

<210> SEQ ID NO 185
 <211> LENGTH: 456
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(456)
 <223> OTHER INFORMATION: AffymetrixID: 200860_s_at

<400> SEQUENCE: 185

acttcagttg	caccatgctg	tacctttttg	cagaggccaa	tacggaagcc	atccaagaac	60
agatcacaag	agttctcttg	gaacgggtga	ttgtaaatag	gccacatcct	tgggggtcttc	120
ttattacctt	cattgagctg	attaaaaacc	cagcgtttaa	gttctggaac	catgaatttg	180
tacactgtgc	cccagaaatc	gaaaagttaa	tccagtcggt	cgcacagtgc	tgcatgggac	240
agaagcaggc	ccagcaagta	atggaaggga	caggtgccag	ttagacgaaa	ctgcatctct	300
gttgtacgtg	tcagtctaga	ggctctcactg	caccgagttc	ataaactgac	tgaagaatcc	360
tttcagctct	tcctgacttt	cccagccctt	tggtttgtgg	gtatctgccc	caactactgt	420
tgggatcagc	ctcctgtctt	atgtgggcac	gttcca			456

<210> SEQ ID NO 186
 <211> LENGTH: 506
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(506)
 <223> OTHER INFORMATION: AffymetrixID: 200983_x_at

-continued

<400> SEQUENCE: 186

```

aggagttgag acctacttca cagtagttct gtggacaatc acaatgggaa tccaaggagg      60
gtctgtcctg ttcgggctgc tgctcgctct ggctgtcttc tgccattcag gtcatagcct    120
gcagtgctac aactgtccta acccaactgc tgactgcaaa acagccgtca attgttcac      180
tgatthttgat gcgtgtctca ttaccaaagc tgggttacaa gtgtataaca agtgttgga      240
gtttgagcat tgcaatttca acgacgtcac aaccgcttg agggaaaatg agctaacgta      300
ctactgctgc aagaaggacc tgtgtaactt taacgaacag cttgaaaatg gtgggacac      360
cttatcagag aaaacagttc ttctgctggt gactccattt ctggcagcag cctggagcct    420
tcatacctaa gtcaacacca ggagagcttc tcccaaatc cccgttctcg cgtagtcggc      480
tttctcttgc tgccacattc taaagg                                           506

```

<210> SEQ ID NO 187

<211> LENGTH: 375

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(375)

<223> OTHER INFORMATION: AffymetrixID: 200991_s_at

<400> SEQUENCE: 187

```

tgccacccgg gagtctatgg tcaaactctc aagtaagctg agtgccgtga gcttgccggg      60
aattggcagt cccagcacag atgccagtgc cagtgatgac cagggaatt tcgccttcga    120
gggcattgga gatgaggatc tgtaatctcc actgcttgga tgtctgccct ctacccacaga    180
ggaatttaca gaaacttgcc ctgtgcctgt gtcccccatt ctaggggcgg aggggtcttt    240
tccttcttct ttctaccta ccccttttct cttggccagg ggctctgtat cctacctttc    300
cttggtccct gggtggctg cacagaggat tgcccttct cttttcagag ctggccctcg    360
atgccaatt agcat                                                         375

```

<210> SEQ ID NO 188

<211> LENGTH: 312

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(312)

<223> OTHER INFORMATION: AffymetrixID: 201112_s_at

<400> SEQUENCE: 188

```

agatctgtgc ggttggcata accaacttac taacagaatg tccccaatg atggacactg      60
agtatacaa actgtggact ccattattac agtctttgat tggctttttt gagttaccg      120
aagatgatac cattcctgat gaggaacatt ttattgacat agaagatata ccaggatata    180
agactgcctt ctcacagttg gcatttgctg ggaaaaaaga gcatgatcct gtaggtcaaa    240
tggtgaataa ccccaaatc cacctggcac agtcacttca catgttgtct accgcctgtc    300
caggaagggt tc                                                         312

```

<210> SEQ ID NO 189

<211> LENGTH: 338

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

-continued

<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(338)
<223> OTHER INFORMATION: AffymetrixID: 201214_s_at

<400> SEQUENCE: 189

agagctgcaa gagttctgga tgaacgacaa tctccttgag agctggagcg acctcgacga	60
gctgaaggga gccaggagcc tggagacagt gtacctggag cggaaccctc tgcagaagga	120
cccccagtac cggcggaagg tcatgctcgc cctccccctcc gtgcggcaga tcgatgccac	180
gttcgtcagg ttctgagtc ttcttggtc ctcctgtggt cctctctctc ggaagaactg	240
cccagccacg ggtttttaac ccacctgttg ctcctgaggt cgtcactata tcaacagtca	300
caaacccaat ggcaataaag gcactgacga tagctggc	338

<210> SEQ ID NO 190
<211> LENGTH: 385
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(385)
<223> OTHER INFORMATION: AffymetrixID: 201241_at

<400> SEQUENCE: 190

aggatgggtc tggcaatttc cctggtggca acagaaaaag aaaaggtttg gtaccatgta	60
tgtagcagcc gtggaaaagg gtgttataac acaagactca aggaagatgg aggctgtacc	120
atatggtaca acgagatgca gttactatct gagatagaag aacacctgaa ctgtaccatt	180
tctcaggttg agccgatat aaaggtacca gtggatgaat ttgatgggaa agttacctac	240
ggtcagaaaa gggctgctgg tgggtgaagc tataaaggcc atgtggatat tttggcacct	300
actgttcaag agttggctgc ccttgaaaag gaggcgcaga catctttcct gcactctggc	360
taccttccta accagctgtt cagaa	385

<210> SEQ ID NO 191
<211> LENGTH: 371
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(371)
<223> OTHER INFORMATION: AffymetrixID: 201263_at

<400> SEQUENCE: 191

gatctggatc caggctgtac attgaataaa aagattcgaa atgcacagtt agcacagtat	60
aacttcattt tagttgttgg tgaaaaagag aaaatcactg gcactgttaa tatccgcaca	120
agagacaata aggtccacgg ggaacgcacc atttctgaaa ctatcgagcg gctacagcag	180
ctcaaagagt tccgcagcaa acaggcagaa gaagaatttt aatgaaaaaa ttaccagat	240
tggctccatg gaaaaggagg aacagcgttt ccgtaaaatt gactttgtac tcgaaaacgt	300
caatttatat tgaacttga ggaggagttt ggcaaagtct gaaataggtc aacctgcagg	360
cgtaactatt t	371

<210> SEQ ID NO 192
<211> LENGTH: 492
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(492)
<223> OTHER INFORMATION: AffymetrixID: 201386_s_at

<400> SEQUENCE: 192
ggagatcatc tgacactgct gaacgtctac catgctttta aacaaaatca tgaatcggtt      60
cagtgggtgtt atgacaactt cattaactac aggtccctga tgtccgcaga caatgtacgc      120
cagcagctat ctcgaattat ggacagattt aatttgcttc gtcgaagtac tgactttaca      180
agcaggggact attatattaa tataagaaaa gctttgggta ctgggtatgt tatgcagggtg      240
gcacatttag aacgaacagg gcattactta actgtgaaag ataaccagggt ggttcagttg      300
catccctcta ctgttcttga ccacaaacct gaatgggtgc tttataatga gtttgttcta      360
acaacaaaga attacatccg gacatgtaca gatatcaagc cagaatgggt ggtgaaaatt      420
gcccctcaat attatgacat gagcaatttc ccacagtgtg aagcaaagag acagttggac      480
cgcatcattg cc                                                                492

<210> SEQ ID NO 193
<211> LENGTH: 408
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(408)
<223> OTHER INFORMATION: AffymetrixID: 201417_at

<400> SEQUENCE: 193
gtaaaccaca tctttttttg acttttttta taagcaaaaa cgtgccgttt aaaccactgg      60
atctatctaa atgccgattt gagttcgcca cactatgtac tgcgtttttc attcttgtat      120
ttgactatgt aatcctttct acttgcgtct aaatataatt gttttagtct tatggcatga      180
tgatagcata tgtgttcagg tttatagctg ttgtgtttta aaattgaaaa aagtggaaaa      240
catcttttga catttaagtc tgtattataa taagcaaaaa gattgtgtgt atgtatgttt      300
aatataacat gacaggcact aggacgtctg cctttttaag gcagttccgt taagggtttt      360
tgttttttaa cttttttttg ccatccatcc tgtgcaatat gccgtgta                    408

<210> SEQ ID NO 194
<211> LENGTH: 422
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(422)
<223> OTHER INFORMATION: AffymetrixID: 201576_s_at

<400> SEQUENCE: 194
aatggcttta accttggccg ctattggcca gcccggggcc ctcagttgac cttgtttgtg      60
ccccgcaca tcctgatgac ctcggcccca aacaccatca ccgtgctgga actggagtgg      120
gcaccctgca gcagtgatga tccagaacta tgtgctgtga cgttcgtgga caggccagtt      180
attggctcat ctgtgacctc cgatcatccc tccaaacctg ttgaaaaaag actcatgccc      240
ccacccccgc aaaaaacaaa agattcatgg ctggacctg tatgatgatg aaagcctgtg      300
tctttgaggg attctacctt gaacatacct cacagatcct cctgtcatg ccacatttca      360
ctgattggaa tgtggaaatg gaaaaggaat ttaggatgtg cattttcacc tgaggtttcc      420

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ct 422

<210> SEQ ID NO 195
<211> LENGTH: 551
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(551)
<223> OTHER INFORMATION: AffymetrixID: 201872_s_at

<400> SEQUENCE: 195

```
gagatccaaa caactatagg ccacgaataa acaaacttaa ttcaattaag gatgtagaac      60
aaaagaagag tggaaactac tttttcttgg atgattagac tgactctgag aatattgata      120
agccatttat taaaaggagt atttactaga attttttgtc atataaaact tgaatcagga      180
ttttatgccc cacatactct ggaacttgaa gtataatata cttaatatata cataaaaagc      240
cagttggggtt ctaaattgta gttgaaacac agaaaatgcc acttttctgt tctgaagag      300
gctcttttgt gcataatatt ctaaaatgaa gacatttcaa gctatacaaa ttacttccaa      360
gttttcatga tgtatgggaa gattttcagt aggtgtatta tattcacggg accaaatgct      420
gaccagtgtt gtcctatttt ttaaactctg aaaaggggtt ctgtacttac ctgggttgcc      480
aagtatgcca gtgtaatgaa actgccctta ttttaaaagc cagtcaaaga ttccactgat      540
tgacatttga t                                     551
```

<210> SEQ ID NO 196
<211> LENGTH: 519
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(519)
<223> OTHER INFORMATION: AffymetrixID: 201892_s_at

<400> SEQUENCE: 196

```
tgtcagagta tgcacggcgc tttggtgttc cggtcattgc tgatggagga atccaaaatg      60
tgggtcatat tgcgaaagcc ttggcccttg gggcctccac agtcatgatg ggctctctcc      120
tggctgccac cactgaggcc cctggtgaat acttcttttc cgatgggatc cggctaaaga      180
aatatcgagg tatgggttct ctcatgcca tggacaagca cctcagcagc cagaacagat      240
atttcagtga agctgacaaa atcaaagtgg ccaggggagt gtctggtgct gtgcaggaca      300
aagggtcaat ccacaaattt gtcccttacc tgattgctgg catccaacac tcatgccagg      360
acattggtgc caagagcttg acccaagtcc gagccatgat gtactctggg gagcttaagt      420
ttgagaagag aacgtcctca gccaggtgg aaggtggcgt ccatagcctc cattcgtatg      480
agaagcggct tttctgaaaa gggatccagc acacctcct                                     519
```

<210> SEQ ID NO 197
<211> LENGTH: 283
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(283)
<223> OTHER INFORMATION: AffymetrixID: 202174_s_at

<400> SEQUENCE: 197

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caacctttaa atagtgtctgc ccataaggag tcacctccta ctgttgattc aactcaacag	60
cctaaccctt tgccgttacg ttacctgaa atggaaccct tagtgcctag agtcaaagaa	120
gttaaactctg ctccagaaac tcctgaaagc tctctggctg gaagtccctga tactgaatct	180
ccagtgttag tgaatgacta tgaagcagaa tctggtaata taagtcaaaa gtctgatgaa	240
gaagattttg taaaagttga agatttacca ctgaaactga caa	283

<210> SEQ ID NO 198
 <211> LENGTH: 522
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(522)
 <223> OTHER INFORMATION: AffymetrixID: 202176_at

<400> SEQUENCE: 198

ggtgatcacg aaactcgctg gcatggagga ggaagacttg gcgttttcga caaaagaaga	60
gcaacagcag ctcttacaga aagtccctggc agccactgac ctggatgccg aggaggaggt	120
ggtggctggg gaattttgct ccagatccag ccaggcatct cggcgctttg gcaccatgag	180
ttctatgtct ggggcccagc acactgtgta catggagtac cactcatcgc ggagcaaggc	240
gcccagcaaa catgtacacc cgctcttcaa gcgctttagg aaatgatgct taggcagggt	300
acttcgttca agaccggcgc ttggcaccct tgttggaag ggattttcag cataacattt	360
tccttcaccc tctttgacct tccctccagc gttggccaaa ttgtgctgag gaagatgcat	420
caagggcttg gctgtgcctt cataggtcat ctagggtttt ataaaggagg aggagacaat	480
attttttcaa actttttggg gagtggggtc atttctgtat at	522

<210> SEQ ID NO 199
 <211> LENGTH: 423
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(423)
 <223> OTHER INFORMATION: AffymetrixID: 202220_at

<400> SEQUENCE: 199

tgatccaaag ctggcacctt caggcacatt ggtctcatag ccattactgt ttttattgcc	60
cttetaagat cctgtcttca gctgggtcag agaaaacttc ttgactaaaa ctggtcagaa	120
ctcatcacag aaatgaaata cagtggctct tctctcccag aactggttgc agctaaaaca	180
gagagatctg actgtggctt ataggatttt ggacttaatg actgaaattg caaattgtcc	240
tttttcttgg cattacagat ttgccccaaa taactttttg tatcaaatat tgatgtgtga	300
aagtgaagga gctagtctgc tgaaccagga atagtttgag atattgaact gtcatttttg	360
cacatttgaa tactttgcag gctggctttg tataaactta tcctctgggt tcctatatgt	420
tgt	423

<210> SEQ ID NO 200
 <211> LENGTH: 344
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (106)..(106)

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```
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (108)..(113)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(344)
<223> OTHER INFORMATION: AffymetrixID: 202225_at

<400> SEQUENCE: 200
gatactgtaa agtcacaca cacattaaat cttgttttcc tgaaagtatg gcatcaaaaa    60
tacttgtaga aaaaccttgt cacaactgat ttgaatgttc ctattntnnn nnnctttgac   120
tttgatattg gcttgtaatg tctcttttca tcatatgtaa tatcagtgga acaggcagcg   180
ctactcaagt cctaaggatt cctcagtgat cagtgatcca gggccgttca tgaaccactg   240
ggctggattt gactgttgag tgtggcagtt aatgcccctc aagaaatcaa aggatgtctt   300
ataagtgctt tccaaaaaaa agcaaatgct gaaatcctat tggc                    344

<210> SEQ ID NO 201
<211> LENGTH: 371
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(371)
<223> OTHER INFORMATION: AffymetrixID: 202464_s_at

<400> SEQUENCE: 201
tattctgtcc tgagaccacg ggcaaagctc ttccattttg agagagaaga aaaactgttt    60
ggaaccacac caatgatatt tttctttgta atacttgaaa tttatttttt tattattttg   120
atagcagatg tgctatttat ttatttaata tatgtataag gagtcctaaa caatagaaag   180
ctgtagaagc tgtagagata ggcttcagtt gttaattggg ttggagcctc ctatgtgtga   240
cttatgactc tctgtgttct gtgtatttgt ctgaattaat gacctgggat ataaagctat   300
gctagctttc aaacaggaga tgccttcaga aagctttgta tattttgcag ttgccagacc   360
aataaaaatac c                                                    371

<210> SEQ ID NO 202
<211> LENGTH: 445
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(445)
<223> OTHER INFORMATION: AffymetrixID: 202545_at

<400> SEQUENCE: 202
atcgcccctg agatcctaca gggcctgaag tacacattct ctgtggactg gtggctcttc    60
ggggtccttc tgtacagat getcattggc cagtcccctt tccatggtga tgatgaggat   120
gaactcttcg agtccatccg tgtggacacg ccacattatc cccgctggat caccaaggag   180
tccaaggaca tcctggagaa gctctttgaa agggaaccaa ccaagaggct gggaatgacg   240
ggaaacatca aaatccacc cttcttcaag accataaact ggactctgct ggaaaagcgg   300
aggttggagc cacccttcag gcccaaagtg aagtcacca gagactacag taactttgac   360
caggagttcc tgaacgagaa ggcgcgcctc tcctacagcg acaagaacct catcgactcc   420
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atggaccagt ctgcattcgc tggct 445

```

<210> SEQ ID NO 203
<211> LENGTH: 482
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(482)
<223> OTHER INFORMATION: AffymetrixID: 202838_at

```

<400> SEQUENCE: 203

```

agaaagaggc gctgctcact gttttcctgc ttcagttttt ctcttatagt accatcacta    60
taatcaacga acttctcttc tccaccaga gatggctttt ccaacacatt ttaattaaag    120
gaactgagta cattaccctg atgtctaaat ggaccaaaga tctgagatcc attgtgatta    180
tatctgtatc aggtcagcag aagaaggaaac tgagcagttg aactctgagt tcatcaattc    240
taatatattg aaattatcta caatggaatc ttccctctgt tctctgataa cctacttgct    300
tactcaatgc cttaagcca agtcaccctg ttgcctatgg gaggaggtgg aaggatttgg    360
caagctcaac cacatgctat ttagttagca tcagttgtca ccaacagtct ttctgcaaag    420
ggcaggagag ctttggggga aaggaaaagg cttaccaggc tgctatggtc aactcttcag    480
aa                                         482

```

```

<210> SEQ ID NO 204
<211> LENGTH: 386
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(386)
<223> OTHER INFORMATION: AffymetrixID: 202896_s_at

```

<400> SEQUENCE: 204

```

ccaccacca actggggcta gagtgggaa gatttccct ttagatcaaa ctgcccttc    60
catggaaaag ctggaaaaa actctggaac ccatatccag gcttggtag gttgctgcca    120
acagtcttg cctcccccac ccctaggcaa agagccatga gtctggagg aggagaggac    180
cctcccaaa ggactggaag caaaaccctc tgcttccttg ggccctcca agactcctg    240
gggccaact gtgttgcctc acccggaacc atctctcct tctagacctg agcttgcccc    300
tccagctagc actaagcaac atctcgtgt aagcgctgt aaattactgt gaaatgtgaa    360
acgtgcaatc ttgaaactga ggtgtt          386

```

```

<210> SEQ ID NO 205
<211> LENGTH: 486
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(486)
<223> OTHER INFORMATION: AffymetrixID: 202950_at

```

<400> SEQUENCE: 205

```

taacatgtta gttgtcattt ggcattgagt tgcattccag taattcttaa ttgatatttg    60
attaattcca tacctttgat taaaacatgc tagttcaaaa taagactgct cagtttccaa    120
gggttttcaa gcctacttac ctttataaag gttctctagt ctctgattag ccatgactgt    180

```


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attggacttt gaacattttc tgaactaaaa acctctattc taaactaatc tcatttggat	240
gtgtaagtct tttgtaaagg caagaataaa taatatccag gacaatttat tagttttctc	300
agtttttcc caaatattag aatatttact tcattattgg ttggctgcc aatgaccccat	360
atgttctgtg agaatagtag ctttatcttt gatataatac atagtctcca aataggtaat	420
acttcgcaat tgattagatt ttcagagtag atttagagtt atctgttttt ctggtgaggg	480
tcaaat	486

<210> SEQ ID NO 206
 <211> LENGTH: 466
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(466)
 <223> OTHER INFORMATION: AffymetrixID: 203037_s_at

<400> SEQUENCE: 206

agtagtgct gtggtttagc ccaccaatct tgatgactaa aagtagctga tgcattgtgc	60
atatgatgct tgagatgggt tttgcaaaag cagaaatcgc tgcaaggtaa tcacaataga	120
taaaagtggt attttaaacc ttgaaataa atggatgtaa ctgtaccttg gtacagcttt	180
tcacttgttt agtttttaaa cgtagtata atctgaataa ataaaatgtt gccaaattca	240
atgtagaaag aatgtgacaa cacaccttgg gtagttctgc ttgtgttttt gcatattgta	300
aaagcagtgt cacagctaaa aagaagaaa tcgtttctaa cagtaaatta ttgtgcttta	360
gttgctagtt tgtactgaga gttgacctc cctgtgcag tttttgttc taaacttgta	420
taaataacaa ttgtgtaatg tgtctccctc ctacattgta acaatt	466

<210> SEQ ID NO 207
 <211> LENGTH: 497
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(497)
 <223> OTHER INFORMATION: AffymetrixID: 203155_at

<400> SEQUENCE: 207

gtcttcgtgg ataccatga tcttcgttc ccctgggtgg ccttctttgc cagcaaaaga	60
atccgggctg ggacagaact tacttgggac tacaactacg aggtgggcag tgtggaaggc	120
aaggagctac tctgttgctg tggggccatt gaatgcagag gacgtcttct ttagaggaca	180
gccttcttcc caaccttct tgaactgtcg tttcctcagg aactgggtct tctgattgt	240
tgaacctga cccgaagtct ctgggctagc tactcccccc agctcctagt tgatagaaat	300
gggggttctg gaccagatga tcccttccaa tgtggtgcta gcaggcagga tcccttctcc	360
acctccaaag gcctaaagg gtggggagag atcaccactc taacctcggc ctgacatccc	420
tcccatccca tatttgtcca agtgttctcg cttctaacag actttgttct tagaatggag	480
cctgtgtatc tactatc	497

<210> SEQ ID NO 208
 <211> LENGTH: 478
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(478)
<223> OTHER INFORMATION: AffymetrixID: 203371_s_at

<400> SEQUENCE: 208

```
ctttcctgcc gtgagaaact cgaggtgacc aacctccgtt tccggttggc tccggttgca    60
gagttgagtg tcttgagagg tcagattgct gtcagacatg gcccatgaac atggacatga    120
gcatggacat cataaaatgg aacttccaga ttatagacaa tggaagatag aagggacacc    180
attagaaact atccagaaga agctgggtgc aaaagggcta agggatccat ggggccgcaa    240
tgaagcttgg agatacatgg gtggctttgc aaagagtgtt tccttttctg atgtattctt    300
taaaggattc aaatggggat ttgctgcatt tgtggtagct gtaggagctg aatattacct    360
ggagtccttg aataagata agaagcatca ctgaagataa tacctggaag catcatagtg    420
gtttcttaac tctccaaaat aagattttct ctctgtagcc tacttgtctg gtttatcc    478
```

<210> SEQ ID NO 209
<211> LENGTH: 510
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(510)
<223> OTHER INFORMATION: AffymetrixID: 203821_at

<400> SEQUENCE: 209

```
gagccactct atgagttgga cttcagtcct gcctaggcga ttttgtctac cattttgtgt    60
ttgaaagccc aaggtgctga tgtcaaatg taacagatat cagtgtctcc ccgtgtcctc    120
tccctgccaa gtctcagaag aggttgggct tccatgcctg tagctttcct ggtccctcac    180
ccccatggcc ccaggccaca gcgtgggaac tcactttccc ttgtgtcaag acattttctct    240
aactcctgcc attcttctgg tgctactcca tgcaggggtc agtgcagcag aggacagtct    300
ggagaaggta ttagcaaaagc aaaaggctga gaaggaacag ggaacattgg agctgactgt    360
tcttggtaac tgattacctg ccaattgcta ccgagaaggt tggaggtggg gaaggctttg    420
tataatccca cccacctcac caaaacgatg aaggtatgct gtcatggtcc tttctggaag    480
tttctggtgc catttctgaa ctgttacaac                    510
```

<210> SEQ ID NO 210
<211> LENGTH: 419
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(419)
<223> OTHER INFORMATION: AffymetrixID: 203966_s_at

<400> SEQUENCE: 210

```
gatgcaacag atatatagcc ctttcaagtc atgttgtgtt tggacttggg gttggaacag    60
ggagagcagc agccatgtca gctacacgct caaatgtgca gatgattatg gaaaataacc    120
tcaaaatctt acaaagctga acatccaagg agttattgaa aactatctta aatgttcttg    180
gtaggggagt tggcattgtt gataaagcca gtcccttcat ttaactgtct ttcaggatgt    240
tccttcgttg tttccatgag tattgcaggt aataatacag tgtgttccat aagaatctca    300
atcttggggc taaatgcctt gtttctttgc acctcttttc aagtccttac atttaattac    360
```

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taattgataa gcagcagctt cctacatata gtaggaaact gccacatttt tgetatcat 419

```

<210> SEQ ID NO 211
<211> LENGTH: 356
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(356)
<223> OTHER INFORMATION: AffymetrixID: 204192_at

```

<400> SEQUENCE: 211

```

taccgcgagg actggttcca agtcctcatc ctgagaggta acgggtcgga ggcgaccgc 60
gtgcctgct cctgtacaa cttgtcgcg accaacgact ccacaatcct agataagggtg 120
atcttgcccc agctcagcag gcttggacac ctggcgcggt ccagacacag tgcagacatc 180
tgcgctgtcc ctgcagagag ccacatctac cgcgagggt gcgcgcagg cctccagaag 240
tgggtgcaca acaaccttat ttccatagtg ggcatTTGCC tgggcgtcgg cctactcgag 300
ctcggttca tgacgtctc gatattctg tgcagaaacc tggaccacgt ctacaa 356

```

```

<210> SEQ ID NO 212
<211> LENGTH: 507
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(507)
<223> OTHER INFORMATION: AffymetrixID: 204419_x_at

```

<400> SEQUENCE: 212

```

acactcgctt ctggaacgct tgaggttatc aataagctcc tagtccagac gccatgggtc 60
atttcacaga ggaggacaag gctactatca caagcctgtg gggcaagggt aatgtggaag 120
atgtggagg agaaacctg ggaaggctcc tggttgtcta cccatggacc cagaggttct 180
ttgacagctt tggcaacctg tcctctgcct ctgccatcat gggcaacccc aaagtcaagg 240
cacatggcaa gaagggtgct acttccttgg gagatgccat aaagcacctg gatgatctca 300
agggcacctt tgcccagctg agtgaactgc actgtgacaa gctgcatgtg gatcctgaga 360
acttcaagct cctgggaaat gtgctggtga cggttttggc aatccatttc ggcaaagaat 420
tcacctctga ggtgcaggct tcctggcaga agatgggtgac tggagtggcc agtgcctgt 480
cctccagata cactgagct cactgcc 507

```

```

<210> SEQ ID NO 213
<211> LENGTH: 463
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(463)
<223> OTHER INFORMATION: AffymetrixID: 204566_at

```

<400> SEQUENCE: 213

```

gccacttgtc ttgaaaactg tgcaactttt taaagtaaat tattaagcag actggaaaag 60
tgatgtattt tcatagtgc ctgtgtttca cttaatgttt cttagagcca agtgtctttt 120
aaacattatt ttttatttct gatttcataa ttcagaacta aatttttcat agaagtgttg 180
agccatgcta cagttagtct tgtcccaatt aaaatactat gcagtatctc ttacatcagt 240

```

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```

agcatttttc taaaacctta gtcacagat atgcttacta aatcttcagc atagaaggaa 300
gtgtgtttgc ctaaaacaat ctaaaacaat tcccttcttt ttcacccag accaatggca 360
ttattaggtc ttaaagtagt tactcccttc tcgtgtttgc ttaaaatatg tgaagttttc 420
cttgctattt caataacaga tgggtctgct aattcccaac att 463

```

```

<210> SEQ ID NO 214
<211> LENGTH: 304
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(304)
<223> OTHER INFORMATION: AffymetrixID: 204689_at

```

<400> SEQUENCE: 214

```

cttttctgta atctgtttat ctcccactta atggaaaggc aaaggggtac cccaaatcca 60
gagggtgccta catttcaggc agccttggag tattttaaaa ggaaaacatt ctttactttt 120
atatgacatt cttatactgc tgtctcaaat cctttttcat ttcagagctc ttgtctcaga 180
gatgtgtgtt ctttttgtca gagatatggt tgatgagaat cttaaatgct tgttttgcac 240
tatcacttag tacctgtttg accaagggtg taagggatag tacctcccat cagcagagaa 300
actg 304

```

```

<210> SEQ ID NO 215
<211> LENGTH: 524
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(524)
<223> OTHER INFORMATION: AffymetrixID: 205249_at

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<400> SEQUENCE: 215

```

ggaacgtagc aatatctgct ccttttcgag ttgtttgaga aatgtaggct attttttcag 60
tgtatatcca ctcagatttt gtgtatttt gatgtacca cactgttctc taaattctga 120
atctttggga aaaaatgtaa agcatttatg atctcagagg ttaacttatt taagggggat 180
gtacatattc tctgaaacta ggatgcatgc aattgtgttg gaagtgtcct tggtcgcctt 240
gtgtgatgta gacaaatgtt acaaggctgc atgtaaatgg gttgccttat tatggagaaa 300
aaaatcactc cctgagttta gtatggctgt atatttatgc ctattaatat ttggaatttt 360
ttttagaaag tatatttttg tatgctttgt tttgtgactt aaaagtgtta cctttgtagt 420
caaatctcag ataagaatgt acataatgtt accggagctg attgttttg tcattagctc 480
ttaatagttg tgaaaaaata aatctattct aacgcaaaac cact 524

```

```

<210> SEQ ID NO 216
<211> LENGTH: 307
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(307)
<223> OTHER INFORMATION: AffymetrixID: 205552_s_at

```

<400> SEQUENCE: 216

```

gctcctgacg gtctatgctt gggagcgagg gagcatgaaa acacatttca acacagccca 60

```

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```

gggatttcgg acggtcttgg aattagtcac aaactaccag caactctgca tctactggac 120
aaagtattat gacttttaaa accccattat tgaaaagtac ctgagaaggc agctcacgaa 180
accacgcct gtgatcctgg acccggcgga ccctacagga aacttgggtg gtggagaccc 240
aaagcgttgg aggcagctgg cacaagaggc tgaggcctgg ctgaattacc catgctttaa 300
gaattgg 307

```

```

<210> SEQ ID NO 217
<211> LENGTH: 525
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(525)
<223> OTHER INFORMATION: AffymetrixID: 206115_at

```

```

<400> SEQUENCE: 217

```

```

ctcgctcctt ctggtatctg catgtcactg catgataatt gagttttcct ttgttttaat 60
aaaaactgttc tcagacatta agctaaacta agagaaaaat aactttgttg ccaaaagggt 120
gtgctatcca gattttttat atgtctgcat gtttaaaaaa aaaaagcaa caaaagaaaa 180
tgcaactctaa cttatgtgaa ctgagagaaa aaaatcaggt tttaaacagg aaaacctatg 240
gggaatgata ttttttgaaa gacttttgta taaagttgag tacttagaaa aaagacaaac 300
cagatgtaat atattttgtg gatgttttta tttcttggtt ttatagtacc ttatactaag 360
gttaaaaaaa tatgcttgat attgtgaaaa ggtgaaattc ttcaccaaca tttcatttgc 420
tcctttgtca tattgtaatg ccaatataat atagttaatg aaaacagcat ttttaaaaac 480
cgaaatattg aaatggtgta atgttgtacc atttgcactg tgagc 525

```

```

<210> SEQ ID NO 218
<211> LENGTH: 509
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(509)
<223> OTHER INFORMATION: AffymetrixID: 206584_at

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```

<400> SEQUENCE: 218

```

```

tgatgattag ttactgatcc tctttgcatt tgtaaagctt tggagatatt gaatcatgtt 60
accattttctg tttttttcca ccctgttttc ttccatattt actgaagctc agaagcagta 120
ttgggtctgc aactcatccg atgcaagtat ttcatacacc tactgtgata aaatgcaata 180
cccaatttca attaatgtta acccctgtat agaattgaaa ggatccaaag gattattgca 240
cattttctac attccaagga gagatttaaa gcaattatat ttcaatctct atataactgt 300
caacaccatg aatcttccaa agcgcaaaga agttatttgc cgaggatctg atgacgatta 360
ctctttttgc agagctctga agggagagac tgtgaataca acaatatcat tctccttcaa 420
gggaataaaa ttttctaagg gaaaatacaa atgtgttgtt gaagctatct ctgggagccc 480
agaagaaatg ctcttttgct tggagtttg 509

```

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<210> SEQ ID NO 219
<211> LENGTH: 431
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(431)
<223> OTHER INFORMATION: AffymetrixID: 206877_at

<400> SEQUENCE: 219

gaaaagccgt tcaccaaattc gaccagcttc agcgagagca ggcacacctg aagaggcagc	60
tggagaagct gggcattgag aggatccgga tggacagcat cggtccacc gtctcctcgg	120
agcgctccga ctccgacagg gaagaaatcg acgttgacgt ggagagcacg gactatctca	180
cagggtgatct ggactggagc agcagcagtg tgagcgactc tgacgagcgg ggcagcatgc	240
agagcctcgg cagtgtatgag ggctattcca gcaccagcat caagagaata aagctgcagg	300
acagtcacaa ggctgtctct ggtctctaag agagtgggca ctgcggctgt ctcttggaag	360
gttctccctg ttggttctga ttaggtaacg tattggacct gccacaaact ccttgccacg	420
taaacttcag t	431

<210> SEQ ID NO 220
<211> LENGTH: 377
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(377)
<223> OTHER INFORMATION: AffymetrixID: 207170_s_at

<400> SEQUENCE: 220

aaaacagcac tcctttggct ggagcacttg tgtccgtgca tgtactggg tgtttccctc	60
catectttct gatatgacca aaaatcaagt tgttttgttt tttgtcacct tcactggcat	120
gggctaacca cttcttttcc aaaccctctg aacacctttt tctgatgggt aacttgccag	180
aatattctat tggaaaagat aacaggaagt acaagtgcct cttgaccctt tctcaatgt	240
ttctagcctt cactctccat tgtcttttct gggctgtatt acagccctct gtggatcttc	300
aactctgctg cctccactgt gatgcagcag tccaactgta actgacagtg gctgccttct	360
ctgggccatg gatcaca	377

<210> SEQ ID NO 221
<211> LENGTH: 518
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(518)
<223> OTHER INFORMATION: AffymetrixID: 208631_s_at

<400> SEQUENCE: 221

ccagaactgc tgacacagat ggtgtccaag ggcttcctag gtcgtaaatc tgggaagggc	60
ttttacatct atcaggagggt tgtgaagagg aaggatttga attctgacat ggatagtatt	120
ttagcgagtc tgaagctgcc tctaagtct gaagtctcat cagacgaaga catccagttc	180
cgcttggtga caagatttgt gaatgaggca gtcattgtgc tgcaagaggg gatcttgccc	240
acacctgcag agggagacat cggagccgtc tttgggcttg gcttcccgcc ttgtctggga	300
gggcctttcc gctttgtgga tctgtatggc gccagaaga tagtggaacc gctcaagaaa	360
tatgaagctg cctatggaaa acagttcacc ccatgccagc tgctagtga ccatgctaac	420
agccctaaca agaagttcta ccagtgcagc ggcctcatgc ctgcctcagt cagtgcacta	480

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accccagctg ccggcagtg tggttctcca acagagtg 518

```

<210> SEQ ID NO 222
<211> LENGTH: 168
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(168)
<223> OTHER INFORMATION: AffymetrixID: 208691_at

```

<400> SEQUENCE: 222

```

gagttctgtc atgattcact attctagaac ttgcatgacc tttactgtgt tagctctttg 60
aatgttcttg aaattttaga ctttctttgt aaacaaataa tatgtcctta tcattgtata 120
aaagctgtta tgtgcaacag tgtggagatt ccttgtctga ttaataaa 168

```

```

<210> SEQ ID NO 223
<211> LENGTH: 555
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(555)
<223> OTHER INFORMATION: AffymetrixID: 208868_s_at

```

<400> SEQUENCE: 223

```

acatctagaa acattacacc acacacaccg tcatcacatt ttcacatgct caattgatat 60
tttttctgct ttcctcggcc caggagagaa gcatgtcagg acagagctgt tggattggct 120
ttgatagagg aatggggatg atgtaagttt acagtattcc tgggggttaa ttgttgtgca 180
gtttcataga tgggtcagga ggtggacaag ttggggccag agatgatggc agtccagcag 240
caactccctg tgctcccttc tctttgggca gagattctat ttttgacatt tgcacaagac 300
aggtagggaa aggggacttg tggtagtgga ccatacctgg ggacaaaag agaccactg 360
taattgatgc attgtggccc ctgatcttcc ctgtctcaca cttcttttct cccatcccg 420
ttgcaatctc actcagacat cacagtacca cccagggggt ggcagtagac aacaacccag 480
aaatttagac agggatctct tacctttgga aaataggggt taggcataaa ggtggttg 540
attaagaaga tgggt 555

```

```

<210> SEQ ID NO 224
<211> LENGTH: 456
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(456)
<223> OTHER INFORMATION: AffymetrixID: 208869_s_at

```

<400> SEQUENCE: 224

```

gactaaaacc actcttagca tctcctctag tattttccat gtatcaggac agaggtgtct 60
tatgtaggga gggggcaagt atgaagtaag gtaattatat actactctca ttcaggattc 120
ttgtcccat gctgctgtcc cttcaggctc acatgcacag gaatgctaca tgatggccag 180
ctgttccct ccttggttat catccactgc agctgctagt tagaaagggt tggagggatg 240
acttttagta aatcatgggg attttattga tttattttca cttttgggat tttgtgggt 300
gggagtgagg agcaggaatt gcactcagac atgacatttc aattcatctc tgctaataaa 360

```

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```
aagggttctt tctcttgggg gaaatgtgtg tgtcagttct gtcagctgca agttcttgta 420
taatgaagtc aatgccatca ggccaaggaa ataaaa 456
```

```
<210> SEQ ID NO 225
<211> LENGTH: 298
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(298)
<223> OTHER INFORMATION: AffymetrixID: 208942_s_at

<400> SEQUENCE: 225
```

```
caacatggcg gaacgcagga gacacaagaa gcggatccag gaagttgggtg aaccatctaa 60
agaagagaag gctgtggcca agtatcttcg attcaactgt ccaacaaagt ccaccaatat 120
gatgggtcac cgggttgatt attttattgc ttcaaaagca gtggactgtc ttttgattc 180
aaagtgggca aaggccaaga aaggagagga agctttattt acaaccaggg agtctgtggt 240
tgactactgc aacaggcttt taaagaagca gttttttcac cgagccctaa aagtaatg 298
```

```
<210> SEQ ID NO 226
<211> LENGTH: 454
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(454)
<223> OTHER INFORMATION: AffymetrixID: 209092_s_at

<400> SEQUENCE: 226
```

```
aaatccaatc atgagtcag gtagagaacg cctgctgtaa tctacactgt tgctgggact 60
gcgcattctg tatataactg tgttggatga gtgacagatg attgtccaga ctaggacagc 120
ggcatgaaca tgactttggt tgggattgcy gatagttagg gttacctctg aatcgtgtag 180
cttttatgag agcagctgtg caagtgaatc cacattaatg ccttgctcgtg gtgccattcc 240
cagcgctga cgatacgtc ttctattgtc ttattctggc aggttttgac gttttaaatt 300
ttttaaagaa attttattcc ttggacaaa aggtttggtt aaccaccccc ctcttacttg 360
ctttcacatt ttgagtgtcc agaggaaaca gaaaggaatg agtgtgtgac gttgctgcac 420
gectgactct gtgcgagctt ctttctgtgt atat 454
```

```
<210> SEQ ID NO 227
<211> LENGTH: 465
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(465)
<223> OTHER INFORMATION: AffymetrixID: 209193_at

<400> SEQUENCE: 227
```

```
gattgtagtg gatctaattt ttcagaaatt ttgcctttaa gttattttac ctgtttttgt 60
ttcttgtttt gaaagatgcy cattctaacc tggagggtcaa tgttatgtat ttattttatt 120
atatttttgg ttcccttctc attccaagct tccatagctg ctgccctagt tttcttctct 180
cctttctctc tctgacttgg ggaccttttg ggggagggtc gcgacgcttg ctctgtttgt 240
ggggtgacgg gactcaggcg ggacagtgtc gcagctccct ggcttctgtg gggccctca 300
```


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```

cctacttacc caggtgggtc cgggtctgt gggatgatgg gaggggcatt gctgactgtg 360
tatataggat aattatgaaa agcagttctg gatgggtgtgc cttccagatc ctctctgggg 420
ctgtgttttg agcagcaggt agcctggctg gttttatctg agtga 465

```

```

<210> SEQ ID NO 228
<211> LENGTH: 447
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(447)
<223> OTHER INFORMATION: AffymetrixID: 209200_at

```

```

<400> SEQUENCE: 228
ggagcaatcc aagccacata tcttctacat caaatttttc cattttgggt attttcataa 60
tctggatttg cattttgcct tccctgttca tacctcaaat tgattcatat ctcagtttaa 120
ttcagagagg tcagttaagt gacggattct gttgtggttt gaatgcagta ccagtgttct 180
cttcagagcaa agtagacctg ggtcactgta ggcataggac ttggattgct tcagatgggt 240
tgctgtatca tttttcttct tttttcttct ctggggactt gtttccatta aatgagagta 300
attaaaaatcg cttgtaaatg agggcatata agcattttgca acaaatattc aaatagaggc 360
tcacagcggc ataagctgga cttgtgcgcc actagatgac aagatgttat aactaagtta 420
aaccacatct gtgtatctca agggact 447

```

```

<210> SEQ ID NO 229
<211> LENGTH: 337
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(337)
<223> OTHER INFORMATION: AffymetrixID: 209861_s_at

```

```

<400> SEQUENCE: 229
aagtaataac ttgatggctc tgaagaatct gtgtgacttg ggcattgtag atccatatcc 60
accattatgt gacattaaag gatcatatac agcgcaattt gaacatacca tctgtttgcg 120
tccaacatgt aaagaagttg tcagcagagg agatgactat taaacttagt ccaaagccac 180
ctcaacacct ttattttctg agctttgttg gaaaacatga taccagaatt aatttgccac 240
atgttgtctg ttttaacagt ggacccatgt aatactttta tccatgttta aaaagaagga 300
atttggacaa aggcaaaccg tctaattgtta ttaacca 337

```

```

<210> SEQ ID NO 230
<211> LENGTH: 196
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(196)
<223> OTHER INFORMATION: AffymetrixID: 209967_s_at

```

```

<400> SEQUENCE: 230
ttcctaaaaa tgcttcaactg tacgtagtta agtcgtagct ataacttcaa attttttaa 60
agggacaaac tgtaaaaaat gtgtgtattc ttaaaatgca atatttgtta ggcttgttcc 120
aatgccacat acttgacgt cccattctat gtgtcatcaa tagtgtccta tgcaataaat 180

```

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tatttgcagg tcttta 196

<210> SEQ ID NO 231
<211> LENGTH: 535
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(535)
<223> OTHER INFORMATION: AffymetrixID: 210027_s_at

<400> SEQUENCE: 231

tgggatgaag cctttcgcaa gttcctgaag ggcctggctt cccgaaagcc ccttgctgtg 60
tgtggagacc tcaatgtggc acatgaagaa attgaccttc gcaaccccaa ggggaacaaa 120
aagaatgctg gcttcacgcc acaagagcgc caaggcttcg ggggaattact gcaggctgtg 180
ccactggctg acagcttttag gcacctctac cccaacacac cctatgccta cactttttgg 240
acttatatga tgaatgctcg atccaagaat gttggttggc gccttgatta ctttttgttg 300
tcccactctc tgttacctgc attgtgtgac agcaagatcc gttccaaggc cctcgcgagt 360
gatcactgtc ctatcacctc atacctagca ctgtgacacc acccctaaat cactttgagc 420
ctgggaaata agccccctca actaccattc cttctttaaa cactcttcag agaaatctgc 480
attctatttc tcatgtataa aacgaggaat cctccaacca ggctcctgtg ataga 535

<210> SEQ ID NO 232
<211> LENGTH: 358
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(358)
<223> OTHER INFORMATION: AffymetrixID: 210053_at

<400> SEQUENCE: 232

aacgtagtta ctgtatggca ctcaaaaact atgttaaagt atccactaac tttttttttc 60
ttggcccatg attaatggaa tgtatgtaac taggtagggt tcctttctta gatctagagg 120
aagtacagcc acccactgac atctgaattt atatacctgt tgagttttga gtgcacccaa 180
acactcgata aaccagggtga agaaatttag cttccatggt ctacttcagc taaaacagct 240
acatacaacc tagtacactt gaagtcagac agacatttca gttgcttacc tccagtactg 300
agccttgctt tgggaaacta aaagatttag accaagtcac tgccagtttt tgcctttg 358

<210> SEQ ID NO 233
<211> LENGTH: 391
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(391)
<223> OTHER INFORMATION: AffymetrixID: 210172_at

<400> SEQUENCE: 233

ggtaaatata cgttctgcat ccaaatgcac tttgagattg ttacgattta tttgagcaa 60
gatctgcatt ttttgaaagt ttgagattgt agttatcttt tttgagatga gatactttca 120
cgactttggt atcatctgtc agtttttgcc cagtgaagtc tgcatttgca gctccttggt 180
ttggtctggt cgtaactgca gtgttctcca tgagtatcag gaaggtaggg tttcacttag 240

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gagtaagaac agtccccagt ccagcagcca ccccttttcag ctgtgtgtca ttgccagttg	300
atgaggtgag tgtcatctgc ctctctggac agggccccagt ggagaacacc gcaggtactg	360
taaaccaagt acttttcaca gcgtggcctt t	391

<210> SEQ ID NO 234
 <211> LENGTH: 164
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (105)..(105)
 <223> OTHER INFORMATION: n is a, c, g, or t
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(164)
 <223> OTHER INFORMATION: AffymetrixID: 210766_s_at

<400> SEQUENCE: 234

ggttccatca atggtgagca ccagcctgaa tgcagaagcg ctccagtatc tccaagggtg	60
cccttcaggca gccagtgtga cactgcttta aactgcattt ttctnaatgg gctaaaccca	120
gatgggtttcc taggaaatca caggcttctg agcacagctg catt	164

<210> SEQ ID NO 235
 <211> LENGTH: 381
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(381)
 <223> OTHER INFORMATION: AffymetrixID: 210949_s_at

<400> SEQUENCE: 235

acaaagtccg caccatgctg gttaggaaga tccaggaaga gtcactgagg acctacctct	60
tcacctacag cagtgtctat gactccatca gcattggagac gctgtcagac atgtttgagc	120
tggatctgcc cactgtgcac tccatcatca gcaaaatgat cattaatgag gagctgatgg	180
cctccctgga ccagccaaca cagacagtgg tgatgcaccg cactgagccc actgcccagc	240
agaacctggc tctgcagctg gccgagaagc tgggcagcct ggtggagaac aacgaacggg	300
tgtttgacca caagcagggc acctacgggg gctacttccg agaccagaag gacggctacc	360
gcaaaaacga gggctacatg c	381

<210> SEQ ID NO 236
 <211> LENGTH: 545
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(545)
 <223> OTHER INFORMATION: AffymetrixID: 211458_s_at

<400> SEQUENCE: 236

aaatagcatt aaactggaat tgacagagtg agttgagcat ctctgtctaa cctgctcttt	60
ctctctgggtg ctctctcatc caccctacc ttggaattta ataagcttca ggcatattcca	120
attgcagact aaaaccatt ctaccatctc ctctagtatt ttccatgtat caggacagag	180
atgtcttatg tagggaaggg gcaggtatga agtgaggtag attatctata cctctcactc	240
attcaggatt ctctgtccca tgctgtgtgc ccttcattct cacactcaca ggaatgctat	300

-continued

```

gtgatggcca gctgcttccc ttcttggtta tccactgcag ctgctagtta gaaaggtttg 360
cagggatgac ttttagtaaa tcatggggat tttattgatt tattatcact tataggattt 420
tgtgggggtgg gagtggggag caggaattgc actcagacat gacatttcaa ttcattctctg 480
caaatgaaaa gggttcttcc tcttggggga aatctgtgtg tcagttctgt cagctgcaag 540
ttctt 545

```

```

<210> SEQ ID NO 237
<211> LENGTH: 311
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(311)
<223> OTHER INFORMATION: AffymetrixID: 211546_x_at

```

```

<400> SEQUENCE: 237

```

```

gggagttgtg gctgctgctg agaaaaccaa acagggtgtg gcagaagcag caggaaagac 60
aaaaagaggt gttctctatg tagtggctga gaagaccaa gagcaagtga caaatgttgg 120
aggagcagtg gtgacgggtg tgacagcagt agcccagaag acagtggagg gagcaggag 180
cattgcagca gccactggct ttgtcaaaaa ggaccagttg ggcaagaatg aagaaggagc 240
cccacaggaa ggaattctgg aagatatgcc tgtggatcct gacaatgagg cttatgaaat 300
gccttctgag g 311

```

```

<210> SEQ ID NO 238
<211> LENGTH: 482
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (377)..(377)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(482)
<223> OTHER INFORMATION: AffymetrixID: 212199_at

```

```

<400> SEQUENCE: 238

```

```

attttgtgt tacctttgtg acctgattgt tttttggaac acgtcaagac gtgggatcag 60
aatcttccaa cttagaggt gcaatggaag acactacgct acttggttga gcttggtgaa 120
gaatgtatta atgagactgc ttgcataaa actgggaaga aagagaagac agttggagat 180
ggaagatggt ttgtatata ttttggaaact ttagttcctc tgtgagacga aagaggagag 240
ctatgttttg tgtcacattg tctgatatat attgtgtaac ctgtcaggtg agttgattta 300
gacaacatag ctgacctttt atgacaaggc agtttgaata gggactattg taataacctc 360
acacattata ggggcancag agaatggcat ggaagagaca gtctacagag agctttaaga 420
ggcgggagaa aggaaaagac attatcaggg cctggaaagt ctctccaggt tcatcagggt 480
ag 482

```

```

<210> SEQ ID NO 239
<211> LENGTH: 419
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (249)..(249)

```

-continued

<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(419)
<223> OTHER INFORMATION: AffymetrixID: 212224_at

<400> SEQUENCE: 239

```
acagtgttct ctaatgttac agatgagatg cgcattgcc aagaggagat ttttgacca    60
gtgcagcaaa tcatgaagtt taaatcttta gatgacgtga tcaaaagagc aaacaatact    120
ttctatggct tatcagcagg agtgtttacc aaagacattg ataaagccat aacaatctcc    180
tctgctctgc aggcaggaac agtgtgggtg aattgctatg gcgtggtaag tgcccagtgc    240
ccctttggnt gggattcaag atgtctggaa atggaagaga actgggagag tacggtttcc    300
atgaatatac agaggtaaaa acagtcacag tgaatatctc tcagaagaac tcataaagaa    360
aatacaagag tggagagaag ctcttcaata gctaagcatc tccttacagt cactaatat    419
```

<210> SEQ ID NO 240
<211> LENGTH: 438
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (203)..(203)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(438)
<223> OTHER INFORMATION: AffymetrixID: 212388_at

<400> SEQUENCE: 240

```
gtgacagtta tgacaggctt accttggaa agttgtcatt tttactgcca attttttgga    60
tgaagatggt ttataaaacc tttcaaatg gtctgcaaac agagcaggaa ttgcacaatt    120
aactcaataa tgctgtgtgt tctcaagaag ctcccttagt gaggccgac ttaagatggc    180
cgattctgcc cgttgaaggc atncttggga aagaaaacaa gcattcccagc gggcatctca    240
ccacgacttc tcctggagtc ctacacaggt cactgacaac tacagtcagt ttaggaact    300
agagtgcctg atcatcagac ttacctgtc ctgccccacc ttccctgcta acatcgaggt    360
gtgtgcagtt accttctgag cttggaacaa gcagactgga attttcctct gctacctctt    420
gtgtataaaa tcttggtt    438
```

<210> SEQ ID NO 241
<211> LENGTH: 546
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(546)
<223> OTHER INFORMATION: AffymetrixID: 212591_at

<400> SEQUENCE: 241

```
ggcccagatt gcagatggat ttcgtattag agttgatctc gcattctgaga cctcatctag    60
agacaagaga tcggtttttg tggggaatct ccctataaaa gttgaagaat ctgccattga    120
gaagcacttt ctggactgtg gaagtatcat ggccgtgagg attgtgagag acaaaatgac    180
aggcatcgcc aaagggtttg gctatgtgct ctttgagaat acagattctg ttcattctgc    240
tctgaaatta aataattctg aactcatggg gagaaaactc agagtcatgc gttctgttaa    300
```

-continued

taaagaaaaa tttaaacac aaattcaaa tccacgattg aagaatgtca gtaaacctaa	360
gcagggactt aattttactt ccaaaactgc agaaggacat cctaaaagct tattttattgg	420
agaaaaagct gttctcctta aaacgaagaa gaaaggacag aagaaaagtg gacgcctaa	480
gaaacagaga aaacagaaat aacaaccagg aactgctttt tcttttcttg ctgagtactg	540
ctaata	546

```

<210> SEQ ID NO 242
<211> LENGTH: 560
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (49)..(49)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (66)..(66)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (68)..(68)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (72)..(72)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (82)..(82)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (121)..(121)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(560)
<223> OTHER INFORMATION: AffymetrixID: 212696_s_at

```

```

<400> SEQUENCE: 242

```

ctgaaggagt gtccctctc tatgtgaaaa gaaaattggt ttattcttnc attctgactt	60
tttaancngt tnggctcact tnccagttag tttgaatgaa aataataatt ttctacttgg	120
nagttgaaga gggcagaatc cgcagctctc atcattgtga tgtgtagcat gtctgcctc	180
tgactggaca tcattgccat taactttctt ctgggcatca cggcaatgtc acgatgccca	240
gacttggagc aaggcaacct tggagtcagt ccaactcataa aatatggtaa caccatttt	300
aaaatttaag ttttgcctt aaagacaact tcagtgggta attataaaag ttgtgttact	360
tcgtcctaaa ttaaattgat agaaagattt aaaaatgtgt tttgtttcta ctattcagaa	420
actgcgaact agggaaaggt tggatgaaa aaatgtcttt ccttttttca atgtacatag	480
ttcaactctt tctttgttac atttaaaacta tatccatgga tatcagctcg ctttggactc	540
ctctgctagt gttacagatg	560

```

<210> SEQ ID NO 243
<211> LENGTH: 516
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (47)..(47)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:

```

-continued

<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(516)
<223> OTHER INFORMATION: AffymetrixID: 212709_at

<400> SEQUENCE: 243

tgcaaattaa gactcacctt cactttccaa aatagctgag ggttgtnngc ttgtgttagc 60
tgaccaccaa aagcagtcac tgcaaatctt ttaattcttc cctatcacct ttgtatttt 120
aatgcaatta ttttggtcca gaactgacct gtattttctg tattgtacac aaaagctaata 180
aattttgtgt actttttatt tattttggag gttttatatg atcttcaatt gagtattaaa 240
taatttgcct agattaagcc taaaatgatg accagctaata taaagaagat attttgaatc 300
tggttctgag ctaaagtgtg gttaattctt agctaagaaa aaattggaaa tccatcatct 360
atattagcaa cagattctca gagtaaatg ttaacttcta tgatttatga taatcaagct 420
ggacttgatc atacaagtta gtctcataat gtattggacc aaaatgtaaa ctccattggt 480
cagatttaga agcattcatg ctcaagtt ttggga 516

<210> SEQ ID NO 244
<211> LENGTH: 428
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(428)
<223> OTHER INFORMATION: AffymetrixID: 212714_at

<400> SEQUENCE: 244

aacttttaggc ttttgggcat atgctagtct gagcttccga aaagatacat atatgtttcc 60
cttttcatta gctgaatgag gatattttaa gaagttgaaa gagaatttat tttcaagttg 120
tgagtaaatc ctcccttgaa attcacctga ttattagata acttaaagtt tatttttaaa 180
agctgacaac tttttatgaa tcttcgagtt gacagttcct aaaagcgtaa ctccagatatt 240
aatgggctgt gtattaaatg gttttatatt cagttttgca gcacagaaca ctgttgaaat 300
atccatatca acttgatttt tttaacctaa ttcaggtgtc ctttgcattc cttaaatgtt 360
gggggtgggg gtcagagcca gttatccggc ttctgttttg tcgattgctt agatttgttc 420
ctgttgtc 428

<210> SEQ ID NO 245
<211> LENGTH: 489
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(489)
<223> OTHER INFORMATION: AffymetrixID: 212893_at

<400> SEQUENCE: 245

aattgtcctt aattaccaac agtgaagcac tacaggaggc aactgtggca ttgcttcctt 60
aaccagctca tgggtgtgtga atgttataaa attgtcactc agatatattt tttaaatgta 120
atgttatata agatgatcat gtgatgtgta caaactatgg tgaaaagtgc cagtggtagt 180
aactgtgtaa agttttctaata tcacaacatt aattccttta aaatacacag ccttctgcct 240
ctgtatttgg agttgtcagt acaactcatc aaagaaaact gcctaataata aaaatcatat 300
atatggtaat aatttcctc tttttagtgc tgcacaagat ccataaaaaga ttgtattttt 360

-continued

```

attactatattt aaacaagtga ttaaatttag tctgcacagt gagcaagggt tcacatgcat    420
tctttttatac tgctggattt tgttgtgcat catttaaaac attttgtatg tttcttctta    480
tctgtgtat                                           489

```

```

<210> SEQ ID NO 246
<211> LENGTH: 417
<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, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(417)
<223> OTHER INFORMATION: AffymetrixID: 212989_at

```

```

<400> SEQUENCE: 246

```

```

gtcagagcct gttcacatat tgtgatcagg tagcaatgac atgtaccact taaattatatt    60
tatcgctgat ttggtagttc nattttaact actcaatgaa aacagccatg aatatctttt    120
cttaaagaga gttttgaaaa tgatcactta cctaaaactt gaaagctatg aattagttat    180
ccatactctc atgacaattt tgttggtgaa caacaaaaaa gagatctatt tctttaaaag    240
atatttgtgc agaaactgca tgtaactcta agttttactc ctaacataca tatgtttggg    300
gaagtattct attctatact tgccaatgtg gagaacaaaa tagtttttta agaatgaaga    360
agtatatata tccattctgt attttacgtg cagcagaatt atcttccgta ggattttt    417

```

```

<210> SEQ ID NO 247
<211> LENGTH: 448
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(448)
<223> OTHER INFORMATION: AffymetrixID: 213410_at

```

```

<400> SEQUENCE: 247

```

```

gacaaattac ggttgagttc tgtggcttct tcaactgaag tgctaacatc agaatcaaac    60
ttaaagcttc cactatttat gtctttgaga agtatgtagt acctcggtat taacagacct    120
gctgtgatgc agttacactt tcacgtatatt ttgaagtatg tcaagctaca cgggtctaag    180
atatgattat tttggataaa atgttacttt ggtcaagaga acttttatcc agatgacatt    240
acaggttcaa gtgggttaag gagacctcct gtacatctac agtgtttccct tttaaattgt    300
ccagaaaaaa ggtgtgttct tcataagctt cagtgcagga tttttcaaag acgagctgtt    360
gtgcaatttg ctgtatttaa tgcattgtct gaaaggattc acttttgact ttatatgaca    420
gttgatcaag aacagggtact acccctttt                                           448

```

```

<210> SEQ ID NO 248
<211> LENGTH: 234
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (81)..(82)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(234)

```


-continued

<223> OTHER INFORMATION: AffymetrixID: 213515_x_at

<400> SEQUENCE: 248

```

ggatgatctc aagggcacct ttgccagct gagtgaactg cactgtgaca agctgcatgt    60
ggatcctgag aacttcaagc nncctgggaa atgtgctggt gaccgttttg gcaatccatt    120
tcggcaaaga attcaccctc gaggtgcagg cttcctggca gaagatgggtg actggagtgg    180
ccagtgccct gtcctccaga taccactgag ctactgccc atgatgcaga gctt          234

```

<210> SEQ ID NO 249

<211> LENGTH: 407

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(407)

<223> OTHER INFORMATION: AffymetrixID: 213528_at

<400> SEQUENCE: 249

```

aactgcattc aagggagggt ccaaagaaat tcactttcaa gattataaca gtatggtgat    60
tgatgaagta accttaccta atgtagtagc taactccact ttggaagatg aagaaatga    120
tgtaaatgag ccagatgtga aaagatgcag gaaacaaaa gtaacacaac tatataaatg    180
ccgatttttt tctggtgagt ggtctgagtt ttgtaagctt gtactaagta gtgaaaaact    240
ttttgtaaaa tatgatctca ttctcacctc agaaccatt tacaaccag attattatag    300
taatttgcac cagactttcc ttagactggt aagtaaaaat ggacgtgtac ttttgccag    360
caaagcacat tattttggtg taggtggagg tgttcctc tttcaga          407

```

<210> SEQ ID NO 250

<211> LENGTH: 406

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(406)

<223> OTHER INFORMATION: AffymetrixID: 213604_at

<400> SEQUENCE: 250

```

gcaatgtcag tatccatttt ggcacataaa gatttttgat gagecctggt tgcataagagc    60
cagatgtttt cccctcccc aagagtatct acatcaggga tgtgacttgg tgcgaagagt    120
caggggaaag aggaaaaacc caatttctaa atgacctcct tgcccagctt actaaaatgg    180
ctgcagagca gacacaggat gaatttgaac ctgacacagg atgaatttga acctttggtc    240
tcatttatgg aaaaacttgt gcaatttttt ttctgtgcta cactacatac aaatcaccaa    300
attacaaatt acccttttgt gatccttggt gtactgagca gtttctttgg ggctttttct    360
ttctgggaag cgggagggaa aggagcaagg tgtcatcctg ctcttc          406

```

<210> SEQ ID NO 251

<211> LENGTH: 466

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (85)..(85)

<223> OTHER INFORMATION: n is a, c, g, or t

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(466)

-continued

<223> OTHER INFORMATION: AffymetrixID: 213619_at

<400> SEQUENCE: 251

```
aatcaaggcc tcagaatttc atacaacac caagaccaa atcctaagta ttggtattgc      60
gtctcaaatt tttccatta acttnaaaa aaaaaaaagc ttaaaacttac gtgccttaca    120
ggttattaaa tgaaactaga attaacaac atgccaaaat gtttcacttt taatagtaga    180
cacagctcct atattgtttt acaaaaaaat aaaagcatgt ctttcaacat gcatccaaaa    240
cagtgttcaa tttaacgtgg caaagggcaa catttaacat aattcaactg cttttaccta    300
aatacgctta ctgcttaagt acatcctata actaacttga gaaaagctgg aacttaagtt    360
taacagttat agtttactca gcttcactgt tacatcctag atgagtattg tattcaaaaa    420
tactgggcct taagtcttca taacaatcct gatttccact tagagt                    466
```

<210> SEQ ID NO 252

<211> LENGTH: 474

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(474)

<223> OTHER INFORMATION: AffymetrixID: 213655_at

<400> SEQUENCE: 252

```
cttcaacgct aacctgcttc agtgggagag taaagtaggc aagaatgagc agccacggat      60
tgttgaactg ttaccagcac catgcttttc agcaacattt cagcggaggt ggaacatttt    120
tttacagcaa aaccattaca acgaagtccc tcccaaacc acctttaacc atctcaagct    180
aacacccaat tacttgcaaa cactggtata aaacacagtt taaacaatta gaaaaatgaa    240
aactgatacc acttatgcct ctatagtgtg attaacctct ctcttagatg cttgcatcac    300
ctataagtct aatggctttc aaatgtaatt tccatttgc t aatgggtgac ttgccacatc    360
tggcacggag acgacacagt aatgctgaaa aagcctctat gtagtcctgt tagtgtctta    420
aagaacctaa aagctgggac cagtaaaatc cacagaaatt cactcttgcc tttta                    474
```

<210> SEQ ID NO 253

<211> LENGTH: 302

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(302)

<223> OTHER INFORMATION: AffymetrixID: 213743_at

<400> SEQUENCE: 253

```
ttgtgtgagc tattcaaact cttcaacccc tgaacagggt attagcttc caaaataatg      60
atggggataa atatggaaat cctttttaag ttgtatttcc attaaacaaa aacctttata    120
attcactact tcatgaattt gctttatcca totcatttgc ataacagttc atctgtctgg    180
tcccattagg ctctacaaa gaaagactct gatgagtgga cattattact gtgactcttg    240
taagtagcca taaataaacc aaaatagtat caaatttagg tatgaaattc cacatgtgca    300
aa                                                    302
```

<210> SEQ ID NO 254

<211> LENGTH: 549

<212> TYPE: DNA

-continued

<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(549)
<223> OTHER INFORMATION: AffymetrixID: 213788_s_at

<400> SEQUENCE: 254

gtttcagtc	tttccggact	aactgtgaca	acgcgtgagc	agggagcacc	gtgcgagtct	60
ccgggagggg	atcctcctgg	ggcccagaga	ctcctccacc	cctggggagg	gcagacaggc	120
tcgggagggg	ctggccaggc	cactggaggc	tggcagggag	caggcatgtc	cacccgcaag	180
cctgggaggc	taactctggc	attcctggcc	ggagccgcca	tgtcattgg	tgggccagtt	240
tgggacatcc	ccgtactcaa	agaccatatg	gcagcctctg	ggaaaacaaa	acaaaaacat	300
caccttctat	taaactctgt	atattattat	tttttacaat	agaaagttaa	aatcaagac	360
ttagatttac	tatacathtt	ttctctcaga	ttacaaagtt	tatattatat	aactgggggt	420
ccctaaattg	atttctttta	aaacagtctt	aaagagacca	gaagtgaata	caaaagaact	480
aaacaaaata	aaaaattaga	atgtgctgta	gctgaaagct	gtctatacct	gtaagcctcc	540
aagtttcat						549

<210> SEQ ID NO 255
<211> LENGTH: 576
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (99)..(99)
<223> OTHER INFORMATION: n is a, c, g, or t

<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (101)..(101)
<223> OTHER INFORMATION: n is a, c, g, or t

<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(576)
<223> OTHER INFORMATION: AffymetrixID: 213872_at

<400> SEQUENCE: 255

aaactggtca	gctagagatt	cttttttctt	tctaagctga	gcacgtagtc	tgttcagagc	60
ttgtttcttc	cgggagtttg	ggtcccccac	tttgaatnc	nggtggtact	aaagcctttg	120
gaaattgtca	ctaaactatg	ggcacttttt	cttaagactc	aagtacaaca	gaaacaagtc	180
attttttttc	ctgctaatat	gattgattag	cgaaaatcac	gactataacc	caaaaactgc	240
accttctgtc	aatattagca	gactgtcata	ttacagggtc	aagaaacaaa	agctgctgtc	300
cagtcatggt	tggacaataa	cgtttggggg	cagacgggaa	aaaggaggga	aagaaaggaa	360
agaaagagga	gaaaataact	aactttcttg	aaaacacatt	tggcttaact	gccaaaataa	420
aggctttgcg	gagaaatgaa	aagcctataa	tcaggattta	ggtgtgcaat	aaaacacagc	480
tgacaccaga	ccaatcccta	aaatccatcc	ggattttccc	cccttttttag	aaaagggatt	540
aagggaacagg	gagggggaag	tgtgatcctt	gcttttc			576

<210> SEQ ID NO 256
<211> LENGTH: 380
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(380)

-continued

<223> OTHER INFORMATION: AffymetrixID: 213979_s_at

<400> SEQUENCE: 256

```

aaatggttac agtcacaaac atgatttttaa ccaaaatatt gctagcctac cacatcagca      60
ggacggcact ggtgcaggcg gggacgtgc caccctccac gtccccagga cagacgtcga      120
tgggcagcgg gcacgtctgg caccgcccaa gcttttcctt ttggagctgc ttcgtgatgc      180
cgtcttcatt tggaacaagg gggggttcat gccaaaatta ggaaaaacag cctttgtttt      240
gtttttctaa attattctaa aaataagaca agcaggtaga aaaaacaatg cactgtgtgg      300
cataaaaaga aaaacgggaa ggattcattg tcctgagaag tttgccaact gcctcattct      360
ggggcacggt ccaacataca                                     380

```

<210> SEQ ID NO 257

<211> LENGTH: 371

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(371)

<223> OTHER INFORMATION: AffymetrixID: 214257_s_at

<400> SEQUENCE: 257

```

attataacct gggcctgcct ttgttctcat gaagccaggg gcctctccat atcctatact      60
tgctcttacg ctaataacaa accaaatgct gcaaaataaa agtaataatg acccaaaacta      120
atttaagtct ttgtttaag gagtaaatga gagaaacatt ttagcttctt aatcaaggag      180
tgctataatt tcaaggcatc ttaataaat tcacttacct taaagcaatt gtgcaataag      240
caaattataa aaggaaaaca acaaaggta actttctaca ggggccaata gacaagatct      300
gtggagcaca gcaattaacc ttcacatact ggagtcttgt ttaaaaggcc atcaaaaact      360
cagattactg a                                     371

```

<210> SEQ ID NO 258

<211> LENGTH: 244

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (74)..(74)

<223> OTHER INFORMATION: n is a, c, g, or t

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (93)..(93)

<223> OTHER INFORMATION: n is a, c, g, or t

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (164)..(169)

<223> OTHER INFORMATION: n is a, c, g, or t

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (171)..(172)

<223> OTHER INFORMATION: n is a, c, g, or t

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (176)..(176)

<223> OTHER INFORMATION: n is a, c, g, or t

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (180)..(181)

<223> OTHER INFORMATION: n is a, c, g, or t

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(244)

-continued

<223> OTHER INFORMATION: AffymetrixID: 214414_x_at

<400> SEQUENCE: 258

```

tcaacttcaa gctcctaagc cactgcctgc tggtgaccct ggccgcccac ctccccgcgcg      60
agttcaaccc ctgnngtgca cgctccctg ganaagttcc tggtttctgt gagcaccgtg      120
ctgacctcca aataccgtta agctggagcc tcggtagccg ttcnnnnnnc nngctnggcn      180
ntccaacggg ccctctctcc ctccctgcac cgcccttcc tggtctttga ataaagtctg      240
agtg                                           244

```

<210> SEQ ID NO 259

<211> LENGTH: 519

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (118)..(118)

<223> OTHER INFORMATION: n is a, c, g, or t

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (125)..(125)

<223> OTHER INFORMATION: n is a, c, g, or t

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (133)..(133)

<223> OTHER INFORMATION: n is a, c, g, or t

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (136)..(136)

<223> OTHER INFORMATION: n is a, c, g, or t

<220> FEATURE:

<221> NAME/KEY: misc_feature

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

<223> OTHER INFORMATION: AffymetrixID: 214696_at

<400> SEQUENCE: 259

```

gagtatacat cgggtgcaggc ttcctggatg acagttgggt gatatgtgtc atgtggccta      60
aaagcctcca tgtcatttga cctacgaatt ctatctttgg gaatttatcc taagaaanta      120
cttanggatt tanttngtga taagatgttc atcccagcat tgcaatggag aaaaatggga      180
agcaatggtt tggttgggaa tttattcctt ttctgctgta acgaaagttt gcaatagggg      240
attgcttaag taaattattg tatctccatc cagatggtgg agtaccgcgc agacattaaa      300
agtcattgta aagaacatct gactgaaaga aaaatgctcc ttgaatatta aaaggttgta      360
aaaaatgtgc atgttatgtg atttcaattt tgttttttaa aatatgggtg tatgcttgta      420
tacgtagagc agataaaaaa gacggaaggc atactaaaaa atgttgagtg gttatctttg      480
tatggtggaa caaagtcact gtaattttca tctttggtt                                519

```

<210> SEQ ID NO 260

<211> LENGTH: 399

<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, or t

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (48)..(48)

<223> OTHER INFORMATION: n is a, c, g, or t

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (75)..(75)

-continued

```
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(399)
<223> OTHER INFORMATION: AffymetrixID: 214933_at

<400> SEQUENCE: 260

aatctttcct ttccctgatg aagacagctg gtggccgagt gcggaanga agccagaagg      60
aaccagaatc ccagngccct acaccacca ccagacacac tcacaccac acacgttctc      120
agacacacac aagagtgcct gccggttata ccaaacccta ctattactgc ctgcagaaat      180
caatttaaaa aaataataat aacaataaac aattttaaaa aggacaaaaa aattaatgat      240
tgagaaaaga ggcatttttt tctgacattt ggtcctgcctt gaaacaacaa aagaagaaga      300
aaaacccacc atcaccaccg attcctttgc ttcttttttc cttttttcct accttgtttg      360
aaaaccgtgg gcttgggact gtgaattatt gcatgacat                               399

<210> SEQ ID NO 261
<211> LENGTH: 202
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(202)
<223> OTHER INFORMATION: AffymetrixID: 215043_s_at

<400> SEQUENCE: 261

cagtcctttcc cagggaaactc cgatgaagtg ttccaacaaa atgagcgagt gaaccaagaa      60
gaggatgaca ttagatccag gagatacaac agaggagata atctccagga tgcctgtgaa      120
gaaagatccc tggatcccg gatgattata ggacaagttg ttcataatcc agcaggccag      180
aagacttcca gggaaactca tt                                              202

<210> SEQ ID NO 262
<211> LENGTH: 501
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (37)..(37)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (437)..(437)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (452)..(452)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(501)
<223> OTHER INFORMATION: AffymetrixID: 215933_s_at

<400> SEQUENCE: 262

ggacagttcc tgtgatcaga ggcaagattt gcccagnгаа cagaataaag gtgcttcttt      60
ggatagctct caatgttcgc cctccctgc ctcccaggaa gaccttgaat cagagatttc      120
agaggattct gatcaggaag tggacattga gggcgataaa agctatttta atgctggatg      180
atgaccactg gcattggcat gttcagaaaa ctggatttag gaataatggt ttgctacaga      240
aaatcttcat agaagaactg gaaggctata taagaaaggg aatcaattct ctggtattct      300
```

-continued

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ggaacacctaa aaatatattgg tgcactgctc aattaacaaa cctacatgga gaccttaatt 360
ttgacttaac aaatagttta tgtactgctc ttaggttggt ttgataaagt gacattatag 420
tgattaaatt ctttcnctt taaaaaaca gntagtggtt ttcactattt ataaatagga 480
ccttcttgaa cgacttttct g 501

```

```

<210> SEQ ID NO 263
<211> LENGTH: 502
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(502)
<223> OTHER INFORMATION: AffymetrixID: 216199_s_at

```

<400> SEQUENCE: 263

```

ctggagtctg ggggtgtgtg tcatagagat ggtgactggc aaggtttgca cagatgaaga 60
atgaagccta gtagaatatg gacttggaaa attctcttaa tcactactgt atgtaatatt 120
tacataaaga ctgtgctgag aagcagtata agccttttta acctccaag actgaagact 180
gcacagggtga caagcgtcac ttctcctgct gctcctgttt gtctgatgtg gcaaaaggcc 240
ctctggaggg ctggtggcca cgaggttaaa gaagctgcat gttaagtgcc attactactg 300
tacacggacc atgcctctg tctcctcgt gtctcgcgcg actgagaacc gtgacatcag 360
cgtagtgttt tgacctttct aggttcaaaa gaagttgtag tgttatcagg cgtccatac 420
cttgttttta atctcctgtt tgtagtgctg actgactgtg aaacctttac cttttttgtt 480
gttggtggca agctgcaggt tt 502

```

```

<210> SEQ ID NO 264
<211> LENGTH: 158
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(158)
<223> OTHER INFORMATION: AffymetrixID: 216202_s_at

```

<400> SEQUENCE: 264

```

gttcacaaaag agttttggtg cttctggagg atatattgga ggcaagaagg agctgataga 60
ctacctgcga acacattctc atagtgcagt gtatgccacg tcattgtcac ctctgtagt 120
ggagcagatc atcacctcca tgaagtgcac catggggc 158

```

```

<210> SEQ ID NO 265
<211> LENGTH: 490
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(490)
<223> OTHER INFORMATION: AffymetrixID: 216996_s_at

```

<400> SEQUENCE: 265

```

gctgcatact ttggatactt gtctaaaact tgatgatact gtctatctga gggacatagc 60
cttgtcactc ccacagctgc cgcgggagct gccatcgta catacaaatg caaagggtggc 120
agaggtgctg agcagccttc tgggaggtga aggacacttc tcaaaggatg tgcacttgcc 180
acacaattat catattgatt ttgaaatcag aatggacact aacaggaatc aagtgtctacc 240

```

-continued

```

actttctgat gtgatacaac ttctgctaca gatattcaaa gagtagctgt gctatgtgtt    300
tccagatctg cttattgttt gggttcaagc caccacagag gattccttgc tatgaaaatg    360
cggcatttga atgcaatggg ttttcatgtg atcttggtca ataactggga gatggacaaa    420
ctagagatgg aagatgcagt cacatttttg aagactaaaa tctattcagt agaagctctt    480
cctgttgctg                                     490

```

```

<210> SEQ ID NO 266
<211> LENGTH: 374
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (315)..(315)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(374)
<223> OTHER INFORMATION: AffymetrixID: 217554_at

```

```

<400> SEQUENCE: 266

```

```

aatgctcacc aaattcacag gaaagaagtg cctagggtgat catttactgc tatttactgc    60
ttcctgggtat ggagcaaaat tgccctctgg taggtaacta catttctaata tagtatgaaa    120
ggttctacta ttttcttttc ttttgcttat tcccccttaa gcacaatttg cagaccctac    180
ttctatttaa ctgatcatac ccttttaaat gccttgteat catttttcat agttcctgca    240
tcttagaaaa aataaaaaat catttaaaat attccttggt gtctagaaaa gaaaatttct    300
ctaacaatag agatnatcat tttgctttct cacttaagct gatctgaatg atgatttggg    360
actgccttta tgag                                     374

```

```

<210> SEQ ID NO 267
<211> LENGTH: 462
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (119)..(119)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (203)..(204)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (286)..(286)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(462)
<223> OTHER INFORMATION: AffymetrixID: 217682_at

```

```

<400> SEQUENCE: 267

```

```

cacgaggtea atttatggtt atcaaatagg tttttttttt tttttttgag actgagtgtc    60
gctctatagc ccaggctgga gtgtagtgct cactgcgact tccgcctcct gggttcaant    120
gattctcgtg cctcagtcct ccgagtagct gggattgtag gcgcctgccca ccacgcccag    180
ctaatttttg tatttgtagt agnnatgggg tttcatcatg ttggcgaagc tggctctgaa    240
cacctgacct caagtgatct gccttagcct cactgcttgc ccctangtgg tgggattgca    300
gggtgtgagcc actgtgctgg cctcaaatag tttttatcaa agctacttca attagtgggt    360

```

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agcaaggctt aaagactaat tcagtgcctt attttgacac ttgttcgcaa catgttgctt 420

tttttcctgt gtcctatggg acctagtcac ctgtatgtta ga 462

<210> SEQ ID NO 268

<211> LENGTH: 482

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

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

<223> OTHER INFORMATION: AffymetrixID: 217840_at

<400> SEQUENCE: 268

gccatccagc acgtcatcaa ttatgacatg ccagaggaga ttgagaacta tgtacaccgg 60

attggccgca cggggcgctc gggaaacaca ggcacgcgca ctaccttcat caacaaagcg 120

tgatgatgagt cagtgcgtgat ggacctcaaa gcgctgctgc tagaagccaa gcagaagggtg 180

ccgcccgtgc tgcagggtgc gcattgcggg gatgagtcca tgctggacat tggaggagag 240

cgcggtgtgt ctttctgcgg gggcctgggt catcgatca ctgactgcc caaactcgag 300

gctatgcaga ccaagcaggt cagcaacatc ggtcgcaagg actacctggc ccacagctcc 360

atggacttct gagccgacag tcttcccttc tctccaagag gcctcagtc ccaagactgc 420

caccagtcta cacatacagc agccccctgg acagaatcag catttcagct cagctggcct 480

gg 482

<210> SEQ ID NO 269

<211> LENGTH: 492

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(492)

<223> OTHER INFORMATION: AffymetrixID: 218229_s_at

<400> SEQUENCE: 269

gacctcacag acaaagccat tgctagaaat gtcattccaa tgatcagatc tggaaacagg 60

ctgcataac cacttttctt tctttagac tcagctcacc tgtatattta aactgttctt 120

ggcatcttga aacacctatt tctactcagg tactcattgt cctgttactg attcaccttt 180

ctgatccttt tcaaccaggt ttcccccaag gggggaaatt ttacttaacc tctagtattt 240

gaacaactca atatttgaat tggtgcccga tttgctttta cctgtactgt attcttggtc 300

atctcaaagt gcgtctaaac ccagctactt tgcattccag aagtttccat tccctccaat 360

tccacctaat ttttcatctg tcttagttac tggctctttc ttcattgttt atttctcttg 420

ctttgggagc ttaaaagatt ttacaagacc taattttggg ttccttcctt ggagccatag 480

ttacctgccc aa 492

<210> SEQ ID NO 270

<211> LENGTH: 177

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(177)

<223> OTHER INFORMATION: AffymetrixID: 218356_at

<400> SEQUENCE: 270

-continued

ctgaaatttc catctgggga ttaacttctg tctttctggt gaacaatata gcaattcacg	60
cattcttcaa gcagcaaaag ttcccgaac aattaggga gacgtatggt ctgaatttat	120
ccaggcagtg ggtctgcttt ggtttttgct ggaaatttat atcagtgtct gggctcc	177

<210> SEQ ID NO 271
 <211> LENGTH: 453
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(453)
 <223> OTHER INFORMATION: AffymetrixID: 218432_at

<400> SEQUENCE: 271

gaaactatgt gactcattct gtgaaaagac ttcttgacgt tgtgagttat ttagaaatga	60
tcaaaatttg taattaggct aatccattta gtgattccta atattttgta ctacacagaga	120
actaattgac taaacaactt gaacgctagt ggtttgtcct tagacaatct gtctttgaat	180
ttaaagtctt tatcgctaag accttgactt taaatttttc atcactacaa ccttgaattt	240
aatttcaggt cttcaacatg atgaccttgg atttaattta aagcttcaa cactatgcgc	300
tttatcatat tttcacaga tgcatttttg aaatgtagta tgtaaaagta tgtaacgtgc	360
tgtttattaa caaaagattg ttcacaacat ctcatgtagt ttaaatttgt aaatactgct	420
tctgttttgt ttctccttta tacacttgac tgt	453

<210> SEQ ID NO 272
 <211> LENGTH: 557
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(557)
 <223> OTHER INFORMATION: AffymetrixID: 218589_at

<400> SEQUENCE: 272

gggtaacaat gcctcagaag cctgctttga aaattttcca gaagccacat ggaaaacata	60
tctctcaagg attgtaattt tcatcgaaat agtgggattt tttattcctc taattttaaa	120
tgtaacttgt tctagtagtg tgctaaaaac tttaaccaa ccagttacat taagtagaag	180
caaaataaac aaaactaagg ttttaaaat gatttttgta catttgatca tattctgttt	240
ctgttttggt cttacaata tcaatcttat tttatattct cttgtgagaa cacaaacatt	300
tgtaattgac tcagtagtgg cagcagtaag gacaatgtac ccaatcactc tctgtattgc	360
tgtttccaac tggtgttttg accctatagt ttactacttt acatcgagaa caattcagaa	420
ttcaataaaa atgaaaaact ggtctgtcag gagaagtac ttcagattct ctgaagttca	480
tggtgcagag aattttattc agcataacct acagacctta aaaagtaaga tatttgacaa	540
tgaatctgct gcctgaa	557

<210> SEQ ID NO 273
 <211> LENGTH: 500
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(500)
 <223> OTHER INFORMATION: AffymetrixID: 218604_at

-continued

<400> SEQUENCE: 273

```

tttgttttat tgtatgcgtt gggtttgacg catgaacttg cacagataat gcacgttttc      60
tgggtaagta aacatgatgc acactattct gtaacagaaa gccctattgt gccttacctg      120
tgtgcttttg tgggcacctt gtttatgaag aataaaaaat gatttgttat ctgaagagaa      180
taaattttaa attctcagtt tatgtctcag atgctaactg gtgaaaatat aaatatatat      240
aatatataaa gtaaccagtc ttccgtgatt ttatgtgcat catagtgatt tatctgagct      300
tagtgacccc catcttgtaa cctgttgcaa gagtgaatgt aaaaaatagt tgtggcattt      360
taaaaggctg cctttgatgc agatgcatct ttttcttgct tctaaaacat atttcatgta      420
aacattgtac atttattatt gtaatatata ctattatgca gcttatttta cctgaaactg      480
ttaagccgac caagatccct                                     500

```

<210> SEQ ID NO 274

<211> LENGTH: 558

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(558)

<223> OTHER INFORMATION: AffymetrixID: 218689_at

<400> SEQUENCE: 274

```

cctgggtggt ccacagctga tagtgattgc cttgaataaa ttcaagggca atttattcat      60
ttttactagg gagatagacc ttacagcaa tcaagatatt tttgtccata tccaggttag      120
ctggtaagag gatttttttg gagaaaaaaa atgatattta gaaagttaat ttctaattcc      180
ggaatggaat aaaaacaata tgagtagtgt aatctttagt aaaaagagtt gtataatcct      240
gtagaatttc tcattctgtg gtacaacca ggggtaaact attattccag tagtcagtac      300
acttttctag ataaatcttg agtgaaaacc agcaatttct ttttccttgt ggtctgattc      360
ctttttctaa tccatgaagg ccattctgta gattacattt atcattaatg caagaataaa      420
gacaattcct cctgtcagtt gcgtgaattt tttttaagaa acaaccaggt gaagagttct      480
accatagcaa ggccaatagt tagctttagc tttagaaaat aacagtttgt gaacttactt      540
ccctatattt gcagctgt                                     558

```

<210> SEQ ID NO 275

<211> LENGTH: 385

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(385)

<223> OTHER INFORMATION: AffymetrixID: 218889_at

<400> SEQUENCE: 275

```

gcttgatttc aggttcattg gcttttgctg gatgatccac ctaaagaagt tacctaattt      60
ggccttttaa aaaagggtgt agtgtttatt atagctactt tcaaggaaag tttgaatatg      120
attctagtct ctaaagtctt tcacgttttc tgacattccc tggagggtga ctggggaaga      180
attgctccag ggtagaagaa ccaggcccaa gactttacca ttctgatcta gagacaaagg      240
atactcaatg aggagctttt ttccctcttt ggaacaggta aatgctttt tcttattaat      300
ataattataa aacagtatct tatgtaacag ctattcccat attctaggag tggcctaaga      360

```

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aatgcgtggt tcagtgacta gatta 385

<210> SEQ ID NO 276
<211> LENGTH: 554
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(554)
<223> OTHER INFORMATION: AffymetrixID: 218973_at

<400> SEQUENCE: 276

ctgcaagtga aacctcagcg cctgatggca gctatgtaca catgtgacat catggccact 60
ggtgatgttc tcggtcgagt ctatgctgtc ttgtcaaaga gagaaggtcg ggtacttcaa 120
gaagaaatga aagaaggac agacatgttc atcatcaagg ctgtgctgcc tgttcttgaa 180
agctttgggt ttgctgatga aatcaggaag aggacaagtg gcctggccag cccacaacta 240
gtattcagcc attgggagat cattcccagt gaccccttct gggtgccaac tactgaggag 300
gaatacttgc actttgggga gaaggctgac tctgagaacc aagcccgaa gtacatgaac 360
gcagtacgaa agcggaagg gctttatgtg gaagaaaaga ttgtggagca tgcagaaaag 420
cagaggacac tcagcaaaaa taagtagcta cctactactg gtggattctt ttccttatag 480
tgaatttaaa agtatcatca agggtttaat attgggaaaa tttctttttg ccacattatc 540
tctgtttatt cact 554

<210> SEQ ID NO 277
<211> LENGTH: 262
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(262)
<223> OTHER INFORMATION: AffymetrixID: 219069_at

<400> SEQUENCE: 277

gaatattgta tactgcatcc cctaccacaa tttacacaat cctgtggata gtccctacctc 60
accctggta acctacatga tccttaagct aatggcgaat cacgatgacc ttgtagacat 120
gcacacaact atacctttgt ccaacagatc ataatatatc tgctatccaa ctgggtttac 180
ctgcctaate ctactgattt gggcactgct tgtatagtct ctcaagttca caggaaatgt 240
tgattttcta aggtcctcat tt 262

<210> SEQ ID NO 278
<211> LENGTH: 490
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(490)
<223> OTHER INFORMATION: AffymetrixID: 219093_at

<400> SEQUENCE: 278

tagagaccca tgatcatctta acctaaagg aaatcttatt gcgttatcat aaaattgatg 60
atatcttagg gtcagaattg cccctttttt tattttgaat ggggaagctct cactaaaaca 120
atcctgagat ttcttaattt catggttctt taaatattat aaacacagag tcaacataga 180
atgaaattgt atttgtaaaa atacacacat tggaggacaa gagcagatga ctacttttcg 240

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```

aagtaatgct gctccttctt aaaagtctgt tttcaatcct ggtaaatatta ggggcactgc 300
ggcacctaag aagccttaaa tgagagctaa tccaatttag agagcgatgg tgcagcatt 360
tcggctctgca tatctgtgtg tccgtatctg cgtttgtgtg cgtgtacgtg tgccccctgtg 420
tgtgggcccc gttttcaggc atgtagaata agcatggagt catattgagg aggactcact 480
tcttgaagat 490

```

```

<210> SEQ ID NO 279
<211> LENGTH: 442
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(442)
<223> OTHER INFORMATION: AffymetrixID: 219099_at

```

```

<400> SEQUENCE: 279

```

```

aatggactga ctgaaactcg ctaagggttaa atctgcatca aaatctaacc aatttgagcc 60
tctgaagggg gtgccattgg ctttatattac ttctctctc tgctagtcct gatttggaaa 120
cagttaaaag ccaattttta gctccagtgg aaccatagcc acataaaact ttaatggaca 180
accatataga attaacttat ttgtccaag tacagttggc attttccaga ataattttac 240
cacccctgcta gatgtcatct ctggattgca catggatgat gaaggaaactc agcattgaaa 300
gttgggggat tagtaacctt gttacaacgg tttcttttcc attttagcct attttaatgg 360
ctattggtaa gatactgtat gtttttagta tctcatccag tgcttagaag aaagaatggt 420
ttataattcc cagtacatgt tt 442

```

```

<210> SEQ ID NO 280
<211> LENGTH: 454
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(454)
<223> OTHER INFORMATION: AffymetrixID: 219176_at

```

```

<400> SEQUENCE: 280

```

```

caacaggagg catctccatt tactatgatg agaaaggaag gaagtgtgtt aacatcctga 60
tgtgtctttt gtatctaacc agtgccaaca tccccagtga aactttaaga ggagccagtg 120
tattccaggt taagtggggg aatcagaatg tggaaactaa acaacttctt agtgcaagct 180
atgagtttca gagggagttc acacaaggag taaagcctga ctggaccatt gcacggattg 240
aacactcaaa attattagaa taattttctt ggaaaaatca gcttatggac tttagcagtt 300
gctgtgaaaa actaaggaag aaaaattttg gggtcatttg atcttcactt aatctaagtc 360
tgtgaattac ttttatatta ttttgaaata ctccttgacg tatattggca tgatacagta 420
aaagcatttt ccacagattg ttatcacctt cttt 454

```

```

<210> SEQ ID NO 281
<211> LENGTH: 517
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(517)
<223> OTHER INFORMATION: AffymetrixID: 219243_at

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<400> SEQUENCE: 281

```
tcttctagat tctctctatg ttggcagata atctcccctt gtagcttcca ctcaacttatt    60
cttgcatcca gagtcacaat gatcatctta cccatgtggg ttttgagaaa gaaagatcaa    120
ttctttgttt gcagtgggta atcttagaga tggagatgat tgtagaatta ttcttagatg    180
agtggtcaatt tattaattc cattgtcata taaggagtca aattgtttct tatcatttgt    240
tcattgaaga acagagacct gtctggaaaa tcgatctcta caaattcaat taaataatga    300
tccccaaatg ctgaaaaagt gaaatacagc aattcaacag ataatagagc aatgtttagt    360
atattcagct gtatctgtag aaactctttg acgaacctca atttaaccaa tttgatgaat    420
accagttctt ctctctttct agagaaagat agttgcaacc tcacctccct cactcaacac    480
ttgaataact tattgtttgg caggtcatcc acacact                                517
```

<210> SEQ ID NO 282

<211> LENGTH: 501

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(501)

<223> OTHER INFORMATION: AffymetrixID: 219363_s_at

<400> SEQUENCE: 282

```
tggtcagaaa agcaccattt ttgctgaact tttcagtga aagactggat aaccagattg    60
gattttttca gaaggaactg gaacttagtg tgaagaagac tagagatctg gtagttcgtc    120
tccccaggct gctaactgga agtctggaac ccgtgaagga aaatatgaag gtttatcgtc    180
ttgaacttgg ttttaaacat aacgaaatc aacatatgat caccagaatc ccaaagatgt    240
taactgcaaa taaaatgaaa cttaccgaga cgtttgattt tgtgcacaat gtgatgagca    300
ttccccacca catcattgtc aagttccac aggtatttaa tacaaggctg ttaagggtca    360
aagaaagaca cttgtttctt acctatttag gaagagcaca gtatgatcca gcaaaaccta    420
actacatctc ttggacaaa ctagtatcta ttctgatga aatattttgt gaagagattg    480
ccaaagcatc agtacaggac t                                              501
```

<210> SEQ ID NO 283

<211> LENGTH: 467

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(467)

<223> OTHER INFORMATION: AffymetrixID: 219434_at

<400> SEQUENCE: 283

```
ccatgatcat ggtttactgc gcgtccgaat ggtcaacctt caagtgaag attctggact    60
gtatcagtgt gtgatctacc agcctcccaa ggagcctcac atgctgttcg atcgatccg    120
cttggtgggt accaagggtt tttcagggac ccttggtctc aatgagaatt ctaccagaa    180
tgtgtataag attcctccta ccaccactaa ggccttgtgc ccactctata ccagccccag    240
aactgtgacc caagctccac ccaagtcaac tgccgatgtc tccactcctg actctgaaat    300
caaccttaca aatgtgacag atatcatcag ggttcgggtg ttcaacattg tcattctcct    360
ggctgggtgga ttctctagta agagcctggt cttctctgtc ctgtttgtctg tcacgtctgag    420
```

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gtcatttgta ccctaggccc acgaaccac gagaatgtcc tctgact 467

<210> SEQ ID NO 284
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(354)
<223> OTHER INFORMATION: AffymetrixID: 221485_at

<400> SEQUENCE: 284

aatgtgacct tgtgcatata ttggtagctg aaaatcttca aggctactga tgggtggccc 60
cttaatcttg tctttgattg ctgtgtgcag ggaaagggtgt ccccgtttgt tcatgctgtt 120
ttgggggggtg ggggggtatt tgcaagaata ctcatcttga cataataggt cctcttgtca 180
gagatcctct accacagaca ttaatagctg agcaggagcc acatggattg attgtatcca 240
ctcaccattg acgatggcat tgagcgtagc tagcttattt ccatcactac gtgtttttga 300
gcttgcctct acgtttttaag aggtgccagg ggtacatttt tgcactgaaa tcta 354

<210> SEQ ID NO 285
<211> LENGTH: 465
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(465)
<223> OTHER INFORMATION: AffymetrixID: 221652_s_at

<400> SEQUENCE: 285

ggccagtgtc gttattatcc ttgtggagaa tagaatcaat actgccaatt ccagaaaaca 60
tcaggaattt gctggacgtt tgaactctgt taataacaga gctgaactat atcaacatct 120
taaagaggaa aatgggatgg agacaacaga aaatggaaaa gccagccggc agtgaagagt 180
gacttgaaga actaaattta gcatattgca aaaatatttt gtgcggaatt cgatataagt 240
acttttacag caagatggta tagttatgtt gcctggactg gtttttcat ttttaaaata 300
tttcagctgt catttttgta ctaattataa aattggcaca taattcaaaa atatacattt 360
gagatgattt gtctctccaa attatacaag tttattttat ggtataaagt gttctctctg 420
gaaatgtttt taaaaaaatt cttaggcttc tctttgcgaa ataaa 465

<210> SEQ ID NO 286
<211> LENGTH: 392
<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, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (93)..(95)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (97)..(98)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (101)..(103)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (106)..(106)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (109)..(110)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (112)..(118)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(392)
<223> OTHER INFORMATION: AffymetrixID: 221755_at

<400> SEQUENCE: 286

```
ggagcctcat ggagtcaggt gccacaagc tgcaggagga ggtgctgac caggagtgg      60
tcacctggt caacaagaag nacgctctca tcnnnannca nnnccngcnn cnnnnnnnca    120
tggaggagca ggacttggag cgaaggttcg agctgctgag ccgagagctg cgggccatgc    180
tggccatcga agactggcag aaaacgtccg ctcagcagca ccgagagcag ctcctactgg    240
aggagctggt gtcgctggtg aaccagcgcg atgagctagt ccgggacctg gaccacaagg    300
agcggatcgc cctggaggag gacgagcgcc tggagcgcgg cctggaacag cggcgccgca    360
agctgagccg gcagttgagc cggcgggagc gc                                  392
```

<210> SEQ ID NO 287
<211> LENGTH: 488
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (101)..(101)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (463)..(463)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(488)
<223> OTHER INFORMATION: AffymetrixID: 221970_s_at

<400> SEQUENCE: 287

```
gcgaaaatgc tactatgact ctctctggaa tacacccacc taccttgaac cagattatgg    60
attggatatg tctacttctg gatgcgaatt ttactgttgt ngtaatgatg ccagaagcaa    120
agaggctact gataaatctt tacaagcttg taaaatctca gatatctggt tattctgagc    180
tcaacaagat tgaagtaagt ttctgggagc tacagaaatt aaatcaagaa aagaataata    240
gaggattata ttcaattgaa gtgctggagc tcttctgata ttatcaattc tccttcatag    300
acattttata aagctctttt atgtgaactc ttgcttcac caggcaagaa cgggtgtttg    360
tttgcgacca tctcagtgtc aagagaaaac gtgcagtgtg tacctggacc atcactaac     420
tgatgctccg gggtaggact gcaggtttca catgaacctg ttntagctg tggacattgg    480
tgtggaga                                           488
```

<210> SEQ ID NO 288
<211> LENGTH: 462
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:

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```
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(462)
<223> OTHER INFORMATION: AffymetrixID: 222127_s_at

<400> SEQUENCE: 288

ctcgcgtgtta tcctggatct ggtgttacaa tggaattcac tattcaggac attctggatt      60
attgttccag cattgcacag tcccactaaa ccttgtgaaa gaagaaaaga taactgaatg      120
aagcatttga gtataacaga cactatacca aaataccaag caactgtttt gagaacccag      180
acttaaaatt ttatgtatta ttaaattgta gataaatggg tagtaccata ctacaaatat      240
ttaaatgcaa aattaccaac ctatatagca gttttatttg ccctataggt tgcatactaa      300
cttaagcatt catgtacca taaaatgcct ttagcatttc tcaatgactg gatgggaaat      360
tttcctttaa tgcttagctg cttgtgtttg agtgggtgtc ctatgagcaa tgcatttgga      420
gttcttcagc ttctactact tctctgtgtc ttgctaatca tg                          462
```

```
<210> SEQ ID NO 289
<211> LENGTH: 535
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (39)..(39)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (43)..(44)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (53)..(53)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (62)..(62)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (70)..(70)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (74)..(74)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (86)..(86)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (113)..(113)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (124)..(124)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (127)..(127)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (142)..(142)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (148)..(148)
<223> OTHER INFORMATION: n is a, c, g, or t
<220> FEATURE:
```

<221> NAME/KEY: misc_feature	
<222> LOCATION: (171)..(465)	
<223> OTHER INFORMATION: n is a, c, g, or t	
<220> FEATURE:	
<221> NAME/KEY: misc_feature	
<222> LOCATION: (1)..(535)	
<223> OTHER INFORMATION: AffymetrixID: 36711_at	
<400> SEQUENCE: 289	
ttgcacggat ctaagtatt ctccccagcc agagcccgng ctinntgtct ccngggaaaa	60
gntggcgtn tggncctgag ctgggnttta tattttatat ctgcaaataa atnacatttt	120
atcntanatt tagggaaaagc cngagagnaa caacaaaaaa tgtttaagcc nnnnnnnnnn	180
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn	240
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn	300
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn	360
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn	420
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnntattg cccggtcct	480
agaatttatt tatttctga cttacagcaa gcgagttatc gtcttctgta ttttg	535
<210> SEQ ID NO 290	
<211> LENGTH: 494	
<212> TYPE: DNA	
<213> ORGANISM: Homo sapiens	
<220> FEATURE:	
<221> NAME/KEY: misc_feature	
<222> LOCATION: (124)..(124)	
<223> OTHER INFORMATION: n is a, c, g, or t	
<220> FEATURE:	
<221> NAME/KEY: misc_feature	
<222> LOCATION: (184)..(184)	
<223> OTHER INFORMATION: n is a, c, g, or t	
<220> FEATURE:	
<221> NAME/KEY: misc_feature	
<222> LOCATION: (237)..(262)	
<223> OTHER INFORMATION: n is a, c, g, or t	
<220> FEATURE:	
<221> NAME/KEY: misc_feature	
<222> LOCATION: (447)..(464)	
<223> OTHER INFORMATION: n is a, c, g, or t	
<220> FEATURE:	
<221> NAME/KEY: misc_feature	
<222> LOCATION: (1)..(494)	
<223> OTHER INFORMATION: AffymetrixID: 38037_at	
<400> SEQUENCE: 290	
ccactctatg agttggactt cagtcttgcc taggcgattt tgtctaccat ttgtgttttg	60
aaagcccaag gtgctgatgt caaagtgtaa cagatatcag tgtctccccg tgcctctccc	120
ctgncaagtc tcagaagagg ttgggcttcc atgcctgtag ctttctgggt ccttcacccc	180
catngcccca ggcccacagc gtgggaactc actttccett gtgtcaagac atttctnnnn	240
nnnnnnnnnn nnnnnnnnnn nnaactccatg caggggtcag tgcagcagag gacagctcgg	300
agaaggtatt agcaaagcaa aaggctgaga aggaacaggg aacattggag ctgactgttc	360
ttggtaactg attacctgcc aattgtctacc gagaaggttg gaggtgggga aggctttgta	420
taatcccacc cacctcacca aaacgannnn nnnnnnnnnn nnnngtcctt tctggaagtt	480
tctggtgccca ttcc	494
<210> SEQ ID NO 291	

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<211> LENGTH: 258
<212> TYPE: DNA
<213> ORGANISM: *E. coli*
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(258)
<223> OTHER INFORMATION: AffymetrixID: AFFX-BioB-M_at

<400> SEQUENCE: 291

gccggagttt tacggcaata tcatcaccac acgcacttat caggaacgcc tcgatacgct 60
ggaaaaagtg cgcgatgccg ggatcaaagt ctgttctggc ggcattgtgg gcttaggcga 120
aacggtaaaa gatcgcgccg gattattgct gcaactggca aacctgccga cgccgccgga 180
aagcgtgccca atcaaatgct tgggtgaagg gaaaggcacg ccgcttgccg ataacgatga 240
tgtcgatgcc ttgatatt 258

<210> SEQ ID NO 292
<211> LENGTH: 276
<212> TYPE: DNA
<213> ORGANISM: *E. coli*
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(276)
<223> OTHER INFORMATION: AffymetrixID: AFFX-r2-Ec-bioC-3_at

<400> SEQUENCE: 292

cgctggtgca gggatcgtaa cccgaacgtc atcaggcgtg gcaggcgtg gacgagcgtc 60
cgcatgctaa tcgcttttta ccgccagatg aaatcgaaca gtcgctgaac ggcgtgcatt 120
atcaaatca tattcagccc atcacgtgt ggtttgatga tgcgctcagt gccatgcgtt 180
cgctgaaagg catcggtgcc acgcatcttc atgaaggcg cgacccgcga atattaacgc 240
gttcgcagtt gcagcgattg caactggcct ggccgc 276

<210> SEQ ID NO 293
<211> LENGTH: 462
<212> TYPE: DNA
<213> ORGANISM: *Homo sapiens*
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(462)
<223> OTHER INFORMATION: AffymetrixID: 204018_x_at

<400> SEQUENCE: 293

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tcaaggccgc ctggggtaag gtcggcgccg acgctggcga gtatggtgcg gaggccctgg 120
agaggatggt cctgtccttc cccaccacca agacctactt cccgcacttc gacctgagcc 180
acggctctgc ccaggttaag ggccacggca agaaggtggc cgacgcccctg accaacgccg 240
tggcgcacgt ggacgacatg cccaacggcg tgtccgcctt gagcgacctg cacgcgcaca 300
agcttcgggt ggaccgggtc aacttcaagc tctaagcca ctgcctgctg gtgacctgg 360
ccgccacct ccccgccgag ttcaccttg cggtgcacgc ctccctggac aagttcctgg 420
cttctgtgag caccgtgctg acctccaat accgttaagc tg 462

<210> SEQ ID NO 294
<211> LENGTH: 323
<212> TYPE: DNA
<213> ORGANISM: *Homo sapiens*
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(323)
<223> OTHER INFORMATION: AffymetrixID: 222043_at

<400> SEQUENCE: 294

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ctgtcttgtg agctgacgc ttggagggtc ctctttttat gttgagttgc tgcttcccgg 120
catgccttca ttttgctatg gggggcaggc aggggggatg gaaaaataagt agaaacaaaa 180
aagcagtggc taagatggta tagggactgt cataccagtg aagaataaaa gggatgaagaa 240
taaaagggat atgatgacaa ggttgatcca cttcaagaat tgcttgcttt caggaagaga 300
gatgtgtttc aacaagccaa cta 323

<210> SEQ ID NO 295
<211> LENGTH: 540
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(540)
<223> OTHER INFORMATION: AffymetrixID: 206026_s_at

<400> SEQUENCE: 295

tacaagtact acttctactg gaaataaaaa ctttttagct ggaagattta gccacttata 60
aaaaaaaaa aggatgatca aaacacacag tgtttatggt ggaatctttt ggaactcctt 120
tgatctcact gttattatta acattttttt attatttttc taaatgtgaa agaaatacat 180
aatttaggga aaattggaaa atataggaaa ctttaaacga gaaaatgaaa cctctcataa 240
tcccactgca tagaaataac aagcgtaaac attttcatat ttttttcttt cagtcatttt 300
tgtatttgtg gtatatgtat atatgtacct atatgtattt gcatttgaaa ttttggaaac 360
ctgctctatg tacagttttg tattatactt tttaaatctt gaactttatg aacattttct 420
gaaatcattg attattctac aaaaacatga ttttaaacag ctgtaaaata ttctatgata 480
tgaatgtttt atgcattatt taagcctgtc tctattgttg gaatttcagg tcattttcat 540

<210> SEQ ID NO 296
<211> LENGTH: 101
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(101)
<223> OTHER INFORMATION: AffymetrixID: 208894_at

<400> SEQUENCE: 296

cgatcaccaa tgtacctca gaggtaactg tgctcacgaa cagccctgtg gaactgagag 60
agcccaacgt cctcatctgt ttcatagaca agttcacccc a 101

<210> SEQ ID NO 297
<211> LENGTH: 491
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(491)
<223> OTHER INFORMATION: AffymetrixID: 222150_s_at

<400> SEQUENCE: 297

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cagaactgct gtatcacatt ccaattttga atagccagtg agcaatcaag tgtagagaaa	180
tgataaatgg cctaagaagg catacagtgg cataaacgat gctcttccta gtagcttaat	240
aggccacaag ctagtcttctg ttgccctctg aaataaaaata tgctttaaaa atgtagggac	300
cagtgccttag aaaagcaaaa actaggtgtg tcattgaaat aataggcata aaaattaaat	360
gttacataag acccctattt ggaaaaaggg tcctttttaa aactgaattt gtactaaatc	420
agatttgcca tgtccagtag agaataattt gtacttagta tttgcagcag ggtttgtctt	480
tgtgaattca g	491

<210> SEQ ID NO 298
 <211> LENGTH: 485
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(485)
 <223> OTHER INFORMATION: AffymetrixID: 207113_s_at

<400> SEQUENCE: 298

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aagtggacct taggccttcc tctctccaga tgtttccaga cttccttgag acacggagcc	180
cagccctccc catggagcca gctccctcta tttatgtttg cacttgatgat tatttattat	240
ttatttatta tttatttatt tacagatgaa tgtatttatt tgggagaccg gggatatctg	300
ggggacccaa ttagagagct gccttggtc agacatgttt tccgtgaaaa cggagagctga	360
acaataggct gttcccatgt agccccctgg cctctgtgcc ttcttttgat tatgtttttt	420
aaaaatattat ctgattaagt tgtctaaaca atgctgattt ggtgaccaac tgctactcat	480
tgctg	485

<210> SEQ ID NO 299
 <211> LENGTH: 491
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(491)
 <223> OTHER INFORMATION: AffymetrixID: 205067_at

<400> SEQUENCE: 299

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ccaactgcct gccttagggt agtgctaaga ggatctcttg tccatcagcc aggacagtca	180
gctctctcct ttcagggccca atccccagcc cttttgttga gccaggcctc tctcacctct	240
cctactcact taaagcccg ctagacagaaa ccacggccac atttgggtct aagaaaccct	300
ctgtcattcg ctcccacatt ctgatgagca accgcttccc tatttattta tttatttgtt	360
tgtttgtttt attcattggt ctaatttatt caaagggggc aagaagtagc agtgtctgta	420
aaagagccta gtttttaata gctatggaat caattcaatt tggactgggtg tgctctcttt	480

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aaatcaagtc c 491

<210> SEQ ID NO 300
<211> LENGTH: 356
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(356)
<223> OTHER INFORMATION: AffymetrixID: 201290_at

<400> SEQUENCE: 300

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caggatttca taattgtcat tgtcacactt tcaaattttt gtacatcagt gaattttttt 180
atattaaaag gttgagccaa aaagccccc gtgtttgtat tttgaagcca agcttcactt 240
ctaaagtgcc tacagagact tgtaaatgaa aatgcagctc tgcacgagtt tgaaccgctc 300
atacctcctt ctattaggaa tggcatatac tgaggtgggc gtaagtctta acttct 356

<210> SEQ ID NO 301
<211> LENGTH: 4666
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(4666)
<223> OTHER INFORMATION: CD11c full-length n.t.

<400> SEQUENCE: 301

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aggtttcaac ttggacacag aggagctgac agccttccgt gtggacagcg ctgggttttg 180
agacagcgtg gtccagtatg ccaactcctg ggtgggtggt ggagccccc aaaagataac 240
agctgccaac caaacgggtg gcctctacca gtgtggctac agcactgggt cctgtgagcc 300
catcggcctg caggtgcccc cggaggccgt gaacatgtcc ctgggcctgt ccttgccgtc 360
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gaacatgtac ctcaccggac tctgttctct cctgggcccc acccagctca cccagaggct 480
cccgggtgcc aggcaggagt gcccagaca ggagcaggac attgtgttcc tgatcgatgg 540
ctcaggcagc atctcctccc gcaactttgc cacgatgatg aacttcgtga gagctgtgat 600
aagccagtgc cagagaccca gcaccaggt ttccctgatg cagttctcca acaaattcca 660
aacacacttc actttcgagg aattcaggcg cagctcaaac cccctcagcc tgttggttc 720
tgttcaccag ctgcaagggt ttacatacac ggccaccgcc atccaaaatg tcgtgcaccg 780
attgttccat gcctcatatg gggcccgtag ggatgccgcc aaaattctca ttgtcatcac 840
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ctttgatgct ctgaaagata ttcaaaacca actgaaggag aagatctttg ccattgaggg 1080
tacggagacc acaagcagta gctccttcga attggagatg gcacaggagg gcttcagcgc 1140

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gtactccag cttccaggac aggaggcatt tatgagagct cagacgacaa cgtgtctgga	3360
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cccgccagct gagaaatgat cccctctttg ccttggaactt cttctcccc gcgagttttc 3600
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aggctgggat gggcctgctt cctgtctttg ggagaaaacg tcttgcttg gaaggggcct 3720
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aaggtctaaa aataaaaaag cttctgtga aaaaaaaaa aaaaaa 4666

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<210> SEQ ID NO 302

<211> LENGTH: 1163

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(1163)

<223> OTHER INFORMATION: CD11c full-length a.a.

<400> SEQUENCE: 302

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Met Thr Arg Thr Arg Ala Ala Leu Leu Leu Phe Thr Ala Leu Ala Thr
1           5           10           15

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```

Ser Leu Gly Phe Asn Leu Asp Thr Glu Glu Leu Thr Ala Phe Arg Val
20           25           30

```

```

Asp Ser Ala Gly Phe Gly Asp Ser Val Val Gln Tyr Ala Asn Ser Trp
35           40           45

```

```

Val Val Val Gly Ala Pro Gln Lys Ile Thr Ala Ala Asn Gln Thr Gly
50           55           60

```

```

Gly Leu Tyr Gln Cys Gly Tyr Ser Thr Gly Ala Cys Glu Pro Ile Gly
65           70           75           80

```

```

Leu Gln Val Pro Pro Glu Ala Val Asn Met Ser Leu Gly Leu Ser Leu
85           90           95

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```

Ala Ser Thr Thr Ser Pro Ser Gln Leu Leu Ala Cys Gly Pro Thr Val
100          105          110

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His His Glu Cys Gly Arg Asn Met Tyr Leu Thr Gly Leu Cys Phe Leu

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115					120					125					
Leu	Gly	Pro	Thr	Gln	Leu	Thr	Gln	Arg	Leu	Pro	Val	Ser	Arg	Gln	Glu
130					135						140				
Cys	Pro	Arg	Gln	Glu	Gln	Asp	Ile	Val	Phe	Leu	Ile	Asp	Gly	Ser	Gly
145					150					155					160
Ser	Ile	Ser	Ser	Arg	Asn	Phe	Ala	Thr	Met	Met	Asn	Phe	Val	Arg	Ala
				165					170					175	
Val	Ile	Ser	Gln	Phe	Gln	Arg	Pro	Ser	Thr	Gln	Phe	Ser	Leu	Met	Gln
			180					185					190		
Phe	Ser	Asn	Lys	Phe	Gln	Thr	His	Phe	Thr	Phe	Glu	Glu	Phe	Arg	Arg
		195					200					205			
Ser	Ser	Asn	Pro	Leu	Ser	Leu	Leu	Ala	Ser	Val	His	Gln	Leu	Gln	Gly
	210					215						220			
Phe	Thr	Tyr	Thr	Ala	Thr	Ala	Ile	Gln	Asn	Val	Val	His	Arg	Leu	Phe
225					230					235					240
His	Ala	Ser	Tyr	Gly	Ala	Arg	Arg	Asp	Ala	Ala	Lys	Ile	Leu	Ile	Val
				245					250					255	
Ile	Thr	Asp	Gly	Lys	Lys	Glu	Gly	Asp	Ser	Leu	Asp	Tyr	Lys	Asp	Val
			260					265					270		
Ile	Pro	Met	Ala	Asp	Ala	Ala	Gly	Ile	Ile	Arg	Tyr	Ala	Ile	Gly	Val
		275					280					285			
Gly	Leu	Ala	Phe	Gln	Asn	Arg	Asn	Ser	Trp	Lys	Glu	Leu	Asn	Asp	Ile
	290					295						300			
Ala	Ser	Lys	Pro	Ser	Gln	Glu	His	Ile	Phe	Lys	Val	Glu	Asp	Phe	Asp
305					310					315					320
Ala	Leu	Lys	Asp	Ile	Gln	Asn	Gln	Leu	Lys	Glu	Lys	Ile	Phe	Ala	Ile
				325						330				335	
Glu	Gly	Thr	Glu	Thr	Thr	Ser	Ser	Ser	Ser	Phe	Glu	Leu	Glu	Met	Ala
			340					345					350		
Gln	Glu	Gly	Phe	Ser	Ala	Val	Phe	Thr	Pro	Asp	Gly	Pro	Val	Leu	Gly
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Ala	Val	Gly	Ser	Phe	Thr	Trp	Ser	Gly	Gly	Ala	Phe	Leu	Tyr	Pro	Pro
	370					375						380			
Asn	Met	Ser	Pro	Thr	Phe	Ile	Asn	Met	Ser	Gln	Glu	Asn	Val	Asp	Met
385					390					395					400
Arg	Asp	Ser	Tyr	Leu	Gly	Tyr	Ser	Thr	Glu	Leu	Ala	Leu	Trp	Lys	Gly
				405					410					415	
Val	Gln	Ser	Leu	Val	Leu	Gly	Ala	Pro	Arg	Tyr	Gln	His	Thr	Gly	Lys
			420					425					430		
Ala	Val	Ile	Phe	Thr	Gln	Val	Ser	Arg	Gln	Trp	Arg	Met	Lys	Ala	Glu
		435					440					445			
Val	Thr	Gly	Thr	Gln	Ile	Gly	Ser	Tyr	Phe	Gly	Ala	Ser	Leu	Cys	Ser
	450					455						460			
Val	Asp	Val	Asp	Ser	Asp	Gly	Ser	Thr	Asp	Leu	Val	Leu	Ile	Gly	Ala
465					470					475					480
Pro	His	Tyr	Tyr	Glu	Gln	Thr	Arg	Gly	Gly	Gln	Val	Ser	Val	Cys	Pro
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Leu	Pro	Arg	Gly	Trp	Arg	Arg	Trp	Trp	Cys	Asp	Ala	Val	Leu	Tyr	Gly
			500					505					510		
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Gly	Asp	Val	Asn	Gly	Asp	Lys	Leu	Thr	Asp	Val	Val	Ile	Gly	Ala	Pro
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545				550						555					560
Gly	Pro	Ser	Ile	Ser	Pro	Ser	His	Ser	Gln	Arg	Ile	Ala	Gly	Ser	Gln
			565						570					575	
Leu	Ser	Ser	Arg	Leu	Gln	Tyr	Phe	Gly	Gln	Ala	Leu	Ser	Gly	Gly	Gln
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Asp	Leu	Thr	Gln	Asp	Gly	Leu	Val	Asp	Leu	Ala	Val	Gly	Ala	Arg	Gly
	595					600						605			
Gln	Val	Leu	Leu	Leu	Arg	Thr	Arg	Pro	Val	Leu	Trp	Val	Gly	Val	Ser
610					615						620				
Met	Gln	Phe	Ile	Pro	Ala	Glu	Ile	Pro	Arg	Ser	Ala	Phe	Glu	Cys	Arg
625				630					635						640
Glu	Gln	Val	Val	Ser	Glu	Gln	Thr	Leu	Val	Gln	Ser	Asn	Ile	Cys	Leu
			645					650						655	
Tyr	Ile	Asp	Lys	Arg	Ser	Lys	Asn	Leu	Leu	Gly	Ser	Arg	Asp	Leu	Gln
		660					665						670		
Ser	Ser	Val	Thr	Leu	Asp	Leu	Ala	Leu	Asp	Pro	Gly	Arg	Leu	Ser	Pro
		675				680						685			
Arg	Ala	Thr	Phe	Gln	Glu	Thr	Lys	Asn	Arg	Ser	Leu	Ser	Arg	Val	Arg
690					695						700				
Val	Leu	Gly	Leu	Lys	Ala	His	Cys	Glu	Asn	Phe	Asn	Leu	Leu	Leu	Pro
705				710					715						720
Ser	Cys	Val	Glu	Asp	Ser	Val	Thr	Pro	Ile	Thr	Leu	Arg	Leu	Asn	Phe
			725					730					735		
Thr	Leu	Val	Gly	Lys	Pro	Leu	Leu	Ala	Phe	Arg	Asn	Leu	Arg	Pro	Met
		740					745					750			
Leu	Ala	Ala	Asp	Ala	Gln	Arg	Tyr	Phe	Thr	Ala	Ser	Leu	Pro	Phe	Glu
		755				760					765				
Lys	Asn	Cys	Gly	Ala	Asp	His	Ile	Cys	Gln	Asp	Asn	Leu	Gly	Ile	Ser
770					775					780					
Phe	Ser	Phe	Pro	Gly	Leu	Lys	Ser	Leu	Leu	Val	Gly	Ser	Asn	Leu	Glu
785				790						795					800
Leu	Asn	Ala	Glu	Val	Met	Val	Trp	Asn	Asp	Gly	Glu	Asp	Ser	Tyr	Gly
			805					810						815	
Thr	Thr	Ile	Thr	Phe	Ser	His	Pro	Ala	Gly	Leu	Ser	Tyr	Arg	Tyr	Val
		820					825						830		
Ala	Glu	Gly	Gln	Lys	Gln	Gly	Gln	Leu	Arg	Ser	Leu	His	Leu	Thr	Cys
		835				840					845				
Asp	Ser	Ala	Pro	Val	Gly	Ser	Gln	Gly	Thr	Trp	Ser	Thr	Ser	Cys	Arg
		850				855					860				
Ile	Asn	His	Leu	Ile	Phe	Arg	Gly	Gly	Ala	Gln	Ile	Thr	Phe	Leu	Ala
865				870					875						880
Thr	Phe	Asp	Val	Ser	Pro	Lys	Ala	Val	Leu	Gly	Asp	Arg	Leu	Leu	Leu
			885					890						895	
Thr	Ala	Asn	Val	Ser	Ser	Glu	Asn	Asn	Thr	Pro	Arg	Thr	Ser	Lys	Thr
		900					905						910		
Thr	Phe	Gln	Leu	Glu	Leu	Pro	Val	Lys	Tyr	Ala	Val	Tyr	Thr	Val	Val
		915				920						925			

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Ser Ser His Glu Gln Phe Thr Lys Tyr Leu Asn Phe Ser Glu Ser Glu
 930                      935                      940

Glu Lys Glu Ser His Val Ala Met His Arg Tyr Gln Val Asn Asn Leu
945                      950                      955                      960

Gly Gln Arg Asp Leu Pro Val Ser Ile Asn Phe Trp Val Pro Val Glu
                      965                      970                      975

Leu Asn Gln Glu Ala Val Trp Met Asp Val Glu Val Ser His Pro Gln
                      980                      985                      990

Asn Pro Ser Leu Arg Cys Ser Ser Glu Lys Ile Ala Pro Pro Ala Ser
 995                      1000                      1005

Asp Phe Leu Ala His Ile Gln Lys Asn Pro Val Leu Asp Cys Ser
1010                      1015                      1020

Ile Ala Gly Cys Leu Arg Phe Arg Cys Asp Val Pro Ser Phe Ser
1025                      1030                      1035

Val Gln Glu Glu Leu Asp Phe Thr Leu Lys Gly Asn Leu Ser Phe
1040                      1045                      1050

Gly Trp Val Arg Gln Ile Leu Gln Lys Lys Val Ser Val Val Ser
1055                      1060                      1065

Val Ala Glu Ile Thr Phe Asp Thr Ser Val Tyr Ser Gln Leu Pro
1070                      1075                      1080

Gly Gln Glu Ala Phe Met Arg Ala Gln Thr Thr Thr Val Leu Glu
1085                      1090                      1095

Lys Tyr Lys Val His Asn Pro Thr Pro Leu Ile Val Gly Ser Ser
1100                      1105                      1110

Ile Gly Gly Leu Leu Leu Leu Ala Leu Ile Thr Ala Val Leu Tyr
1115                      1120                      1125

Lys Val Gly Phe Phe Lys Arg Gln Tyr Lys Glu Met Met Glu Glu
1130                      1135                      1140

Ala Asn Gly Gln Ile Ala Pro Glu Asn Gly Thr Gln Thr Pro Ser
1145                      1150                      1155

Pro Pro Ser Glu Lys
1160

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<210> SEQ ID NO 303
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(107)
<223> OTHER INFORMATION: Adalimumab VL

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<400> SEQUENCE: 303

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1                      5                      10                      15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
 20                      25                      30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35                      40                      45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50                      55                      60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65                      70                      75                      80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr

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-continued

	85		90		95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys					
	100		105		

<210> SEQ ID NO 304
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(121)
<223> OTHER INFORMATION: Adalimumab VH

<400> SEQUENCE: 304

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg					
1	5		10		15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr					
	20		25		30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val					
	35		40		45
Ser Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val					
	50		55		60
Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr					
65	70		75		80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys					
	85		90		95
Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly					
	100		105		110
Gln Gly Thr Leu Val Thr Val Ser Ser					
	115		120		

<210> SEQ ID NO 305
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic consensus motif for adalimumab VL CDR3
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9)..(9)
<223> OTHER INFORMATION: Xaa is Thr or Ala

<400> SEQUENCE: 305

Gln Arg Tyr Asn Arg Ala Pro Tyr Xaa	
1	5

<210> SEQ ID NO 306
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic consensus motif for adalimumab VH CDR3
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: Xaa is Tyr or Asn

<400> SEQUENCE: 306

Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Xaa		
1	5	10

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<210> SEQ ID NO 307
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(7)
<223> OTHER INFORMATION: Adalimumab VL CDR2

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<400> SEQUENCE: 307

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Ala Ala Ser Thr Leu Gln Ser
1             5

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<210> SEQ ID NO 308
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(17)
<223> OTHER INFORMATION: Adalimumab VH CDR2

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<400> SEQUENCE: 308

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Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu
1             5             10             15

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Gly

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<210> SEQ ID NO 309
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(11)
<223> OTHER INFORMATION: Adalimumab VL CDR1

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<400> SEQUENCE: 309

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Arg Ala Ser Gln Gly Ile Arg Asn Tyr Leu Ala
1             5             10

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<210> SEQ ID NO 310
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(5)
<223> OTHER INFORMATION: Adalimumab VH CDR1

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<400> SEQUENCE: 310

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Asp Tyr Ala Met His
1             5

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What is claimed is:

1. A method for predicting responsiveness to a TNF α inhibitor in a subject having an autoimmune disorder, the method comprising: (i) assaying the subject for expression of one or more biomarkers predictive of responsiveness to a TNF α inhibitor in an autoimmune disorder, and (ii) predicting responsiveness of the subject to the TNF α inhibitor based on expression of the one or more biomarkers in the subject, wherein the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected

from the group consisting of SEQ ID NO: 1-10, 12-28, 30-43, 45-61, 63, 64, 66-73, and 75-82,

wherein decreased expression of the one or more biomarkers encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-5, 8, 9, 12-14, 18, 20, 21, 23, 25, 26, 28, 30, 32, 33, 40-42, 48, 50, 52, 53, 56, 58, 60, 63, 66-69, 71-73, 76-78, 80 and 81 is predictive of responsiveness of the subject to a TNF α inhibitor; and/or

wherein increased expression of the one or more biomarkers encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 6, 7, 10, 15-17, 19, 22, 24, 27, 31, 34-39, 43, 45-47, 49, 51, 54, 55, 57, 59, 61, 64, 70, 75, 79 and 82 is predictive of responsive of the subject to a TNF α inhibitor.

2. A method for predicting responsiveness to a TNF α inhibitor in a subject having an autoimmune disorder, the method comprising:

- (i) assaying the subject for expression of one or more biomarkers predictive of responsiveness to a TNF α inhibitor in an autoimmune disorder, and
- (ii) predicting responsiveness of the subject to the TNF α inhibitor based on expression of the one or more biomarkers in the subject, wherein the one or more biomarkers is selected from the group consisting of Aquaporin 3 (Genbank Accession No. NM_004925); Similar to ribosomal protein S24, clone MGC:8595 (Genbank Accession No. NM_033022); Transmembrane emp24 domain trafficking protein 2 (Genbank Accession No. NM_006815); Superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (Genbank Accession No. NM_000454); Calmodulin 1 (phosphorylase kinase, delta) (Genbank Accession No. NM_006888); Guanine nucleotide binding protein (G protein), beta polypeptide 1 (Genbank Accession No. NM_002074); Prothymosin, alpha (gene sequence 28) (Genbank Accession No. NM_002823); *Homo sapiens* isocitrate dehydrogenase 1 (NADP⁺) soluble (IDH1) (Genbank Accession No. NM_005896); Tumor protein D52 (Genbank Accession Nos. NM_001025252, NM_001025253, NM_005079); Early growth response 1 (Genbank Accession No. NM_001964); Cytochrome c oxidase subunit VIIb (Genbank Accession No. NM_001866); CUG triplet repeat, RNA binding protein 2 (Genbank Accession No. NM_001025077, NM_001025076, NM_006561); Ubiquinol-cytochrome c reductase hinge protein (Genbank Accession No. NM_006004); *Homo sapiens* leptin receptor gene-related protein (HS0BRGRP) (Genbank Accession No. NM_017526); Wiskott-Aldrich syndrome protein interacting protein (Genbank Accession Nos. NM_001077269, NM_003387); CD97 antigen (Genbank Accession Nos. NM_001025160, NM_001784, NM_078481); Glutamate-cysteine ligase, catalytic subunit (Genbank Accession No. NM_001498); Crystallin, zeta (quinone reductase) (Genbank Accession No. NM_001889); Rap guanine nucleotide exchange factor (GEF) 2 (Genbank Accession No. NM_014247); Ataxin 1 (Genbank Accession No. NM_000332); Adaptor-related protein complex 1, sigma 2 subunit (Genbank Accession No. NM_003916); Ectonucleotide pyrophosphatase/phosphodiesterase 4 (Genbank Accession No. NM_014936); Desmocollin 2 (Genbank Accession Nos. NM_024422, NM_004949); MAL, T-cell differentiation protein (Genbank Accession Nos. NM_002371, NM_022438, NM_022439, NM_022440); Glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase (Genbank Accession No. NM_005476); Chemokine (C—C motif) ligand 3 (Genbank Accession Nos. NM_001001437, NM_021006); Carboxypeptidase A3 (Genbank Accession No. NM_001870); NADH dehydrogenase

(ubiquinone) 1 beta subcomplex, 1, 7 kDa (Genbank Accession No. NM_004545); Interleukin 8 receptor, beta (Genbank Accession No. NM_001557); Platelet factor 4 variant 1 (Genbank Accession No. NM_002620); Poly(A) binding protein interacting protein 1 (Genbank Accession No. NM_006451); ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (Genbank Accession No. NM_003786); Actinin, alpha 1 (Genbank Accession No. NM_001102); NAD kinase (Genbank Accession No. NM_023018); Platelet/endothelial cell adhesion molecule (CD31 antigen) (Genbank Accession No. NM_000442); Esterase D/formylglutathione hydrolase (Genbank Accession No. NM_001984); Chromosome 20 open reading frame 111 (Genbank Accession No. NM_016470); Sterol-C4-methyl oxidase-like (Genbank Accession Nos. NM_001017369, NM_006745); PIM-1 oncogene (Genbank Accession No. NM_002648); GATA binding protein 2 (Genbank Accession No. NM_032638); Cathepsin Z (Genbank Accession No. NM_001336); Lectin, galactoside-binding, soluble, 8 (galectin 8) (Genbank Accession Nos. NM_006499, NM_201545); CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) (Genbank Accession Nos. NM_006889, NM_175862); Interleukin 8 (Genbank Accession No. NM_000584); Fc fragment of IgE, high affinity I, receptor for alpha polypeptide (Genbank Accession No. NM_002001); Actin, gamma 1 (Genbank Accession No. NM_001614); KIAA0746 protein (Genbank Accession No. NM_015187); Glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID) (Genbank Accession No. NM_002076); Transcription factor 4 (Genbank Accession Nos. BF592782, CR612521); Major histocompatibility complex, class II, DQ alpha 1 (Genbank Accession Nos. NM_002122, NM_020056); Cell division cycle 2-like 6 (CDK8-like) (Genbank Accession No. NM_015076); Major histocompatibility complex, class II, DQ beta 1 (Genbank Accession No. XM_942240); Phospholipase C-like 2 (Genbank Accession No. NM_015184); Coagulation factor II (thrombin) receptor-like 1 (Genbank Accession No. NM_005242); TM2 domain containing 1 (Genbank Accession No. NM_032027); Splicing factor 3b, subunit 1, 155 kDa (Genbank Accession No. NM_012433); SUB1 homolog (*S. cerevisiae*) (Genbank Accession No. NM_006713); MRNA, cDNA DKFZp564O0862 (Genbank Accession No. A1278204); Cytochrome b-5 (Genbank Accession Nos. NM_001914, NM_148923); Cold autoimmune syndrome 1 (Genbank Accession No. NM_183395); Ribosomal protein S26, 40S ribosomal protein (Genbank Accession No. XM_941927); CCR4-NOT transcription complex, subunit 6 (Genbank Accession No. NM_015455); Ubiquinol-cytochrome c reductase complex (7.2 kD) (Genbank Accession Nos. NM_013387, NM_001003684); Hepatocellular carcinoma-associated antigen 112 (Genbank Accession No. NM_018487); Kruppel-like factor 11 (Genbank Accession No. XM_001129527); GGA binding partner (Genbank Accession No. NM_018318); Cornichon homolog 4 (*Drosophila*) (Genbank Accession No. NM_014184); Hypothetical protein FLJ21616 (Genbank Accession No. NM_024567); Nuclear prelamin A recognition factor (Genbank Accession Nos. NM_012336,

NM_001038618); Erythroblast membrane-associated protein (Genbank Accession Nos. NM_018538, NM_001017922); LR8 protein (Genbank Accession No. NM_014020); Likely ortholog of mouse limb-bud and heart gene (LBH) (Genbank Accession No. NM_030915); Calmin (calponin-like, transmembrane) (Genbank Accession No. NM_024734); Chromosome 14 open reading frame 156 (Genbank Accession No. NM_031210); Guanine nucleotide binding protein (G protein) alpha 12 (Genbank Accession No. NM_007353); and SRY (sex determining region Y)-box 18 (Genbank Accession No. NR_003287).

3. A method for predicting responsiveness to a TNF α inhibitor, which TNF α inhibitor is adalimumab, in a subject having an autoimmune disorder, the method comprising:

- (i) assaying the subject for expression of one or more biomarkers predictive of responsiveness to adalimumab in an autoimmune disorder, and
- (ii) predicting responsiveness of the subject to adalimumab based on expression of the one or more biomarkers in the subject,

wherein decreased expression of the one or more biomarkers encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-5, 8, 9, 12-14, 18, 20, 21, 23, 25, 26, 28, 30, 32, 33, 40-42, 48, 50, 52, 53, 56, 58, 60, 63, 66-69, 71-73, 76-78, 80 and 81 is predictive of responsiveness of the subject to a TNF α inhibitor; and/or

wherein increased expression of the one or more biomarkers encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 6, 7, 10, 15-17, 19, 22, 24, 27, 31, 34-39, 43, 45-47, 49, 51, 54, 55, 57, 59, 61, 64, 70, 75, 79 and 82 is predictive of responsive of the subject to a TNF α inhibitor.

4. The method of any of claims 1-3, wherein a sample from the subject is assayed for expression of mRNA encoding the one or more biomarkers.

5. The method of any of claims 1-3, wherein a sample from the subject is assayed for protein expression of the one or more biomarkers.

6. The method of any of claims 1-3, which further comprises selecting a treatment regimen with the TNF α inhibitor based upon expression of the one or more biomarkers in the subject.

7. The method of claim 6, which further comprises administering the TNF α inhibitor to the subject according to the treatment regimen such that the autoimmune disorder is inhibited in the subject.

8. The method of any of claims 1-3, wherein the TNF α inhibitor is an anti-tumor necrosis factor-alpha (TNF α) antibody, or antigen-binding portion thereof.

9. The method of claim 8, wherein the anti-TNF α antibody, or antigen-binding portion thereof, is a human antibody, a humanized antibody, a chimeric antibody or a multivalent antibody.

10. The method of claim 8, wherein the anti-TNF α antibody, or antigen-binding portion thereof, is adalimumab.

11. The method of claim 9, wherein the anti-TNF α antibody, or antigen-binding portion thereof, is selected from the group consisting of

- i) an isolated human antibody that dissociates from human TNF α with a K_d of 1×10^{-8} M or less and a K_{off} rate constant of 1×10^{-3} s⁻¹ or less, both determined by sur-

face plasmon resonance, and neutralizes human TNF α cytotoxicity in a standard in vitro L929 assay with an IC₅₀ of 1×10^{-7} M or less;

- ii) an isolated human antibody with the following characteristics:

- a) dissociates from human TNF α with a K_{off} rate constant of 1×10^{-3} s⁻¹ or less, as determined by surface plasmon resonance;
- b) has a light chain CDR3 domain comprising the amino acid sequence of SEQ ID NO: 305, or modified from SEQ ID NO: 305 by a single alanine substitution at position 1, 4, 5, 7 or 8 or by one to five conservative amino acid substitutions at positions 1, 3, 4, 6, 7, 8 and/or 9;
- c) has a heavy chain CDR3 domain comprising the amino acid sequence of SEQ ID NO: 306, or modified from SEQ ID NO: 306 by a single alanine substitution at position 2, 3, 4, 5, 6, 8, 9, 10 or 11 or by one to five conservative amino acid substitutions at positions 2, 3, 4, 5, 6, 8, 9, 10, 11 and/or 12; and

- iii) an isolated human antibody with a light chain variable region (LCVR) comprising the amino acid sequence of SEQ ID NO: 303 and a heavy chain variable region (HCVR) comprising the amino acid sequence of SEQ ID NO: 304.

12. The method of claim 1, wherein the TNF α inhibitor is etanercept.

13. The method of any one of claims 1-3, wherein the subject is a human.

14. The method of any one of claims 1-3, wherein the autoimmune disorder is rheumatoid arthritis.

15. A kit for predicting responsiveness to a TNF α inhibitor in a subject having an autoimmune disorder, the kit comprising:

- a) means for isolating monocytes;
- b) means for measuring expression in the subject of one or more biomarkers predictive of responsiveness to a TNF α inhibitor in an autoimmune disorder;
- c) means for measuring expression of at least one house-keeping gene; and
- d) instructions for use of the kit to predicting responsiveness to a TNF α inhibitor in a subject having an autoimmune disorder, wherein decreased expression of the one or more biomarkers encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-5, 8, 9, 11-14, 18, 20, 21, 23, 25, 26, 28-30, 32, 33, 40-42, 48, 50, 52, 53, 56, 58, 60, 63, 65-69, 71-74, 76-78, 80 and 81 is predictive of responsiveness of the subject to a TNF α inhibitor and/or wherein increased expression of the one or more biomarkers encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 6, 7, 10, 15-17, 19, 22, 24, 27, 31, 34-39, 43, 44-47, 49, 51, 54, 55, 57, 59, 61, 62, 64, 70, 75, 79 and 82 is predictive of responsive of the subject to a TNF α inhibitor.

16. A method of monitoring an autoimmune disorder in a subject having the autoimmune disorder, the method comprising: assaying the subject for expression of one or more biomarkers, wherein the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 83-133, thereby monitoring the autoimmune disorder in the subject.

17. A method of monitoring an autoimmune disorder in a subject having the autoimmune disorder, the method comprising: assaying the subject for expression of one or more biomarkers, wherein the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 134-177, 110, 112, 118, 123 and 131, thereby monitoring the autoimmune disorder in the subject.

18. A method of monitoring an autoimmune disorder in a subject having an autoimmune disorder, the method comprising: assaying the subject for expression of one or more biomarkers, wherein the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 178-292, 91 and 97, thereby monitoring the autoimmune disorder in the subject.

19. A method of monitoring an autoimmune disorder in a subject having the autoimmune disorder, the method comprising: assaying the subject for expression of one or more biomarkers, wherein the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 87, 97, 101, 293, 92, 272, 93, 107, 108, 121 and 123, and wherein the subject is monitored prior to treatment with a TNF α inhibitor, thereby monitoring the autoimmune disorder in the subject.

20. A method of monitoring an autoimmune disorder in a subject having the autoimmune disorder, the method comprising: assaying the subject for expression of one or more biomarkers, wherein the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence

selected from the group consisting of SEQ ID NO: 290, 209, 98, 112, 116, 121, 130, 155, 92, 289, 216 and 131, and wherein the subject is monitored after treatment with a TNF α inhibitor, thereby monitoring the autoimmune disorder in the subject.

21. A method of monitoring an autoimmune disorder in a subject having the autoimmune disorder, the method comprising: assaying the subject for expression of one or more biomarkers, wherein the one or more biomarkers is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 97, 102, 29, 294, 295, 91, 131, 290, 100, 134, 296, 297, 298, 299, 136, 174 and 300, thereby monitoring the autoimmune disorder in the subject.

22. A method of selecting an autoimmune disorder subject for a treatment with a TNF α inhibitor, the method comprising:

- (i) identifying, in a database comprising a plurality of autoimmune disorder subjects, a subject whose database entry is associated with a biomarker expression pattern that is predictive of responsiveness to treatment with a TNF α inhibitor, and
- (ii) selecting the subject for treatment with a TNF α inhibitor, wherein the biomarker expression pattern reports expression in the subject of one or more biomarkers encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-82.

* * * * *