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(54) Titre : IDENTIFICATION DE SEQUENCES PARTICULIEREMENT UTILES AU DIAGNOSTIC ET A L'IDENTIFICATION DE CIBLES THERAPEUTIQUES POUR L'OSTEO-ARTHRITE

(54) Title: IDENTIFICATION OF SEQUENCES PARTICULARLY USEFUL FOR THE DIAGNOSIS AND IDENTIFICATION OF THERAPEUTIC TARGETS FOR OSTEOARTHRITIS

(57) Abrégé/Abstract:

The invention relates to the identification and selection of sequences which demonstrate particular advantage in identifying individuals having osteoarthritis (OA). The invention also provides a selection of sequences particularly useful in diagnosing the degree of advancement of osteoarthritis of an individual and in the identification of novel therapeutic targets for OA. The invention further provides for the use of these sequences as a tool to diagnose disease progression and to monitor the efficacy of therapeutic regimens.

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(54) Title: IDENTIFICATION OF SEQUENCES PARTICULARLY USEFUL FOR THE DIAGNOSIS AND IDENTIFICATION OF THERAPEUTIC TARGETS FOR OSTEOARTHRITIS

(57) Abstract: The invention relates to the identification and selection of sequences which demonstrate particular advantage in identifying individuals having osteoarthritis (OA). The invention also provides a selection of sequences particularly useful in diagnosing the degree of advancement of osteoarthritis of an individual and in the identification of novel therapeutic targets for OA. The invention further provides for the use of these sequences as a tool to diagnose disease progression and to monitor the efficacy of therapeutic regimens.

IDENTIFICATION OF SEQUENCES PARTICULARLY USEFUL FOR THE DIAGNOSIS AND IDENTIFICATION OF THERAPEUTIC TARGETS FOR OSTEOARTHRITIS

RELATED APPLICATION(S)

This application claims the benefit of U.S. Provisional Application No. 60/410,180 filed on September 12, 2002. The entire teachings of the above application are incorporated herein by reference.

FIELD OF THE INVENTION

The invention relates to the identification and selection of sequences which demonstrate particular advantage in identifying individuals having osteoarthritis (OA). The invention also provides a selection of sequences particularly useful in diagnosing the degree of advancement of osteoarthritis of an individual and in the identification of novel therapeutic targets for OA. The invention further provides for the use of these sequences as a tool to diagnose disease progression and to monitor the efficacy of therapeutic regimens.

BACKGROUND

Osteoarthritis (OA) is a chronic disease in which the articular cartilage that lies on the ends of bones that forms the articulating surface of the joints gradually degenerates over time. There are many factors that are believed to predispose a patient to osteoarthritis including genetic susceptibility, obesity, accidental or athletic trauma, surgery, drugs and heavy physical demands. Osteoarthritis is initiated by damage to the cartilage of joints. The two most common injuries to joints are sports-related injuries and long term “repetitive use” joint injuries. Joints most commonly affected by osteoarthritis are the knees, hips and hands. In most cases, due to the essential weight-bearing function of the knees and hips, osteoarthritis in these joints causes much more disability than osteoarthritis of the hands. As cartilage degeneration progresses, secondary changes occur in other tissues in and around joints including bone, muscle, ligaments, menisci and synovium. The net effect of the primary failure of cartilage tissue and secondary damage to other tissues is that the patient experiences pain, swelling, weakness and loss of functional ability in the afflicted joint(s). These symptoms frequently progress to the point that they have a significant impact in terms of lost productivity and or quality of life consequences for the patient.

Articular cartilage is predominantly composed of chondrocytes, type II collagen, proteoglycans and water. Articular cartilage has no blood or nerve supply and chondrocytes are the only type of cell in this tissue. Chondrocytes are responsible for manufacturing the type II collagen and proteoglycans that form the cartilage matrix. This matrix in turn has physical-chemical properties that allow for saturation of the matrix with water. The net effect of this structural-functional relationship is that articular cartilage has exceptional wear characteristics and allows for almost frictionless movement between the articulating cartilage surfaces. In the absence of osteoarthritis, articular cartilage often provides a lifetime of pain-free weight bearing and unrestricted joint motion even under demanding physical conditions.

During fetal development, articular cartilage is initially derived from the interzone of mesenchymal condensations. The mesenchymal cells cluster together and synthesize matrix proteins. The tissue is recognized as cartilage when the accumulation of matrix separates the cells, which are spherical in shape and are now called chondrocytes. During cartilage formation and growth, chondrocytes proliferate rapidly and synthesize large volumes of matrix. Prior to skeletal maturity, chondrocytes are at their highest level of metabolic activity. As skeletal maturation is reached, the rate of chondrocyte metabolic activity and cell division declines. After completion of skeletal growth, most chondrocytes do not divide but do continue to synthesize matrix proteins such as collagens, proteoglycans and other noncollagenous proteins. (Zaleske DJ. Cartilage and Bone Development. Instr Course Lect 1998;47:461-); (Buckwalter JA, Mankin HJ. Articular Cartilage: Tissue Design and Chondrocyte-Matrix Interactions. Instr Course Lect 1998;47:477-86.)

Like all living tissues, articular cartilage is continually undergoing a process of renewal in which “old” cells and matrix components are being removed (catabolic activity) and “new” cells and molecules are being produced (anabolic activity). Relative to most tissues, the rate of anabolic/catabolic turnover in articular cartilage is low. Long-term maintenance of the structural integrity of mature cartilage relies on the proper balance between matrix synthesis and degradation. Chondrocytes maintain matrix equilibrium by responding to chemical and mechanical stimuli from their environment. Appropriate and effective chondrocyte responses to these stimuli are essential for cartilage homeostasis. Disruption of homeostasis through either inadequate anabolic activity or excessive catabolic activity can result in cartilage degradation and osteoarthritis. (Westacott CI, Sharif M. Cytokines in Osteoarthritis: Mediators or Markers of Joint Destruction? Semin Arthritis Rheum 1996;25:254-72). Most tissues that are damaged and have increased catabolic activity are able to mount an increased anabolic response that allows for tissue healing. Unfortunately, chondrocytes have very limited ability to up-regulate their anabolic activity and increase the synthesis of proteoglycan and type II collagen in response to damage or loss of cartilage matrix. This fundamental limitation of chondrocytes is the core problem that has precluded the development of therapies that can prevent and cure osteoarthritis. Additionally, there is a need for a definitive diagnostic test for detecting early osteoarthritis, and a prognostic test that effectively monitors a patient's response to therapy.

Joint pain is the most common manifestation of early osteoarthritis. The pain tends to be episodic lasting days to weeks and remitting spontaneously. Although redness and swelling of joints is uncommon, joints become tender during a flare-up of osteoarthritis.

"Mild" or "early stage osteoarthritis" is difficult to diagnose. The physician relies primarily on the patient's history and physical exam to make the diagnosis of mild osteoarthritis. X-rays do not show the underlying early changes in articular cartilage. There are no recognized biochemical markers used to confirm the diagnosis of early stage osteoarthritis.

X-ray changes confirm the diagnosis of moderate osteoarthritis. X-rays of normal joints reveal well preserved symmetrical joint spaces. Changes seen on the x-rays of patients with osteoarthritis include new bone formation (osteophytes), joint space narrowing and sclerosis (bone thickening). There are no recognized biochemical markers used to confirm the diagnosis of "moderate osteoarthritis" at this stage.

The clinical exam of a joint with severe osteoarthritis reveals tenderness, joint deformity and a loss of mobility. Passive joint movement during examination may elicit crepitus or the grinding of bone-on-bone as the joint moves. X-ray changes are often profound: the joint space may be obliterated and misalignment of the joint can be seen. New bone formation (osteophytes) is prominent. Again, there are no recognized biochemical markers used to confirm the diagnosis of "severe osteoarthritis".

"Osteoarthritis" is the most common chronic joint disease. It is characterized by progressive degeneration and eventual loss of cartilage. Currently, there is a need for an effective therapy that will alter the course of osteoarthritis. Further advances in preventing, modifying or curing the osteoarthritic disease process critically depends, at least in part, on a thorough understanding of the molecular mechanisms underlying anabolic and catabolic processes in cartilage. Since cellular functions are substantially determined by the genes that the cells express, elucidating the genes expressed in articular cartilage at different developmental and disease stages will inevitably provide new insights into the molecules and mechanisms involved in cartilage formation, injury, disease and repair.

cDNA libraries from putatively normal and severely osteoarthritic human cartilage tissue have been constructed (Kumar et al., 46th Annual Meeting, Orthopaedic Res. Soc., Abstract, p. 1031). However, this work does not adequately address the differentiation of chondrocyte gene expression from differing severities of osteoarthritic human cartilage (mild, moderate, marked and severe). In addition, the "normal cartilage" samples were obtained from deceased donors more than 24 hours after death. Thus, this cDNA library does not truly reflect normal chondrocyte gene expression due to the rapid degeneration of RNA that occurs after cessation of perfusion to the sampled joint, as demonstrated by baboon studies, presented herein below.

Even upon construction of cDNA libraries from individuals demonstrating differing severities of osteoarthritis, it has been difficult to identify sequences which will be particularly useful in the diagnosis of osteoarthritis. More importantly previous studies have not identified sequences which will be either effective in diagnosing the degree of advancement of osteoarthritis so as to aid in both early detection and treatment, or in identifying novel therapeutic targets.

Even upon construction of cDNA libraries from individuals demonstrating differing severities of osteoarthritis, it has been difficult to identify sequences which will be particularly useful in the diagnosis of osteoarthritis. More importantly previous studies have not identified sequences which will be effective in diagnosing the degree of advancement of osteoarthritis so as to aid in both early detection, and treatment. Additionally previous studies have not identified sequences which will be effective in identifying agents which will be useful in treating osteoarthritis.

SUMMARY OF THE INVENTION

The invention relates to the identification and selection of sequences which demonstrate particular advantage in identifying individuals having osteoarthritis (OA). The invention also provides a selection of sequences particularly useful in diagnosing the degree of advancement of osteoarthritis of an individual and in the identification of novel therapeutic targets for OA. The invention further provides for the use of these sequences as a tool to diagnose disease progression and to monitor the efficacy of therapeutic regimens.

In one embodiment, the invention provides for an isolated biomarker comprising 51% or more genes selected from the group consisting of the nucleic acids identified in Figures 1, 3, 5, 6a and 7a.

In one embodiment, the invention provides for an isolated biomarker comprising two or more genes selected from the group consisting of the nucleic acids identified in Figures 1, 3, 5, 6a and 7a.

In one embodiment, the invention provides for an isolated biomarker consisting essentially of the nucleic acids identified in Figures 1, 3, 5, 6a and 7a.

In one embodiment, the invention provides for an isolated biomarker comprising 51% or more genes selected from the group consisting of the nucleic acids identified in Figures 6b.

In one embodiment, the invention provides for an isolated biomarker comprising two or more genes selected from the group consisting of the nucleic acids identified in Figures 6b.

In one embodiment, the invention provides for an isolated biomarker consisting essentially of the nucleic acids identified in Figures 6b.

In one embodiment, the invention provides for an isolated biomarker comprising 51% or more genes selected from the group consisting of the nucleic acids identified in Figures 6c.

In one embodiment, the invention provides for an isolated biomarker comprising two or more genes selected from the group consisting of the nucleic acids identified in Figures 6c.

In one embodiment, the invention provides for an isolated biomarker consisting essentially of the nucleic acids identified in Figures 6c.

In one embodiment, the invention provides for an isolated biomarker comprising 51% or more genes selected from the group consisting of the nucleic acids identified in Figures 2, 4, 5, 6d and 7b.

In one embodiment, the invention provides for an isolated biomarker comprising two or more genes selected from the group consisting of the nucleic acids identified in Figures 2, 4, 5, 6d and 7b.

In one embodiment, the invention provides for an isolated biomarker consisting essentially of the nucleic acids identified in Figures 2, 4, 5, 6d and 7b.

In another embodiment, the invention teaches a method of diagnosing mild osteoarthritis in an individual, comprising determining the level of expression of a biomarker in a sample where the biomarker comprises one or more polynucleotide sequences selected from the group consisting of the nucleic acids identified in Figures 1, 3, 5, 6a, 7a , whereby a difference in the level of expression of the biomarker compared to a biomarker control is indicative or predictive of mild osteoarthritis.

In yet another embodiment, the polynucleotide sequences are from the 5' region of a gene selected from the group consisting of the nucleic acids identified in Figures 1, 3, 5, 6a, 7a.

In yet another embodiment, the polynucleotide sequences are from the 3' region of a gene selected from the group consisting of the nucleic acids identified in Figures 1, 3, 5, 6a, 7a.

In yet another embodiment, the polynucleotide sequences are from the internal coding region of a gene selected from the group consisting of the nucleic acids identified in Figures 1, 3, 5, 6a, 7a.

In another embodiment, the invention teaches a method of diagnosing severe osteoarthritis in an individual, comprising determining the level of expression of a biomarker in a sample where the biomarker comprises one or more polynucleotide sequences selected from the group consisting of the nucleic acids identified in Figures 2, 4, 5, 6d, 7b whereby a difference in the level of expression of the biomarker compared to a biomarker control is indicative or predictive of severe osteoarthritis.

In yet another embodiment, the polynucleotide sequences are from the 5' region of a gene selected from the group consisting of the nucleic acids identified in Figures 2, 4, 5, 6d, 7b.

In yet another embodiment, the polynucleotide sequences are from the 3' region of a gene selected from the group consisting of the nucleic acids identified in Figures 2, 4, 5, 6d, 7b.

In yet another embodiment, the polynucleotide sequences are from the internal coding region of a gene selected from the group consisting of the nucleic acids identified in Figures 2, 4, 5, 6d, 7b.

In another embodiment, the invention teaches a method of diagnosing moderate osteoarthritis in an individual, comprising determining the level of expression of a biomarker in a sample where the biomarker comprises one or more polynucleotide sequences selected from the group consisting of the nucleic acids identified in Figures 6b, whereby a difference in the level of expression of the biomarker compared to a biomarker control is indicative or predictive of moderate osteoarthritis.

In yet another embodiment, the polynucleotide sequences are from the 5' region of a gene selected from the group consisting of the nucleic acids identified in Figures 6b.

In yet another embodiment, the polynucleotide sequences are from the 3' region of a gene selected from the group consisting of the nucleic acids identified in Figures 6b.

In yet another embodiment, the polynucleotide sequences are from the internal coding region of a gene selected from the group consisting of the nucleic acids identified in Figures 6b.

In another embodiment, the invention teaches a method of diagnosing marked osteoarthritis in an individual, comprising determining the level of expression of a biomarker in a sample where the biomarker comprises one or more polynucleotide sequences selected from the group consisting of the nucleic acids identified in Figures 6c, whereby a difference in the level of expression of the biomarker compared to a biomarker control is indicative or predictive of marked osteoarthritis.

In yet another embodiment, the polynucleotide sequences are from the 5' region of a gene selected from the group consisting of the nucleic acids identified in Figures 6c.

In yet another embodiment, the polynucleotide sequences are from the 3' region of a gene selected from the group consisting of the nucleic acids identified in Figures 6c.

In yet another embodiment, the polynucleotide sequences are from the internal coding region of a gene selected from the group consisting of the nucleic acids identified in Figures 6c.

In another embodiment, the invention teaches a method for monitoring efficacy of a drug for treatment of mild osteoarthritis in a patient, comprising the steps of obtaining a sample from a patient before treatment and a second sample from the patient after treatment; detecting the level of expression of an isolated biomarker comprising two or more genes selected from the group consisting of the nucleic acids identified in Figures 1, 3, 5, 6a and 7a. in the first sample and the second sample; and determining a difference in the level of expression of the biomarker in the first sample as compared with the second sample, where the difference in the level of expression is indicative of the efficacy of the drug for treatment of mild osteoarthritis in the patient.

In another embodiment, the invention teaches a method for monitoring efficacy of a drug for treatment of moderate osteoarthritis in a patient, comprising the steps of obtaining a sample from a patient before treatment and a second sample from the patient after treatment; detecting the level of expression of an isolated biomarker comprising two or more genes selected from the group consisting of the nucleic acids identified in Figures 6b in the first sample and the second sample; and determining a difference in the level of expression of the biomarker in the first sample as compared with the second sample, where the difference in the level of expression is indicative of the efficacy of the drug for treatment of moderate osteoarthritis in the patient.

In another embodiment, the invention teaches a method for monitoring efficacy of a drug for treatment of marked osteoarthritis in a patient, comprising the steps of obtaining a sample from a patient before treatment and a second sample from the patient after treatment; detecting the level of expression of an isolated biomarker comprising two or more genes selected from the group consisting of the nucleic acids identified in Figures 6c in the first sample and the second sample; and determining a difference in the level of expression of the biomarker in the first sample as compared with the second sample, where the difference in the level of expression is indicative of the efficacy of the drug for treatment of marked osteoarthritis in the patient.

In another embodiment, the invention teaches a method for monitoring efficacy of a drug for treatment of severe osteoarthritis in a patient, comprising the steps of obtaining a sample from a patient before treatment and a second sample from the patient after treatment; detecting the level of expression of an isolated biomarker comprising two or more genes selected from the group consisting of the nucleic acids identified in Figures 2, 4, 5, 6d and 7b in the first sample and the second sample; and determining a difference in the level of expression of the biomarker in the first sample as compared with the second sample, where the difference in the level of expression is indicative of the efficacy of the drug for treatment of severe osteoarthritis in the patient.

In another embodiment, the invention teaches a method of identifying a therapeutic agent for the treatment of osteoarthritis, the method comprising providing a sample from a patient diagnosed with osteoarthrtis, measuring the level of expression of a biomarker as set out in Figures 1 - 7 in the presence and the absence of the therapeutic agent; and comparing the level of expression measured in the presence of the therapeutic agent to the level of expression measured in the absence of the therapeutic agent, wherein a decrease in the differential expression of the biomarker is indicative of a therapeutic agent for the treatment of osteoarthritis.

In another embodiment, the sample is human cartilage.

In another embodiment, the biomarker is immobilized to a microarray.

In another embodiment, the level of expression of the biomarker is determined by hybridization to a microarray or real time RT-PCR.

In another embodiment, the invention provides for a kit comprising an isolated biomarker of one or more of the subject isolated biomarkers described above and packaging means therefore.

In another embodiment, the invention provides for a microarray comprising an isolated biomarker of one or more of the subject isolated biomarkers, described above, bound to a solid support.

BRIEF DESCRIPTION OF THE DRAWINGS

The objects and features of the invention can be better understood with reference to the following detailed description and drawings.

Figure 1 depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being down regulated in cartilage isolated from patients having mild osteoarthritis, but which are not down-regulated in patients having severe osteoarthritis, when compared with cartilage isolated from normal individuals. EST sequences matching to regions of greater than 100Kb or that are novel are identified by SEQ ID NO.

Figure 2 depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being down regulated in cartilage isolated from patients having severe osteoarthritis, but which are not down regulated in patients having mild osteoarthritis, when compared with cartilage isolated from normal individuals. EST sequences matching to regions of greater than 100Kb or that are novel are identified by SEQ ID NO.

Figure 3 depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being up regulated in cartilage in patients having mild osteoarthritis, but which are not up regulated in patients having severe osteoarthritis, when compared with cartilage isolated from normal individuals. EST sequences matching to regions of greater than 100Kb or that are novel are identified by SEQ ID NO.

Figure 4 depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being up regulated in cartilage isolated from patients having severe osteoarthritis, but which are not up regulated in patients having mild osteoarthritis, when compared with cartilage isolated from normal individuals. EST sequences matching to regions of greater than 100Kb or that are novel are identified by SEQ ID NO.

Figure 5 depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being up regulated in cartilage isolated from patients having severe osteoarthritis, but which are down regulated in patients having mild osteoarthritis, when compared with cartilage isolated from normal individuals. EST sequences matching to regions of greater than 100Kb or that are novel are identified by SEQ ID NO.

Figure 6 depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being OA stage specific markers for (a) mild OA only, (b) moderate OA only, (c) marked OA only and (d) severe OA only in OA cartilage as compared to cartilage isolated from normal individuals using the 15K ChondroChip^{TM} microarray analyis as disclosed herein.

Figure 7 depicts a chart listing the names of EST sequences and corresponding gene (Genbank Accession Number or Unigene No) and polypeptide sequences (Protein Accession Number), where known, which have been identified as being OA stage specific markers for (a) mild OA only and (b) severe OA only in OA cartilage as compared to cartilage isolated from normal individuals using the Affymetrix® U133A Array analyis as disclosed herein.

DETAILED DESCRIPTION

The invention relates to methods of profiling gene sequences expressed in human chondrocytes to identify differential gene expression in chondrocytes at different stages of disease progression. Differentially expressed genes and their products (e.g., mRNAs and proteins) can be used in methods for diagnosis, prognosis, screening, or treatment of osteoarthritis.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology and recombinant DNA techniques, which are within the skill of the art. Such techniques are explained fully in the literature. See, e.g., Sambrook, Fritsch & Maniatis, 1989, Molecular Cloning: A Laboratory Manual, Second Edition ; Oligonucleotide Synthesis (M.J. Gait, ed., 1984); Nucleic Acid Hybridization (B.D. Harnes & S.J. Higgins, eds., 1984); A Practical Guide to Molecular Cloning (B. Perbal, 1984); and a series, Methods in Enzymology (Academic Press, Inc.); Short Protocols In Molecular Biology, (Ausubel et al., ed., 1995).

Definitions

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology and recombinant DNA techniques, which are within the skill of the art. Such techniques are explained fully in the literature. See, e.g., Sambrook, Fritsch & Maniatis, 1989, Molecular Cloning: A Laboratory Manual, Second Edition ; Oligonucleotide Synthesis (M.J. Gait, ed., 1984); Nucleic Acid Hybridization (B.D. Harnes & S.J. Higgins, eds., 1984); A Practical Guide to Molecular Cloning (B. Perbal, 1984); and a series, Methods in Enzymology (Academic Press, Inc.); Short Protocols In Molecular Biology, (Ausubel et al., ed., 1995). All patents, patent applications, and publications mentioned herein, both supra and infra, are hereby incorporated by reference in their entireties.

The following definitions are provided for specific terms which are used in the following written description.

As used herein, "osteoarthritis" refers to a particular form of arthritis, and in particular a chronic disease in which the articular cartilage that lies on the ends of bones that form the articulating surface of the joints gradually degenerates over time. Cartilage degeneration can be caused by an imbalanced catabolic activity (removal of "old" cells and matrix components) and anabolic activity (production of "new" cells and molecules) (Westacott et al., 1996, *Semin Arthritis Rheum*, 25:254-72).

As used herein, "cartilage" or "articular cartilage" refers to elastic, translucent connective tissue in mammals, including human and other species. Cartilage is composed predominantly of chondrocytes, type II collagen, small amounts of other collagen types, other noncollagenous proteins, proteoglycans and water, and is usually surrounded by a perichondrium, made up of fibroblasts, in a matrix of type I and type II collagen as well as other proteoglycans. Although most cartilage becomes bone upon maturation, some cartilage remains in its original form in locations such as the nose, ears, knees, and other joints. The cartilage has no blood or nerve supply and chondrocytes are the only type of cell in this tissue.

As used herein, "chondrocyte" refers to cells from cartilage.

As used herein, "synovial fluid" refers to fluid secreted from the "synovial sac" which surrounds each joint. Synovial fluid serves to protect the joint, lubricate the joint and provide nourishment to the articular cartilage. Synovial fluid useful according to the invention contains cells from which RNA can be isolated according to methods well known in the art as described herein.

As used herein, the term "osteoarthritis (OA) staging" or "osteoarthritis (OA) grading" refers to determining the onset and or the degree of advancement or progression of the disease in the cartilage. In order to classify cartilage into different disease stages, a scoring system is used according to known methods in the art. Preferably the scoring system described in Marshall (Marshall W., 1996, *The Journal of Rheumatology*, 23:582-584, incorporated by reference) is used. According to this method, each of the 6 articular surfaces (patella, femoral trochlea, medial femoral condyle, medial tibial plateau, lateral femoral condyle and lateral tibial plateau) is assigned a cartilage grade based on the worst lesion present on that specific surface. A scoring system is then applied in which each articular surface receives an OA severity number value that reflects the cartilage severity grade for that surface. For example, if the medial femoral condyle has a grade I lesion as its most severe cartilage damage a value of 1 is assigned. A total score for the patient is then derived from the sum of the scores on the 6 articular surfaces. Based on the total score, each patient is placed into one of 4 OA groups: "mild" (early) is defined as having a Marshall score of 1-6, "moderate" is defined as having a Marshall score of 7-12, "marked" is defined as having a Marshall score of 13-18 and "severe" is defined as having a Marshall score of greater than 18.

As used herein, "diagnosis" refers to a process of determining if an individual is afflicted with a disease or ailment. "Diagnosis of OA" or "OA diagnosis", according to the invention, means determining if an individual is afflicted with OA, or, once a patient is diagnosed as having OA, determining the OA stage or grade based on the medical history and physical examination of the patient using methods known in the art (i.e., joint X ray). Preferably, OA stages are measured using the scoring system described by Marshall, *supra*. "Prognosis of OA" refers to a prediction of the probable occurrence and/or progression of OA in a patient, as well as the likelihood of recovery from OA, or the likelihood of ameliorating symptoms of OA or the likelihood of reversing the effects of OA.

As used herein, "patient" refers to a mammal who is diagnosed with arthritis and further includes a mammal who is diagnosed with the mild, moderate, marked, or severe form of OA.

As used herein, "normal" refers to an individual or group of individuals who have not shown any OA symptoms, including joint pain, and have not been diagnosed with cartilage injury or OA. Preferably said normal individual(s) is not on medication affecting OA and has not been diagnosed with any other disease. More preferably normal individuals have similar sex, age and body mass index (BMI) as compared with the test samples. "Normal", according to the invention, also refers to a samples isolated from normal individuals and includes total RNA or mRNA isolated from normal individuals. A sample taken from a normal individual can include RNA isolated from a cartilage tissue sample wherein RNA is isolated from a whole or a piece of cartilage isolated from cartilage tissue from an individual who was not diagnosed with OA and does not show any symptoms of OA at the time of tissue removal. In one embodiment of the invention, the "normal" cartilage sample is isolated at 14 hours post-mortem and the integrity of mRNA samples extracted is confirmed. A sample taken from a normal individual can also include RNA isolated from a sample wherein the sample is from an individual who has not been diagnosed with OA and does not show any symptoms of OA at the time the sampl is isolated.

As used herein, the term "biomarker" refers to a set of genes that are differentially regulated during the course of a disease.

As used herein, “isolated biomarker” means that the biomarker is isolated from and therefore not part of a mixture containing a set of OA genes including those taught in WO-02/070737 , of more than 50 genes.

The term "comprising" means including the recited sequences, i.e. the "biomarker" sequences, and also including unrecited sequences.

The term "consisting of" means that only those sequences recited are present in the biomarker and no other sequences are present in the biomarker.

The term "consisting essentially of" means that the recited sequences are present in the biomarker , i.e. OA stage-specific sequences. The term "consisting essentially of" means that additional unrecited sequences which are OA-specific are not present in the biomarker. Thus "consisting essentially of" does not exclude sequences which are not OA-specific. OA-specific or stage-specific OA, as defined herein, means that a given sequence is differentially expressed in mild, moderate, marked, and/or severe OA relative to normal (not afflicted with OA).

In one embodiment, a biomarker for the diagnosis of osteoarthritis consists essentially of the genes as set out in Figure 1-7.

In another embodiment, a biomarker for the diagnosis of mild osteoarthritis consists essentially of the genes disclosed in Figure 1, 3, 5, 6a or 7a.

In another embodiment, a biomarker for the diagnosis of severe osteoarthritis consists essentially of the genes as set out in Figure 2, 4, 5, 6d or 7b.

In another embodiment, a biomarker for the diagnosis of moderate osteoarthritis consists essentially of the genes disclosed in Figure 6b.

In another embodiment, a biomarker for the diagnosis of marked osteoarthritis consists essentially of the genes disclosed in Figure 6c.

A “gene”, as used herein, refers to DNA encoding mRNA and does not include promoters and enhancers upstream of the coding region.

As used herein, “polypeptide sequences encoded by” refers to the amino acid sequences obtained after translation of the protein coding region of a gene, as defined herein. The mRNA nucleotide sequence for each gene is identified by its Genbank Accession number (see Figures 1-7) and the corresponding polypeptide sequence is identified by a Protein Accession Number or GefSeq or RefSeq (see Figures 1-7). The Genbank Accession numbers identified in Figures 1-7 provide the location of the 5’ UTR, protein coding region (CDS) and 3’ UTR within the mRNA nucleotide sequence of each gene.

When a protein or fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to a given region or three-dimensional structure on the protein; these regions or structures are referred to as epitopes or antigenic determinants. As used herein, “antigenic fragments” refers portions of a polypeptide that contains one or more epitopes. Epitopes can be linear, comprising essentially a linear sequence from the antigen, or conformational, comprising sequences which are genetically separated by other sequences but come together structurally at the binding site for the polypeptide ligand. “Antigenic fragments”may be 5000, 1000, 500, 400, 300, 200, 100, 50 or 25 or 20 or 10 or 5 amino acids in length.

As used herein, the "5' end" refers to the end of an mRNA up to the first 1000 nucleotides or 1/3 of the mRNA(where the full length of the mRNA does not include the poly A tail) , starting at the first nucleotide of the mRNA. The "5' region" of a gene refers to a polynucleotide (double-stranded or single-stranded) located within or at the 5' end of a gene, and includes, but is not limited to, the 5' untranslated region, if that is present, and the 5' protein coding region of a gene. The 5' region is not shorter than 8 nucleotides in length and not longer than 1000 nucleotides in length. Other possible lengths of the 5' region include but are not limited to 10, 20, 25, 50, 100, 200, 400, and 500 nucleotides.

As used herein, the "3' end" refers to the end of an mRNA up to the last 1000 nucleotides or 1/3 of the mRNA, where the 3' terminal nucleotide is that terminal nucleotide of the coding or untranslated region that adjoins the poly-A tail, if one is present. That is, the 3' end of an mRNA does not include the poly-A tail, if one is present. The "3' region" of a gene refers to a polynucleotide (double-stranded or single-stranded) located within or at the 3' end of a gene, and includes, but is not limited to, the 3' untranslated region, if that is present, and the 3' protein coding region of a gene. The 3' region is not shorter than 8 nucleotides in length and not longer than 1000 nucleotides in length. Other possible lengths of the 3' region include but are not limited to 10, 20, 25, 50, 100, 200, 400, and 500 nucleotides.

As used herein, the "internal coding region" of a gene refers to a polynucleotide (double-stranded or single-stranded) located between the 5' region and the 3' region of a gene as defined herein. The "internal coding region" is not shorter than 8 nucleotides in length and not longer than 1000 nucleotides in length. Other possible lengths of the "internal coding region" include but are not limited to 10, 20, 25, 50, 100, 200, 400, and 500 nucleotides.

The 5', 3' and internal regions are non-overlapping and may, but need not be contiguous, and may, but need not, add up to the full length of the corresponding gene.

As used herein, the "amino terminal" region of a polypeptide refers to the polypeptide sequences encoded by polynucleotide sequences (double-stranded or single-stranded) located within or at the 5' end of a gene, and includes, but is not limited to, the 5' protein coding region of a gene. As used herein, the " amino terminal" region refers to the amino terminal end of a polypeptide up to the first 300 amino acids or 1/3 of the polypeptide, starting at the first amino acid of the polypeptide. The "amino terminal" region of a polypeptide is not shorter than 3 amino acids in length and not longer than 350 amino acids in length. Other possible lengths of the "amino terminal" region of a polypeptide include but are not limited to 5, 10, 20, 25, 50, 100 and 200 amino acids.

As used herein, the "carboxy terminal" region of a polypeptide refers to the polypeptide sequences encoded by polynucleotide sequences (double-stranded or single-stranded) located within or at the 3' end of a gene, and includes, but is not limited to, the 3' protein coding region of a gene. As used herein, the " carboxy terminal" region refers to the carboxy terminal end of a polypeptide up to 300 amino acids or 1/3 of the polypeptide from the last amino acid of the polypeptide. The "3' end" does not include the polyA tail, if one is present. The "carboxy terminal" region of a polypeptide is not shorter than 3 amino acids in length and not longer than 350 amino acids in length. Other possible lengths of the "carboxy terminal" region of a polypeptide include, but are not limited to, 5, 10, 20, 25, 50, 100 and 200 amino acids.

As used herein, the "internal polypeptide region" of a polypeptide refers to the polypeptide sequences located between the amino terminal region and the carboxy terminal region of a polypeptide, as defined herein. The "internal polypeptide region" of a polypeptide is not shorter than 3 amino acids in length and not longer than 350 amino acids in length. Other possible lengths of the "internal polypeptide region" of a polypeptide include, but are not limited to, 5, 10, 20, 25, 50, 100 and 200 amino acids.

The amino terminal, carboxy terminal and internal polypeptide regions of a polypeptide are non-overlapping and may, but need not be contiguous, and may, but need not, add up to the full length of the corresponding polypeptide.

As used herein, "polynucleotide" encompasses double-stranded DNA, single-stranded DNA and double-stranded or single-stranded RNA of more than 8 nucleotides in length.

As used herein, the term "oligonucleotide" is defined as a molecule comprised of two or more deoxyribonucleotides and/ or ribonucleotides, and preferably more than three. Its exact size will depend upon many factors which, in turn, depend upon the ultimate function and use of the oligonucleotide. The oligonucleotides may be from about 8 to about 1,000 nucleotides long. Although oliognucleotides of 8 to 100 nucleotides are useful in the invention, preferred oligonucleotides range from about 8 to about 15 bases in length, from about 8 to about 20 bases in length, from about 8 to about 25 bases in length, from about 8 to about 30 bases in length, from about 8 to about 40 bases in length or from about 8 to about 50 bases in length.

The term, "primer", as used herein refers to an oligonucleotide, whether occurring naturally as in a purified restriction digest or produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product, which is complementary to a nucleic acid strand, is induced, i.e., in the presence of nucleotides and an inducing agent such as a DNA polymerase and at a suitable temperature and pH. The primer may be either single-stranded or double-stranded and must be sufficiently long to prime the synthesis of the desired extension product in the presence of the inducing agent. The exact length of the primer will depend upon many factors, including temperature, source of primer and the method used. For example, for diagnostic applications, depending on the complexity of the probe sequence, the oligonucleotide primer typically contains 15-25 or more nucleotides, although it may contain fewer nucleotides. The factors involved in determining the appropriate length of primer are readily known to one of ordinary skill in the art.

As used herein, the term "probe" means oligonucleotides and analogs thereof and refers to a range of chemical species that recognize polynucleotide target sequences through hydrogen bonding interactions with the nucleotide bases of the target sequences. The probe or the target sequences may be single- or double-stranded RNA or single- or double-stranded DNA or a combination of DNA and RNA bases. A probe is at least 8 nucleotides in length and less than the length of a complete gene. A probe may be 10, 20, 30, 50, 75, 100, 150, 200, 250, 400, 500 and up to 2000 nucleotides in length as long as it is less the full length of the target gene.

The oligonucleotides and analogs thereof may be RNA or DNA, or analogs of RNA or DNA, commonly referred to as antisense oligomers or antisense oligonucleotides. Such RNA or DNA analogs comprise but are not limited to 2-'O-alkyl sugar modifications, methylphosphonate, phosphorothiate, phosphorodithioate, formacetal, 3'-thioformacetal, sulfone, sulfamate, and nitroxide backbone modifications, and analogs wherein the base moieties have been modified. In addition, analogs of oligomers may be polymers in which the sugar moiety has been modified or replaced by another suitable moiety, resulting in polymers which include, but are not limited to, morpholino analogs and peptide nucleic acid (PNA) analogs (Egholm, et al. Peptide Nucleic Acids (PNA)--Oligonucleotide Analogues with an Achiral Peptide Backbone, (1992)).

Probes may also be mixtures of any of the oligonucleotide analog types together or in combination with native DNA or RNA. At the same time, the oligonucleotides and analogs thereof may be used alone or in combination with one or more additional oliognucleotides or analogs thereof.

As used herein, a "nucleic acid target " or a “nucleic acid marker” or a “nucleic acid member on an array” or “nucleic acid target on an array” also includes nucleic acid immobilized on an array and capable of binding to a nucleic acid member of complementary sequence through sets of non-covalent bonding interactions, including complementary base pairing interactions. As used herein, a nucleic acid target may include natural (i. e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in nucleic acid target may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization (i.e., the nucleic acid target still specifically binds to its complementary sequence under standard stringent or selective hybridization conditions). Thus, nucleic acid target may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

An “mRNA” means an RNA complimentary to a gene; an mRNA includes a protein coding region and also may include 5’ end and 3’ untranslated regions (UTR).

A “coding region” refers to a DNA encoding mRNA.

A “protein coding region” refers to the portion of the mRNA encoding a polypeptide.

As used herein, “mRNA integrity” refers to the quality of mRNA extracts from cartilage samples. mRNA extracts with good integrity do not appear to be degraded when examined by methods well known in the art, for example, by RNA agarose gel electrophoresis (e.g., Ausubel et al., John Weley & Sons, Inc., 1997, *Current Protocols in Molecular Biology*). Preferably, the mRNA samples have good integrity (e.g., less than 10%, preferably less than 5%, and more preferably less than 1% of the mRNA is degraded) to truly represent the gene expression levels of the cartilage samples from which they are extracted.

As used herein, “nucleic acid(s)” is interchangeable with the term “polynucleotide(s)” and it generally refers to any polyribonucleotide or poly-deoxyribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA or any combination thereof. “Nucleic acids” include, without limitation, single- and double-stranded nucleic acids. As used herein, the term “nucleic acid(s)” also includes DNAs or RNAs as described above that contain one or more modified bases. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are “nucleic acids”. The term “nucleic acids” as it is used herein embraces such chemically, enzymatically or metabolically modified forms of nucleic acids, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including for example, simple and complex cells. A “nucleic acid” or “nucleic acid sequence” may also include regions of single- or double-stranded RNA or DNA or any combinations thereof and can include expressed sequence tags (ESTs) according to some embodiments of the invention. An EST is a portion of the expressed sequence of a gene (i.e., the "tag" of a sequence), made by reverse transcribing a region of mRNA so as to make cDNA.

As used herein, “isolated” or “purified” when used in reference to a nucleic acid means that a naturally occurring sequence has been removed from its normal cellular (e.g., chromosomal) environment or is synthesized in a non-natural environment (e.g., artificially synthesized). Thus, an “isolated” or “purified” sequence may be in a cell-free solution or placed in a different cellular environment. The term “purified” does not imply that the sequence is the only nucleotide present, but that it is essentially free (about 90-95% pure) of non-nucleotide material naturally associated with it, and thus is distinguished from isolated chromosomes.

As defined herein, a "nucleic acid array" refers a plurality of unique nucleic acids (or "nucleic acid members") attached to a support where each of the nucleic acid members is attached to a support in a unique pre-selected region. In one embodiment, the nucleic acid target attached to the surface of the support is DNA. In a preferred embodiment, the nucleic acid target attached to the surface of the support is either cDNA or oligonucleotides. In another preferred embodiment, the nucleic acid target attached to the surface of the support is cDNA synthesized by polymerase chain reaction (PCR). The term "nucleic acid", as used herein, is interchangeable with the term "polynucleotide". In another preferred embodiment, a "nucleic acid array" refers to a plurality of unique nucleic acids attached to nitrocellulose or other membranes used in Southern and/or Northern blotting techniques.

As used herein, the term "amplified", when applied to a nucleic acid sequence, refers to a process whereby one or more copies of a particular nucleic acid sequence is generated from a template nucleic acid, preferably by the method of polymerase chain reaction (Mullis and Faloona, 1987, Methods Enzymol., 155:335). "Polymerase chain reaction" or "PCR" refers to an in vitro method for amplifying a specific nucleic acid template sequence. The PCR reaction involves a repetitive series of temperature cycles and is typically performed in a volume of 50-100 μl. The reaction mix comprises dNTPs (each of the four deoxynucleotides dATP, dCTP, dGTP, and dTTP), primers, buffers, DNA polymerase, and nucleic acid template. The PCR reaction comprises providing a set of polynucleotide primers wherein a first primer contains a sequence complementary to a region in one strand of the nucleic acid template sequence and primes the synthesis of a complementary DNA strand, and a second primer contains a sequence complementary to a region in a second strand of the probe nucleic acid sequence and primes the synthesis of a complementary DNA strand, and amplifying the nucleic acid template sequence employing a nucleic acid polymerase as a template-dependent polymerizing agent under conditions which are permissive for PCR cycling steps of (i) annealing of primers required for amplification to a probe nucleic acid sequence contained within the template sequence, (ii) extending the primers wherein the nucleic acid polymerase synthesizes a primer extension product. "A set of polynucleotide primers" or "a set of PCR primers" can comprise two, three, four or more primers. In one embodiment, an exo- Pfu DNA polymerase is used to amplify a nucleic acid template in PCR reaction. Other methods of amplification include, but are not limited to, ligase chain reaction (LCR), polynucleotide-specific based amplification (NSBA), or any other method known in the art.

According to the invention, an array contemplates a specific set of genes immobilized to a solid support, or a set of corresponding 5' ends or a set of corresponding 3' ends or a set of corresponding internal coding regions. Of course, mixtures of a 5' end of one gene may be used as a target or a probe in combination with a 3' end of another gene to achieve the same result of OA diagnosis.

As used herein, "a plurality of" or "a set of" refers to more than two, for example, 3 or more, 100 or more, or 1000 or more, or 10,000 or more.

As used herein, the term "majority" refers to a number representing more than 50% (e.g., 51%, 60%, or 70%, or 80% or 90% or up to 100%) of the total members of a composition. The term "majority", when referring to an array, it means more than 50% (e.g., 51%, 60%, or 70%, or 80% or 90% or up to 100%) of the total nucleic acid members that are stably associated with the solid substrate of the array.

As used herein, "attaching" or "spotting" refers to a process of depositing a nucleic acid onto a solid substrate to form a nucleic acid array such that the nucleic acid is stably bound to the solid substrate via covalent bonds, hydrogen bonds or ionic interactions.

As used herein, "stably associated" refers to a nucleic acid that is stably bound to a solid substrate to form an array via covalent bonds, hydrogen bonds or ionic interactions such that the nucleic acid retains its unique pre-selected position relative to all other nucleic acids that are stably associated with an array, or to all other pre-selected regions on the solid substrate under conditions in which an array is typically analyzed (i.e., during one or more steps of hybridization, washes, and/or scanning, etc.).

As used herein, "solid substrate" or "solid support" refers to a material having a rigid or semi-rigid surface. The terms "substrate" and "support" are used interchangeably herein with the terms "solid substrate" and "solid support". The solid support may be biological, non-biological, organic, inorganic, or a combination of any of these, existing as particles, strands, precipitates, gels, sheets, tubing, spheres, beads, containers, capillaries, pads, slices, films, plates, slides, chips, etc. Often, the substrate is a silicon or glass surface, (poly)tetrafluoroethylene, (poly)vinylidendifluoride, polystyrene, polycarbonate, a charged membrane, such as nylon 66 or nitrocellulose, or combinations thereof. In a preferred embodiment, the solid support is glass. Preferably, at least one surface of the substrate will be substantially flat. Preferably, the solid support will contain reactive groups, including, but not limited to, carboxyl, amino, hydroxyl, thiol, and the like. In one embodiment, the solid support is optically transparent.

As used herein, “pre-selected region”, “predefined region”, or “unique position” refers to a localized area on a substrate which is, was, or is intended to be used for the deposit of a nucleic acid and is otherwise referred to herein in the alternative as a "selected region" or simply a "region." The pre-selected region may have any convenient shape, e.g., circular, rectangular, elliptical, wedge-shaped, etc. In some embodiments, a pre-selected region is smaller than about 1 cm^2, more preferably less than 1 mm^2, still more preferably less than 0.5 mm^2, and in some embodiments less than 0.1 mm^2. A nucleic acid member at a “pre-selected region”, “predefined region”, or “unique position” is one whose identity (e.g., sequence) can be determined by virtue of its position at the region or unique position.

As used herein “nucleic acid probe” or “nucleic acid probe marker” is defined as a nucleic acid capable of binding to a nucleic acid bound to an array of complementary sequence through sets of non-covalent bonding interactions including complementary base pairing interactions. The nucleic acid probe can either be an isolated nucleic acid sequence corresponding to a gene or portion thereof, or the nucleic acid probe can be total RNA or mRNA isolated from a sample. More preferably, the nucleic acid probes are single- or double-stranded DNA, RNA, or DNA-RNA hybrids, from human cartilage, total RNA extracts, and preferably from mRNA extracts.

In one embodiment, a conventional nucleic acid array of ‘target’ sequences bound to the array can be representative of the entire human genome, e.g. Affymetrix chip, and the isolated biomarker consisting of or comprising two or more of the genes described in Figures 1-7 or gene targets is applied to the conventional array.

In another embodiment, sequences bound to the array can be an isolated biomarker according to the invention and total cellular RNA is applied to the array.

As used herein, a “cartilage nucleic acid sample”, refers to nucleic acids derived from cartilage. Preferably, a cartilage nucleic acid sample is total RNA, mRNA or is a nucleic acid corresponding to RNA, for example, cDNA. A cartilage nucleic acid sample can also include a PCR product derived from total RNA, mRNA or cDNA.

As used herein, the term "hybridizing to" or "hybridization" refers to the sequence specific non-covalent binding interactions with a complementary nucleic acid, for example interactions between a probe nucleic acid sequence and a target nucleic acid member on an array.

As used herein, "specifically hybridizes", "specific hybridization" or "selective hybridization" refers to hybridization which occurs when two nucleic acid sequences are substantially complementary (at least about 65% complementary over a stretch of at least 14 to 25 nucleotides, preferably at least about 75% complementary, more preferably at least about 90% complementary). See Kanehisa, M., 1984, *Nucleic acids Res.*, 12:203, incorporated herein by reference. As a result, it is expected that a certain degree of mismatch is tolerated. Such mismatch may be small, such as a mono-, di- or tri-nucleotide. Alternatively, a region of mismatch can encompass loops, which are defined as regions in which there exists a mismatch in an uninterrupted series of four or more nucleotides. Numerous factors influence the efficiency and selectivity of hybridization of two nucleic acids, for example, the hybridization of a target nucleic acid member on an array to a probe nucleic acid sequence. These factors include nucleic acid member length, nucleotide sequence and/or composition, hybridization temperature, buffer composition and potential for steric hindrance in the region to which the nucleic acid member is required to hybridize. A positive correlation exists between the nucleic acid length and both the efficiency and accuracy with which a probe nucleic acid will anneal to a target sequence. In particular, longer sequences have a higher melting temperature (T_M) than do shorter ones, and are less likely to be repeated within a given probe sequence, thereby minimizing promiscuous hybridization. Hybridization temperature varies inversely with nucleic acid member annealing efficiency. Similarly the concentration of organic solvents, e.g., formamide, in a hybridization mixture varies inversely with annealing efficiency, while increases in salt concentration in the hybridization mixture facilitate annealing. Under stringent annealing conditions, longer nucleic acids, hybridize more efficiently than do shorter ones, which are sufficient under more permissive conditions.

As used herein, the term "differential hybridization" refers to a difference in the quantitative level of hybridization of a nucleic acid target to a first complementary nucleic acid probe as compared with the hybridization of the same nucleic acid target to a control nucleic acid probe. "Differential hybridization" can also refer to a difference in the quantitative level of hybridization of a first nucleic acid target to a nucleic acid probe as compared with a second control nucleic acid target. A "differential hybridization" means that the ratio of the level of hybridization of the first sample as compared with the control is not equal to 1.0. For example, the ratio of the level of hybridization of the target to the first probe as compared to the second probe is greater than or less than 1.0, and includes greater than 1.5 and less than 0.7, greater than 2 and less than 0.5. A differential hybridization also exists if the hybridization is detectable in one sample but not another sample.

As used herein, the term “differential expression” refers to a difference in the level of expression of a gene, as measured by the amount or level of RNA, including mRNA, complementary to the gene, in one sample as compared with the level of expression of the same gene in a second sample. Differential expression can be determined as a result of differential hybridization or through other known methods in the art used to measure the level or amount of mRNA expression.

As used herein the term “differential expression” also refers to a difference in the level of expression of a gene, as measured by the amount or level of protein encoded by the gene, in one sample as compared with the amount or level of protein expression of the same gene in a second sample. Differential protein expression can be determined as a result of binding to monoclonal antibodies that are specific for the particular protein or through other known methods in the art used to measure the level or amount of protein expression.

"Differentially increased expression” refers to 1.1 fold, 1.2 fold, 1.4 fold, 1.6 fold, 1.8 fold or more. "Differentially decreased expression" refers to less than 1.0 fold, 0.8 fold, 0.6 fold, 0.4 fold, 0.2 fold, 0.1 fold or less.

As used herein, the term “control” or “control sample” in the context of this invention refers to one or more cartilage nucleic acid samples isolated from an individual or group of individuals who are classified as normal. A control or control sample can also refer to a sample isolated from a group of patients diagnosed with disease including patients diagnosed with OA, or a patients diagnosed with a specific stage of OA. The term control or control sample can also refer to the compilation of data derived from samples of one or more individuals classified as normal or one or more individuals diagnosed with disease or a stage of disease, or one or more individuals having undergone treatment of disease.

As used herein, the term “up regulated” or “increased level of expression” in the context of this invention refers to a sequence corresponding to a gene which is expressed wherein the measure of the quantity of the sequence demonstrates an increased level of expression of the gene, as can be determined using array analysis or other similar analysis, in cartilage isolated from an individual having osteoarthritis or an identified disease state of osteoarthritis as determined by osteoarthritis staging as compared with the same gene in cartilage isolated from normal individuals or from an individual with a different identified disease state of osteoarthritis as determined by osteoarthritis staging. An "increased level of expression" according to the present invention, is an increase in expression of at least 10% or more, for example, 20%, 30%, 40%, or 50%, 60%, 70%, 80%, 90% or more, or greater than 1-fold, 2-fold, 3-fold, 4-fold, 5-fold, 10-fold, 50-fold, 100-fold or more as measured, for example, by the intensity of hybridization according to methods of the present invention. For example, up regulated sequences includes sequences having an increased level of expression in cartilage isolated from individuals characterized as having mild, moderate, marked or severe OA as compared with cartilage isolated from normal individuals.

As used herein, the term "down regulated" or "decreased level of expression" in the context of this invention refers to a sequence corresponding to a gene which is expressed wherein the measure of the quantity of the sequence demonstrates a decreased level of expression of the gene, as can be determined using microarray analysis or other similar analysis, in cartilage isolated from an individual having osteoarthritis or an identified disease state of osteoarthritis as determined by osteoarthritis staging as compared with the same gene in cartilage isolated from normal individuals or from an individual having a different identified disease state of osteoarthritis as determined by osteoarthritis staging. A "decreased level of expression" according to the present invention, is a decrease in expression of at least 10% or more, for example, 20%, 30%, 40%, or 50%, 60%, 70%, 80%, 90% or more, or a decrease of greater than 1-fold, 2-fold, 3-fold, 4-fold, 5-fold, 10-fold, 50-fold, 100-fold or more as measured, for example, by the intensity of hybridization according to methods of the present invention. For example, down regulated sequences includes sequences having a decreased level of expression in cartilage isolated from individuals characterized as having mild, moderate, marked or severe OA as compared with cartilage isolated from normal individuals.

As herein used, the term "standard stringent conditions" means hybridization will occur only if there is at least 95% and preferably, at least 97% identity between the sequences, wherein the region of identity comprises at least 10 nucleotides. In one embodiment, the sequences hybridize under stringent conditions following incubation of the sequences overnight at 42°C, followed by stringent washes (0.2X SSC at 65° C).

The degree of stringency of washing can be varied by changing the temperature, pH, ionic strength, divalent cation concentration, volume and duration of the washing. For example, the stringency of hybridization may be varied by conducting the hybridization at varying temperatures below the melting temperatures of the probes. The melting temperature of the probe may be calculated using the following formulas:

For oligonucleotide probes, between 14 and 70 nucleotides in length, the melting temperature (Tm) in degrees Celcius may be calculated using the formula: $Tm=81.5+16.6(\log [Na+]) + 0.41(\text{fraction } G+C)-(600/N)$ where N is the length of the oligonucleotide.

For example, the hybridization temperature may be decreased in increments of 5 °C from 68 °C to 42 °C in a hybridization buffer having a Na+ concentration of approximately 1M. Following hybridization, the filter may be washed with 2X SSC, 0.5% SDS at the temperature of hybridization. These conditions are considered to be "moderate stringency" conditions above 50°C and "low stringency" conditions below 50°C. A specific example of "moderate stringency" hybridization conditions is when the above hybridization is conducted at 55°C. A specific example of "low stringency" hybridization conditions is when the above hybridization is conducted at 45°C.

If the hybridization is carried out in a solution containing formamide, the melting temperature may be calculated using the equation $Tm=81.5+16.6(\log [Na^{+}]) + 0.41(\text{fraction } G + C)-(0.63\% \text{ formamide})-(600/N)$, where N is the length of the probe.

For example, the hybridization may be carried out in buffers, such as 6X SSC, containing formamide at a temperature of 42 °C. In this case, the concentration of formamide in the hybridization buffer may be reduced in 5% increments from 50% to 0% to identify clones having decreasing levels of homology to the probe. Following hybridization, the filter may be washed with 6X SSC, 0.5% SDS at 50 °C. These conditions are considered to be "moderate stringency" conditions above 25% formamide and "low stringency" conditions below 25% formamide. A specific example of "moderate stringency" hybridization conditions is when the above hybridization is conducted at 30% formamide. A specific example of "low stringency" hybridization conditions is when the above hybridization is conducted at 10% formamide.

As used herein, the term "level of expression" refers to the measurable quantity of a given nucleic acid as determined by hybridization (relative to a control) or more quantitative measurements such as real-time RT PCR, which includes use of both SYBR® green and TaqMan® technology and which corresponds in direct proportion with the extent to which the gene is expressed. The level of expression of a nucleic acid is determined by methods well known in the art. The term "differentially expressed" or "difference in the level of expression" refers to an increase or decrease in the measurable expression level of a given nucleic acid as compared with a control. As used herein, "differentially expressed" or "change in the level of expression" when referring to microarray analysis, or real-time RT PCR means the ratio of the level of expression of a given polynucleotide in one sample and the expression level of the given polynucleotide in another sample is not equal to 1.0. "Differentially expressed" or "change in the level of expression" when referring to microarray analysis or real-time RT PCR according to the invention also means the ratio of the expression level of a given polynucleotide in one sample and the expression level of the given polynucleotide in another sample where the ratio is greater than or less than 1.0 and includes greater than 1.5 and less than 0.7, as well as greater than 2.0 and less than 0.5. A nucleic acid also is said to be differentially expressed in two samples if one of the two samples contains no detectable expression of the nucleic acid. Absolute quantification of the level of expression of a nucleic acid can be accomplished by including known concentration(s) of one or more control nucleic acid species, generating a standard curve based on the amount of the control nucleic acid and extrapolating the expression level of the "unknown" nucleic acid species from the real-time RT PCR hybridization intensities of the unknown with respect to the standard curve.

As used herein, the "level of expession of a biomarker" refers to the measurable quantity of each gene of the biomarker as determined by hybridization relative to an internal standard.

As used herein, a "difference of the level of expression" when referring to a biomarker indicates a change in the ratio of the level of expression of each gene of the biomarker as compared to a biomarker control wherein the biomarker control is comprised of two populations: a) a population that has been confirmed as not having OA (normal population) using those means known in the art, and b) a control population of individuals having OA or having a specific stage of OA (disease population), wherein the disease population has been confirmed to have OA or a specific stage of OA using those means known in the art, wherein the changes in the ratio of the level of expression of each gene of the biomarker when properly weighted and compared to a normal population and a disease population is such that using a ROC analysis (Basic Principles of ROC Analysis Metz. E. Nuclear Medicine 8, 4 (1978)) or a similar statistical method

(MedCalc Software for Windows, Medcalc^{TM} version 7.2, Belgium) a person of skill in the art can determine that a patient is correctly classified as having OA or having a specific stage of OA.

For microarray analysis, the level of expression is measured by hybridization analysis using labeled probe nucleic acids according to methods well known in the art. The label on the probe nucleic acid can be a luminescent label, an enzymatic label, a radioactive label, a chemical label or a physical label. Preferably, probe nucleic acids are labeled with a fluorescent molecule. Preferred fluorescent labels include, but are not limited to: fluorescein, amino coumarin acetic acid, tetramethylrhodamine isothiocyanate (TRITC), Texas Red, Cyanine 3 (Cy3) and Cyanine 5 (Cy5).

As used herein, the term “significant match”, when referring to nucleic acid sequences, means that two nucleic acid sequences exhibit at least 65% identity, at least 70%, at least 75%, at least 80%, at least 85%, and preferably, at least 90% identity, using comparison methods well known in the art (i.e., Altschul, S.F. et al., 1997, *Nucl. Acids Res.*, 25:3389-3402; Schäffer, A.A. et al., 1999, *Bioinformatics* 15:1000-1011). As used herein, “significant match” encompasses non-contiguous or scattered identical nucleotides so long as the sequences exhibit at least 65%, and preferably, at least 70%, at least 75%, at least 80%, at least 85%, and preferably, at least 90% identity, when maximally aligned using alignment methods routine in the art.

As used herein, a “gene expression pattern” or “gene expression profile” or “nucleic acid array expression profile” comprises the pattern of differential hybridization of a plurality of probe nucleic acid sequences hybridized to a plurality of nucleic acid targets on an array as compared with a control.

As used herein, “indicative of disease” refers to an expression pattern which is diagnostic of disease or a stage of disease such that the expression pattern is found significantly more often in patients with a disease or a stage of disease than in patients without the disease or another stage of disease (as determined using routine statistical methods setting confidence levels at a minimum of 95%). Preferably, an expression pattern which is indicative of disease is found in at least 60% of patients who have the disease and is found in less than 10% of patients who do not have the disease. More preferably, an expression pattern which is indicative of disease is found in at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or more in patients who have the disease and is found in less than 10%, less than 8%, less than 5%, less than 2.5%, or less than 1% of patients who do not have the disease.

As used herein, a "therapeutic agent" or "agent" refers to a compound that increases or decreases the expression of one or more polynucleotide sequence that is differentially expressed in a chondrocyte from any two of the following developmental or osteoarthritis disease stages: (a) mild, (b) moderate, (c) marked and (d) severe, or (e) chondrocyte from a normal individual, as defined herein. A therapeutic agent according to the invention also refers to a compound that increases or decreases the anabolic activity of a chondrocyte. The invention provides for a "therapeutic agent" that 1) prevents the onset of osteoarthritis; 2) reduces, delays, or eliminates osteoarthritis symptoms such as pain, swelling, weakness and loss of functional ability in the afflicted joints; 3) reduces, delays, or eliminates cartilage degeneration, and/or enhances chondrocyte metabolic activity and cell division rates; and/or 4) restores one or more expression profiles of one or more disease-indicative nucleic acids of a patient to a profile more similar to that of an individual having an earlier stage of disease or normal individual when administered to a patient.

As used herein, the term "drug efficacy" refers to the effectiveness of a drug. "Drug efficacy" is usually measured by the clinical response of the patient who has been or is being treated with a drug. A drug is considered to have a high degree of efficacy, if it achieves desired clinical results, for example, the reduction of the symptoms of osteoarthritis or the prevention of osteoarthritis progression as described in the present specification. The amount of drug absorbed may be used to predict a patient's response. A general rule is that as the dose of a drug is increased, a greater effect is seen in the patient until a maximum desired effect is reached. If more drug is administered after the maximum point is reached, the side effects will normally increase.

As used herein, a "ligand" is a molecule that specifically binds to a polypeptide encoded by one of the genes of a biomarker of the invention. A ligand can be a nucleic acid (RNA or DNA), polypeptide, peptide or chemical compound. A ligand of the invention can be a peptide ligand, *e.g.*, a scaffold peptide, a linear peptide, or a cyclic peptide. In a preferred embodiment, the polypeptide ligand is an antibody. The antibody can be a human antibody, a chimeric antibody, a recombinant antibody, a humanized antibody, a monoclonal antibody, or a polyclonal antibody. The antibody can be an intact immunoglobulin, *e.g.*, an IgA, IgG, IgE, IgD, IgM or subtypes thereof. The antibody can be conjugated to a functional moiety (*e.g.*, a compound which has a biological or chemical function (which may be a second different polypeptide, a therapeutic drug, a cytotoxic agent, a detectable moiety, or a solid support. A polypeptide ligand e.g. antibody of the invention interacts with a polypeptide, encoded by one of the genes of a biomarker, with high affinity and specificity. For example, the polypeptide ligand binds to a polypeptide, encoded by one of the genes of a biomarker, with an affinity constant of at least 10^7 M^{-1}, preferably, at least 10^8 M^{-1}, 10^9 M^{-1}, or 10^{10} M^{-1}.

As used herein, the term "specifically binds" refers to the interaction of two molecules, e.g., a ligand and a protein or peptide, wherein the interaction is dependent upon the presence of particular structures on the respective molecules. For example, when the two molecules are protein molecules, a structure on the first molecule recognizes and binds to a structure on the second molecule, rather than to proteins in general. "Specific binding", as the term is used herein, means that a molecule binds its specific binding partner with at least 2-fold greater affinity, and preferably at least 10-fold, 20-fold, 50-fold, 100-fold or higher affinity than it binds a non-specific molecule.

As used herein, the term "immunoglobulin" refers to a protein consisting of one or more polypeptides substantially encoded by immunoglobulin genes. The recognized human immunoglobulin genes include the kappa, lambda, alpha (IgA1 and IgA2), gamma (IgG1, IgG2, IgG3, IgG4), delta, epsilon and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Full-length immunoglobulin "light chains" (about 25 Kd or 214 amino acids) are encoded by a variable region gene at the NH2-terminus (about 110 amino acids) and a kappa or lambda constant region gene at the COOH-terminus. Full-length immunoglobulin "heavy chains" (about 50 Kd or 446 amino acids), are similarly encoded by a variable region gene (about 116 amino acids) and one of the other aforementioned constant region genes, *e.g.*, gamma (encoding about 330 amino acids).

The term "antibody" also encompasses antigen-binding fragments of an antibody. The term "antigen-binding fragment" of an antibody (or simply "antibody portion," or "fragment"), as used herein, refers to one or more fragments of a full-length antibody that retain the ability to specifically bind to a polypeptide encoded by one of the genes of a biomarker of the invention.. Examples of binding fragments encompassed within the term "antigen-binding fragment" of an antibody include (i) a Fab fragment, a monovalent fragment consisting of the VL, VH, CL and CH1 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 VH and CH1 domains; (iv) a Fv fragment consisting of the VL and VH domains of a single arm of an antibody, (v) a dAb fragment (Ward *et al.*, (1989) *Nature* 341:544-546), which consists of a VH domain; and (vi) an isolated complementarity determining region (CDR). Furthermore, although the two domains of the Fv fragment, VL and VH, 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 VL and VH 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 fragment" 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. The antibody is preferably monospecific, *e.g.*, a monoclonal antibody, or antigen-binding fragment thereof. The term "monospecific antibody" refers to an antibody that displays a single binding specificity and affinity for a particular target, *e.g.*, epitope. This term includes a "monoclonal antibody" or "monoclonal antibody composition," which as used herein refer to a preparation of antibodies or fragments thereof of single molecular composition.

Identifying Chondrocyte Enriched and Chondrocyte-Specific Polynucleotide Sequences

cDNA libraries were constructed from human fetal, normal, mild, moderate, marked and/or severe osteoarthritic cartilage samples. The known and novel clones derived from these libraries were then used to construct human chondrocyte-specific microarrays to generate differential gene expression profiles useful as a diagnostic tool for detection of mild (early stage) osteoarthritis. Arrays of the invention are useful as a gold standard for osteoarthritis diagnosis and for use to identify and monitor therapeutic efficacy of new drug targets.

One effective and rapid way of characterizing gene expression patterns in a given tissue is through large-scale partial sequencing of a cDNA library produced from such a tissue to generate expressed sequence tags (ESTs). This approach has provided both quantitative and qualitative information on gene expression in a variety of tissues and cells (Adams MD, Kerlavage AR, Fleischmann RD, Fuldner RA, Bult CJ, Lee NH, et al. Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence. Nature 1995;377 Suppl:3-174.); (Hwang DM, Dempsey AA, Wang RX, Rezvani M, Barrans JD, Dai KS, et al. A Genome-Based Resource for Molecular Cardiovascular Medicine: Toward a Compendium of Cardiovascular Genes. Circulation 1997;96:4146-203.); (Mao M, Fu G, Wu JS, Zhang QH, Zhou J, Kan LX, et al. Identification of genes expressed in human CD34$^+$

hematopoietic stem/progenitor cells by expressed sequence tags and efficient full-length cDNA cloning. Proc Natl Acad Sci 1998;95:8175-80);

(Hillier LD, Lennon G, Becker M, Bonaldo MF, Chiapelli B, Chissoe S, et al. Generation and analysis of 280,000 human expressed sequence tags. Genome Res. 1996;6:807-28).

Since cDNA libraries represent gene transcription in the cells of the tissue used to construct the library, gene expression profiles generated by random sampling and sequencing is used for detailed genetic-level comparison between developmental, normal and pathological states of the tissue examined.

Many human genes are expressed at different levels in cartilage of different disease states. In some cases, a gene is not expressed at all in some disease states, and at high levels in others. According to the invention, differential analysis of chondrocyte gene expression during different stages of cartilage developmental and in different disease states using an EST-based approach has identified genes that play important roles in osteoarthritis pathogenesis and cartilage repair. The advantage of this method is that it provides gene expression information on a larger scale than other methods. The cDNA clones generated by this approach are also useful for functional studies of certain genes. This type of genomic-based approach has provided important novel insights into our understanding of the osteoarthritis disease process and provides for novel diagnostic, prognostic and therapeutic approaches.

Identification of Biomarkers Useful in Diagnosis of OA

Identification of Biomarkers Useful in Diagnosis of OA

The invention provides stage-specific genes identifiable in a sample (Figures 1-7) whose level of expression is indicative of the existence of some degree of mild, moderate, marked or severe osteoarthritis when compared with the level of expression of the same one or more genes in a normal individual. These genes, or the products of these genes, in combination are therefore useful as biomarkers to identify individuals having OA.

It would be understood by a person skilled in the art that two or more of these genes, or the products of these genes in combination are useful as biomarkers.

More specifically the number of useful combinations is described (*Feller, W.F.* , Intro to Probability Theory, 3rd Ed. Volume 1, 1968, ed. J. Wiley) and can be calculated using the general formula:

$$x!/(n)!\,(x-n)!$$

where n is the number of genes to be selected for the combination and x is the number of genes to be considered.

For example there are

$$\frac{21!}{2!\,(21-2)!} = \frac{5.1\ 10^{19}}{2.432\ 10^{17}} = 210$$

possible combinations of two genes amongst the 21 genes that are down regulated in severe OA (Figure 2).

Similarly there are 21!/3!(21-3)! possible combinations of three genes amongst the 21 genes that are down regulated in severe OA (Figure 2).

Identification of Biomarkers Useful in Identification of Stage Specific OA

The invention further provides genes as set forth in Figures 1-7 whose level of expression is distinctive for at least one stage of osteoarthritis as compared with another stage of osteoarthritis. For example, the invention provides for genes which have been identified as being down regulated (Figure 1) or up-regulated (Figure 3) in cartilage isolated from patients having mild osteoarthritis, but which are not neither down-regulated (Figure 1) or up-regulated (Figure 3) in patients having severe osteoarthritis, when compared with cartilage isolated from normal individuals. Similarly, the invention provides for genes which have been identified as being down regulated (Figure 2) or up-regulated (Figure 4) in cartilage isolated from patients having severe osteoarthritis, but which are not down regulated (Figure 2) or up-regulated (Figure 4) in patients having mild osteoarthritis, when compared with cartilage isolated from normal individuals. The invention also provides for genes that are differentially expressed at specific stages of OA e.g. mild OA only (Figure 6a and 7a), moderate OA only (Figure 6b) , marked OA only (Figure 6c) or severe OA only (Figure 6d and 7b). The invention further provides for genes that are up-regulated in severe OA and down regulated in mild OA (Figure 5).

These genes, portions of these genes, or products of these genes, either singly or in combination, are therefore useful as biomarkers to identify the stage of OA of a patient. These genes, portions thereof, or the products of these genes, either singly or in combination, are also useful as biomarkers to identify the efficacy of treatment (e.g. to be able to identify regression of disease stage as a result of successful treatment).

Methods of Using Biomarkers of the Invention to Diagnose OA

The invention contemplates the use of the genes set out in Figures 1-7 as biomarkers of OA whose level of expression is indicative of the existence of osteoarthritis when compared with the level of expression of the same gene in a normal individual. The level of expression of the biomarkers of the invention can be determined by measuring the level of the protein products of the genes, or may be determined by measuring the expression of mRNA utilizing oligonucleotides, ESTs, cDNA, DNA or RNA, or portions thereof, corresponding to one or more genes of the invention to measure the level of expression.

Oligonucleotides, ESTs, cDNA, DNA or RNA or portions thereof, for example, can be used as nucleic acid targets immobilized on an array and hybridized to total RNA, mRNA, cDNA or RT-PCR specific to one or more genes of the invention, or portions thereof, to measure the level of expression of mRNA corresponding to these genes of a test individual as compared with a control wherein differential hybridization as between the sample of the test individual as compared with the control is indicative of OA.

The invention further contemplates the use of total RNA, mRNA, cDNA or RT-PCR products corresponding to one or more genes of the invention, or portions thereof, wherein said nucleic acids can be utilized as nucleic acid probes hybridized with a commercial array (such as Affymetrix Affy U133) or a manufactured array, wherein the array is comprised of oligonucleotides cDNAs, ESTs, or DNA corresponding to one or more of the genes of the human genome. The level of hybridization of the RT-PCR products to the array as compared with a control is measured and differential hybridization of said RT-PCR products as compared with the control is indicative of OA.

The invention further contemplates the use of techniques such as quantitative real-time RT PCR (for example using SYBR®Green or TaqMan® labelled probes complementary to a gene of the invention) to determine levels of mRNA expression of the genes of the invention as compared with a control as a means of diagnosing OA.

The invention further contemplates the use of techniques known to persons skilled in the art (for example, techniques such as Western Blotting, Immunoprecipitation protein microarray analysis and the like) to measure the level of proteins corresponding to the genes of the invention to determine levels of expression of the genes of the invention as compared with a control as a means of diagnosing OA.

Thus, in one embodiment, the method of determining whether a person has OA comprises the steps of (a) hybridizing nucleic acid probes corresponding to RNA, mRNA, cDNA or RT-PCR products from a test individual to an array having one or more oligonucleotides, ESTs, cDNAs, DNA or RNA, or portions thereof corresponding to one or more genes of the invention spotted onto the array; (b) measuring the amount of hybridization of each sample to each unique location on the array; and (c) comparing the amount of hybridization of the nucleic acid probes of the test individual to the array as compared with a control wherein differential hybridization of the test sample as compared with the control is indicative of the test individual having OA.

In another embodiment, the method of determining whether a person has OA comprises the steps of (a) isolating total cellular protein from a test individual; (b) generating monoclonal antibodies specific for the polypeptides encoded by one or more genes, or portions thereof, of the invention for use as an antibody target (c) spotting the antibody targets of step (b) to an array; and (d) incubating the total cellular protein from a test individual to said array; and (e) measuring the amount of binding at each unique location on the array; and (f) comparing the amount of binding of the total cellular protein of the test individual to a control wherein the control uses total cellular protein derived from a normal individual.

Methods of Using Biomarkers of the Invention to Determine Progression of OA

The invention contemplates the use of genes as set out in Figures 1-7, or combinations thereof, whose level of expression is indicative of the existence of a certain stage of osteoarthritis. The expression levels of the marker genes in a sample may be determined by any means known in the art. For example, the level of expression of the biomarkers of the invention can be determined by measuring the level of the protein products of the genes, or may be determined utilizing oligonucleotides, ESTs, cDNA, DNA or RNA, or portions thereof, corresponding to one or more genes of the invention to measure the level of expression.

In one embodiment of the invention, oligonucleotides, ESTs, cDNA, DNA or RNA, or portions thereof, corresponding to one or more genes of the invention, are used as nucleic acid targets on an array to measure the level of expression of mRNA corresponding to these genes of a test individual as compared with a control wherein differential expression of said mRNA as compared with the control is useful as a means of determining the progression or regression of OA of the test individual.

The invention further contemplates the use of total RNA, mRNA, cDNA or RT-PCR products corresponding to one or more genes of the invention, or portions thereof, wherein said nucleic acids can be utilized as nucleic acid targets hybridized with a commercial array (such as Affymetrix Affy U133) or a manufactured array wherein the array is comprised of oligonucleotides, cDNAs or ESTs corresponding to one or more of the genes of the human genome wherein the level of hybridization of the RT-PCR products as compared with a control is useful as a means of determining the progression or regression of OA of the test individual.

The invention further contemplates the use of techniques such as quantitative real-time RT PCR (for example using SYBR®Green or TaqMan® labelled probes complementary to a gene of the invention) to determine levels of mRNA expression corresponding to the genes of the invention as compared with a control as a means of determining the progression or regression of OA of the test individual.

The invention further contemplates the use of techniques known to persons skilled in the art (for example, techniques such as Western Blotting, Immunoprecipitation, Protein arrays and the like) to measure the level of proteins corresponding to the gene of the invention to determine levels of expression of the genes of the invention as compared with a control as a means of determining progression or regression of OA of the test individual.

Thus, in one embodiment, the method of determining whether a person has OA comprises the steps of (a) hybridizing nucleic acid probes corresponding to RNA, mRNA or cDNA or RT-PCR products from a test individual to an array having one or more oligonucleotides, ESTs, cDNAs, DNA, RNA, or portions thereof corresponding to a gene of the invention spotted onto the array; (b) measuring the amount of hybridization of each unique location on the array; and (c) comparing the amount of hybridization of the nucleic acid probes of the test individual to a control wherein the control uses nucleic acid probes derived from a normal individual or derived from an individual having a different stage of OA as a means of determining disease progression or regression.

Thus, in another embodiment, the method of determining whether a person has OA comprises the steps of (a) incubating total protein from a sample of a test individual to a protein array having one or more monoclonal antibodies that specifically bind to a polypeptide encoded by a gene of the invention spotted onto the array; (b) measuring the amount of binding at each unique location on the array; and (c) comparing the amount of binding of the total cellular protein of the test individual to a control wherein the control uses total cellular protein derived from a normal individual or derived from an individual having a different stage of OA as a means of determining disease progression or regression.

Samples

Cartilage

In one aspect, cartilage is obtained from a fetus using methods known in the art. The chondrocytes of fetal cartilage have a higher level of metabolic activity and cell division rates as compared to chondrocytes from cartilage from either a normal adult or from an individual diagnosed with any stage of osteoarthritis (mild, moderate, marked and severe).

In another aspect, cartilage is obtained from a normal individual who is alive or is obtained from cartilage tissue less than 14 hours post mortem, according to methods known in the art and described below. Normal articular cartilage from human adults are obtained using any known method. However, truly normal cartilage cannot generally be sampled from live donors due to ethical considerations. Preferably, normal cartilage samples are obtained from deceased donors, within a fourteen-hour post-mortem window after cessation of perfusion to the sampled joint, to minimize the degradation of RNA observed beyond the window. In other embodiments, the "normal" tissue is obtained less than 14 hours post-mortem, such as 13, 12, 11, 10, 9, 8, 6, 4, 2,or 1 hour post-mortem. A baboon study was conducted to confirm this approach and is described herein below in Example 11. Preferably the normal cartilage is obtained less than 14 hours post-mortem. More prefably, the normal cartilage is obtained less than 12 hours post-mortem.

In another aspect of the invention, cartilage also is isolated from the following disease stages of osteoarthritis: mild, marked, moderate and severe. Human cartilage samples from osteoarthritic individuals are obtained using any known method. Preferably the cartilage is obtained from individuals undergoing arthroscopy or total knee replacements and samples are stored in liquid nitrogen until needed. In a preferred embodiment, a minimum of 0.05 g of cartilage sample is isolated to obtain 2 μg total RNA extract for the construction of a cDNA library. In another preferred embodiment, a minimum of 0.025 g cartilage sample is isolated to obtain 1 μg total RNA extract to use as a probe sample for a microarray. A cartilage sample that is useful according to the invention is in an amount that is sufficient for the detection of one or more nucleic acid sequences according to the invention.

Developmental and Disease Stages of Articular Cartilage

Chondrocytes were preferably obtained from any of the following developmental and disease stages: fetal, normal, mild osteoarthritic, moderate osteoarthritic, marked osteoarthritic or severe osteoarthritic.

Cartilage isolated from a human fetus (e.g., during fetal development) is characterized above, and is useful according to the invention for analysis of fetal chondrocytes.

Cartilage isolated from a "normal" individual, defined herein, also is useful according to the invention for isolation and analysis of "normal" chondrocytes.

Cartilage isolated from a patient diagnosed with any one of: mild, moderate, marked and severe osteoarthritis also is useful in the present invention.

In order to classify cartilage according to disease state, a scoring system is used, whereby subjective decisions by the arthroscopist are minimized. The scoring system which defines disease states described herein is that of Marshall, *supra*, incorporated herein by reference. According to this method, each of the 6 articular surfaces (patella, femoral trochlea, medial femoral condyle, medial tibial plateau, lateral femoral condyle and lateral tibial plateau) is assigned a cartilage grade based on the worst lesion present on that specific surface. A scoring system is then applied in which each articular surface receives an osteoarthritis severity number value that reflects the cartilage severity grade for that surface, as described in Table 1.

Table 1. Articular Cartilage Grading System

Grade	Articular Cartilage	Points
0	Normal	0
I	Surface intact-softening, edema	1
II	Surface-disrupted-partial thickness lesions (no extension to bone)	2
III	Full thickness lesions-extensions to intact bone	3
IV	Bone erosion or eburnation	4

For example, if the medial femoral condyle has a grade I lesion as its most severe cartilage damage, a value of 1 is assigned. A total score for the patient is then derived from the sum of the scores of the 6 articular surfaces. Based on the total score, each patient is placed into one of 4 osteoarthritis groups: mild (1-6), moderate (7-12), marked (13-18) and severe (>18).

RNA Preparation

In one aspect, RNA is isolated from cartilage samples from various disease or developmental stages as described herein. Samples can be from single patients or can be pooled from multiple patients.

Total RNA is extracted from the cartilage samples according to methods well known in the art. In one embodiment, RNA is purified from cartilage tissue according to the following method. Following removal of a tissue of interest from an individual or patient, the tissue is quick frozen in liquid nitrogen, to prevent degradation of RNA. Upon the addition of a volume of tissue guanidinium solution, tissue samples are ground in a tissuemizer with two or three 10-second bursts. To prepare tissue guanidinium solution (1 L) 590.8 g guanidinium isothiocyanate is dissolved in approximately 400 ml DEPC-treated H_2O. 25 ml of 2 M Tris-Cl, pH 7.5 (0.05 M final) and 20 ml Na_2EDTA (0.01 M final) is added, the solution is stirred overnight, the volume is adjusted to 950 ml, and 50 ml 2-ME is added.

Homogenized tissue samples are subjected to centrifugation for 10 min at 12,000 x g at 12°C. The resulting supernatant is incubated for 2 min at 65°C in the presence of 0.1 volume of 20% Sarkosyl, layered over 9 ml of a 5.7M CsCl solution (0.1g CsCl/ml), and separated by centrifugation overnight at 113,000 x g at 22°C. After careful removal of the supernatant, the tube is inverted and drained. The bottom of the tube (containing the RNA pellet) is placed in a

50 ml plastic tube and incubated overnight (or longer) at 4°C in the presence of 3 ml tissue resuspension buffer (5 mM EDTA, 0.5% (v/v) Sarkosyl, 5% (v/v) 2-ME) to allow complete resuspension of the RNA pellet. The resulting RNA solution is extracted sequentially with 25:24:1 phenol/chloroform/isoamyl alcohol, followed by 24:1 chloroform/isoamyl alcohol, precipitated by the addition of 3 M sodium acetate, pH 5.2, and 2.5 volumes of 100% ethanol, and resuspended in DEPC water (Chirgwin et al., 1979, *Biochemistry*, 18:5294).

Alternatively, RNA is isolated from cartilage tissue according to the following single step protocol. The tissue of interest is prepared by homogenization in a glass teflon homogenizer in 1 ml denaturing solution (4M guanidinium thiosulfate, 25 mM sodium citrate, pH 7.0, 0.1M 2-ME, 0.5% (w/v) N-laurylsarkosine) per 100mg tissue. Following transfer of the homogenate to a 5-ml polypropylene tube, 0.1 ml of 2 M sodium acetate, pH 4, 1 ml water-saturated phenol, and 0.2 ml of 49:1 chloroform/isoamyl alcohol are added sequentially. The sample is mixed after the addition of each component, and incubated for 15 min at 0-4°C after all components have been added. The sample is separated by centrifugation for 20 min at 10,000 x g, 4°C, precipitated by the addition of 1 ml of 100% isopropanol, incubated for 30 minutes at -20°C and pelleted by centrifugation for 10 minutes at 10,000 x g, 4°C. The resulting RNA pellet is dissolved in 0.3 ml denaturing solution, transferred to a microfuge tube, precipitated by the addition of 0.3 ml of 100% isopropanol for 30 minutes at -20°C, and centrifuged for 10 minutes at 10,000 x g at 4°C. The RNA pellet is washed in 70% ethanol, dried, and resuspended in 100-200µl DEPC-treated water or DEPC-treated 0.5% SDS (Chomczynski and Sacchi, 1987, *Anal. Biochem.*, 162:156).

Preferably, the cartilage samples are finely powdered under liquid nitrogen and total RNA is extracted using TRIzol® reagent (GIBCO/BRL). Purity and integrity of RNA is assessed by absorbance at 260/280nm and agarose gel electrophoresis followed by inspection under ultraviolet light.

Construction of cDNA libraries

cDNA libraries are constructed according to methods well known in the art (see for example Ausubel, *supra*, and Sambrook, *supra*, incorporated herein by reference).

In one aspect, cDNA samples, i.e., DNA that is complementary to RNA such as mRNA are prepared. The preparation of cDNA is well-known and well-documented in the prior art.

cDNA may be prepared according to the following method. Total cellular RNA is isolated (as described) and passed through a column of oligo(dT)-cellulose to isolate polyA RNA. The bound polyA mRNAs are eluted from the column with a low ionic strength buffer. To produce cDNA molecules, short deoxythymidine oligonucleotides (12-20 nucleotides) are hybridized to the polyA tails to be used as primers for reverse transcriptase, an enzyme that uses RNA as a template for DNA synthesis. Alternatively, or additionally, mRNA species are primed from many positions by using short oligonucleotide fragments comprising numerous sequences complementary to the mRNA of interest as primers for cDNA synthesis. The resultant RNA-DNA hybrid is converted to a double stranded DNA molecule by a variety of enzymatic steps well-known in the art (Watson et al., 1992, *Recombinant DNA*, 2nd edition, Scientific American Books, New York).

To construct a cDNA library, the poly $(A)^+$ RNA fraction may be isolated by oligo-dT cellulose chromatography (Pharmacia), and 3-5 ug poly $(A)^+$ RNA is used to construct a cDNA library in the λ ZAP Express vector (Stratagene). Alternatively, cDNA libraries may be constructed into λTriplEx2 vector through a PCR-based method, using SMART (Switching Mechanism At 5' end of RNA Transcript) cDNA Library Construction Kit (Clontech). First-strand cDNA is synthesized with an Xho I-oligo (dT) adapter-primer in the presence of 5'-methyl dCTP. After second-strand synthesis and ligation of EcoRI adapters, the cDNAs are digested with Xho I, resulting in cDNA flanked by EcoRI sites at the 5'-ends and Xho I sites at the 3'-ends. Digested cDNAs are size-fractionated in Sephacryl S-500 spin columns (Stratagene), then ligated into the λ ZAP Express vector predigested with EcoRI and Xho I. The resulting DNA/cDNA concatomers are packaged using Gigapack Gold packaging extracts. After titration, aliquots of primary packaging mix are stored in 7% DMSO at -80°C as primary library stocks, and the rest are amplified to establish stable library stocks.

From the amplified library, phage plaques are plated onto an appropriate medium. Preferably, phage plaques are plated at a density of 200-500 pfu/150 mm plate onto an *Escherichia coli* XL1-blue MRF' lawn with IPTG/X-gal for color selection. The plaques are then randomly picked and positive inserts are identified by polymerase chain reaction (PCR), according to methods well known in the art and described hereinbelow. Preferably, plaques are picked into 75 ul suspension media buffer (100 mM NaCl, 10 mM $MgSO_4$, 1 mM Tris, pH7.5, 0.02% gelatin). Phage elutes (5 ul) may be used for PCR reactions (50 ul total volume) with 125 umol/L of each dNTP (Pharmacia), 10 pmol each of modified T3 (5'-

GCCAAGCTCGAAATTAACCCTCACTAAAGGG-3' (SEQ ID NO: 19)) and T7 (5'-CCAGTGAATTGTAATACGACTCACTATAGGGCG-3' (SEQ ID NO: 20)) primers, and 2 U of Taq DNA polymerase (Pharmacia). Reactions are cycled in a DNA Thermal Cycler (Perkin-Elmer) [denaturation at 95°C for 5 minutes, followed by 30 cycles of amplification (94°C, 45 seconds; 55°C, 30 seconds; 72°C, 3 minutes) and a terminal isothermal extension (72°C, 3 minutes)]. Agarose gel electrophoresis is used to assess the presence and purity of inserts.

The PCR product is then subjected to DNA sequencing using known methods (see Ausubel et al., *supra* and Sambrook et al., *supra*). Methods of sequencing employ such enzymes as the Klenow fragment of DNA polymerase I, Sequenase® (US Biochemical Corp, Cleveland, OH), Taq polymerase (Perkin Elmer, Norwalk, CT), thermostable T7 polymerase (Amersham, Chicago, IL), or combinations of recombinant polymerases and proofreading exonucleases such as the ELONGASE Amplification System (Gibco BRL, Gaithersburg, MD). Preferably, the process is automated with machines such as the Hamilton Micro Lab 2200 (Hamilton, Reno NV), Peltier Thermal Cycler (PTC200; MJ Research, Watertown, MA), the ABI 377 DNA sequencers (Perkin Elmer), and the PE Biosystems ABI Prism 3700 DNA Analyzer..

PCR products are first subjected to DNA sequencing reactions using specific primers, BigDye™ Terminator Cycle Sequencing v2.0 Ready Reaction (PE Biosystems), Tris MgCl buffer and water in a thermocycler. Sequencing reactions were incubated at 94°C for 2 minutes, followed by 25 cycles of 94°C, 30 seconds; 55°C, 20 seconds; and 72°C, 1 minute; and 15 cycles of 94°C, 30 seconds; and 72°C for 1 minute; and 72°C for 5 minutes. Reactions were then put on hold at 4°C until purified using methods well known in the prior art (i.e. alcohol precipitation or ethanol precipitation). Automated sequencing is preferably carried out with a PE Biosystems ABI Prism 3700 DNA Analyzer.

PCR

In one aspect, nucleic acid sequences of the invention are amplified by the polymerase chain reaction (PCR). PCR methods are well-known to those skilled in the art.

PCR provides a method for rapidly amplifying a particular nucleic acid sequence by using multiple cycles of DNA replication catalyzed by a thermostable, DNA-dependent DNA polymerase to amplify the target sequence of interest. PCR requires the presence of a nucleic acid to be amplified, two single-stranded oligonucleotide primers flanking the sequence to be amplified, a DNA polymerase, deoxyribonucleoside triphosphates, a buffer and salts.

The method of PCR is well known in the art. PCR, is performed as described in Mullis and Faloona, 1987, *Methods Enzymol.,* 155: 335, herein incorporated by reference.

PCR is performed using template DNA (at least 1fg; more usefully, 1-1000 ng) and at least 25 pmol of oligonucleotide primers. A typical reaction mixture includes: 2μl of DNA, 25 pmol of oligonucleotide primer, 2.5 μl of 10H PCR buffer 1 (Perkin-Elmer, Foster City, CA), 0.4 μl of 1.25 μM dNTP, 0.15 μl (or 2.5 units) of Taq DNA polymerase (Perkin Elmer, Foster City, CA) and deionized water to a total volume of 25 μl. Mineral oil is overlaid and the PCR is performed using a programmable thermal cycler.

The length and temperature of each step of a PCR cycle, as well as the number of cycles, are adjusted according to the stringency requirements in effect. Annealing temperature and timing are determined both by the efficiency with which a primer is expected to anneal to a template and the degree of mismatch that is to be tolerated. The ability to optimize the stringency of primer annealing conditions is well within the knowledge of one of moderate skill in the art. An annealing temperature of between 30°C and 72°C is used. Initial denaturation of the template molecules normally occurs at between 92°C and 99°C for 4 minutes, followed by 20-40 cycles consisting of denaturation (94-99°C for 15 seconds to 1 minute), annealing (temperature determined as discussed above; 1-2 minutes), and extension (72°C for 1 minute). The final extension step is generally carried out for 4 minutes at 72°C, and may be followed by an indefinite (0-24 hour) step at 4°C.

Several techniques for detecting PCR products quantitatively without electrophoresis may be useful according to the invention . One of these techniques, for which there are commercially available kits such as Taqman^{TM} (Perkin Elmer, Foster City, CA), is performed with a transcript-specific antisense probe. This probe is specific for the PCR product (e.g. a nucleic acid fragment derived from a gene) and is prepared with a quencher and fluorescent reporter probe complexed to the 5' end of the oligonucleotide. Different fluorescent markers are attached to different reporters, allowing for measurement of two products in one reaction. When Taq DNA polymerase is activated, it cleaves off the fluorescent reporters of the probe bound to the template by virtue of its 5'-to-3' exonuclease activity. In the absence of the quenchers, the reporters now fluoresce. The color change in the reporters is proportional to the amount of each specific product and is measured by a fluorometer; therefore, the amount of each color is measured and the PCR product is quantified. The PCR reactions are performed in 96 well plates so that samples derived from many individuals are processed and measured simultaneously. The Taqman^{TM} system has the additional advantage of not requiring gel electrophoresis and allows for quantification when used with a standard curve.

Nucleic acid Sequences Useful According to the Invention

The invention provides for isolated nucleic acid sequences including ESTs which can be used as targets, arrayed on microarrays, and/or used for the development of therapies to treat osteoarthritis.

In one aspect, the invention is to monitor cartilage gene expression profiles of osteoarthritis patients diagnosed with different stages of osteoarthritis. A second aspect of the invention is to screen for potential therapeutic agents which alter the gene expression profile of diseased cartilage cells. The invention therefore provides for nucleic acid sequences that are present at each of the following disease stages: normal, mild osteoarthritic, moderate osteoarthritic, marked osteoarthritic and severe osteoarthritic. The invention also provides for nucleic acid sequences that are differentially expressed in any two of the following developmental and disease stages: normal, fetal, mild osteoarthritic, moderate osteoarthritic, marked osteoarthritic and severe osteoarthritic.

Nucleic acids useful according to the invention are prepared by isolating cartilage tissue samples from a developmental or disease stage (normal, fetal, mild osteoarthritic, moderate osteoarthritic, marked osteoarthritic and severe osteoarthritic), preparing a cDNA library (as described above), and performing large-scale partial sequencing (described herein) of the cDNA library to generate Expressed Sequence Tags (ESTs). An EST useful according to the invention is preferably in the range of 50-1000 nucleotides and most preferably 50-500 nucleotides in length.

The invention provides for nucleic acid sequences or ESTs that are categorized as "novel" or "known", including "known sequences with a function" and "known sequences without a known function", all defined herein.

Nucleic Acid Members and Targets

In one aspect, the invention provides nucleic acid members and targets that bind specifically to a probe nucleic acid sequence (e.g., present in a cartilage nucleic acid sample).

Nucleic acid members are stably associated with a solid support to comprise an array according to the invention. The length of a nucleic acid member can range from 50 to 6000 nucleotides, 100 to 500 nucleotides, and in other embodiments, from 500 to 1500 nucleotides. The nucleic acid members may be single or double stranded, and/or may be PCR fragments amplified from cDNA.

The invention also provides for nucleic acid sequences comprising a probe. In a certain embodiment, a probe is labeled, according to methods known in the art. A probe according to the invention is 50 to 5000 nucleotides, more preferably 100-500 nucleotides and most preferably 50 to 250 nucleotides in length. The probe may be single or double stranded, and may be a PCR fragment amplified from cDNA.

The nucleic acid members and targets according to the invention can be used to detect probe sequences such as chondrocyte enriched or chondrocyte-specific sequences, and preferably sequences whose presence in a sample are indicative ,or diagnostic or prognostic, of a stage of osteoarthritis.

The probe nucleic acid sequences to be analyzed are preferably from human cartilage and preferably comprise RNA or nucleic acid corresponding to RNA, (i.e., cDNA or amplified products of RNA or cDNAs).

Polypeptides and Antibodies

In one aspect, the invention provides for antibodies that are bound to an array and selectively bind to the polypeptides encoded by two or more of the genes of an isolated biomarker (e.g., labelled proteins encoded by the nucleotide sequences of Figure 1-7). The invention also provides for the production and purification of the polypeptides encoded by the genes of an isolated biomarker as well as the isolation, characterization and production of monoclonal antibodies that bind to the polypeptides encoded by the genes described in Figures 1-7.

Protein production

Standard recombinant nucleic acid methods can be used to express a polypeptide or antibody of the invention. Generally, a nucleic acid sequence encoding the polypeptide is cloned into a nucleic acid expression vector. Of course, if the protein includes multiple polypeptide chains, each chain must be cloned into an expression vector, *e.g.*, the same or different vectors, that are expressed in the same or different cells. If the protein is sufficiently small, *i.e.*, the protein is a peptide of less than 50 amino acids, the protein can be synthesized using automated organic synthetic methods. Polypeptides comprising the 5' region, 3' region or internal coding region of a gene of an isolated biomarker as defined herein, are expressed from nucleic acid expression vectors containing only those nucleotide sequences corresponding to the 5' region, 3' region or internal coding region of a gene of an isolated biomarker. Methods for producing antibodies directed to full length polypeptides encoded by the genes described in Figure 1-7 or polypeptides encoded by the 5' region, 3' region or internal coding regions of the genes described in Figure 1-7 are provided below.

The expression vector for expressing the polypeptide can include, in addition to the segment encoding the polypeptide or fragment thereof, regulatory sequences, including for example, a promoter, operably linked to the nucleic acid(s) of interest. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene, La Jolla, California, USA); pTrc99A, pKK223-3, pKK233-3, pDR540, and pRIT5 (Pharmacia, Uppsala, Sweden). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, and pSVL (Pharmacia). One preferred class of preferred libraries is the display library, which is described below.

Methods well known to those skilled in the art can be used to construct vectors containing a polynucleotide of the invention and appropriate transcriptional/translational control signals. These methods include *in vitro* recombinant DNA techniques, synthetic techniques and *in vivo* recombination/genetic recombination. See, for example, the techniques described in Sambrook & Russell, *Molecular Cloning: A Laboratory Manual*, 3rd Edition, Cold Spring Harbor Laboratory, N.Y. (2001) and Ausubel *et al.*, *Current Protocols in Molecular Biology* (Greene Publishing Associates and Wiley Interscience, N.Y. (1989). Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda P, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, mouse metallothionein-I, and various art-known tissue specific promoters.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* auxotrophic markers (such as *URA3, LEU2, HIS3,* and *TRPl* genes), and a promoter derived from a highly expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The polynucleotide of the invention is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, a nucleic acid of the invention can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product. Useful expression-vectors for bacteria are constructed by inserting a polynucleotide of the invention together with suitable translation initiation and termination signals, optionally in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli, Bacillus subtilis, Salmonella typhimurium* and various species within the genera Pseudomonas, Streptomyces, and Staphylococcus, although others may also be employed as a matter of choice.

As a representative but nonlimiting example, useful expression vectors for bacteria can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and pGEM1 (Promega, Madison, Wisconsin, USA).

The present invention further provides host cells containing the vectors of the present invention, wherein the nucleic acid has been introduced into the host cell using known transformation, transfection or infection methods. For example, the host cells can include members of a library constructed from the diversity strand. The host cell can be a eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected, for example, by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. *et al.*, *Basic Methods in Molecular Biology* (1986)).

Any host/vector system can be used to identify one or more of the target elements of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, CV-1 cell, COS cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular reporter polypeptide or protein or which expresses the reporter polypeptide or protein at low natural level.

The host of the present invention may also be a yeast or other fungi. In yeast, a number of vectors containing constitutive or inducible promoters may be used. For a review see, *Current Protocols in Molecular Biology*, Vol. 2, Ed. Ausubel *et al.*, Greene Publish. Assoc. & Wiley Interscience, Ch. 13 (1988); Grant *et al.* (1987) "Expression and Secretion Vectors for Yeast", *Methods Enzymol.* 153:516-544; Glover, *DNA Cloning*, Vol. II, IRL Press, Wash., D.C., Ch. 3 (1986); Bitter, *Heterologous Gene Expression in Yeast, Methods Enzymol.* 152:673-684 (1987); and *The Molecular Biology of the Yeast Saccharomyces*, Eds. Strathern *et al.*, Cold Spring Harbor Press, Vols. I and II (1982).

The host of the invention may also be a prokaryotic cell such as *E. coli*, other enterobacteriaceae such as *Serratia marescans*, bacilli, various pseudomonads, or other prokaryotes which can be transformed, transfected, and/or infected.

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell.

Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. *et al.*, (1986) *Basic Methods in Molecular Biology*). The host cells containing one of polynucleotides of the invention, can be used in a conventional manner to produce the gene product encoded by the isolated fragment (in the case of an ORF).

Any host/vector system can be used to express one or more of the diversity strands of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, CV-1 cell, COS cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook *et al.*, in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is incorporated herein by reference in its entirety.

Various mammalian cell culture systems can also be employed to express recombinant protein.

Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman (1981) *Cell* 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome-binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences.

DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. In some embodiments, the template nucleic acid also encodes a polypeptide tag, *e.g.*, penta- or hexa-histidine. The recombinant polypeptides encoded by a library of diversity strands can then be purified using affinity chromatography.

Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. A number of types of cells may act as suitable host cells for expression of the protein. Scopes ((1994) *Protein Purification: Principles and Practice*, Springer-Verlag, New York) provides a number of general methods for purifying recombinant (and non-recombinant) proteins. The method include, *e.g.*, ion-exchange chromatography, size-exclusion chromatography, affinity chromatography, selective precipitation, dialysis, and hydrophobic interaction chromatography.

Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli, Bacillus subtilis, Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods. In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods.

Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting, including polyadenylation signals. mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

Monoclonal Antibody production

Methods for generating monoclonal antibodies (mAbs) directed to a polypeptide encoded by a gene of a biomarker are described in U.S. Pat. Nos. RE 32,011, 4,902,614, 4,543,439, 4,411,993 and 4,196,265 which are incorporated herein by reference; see also Monoclonal Antibodies, Hybridomas: A New Dimension in Biological Analyses, Kennett et al (eds.), Plenum Press (1980); and Antibodies. A Laboratory Manual, Harlow and Lane (eds.), Cold Spring Harbor Laboratory Press (1988), which also are incorporated herein by reference). Other techniques that enable the production of antibodies through recombinant techniques (e.g., techniques described by William D. Huse et al., Science, 246: 1275-1281 (1989); L. Sastry et al., Proc. Natl. Acad. Sci. USA, 86: 5728-5732 (1989); and Michelle Alting-Mees et al., Strategies in Molecular Biology, 3: 1-9 (1990) involving a commercial system available from Stratacyte, La Jolla, Calif.) may also be utilized to construct monoclonal antibodies.

In one preferred embodiment, monoclonal antibodies are produced in mammalian cells. Preferred mammalian host cells for expressing the clone antibodies or antigen-binding fragments thereof include Chinese Hamster Ovary (CHO cells) (including dhfr- CHO cells, described in Urlaub and Chasin ((1980) *Proc. Natl. Acad. Sci. USA* 77:4216-4220), used with a DHFR selectable marker, *e.g.*, as described in Kaufman and Sharp ((1982) *Mol. Biol.* 159:601-621), lymphocytic cell lines, *e.g.*, NS0 myeloma cells and SP2 cells, COS cells, and a cell from a transgenic animal, *e.g.*, a transgenic mammal. For example, the cell is a mammary epithelial cell.

In addition to the nucleic acid sequence encoding the diversified immunoglobulin domain, the recombinant expression vectors may carry additional sequences, such as sequences that regulate replication of the vector in host cells (*e.g.*, origins of replication) and selectable marker genes. The selectable marker gene facilitates selection of host cells into which the vector has been introduced (see *e.g.*, U.S. Patents Nos. 4,399,216, 4,634,665 and 5,179,017). For example, typically the selectable marker gene confers resistance to drugs, such as G418, hygromycin or methotrexate, on a host cell into which the vector has been introduced. Preferred selectable marker genes include the dihydrofolate reductase (DHFR) gene (for use in *dhfr*$^-$ host cells with methotrexate selection/amplification) and the *neo* gene (for G418 selection).

In an exemplary system for recombinant expression of an antibody, or antigen-binding portion thereof, of the invention, a recombinant expression vector encoding both the antibody heavy chain and the antibody light chain is introduced into *dhfr*$^-$ CHO cells by calcium phosphate-mediated transfection. Within the recombinant expression vector, the antibody heavy and light chain genes are each operatively linked to enhancer/promoter regulatory elements (*e.g.*, derived from SV40, CMV, adenovirus and the like, such as a CMV enhancer/AdMLP promoter regulatory element or an SV40 enhancer/AdMLP promoter regulatory element) to drive high levels of transcription of the genes. The recombinant expression vector also carries a DHFR gene, which allows for selection of CHO cells that have been transfected with the vector using methotrexate selection/amplification. The selected transformant host cells are cultured to allow for expression of the antibody heavy and light chains and intact antibody is recovered from the culture medium. Standard molecular biology techniques are used to prepare the recombinant expression vector, transfect the host cells, select for transformants, culture the host cells and recover the antibody from the culture medium. For example, some antibodies can be isolated by affinity chromatography with a Protein A or Protein G.

For antibodies that include an Fc domain, the antibody production system preferably synthesizes antibodies in which the Fc region is glycosylated. For example, the Fc domain of IgG molecules is glycosylated at asparagine 297 in the CH2 domain. This asparagine is the site for modification with biantennary-type oligosaccharides. It has been demonstrated that this glycosylation is required for effector functions mediated by Fcγ receptors and complement C1q (Burton and Woof (1992) *Adv. Immunol.* 51:1-84; Jefferis *et al.* (1998) *Immunol. Rev.* 163:59-76). In a preferred embodiment, the Fc domain is produced in a mammalian expression system that appropriately glycosylates the residue corresponding to asparagine 297. The Fc domain can also include other eukaryotic post-translational modifications.

Antibodies can also be produced by a transgenic animal. For example, U.S. Patent No. 5,849,992 describes a method of expressing an antibody in the mammary gland of a transgenic mammal. A transgene is constructed that includes a milk-specific promoter and nucleic acids encoding the antibody of interest and a signal sequence for secretion. The milk produced by females of such transgenic mammals includes, secreted-therein, the antibody of interest. The antibody can be purified from the milk, or for some applications, used directly.

Data Acquisition and Analysis of EST Sequences

The invention provides for EST sequences including “novel sequences”, “novel expressed sequence tags (ESTs)” and “known sequences” including “known sequences with a function” and “known sequences with no known function”.

The generated EST sequences are searched against available databases, including the "nt", "nr", "est", "gss" and "htg" databases available through NCBI to determine putative identities for ESTs matching to known genes or other ESTs. Relative EST frequency level can then be calculated using known methods. Functional characterization of ESTs with known gene matches are made according to any known method. Preferably, generated EST sequences are compared to the non-redundant Genbank/EMBL/DDBJ and dbEST databases using the BLAST algorithm (8). A minimum value of $P = 10^{-10}$ and nucleotide sequence identity >95%, where the sequence identity is non-contiguous or scattered, are required for assignments of putative identities for ESTs matching to known genes or to other ESTs. Construction of a non-redundant list of genes represented in the EST set is done with the help of Unigene, Entrez and PubMed at the National Center for Biotechnology Information (NCBI) site (http://www.ncbi.nlm.nih.gov/). Relative gene expression frequency is calculated by dividing the number of EST copies for each gene by the total number of ESTs analyzed.

Genes are identified from ESTs according to known methods. To identify novel genes from an EST sequence, the EST should preferably be at least 100 nucleotides in length, and more preferably 150 nucleotides in length, for annotation. Preferably, the EST exhibits open reading frame characteristics (i.e., can encode a putative polypeptide).

Because of the completion of the Human Genome Project, a specific EST which matches with a genomic sequence can be mapped onto a specific chromosome based on the chromosomal location of the genomic sequence. However, no function may be known for the protein encoded by the sequence and the EST would then be considered "novel" in a functional sense. In one aspect, the invention is used to identify a novel EST which is part of a larger known sequence for which no function is known is used to determine the function of a gene comprising the EST (e.g., such as the role of expression products produced by the gene in chondrogenesis and/or in a pathology affecting chondrocytes). Alternatively, or additionally, the EST can be used to identify an mRNA or polypeptide encoded by the larger sequence as a diagnostic or prognostic marker of chondrogenesis and/or of a pathology affecting chondrocytes.

Having identified an EST corresponding to a larger sequence, other portions of the larger sequence which comprises the EST can be used in assays to elucidate gene function, e.g., to isolate polypeptides encoded by the gene, to generate antibodies specifically reactive with these polypeptides, to identify binding partners of the polypeptides (receptors, ligands, agonists, antagonists and the like) and/or to detect the expression of the gene (or lack thereof) in chondrocytes in fetal, adult, normal, and/or diseased individuals.

In another aspect, the invention provides for nucleic acid sequences that do not demonstrate a "significant match" to any of the publicly known sequences in sequence databases at the time a query is done. Longer genomic segments comprising these types of novel EST sequences can be identified by probing genomic libraries, while longer expressed sequences can be identified in cDNA libraries and/or by performing polymerase extension reactions (e.g., RACE) using EST sequences to derive primer sequences as is known in the art. Longer fragments can be mapped to particular chromosomes by FISH and other techniques and their sequences compared to known sequences in genomic and/or expressed sequence databases and further functional analysis can be performed as described above.

Identified genes can be catalogued according to their putative function. Functional characterization of ESTs with known gene matches is preferably made according to the categories described by Hwang et al (Hwang DM, Dempsey AA, Wang RX, Rezvani M, Barrans JD, Dai KS, et al. A Genome-Based Resource for Molecular Cardiovascular Medicine: Toward a Compendium of Cardiovascular Genes. Circulation 1997;96:4146-203). The distribution of genes in each of the subcellular categories is indicative of the dynamic state of the tissue and will provide important insights into the osteoarthritis disease process.

Alternative methods for analyzing ESTs are also available. For example, the ESTs from each library may be assembled into contigs with sequence alignment, editing, and assembly programs such as PHRED and PHRAP (Ewing, et al., 1998, *Genome Res.* 3:175, incorporated herein; world wide web bozeman.genome.washington.edu/).Contig redundancy is reduced by clustering nonoverlapping sequence contigs using the EST clone identification number, which is common for the nonoverlapping 5^1 and 3^1 sequence reads for a single EST cDNA clone. In one aspect, the consensus sequence from each cluster is compared to the non-redundant Genbank/EMBL/DDBJ and dbEST databases using the BLAST algorithm with the help of unigene, Entrez and PubMed at the NCBI site.

Known Nucleic acid Sequences or ESTs and Novel Nucleic acid Sequences or ESTs

An EST that exhibits a significant match (> 65%, and preferably 90% or greater, identity) to at least one existing sequence in an existing nucleic acid sequence database is characterized as a "known" sequence according to the invention. Within this category, some known ESTs match to existing sequences which encode polypeptides with known function(s) and are referred to as a "known sequence with a function". Other "known" ESTs exhibit significant match to existing sequences which encode polypeptides of unknown function(s) and are referred to as a "known sequence with no known function".

EST sequences which have no significant match (less than 65% identity) to any existing sequence in the above cited available databases are categorized as novel ESTs. These novel ESTs are considered chondrocyte-specific since they are not matched to any other genes or ESTs derived from any other tissue. To identify a novel gene from an EST sequence, the EST is preferably at least 150 nucleotides in length. More preferably, the EST encodes at least part of an open reading frame, that is, a nucleic acid sequence between a translation initiation codon and a termination codon, which is potentially translated into a polypeptide sequence.

The invention provides for known and novel nucleic acid sequences that are uniquely expressed in mild osteoarthritic, moderate osteoarthritic, marked osteoarthritic and severe osteoarthritic cartilage. Figure 6 and 7 shows OA stage specific markers with Genbank Accesion numbers and corresponding Protein Accession Numbers that are diagnostic for mild OA only (Figure 6a, 7a), moderate OA only (Figure 6b), marked OA (Figure 6c) and severe OA (Figure 6d, 7b) as identified in cartilage cDNA libraries using the methods according to the invention.

The invention also provides for known and novel nucleic acid sequences that are upregulated and downregulated in mild osteoarthritic and severe osteoarthritic cartilage.

Nucleic Acid Molecules of Potential Drug Markers

Many of the novel nucleic acid molecules of the present invention are differentially expressed between the various osteoarthritis disease states and are thus useful as potential drug targets or markers for the osteoarthritis disease process.

Microarrays

Construction of a Microarray

In one aspect, cDNAs generated from human cartilage cDNA libraries are arrayed on a microarray. Preferably, a microarray according to the invention comprises chondrocyte enriched or chondrocyte-specific genes and includes the whole spectrum of genes that are important in the osteoarthritis disease process.

Microarrays according to the invention may be used to show differential expression profiles between different developmental stages and osteoarthritis disease states for novel EST sequences. These novel EST sequences may be further characterized by cluster and alignment analyses to determine how many unique genes are represented by the novel EST sequences. The novel unique genes identified may provide a basis for identifying key markers in osteoarthritis disease progression and treatment.

In the subject methods, an array of nucleic acid members stably associated with the surface of a substantially solid support is contacted with a sample comprising probe nucleic acids under hybridization conditions sufficient to produce a hybridization pattern of complementary nucleic acid members/probe complexes in which one or more complementary nucleic acid members at unique positions on the array specifically hybridize to probe nucleic acids. The identity of probe nucleic acids which hybridize can be determined with reference to location of nucleic acid members on the array.

The nucleic acid members may be produced using established techniques such as polymerase chain reaction (PCR) and reverse transcription (RT). These methods are similar to those currently known in the art (see e.g., *PCR Strategies*, Michael A. Innis (Editor), et al. (1995) and *PCR: Introduction to Biotechniques Series*, C. R. Newton, A. Graham (1997)). Amplified nucleic acids are purified by methods well known in the art (e.g., column purification or alcohol precipitation). A nucleic acid is considered pure when it has been isolated so as to be substantially free of primers and incomplete products produced during the synthesis of the desired nucleic acid. Preferably, a purified nucleic acid will also be substantially free of contaminants which may hinder or otherwise mask the specific binding activity of the molecule.

A microarray according to the invention comprises a plurality of unique nucleic acids attached to one surface of a solid support at a density exceeding 20 different nucleic acids/cm^2, wherein each of the nucleic acids is attached to the surface of the solid support in a non-identical pre-selected region. Each associated sample on the array comprises a nucleic acid composition, of known identity, usually of known sequence, as described in greater detail below. Any conceivable substrate may be employed in the invention.

In one embodiment, the nucleic acid attached to the surface of the solid support is DNA. In a preferred embodiment, the nucleic acid attached to the surface of the solid support is cDNA or RNA. In another preferred embodiment, the nucleic acid attached to the surface of the solid support is cDNA synthesized by polymerase chain reaction (PCR). Preferably, a nucleic acid member in the array, according to the invention, is at least 50 nucleotides in length. In one embodiment, a nucleic acid member is at least 150 nucleotides in length. Preferably, a nucleic acid member is less than 1000 nucleotides in length. More preferably, a nucleic acid member is less than 500 nucleotides in length. In one embodiment, an array comprises at least 10 different nucleic acids attached to one surface of the solid support. In another embodiment, the array comprises at least 100 different nucleic acids attached to one surface of the solid support. In yet another embodiment, the array comprises at least 10,000 different nucleic acids attached to one surface of the solid support. In yet another embodiment, the array comprises at least 15,000 different nucleic acids attached to one surface of the solid support.

In the arrays of the invention, the nucleic acid compositions are stably associated with the surface of a solid support, where the support may be a flexible or rigid solid support. By "stably associated" is meant that each nucleic acid member maintains a unique position relative to the solid support under hybridization and washing conditions. As such, the samples are non-covalently or covalently stably associated with the support surface. Examples of non-covalent association include non-specific adsorption, binding based on electrostatic interactions (e.g., ion pair interactions), hydrophobic interactions, hydrogen bonding interactions, specific binding through a specific binding pair member covalently attached to the support surface, and the like. Examples of covalent binding include covalent bonds formed between the nucleic acids and a functional group present on the surface of the rigid support (e.g., --OH), where the functional group may be naturally occurring or present as a member of an introduced linking group, as described in greater detail below

The amount of nucleic acid present in each composition will be sufficient to provide for adequate hybridization and detection of probe nucleic acid sequences during the assay in which the array is employed. Generally, the amount of each nucleic acid member stably associated with the solid support of the array is at least about 0.001 ng, preferably at least about 0.02 ng and more preferably at least about 0.05 ng, where the amount may be as high as 1000 ng or higher, but will usually not exceed about 20 ng. Where the nucleic acid member is “spotted” onto the solid support in a spot comprising an overall circular dimension, the diameter of the “spot” will generally range from about 10 to 5,000 μm, usually from about 20 to 2,000 μm and more usually from about 100 to 200 μm.

Control nucleic acid members may be present on the array including nucleic acid members comprising oligonucleotides or nucleic acids corresponding to genomic DNA, housekeeping genes, vector sequences, plant nucleic acid sequence, negative and positive control genes, and the like. Control nucleic acid members are calibrating or control genes whose function is not to tell whether a particular "key" gene of interest is expressed, but rather to provide other useful information, such as background or basal level of expression.

Other control nucleic acids are spotted on the array and used as probe expression control nucleic acids and mismatch control nucleotides to monitor non-specific binding or cross-hybridization to a nucleic acid in the sample other than the probe to which the target is directed. Mismatch targets thus indicate whether a hybridization is specific or not. For example, if the probe is present, the perfectly matched targets should be consistently brighter than the mismatched targets. In addition, if all control mismatches are present, the mismatch targets are used to detect a mutation.

Solid Substrate

An array according to the invention comprises either a flexible or rigid substrate. A flexible substrate is capable of being bent, folded or similarly manipulated without breakage. Examples of solid materials which are flexible solid supports with respect to the present invention include membranes, e.g., nylon, flexible plastic films, and the like. By "rigid" is meant that the support is solid and does not readily bend, i.e., the support is not flexible. As such, the rigid substrates of the subject arrays are sufficient to provide physical support and structure to the associated nucleic acids present thereon under the assay conditions in which the array is employed, particularly under high throughput handling conditions.

The substrate may be biological, non-biological, organic, inorganic, or a combination of any of these, existing as particles, strands, precipitates, gels, sheets, tubing, spheres, beads, containers, capillaries, pads, slices, films, plates, slides, chips, etc. The substrate may have any convenient shape, such as a disc, square, sphere, circle, etc. The substrate is preferably flat or planar but may take on a variety of alternative surface configurations. The substrate may be a polymerized Langmuir Blodgett film, functionalized glass, Si, Ge, GaAs, GaP, SiO_2, SIN_4, modified silicon, or any one of a wide variety of gels or polymers such as (poly)tetrafluoroethylene, (poly)vinylidenedifluoride, polystyrene, polycarbonate, or combinations thereof. Other substrate materials will be readily apparent to those of skill in the art upon review of this disclosure.

In a preferred embodiment the substrate is flat glass or single-crystal silicon. According to some embodiments, the surface of the substrate is etched using well-known techniques to provide for desired surface features. For example, by way of formation of trenches, v-grooves, mesa structures, or the like, the synthesis regions may be more closely placed within the focus point of impinging light, be provided with reflective "mirror" structures for maximization of light collection from fluorescent sources, etc.

Surfaces on the solid substrate will usually, though not always, be composed of the same material as the substrate. Alternatively, the surface may be composed of any of a wide variety of materials, for example, polymers, plastics, resins, polysaccharides, silica or silica-based materials, carbon, metals, inorganic glasses, membranes, or any of the above-listed substrate materials. In some embodiments the surface may provide for the use of caged binding members which are attached firmly to the surface of the substrate. Preferably, the surface will contain reactive groups, which are carboxyl, amino, hydroxyl, or the like. Most preferably, the surface will be optically transparent and will have surface Si--OH functionalities, such as are found on silica surfaces.

The surface of the substrate is preferably provided with a layer of linker molecules, although it will be understood that the linker molecules are not required elements of the invention. The linker molecules are preferably of sufficient length to permit nucleic acids of the invention and on a substrate to hybridize to other nucleic acid molecules and to interact freely with molecules exposed to the substrate.

Often, the substrate is a silicon or glass surface, (poly)tetrafluoroethylene, (poly)vinylidendifluoride, polystyrene, polycarbonate, a charged membrane, such as nylon 66 or nitrocellulose, or combinations thereof. In a preferred embodiment, the solid support is glass. Preferably, at least one surface of the substrate will be substantially flat. Preferably, the surface of the solid support will contain reactive groups, including, but not limited to, carboxyl, amino, hydroxyl, thiol, or the like. In one embodiment, the surface is optically transparent. In a preferred embodiment, the substrate is a poly-lysine coated slide or Gamma amino propyl silane-coated Corning Microarray Technology-GAPS or CMT-GAP2 coated slides.

Any solid support to which a nucleic acid member may be attached may be used in the invention. Examples of suitable solid support materials include, but are not limited to, silicates such as glass and silica gel, cellulose and nitrocellulose papers, nylon, polystyrene, polymethacrylate, latex, rubber, and fluorocarbon resins such as TEFLON™.

The solid support material may be used in a wide variety of shapes including, but not limited to slides and beads. Slides provide several functional advantages and thus are a preferred form of solid support. Due to their flat surface, probe and hybridization reagents are minimized using glass slides. Slides also enable the targeted application of reagents, are easy to keep at a constant temperature, are easy to wash and facilitate the direct visualization of RNA and/or DNA immobilized on the solid support. Removal of RNA and/or DNA immobilized on the solid support is also facilitated using slides.

The particular material selected as the solid support is not essential to the invention, as long as it provides the described function. Normally, those who make or use the invention will select the best commercially available material based upon the economics of cost and availability, the expected application requirements of the final product, and the demands of the overall manufacturing process.

Spotting Method

In one aspect, the invention provides for arrays where each nucleic acid member comprising the array is spotted onto a solid support.

Preferably, spotting is carried out as follows. PCR products (~40 ul) of cDNA clones from osteoarthritis, fetal or normal cartilage cDNA libraries, in the same 96-well tubes used for amplification, are precipitated with 4 ul (1/10 volume) of 3M sodium acetate (pH 5.2) and 100 ul (2.5 volumes) of ethanol and stored overnight at –20°C. They are then centrifuged at 3,300 rpm at 4°C for 1 hour. The obtained pellets are washed with 50 ul ice-cold 70% ethanol and centrifuged again for 30 minutes. The pellets are then air-dried and resuspended well in 20ul 3X SSC or in 50% dimethylsulfoxide (DMSO) overnight. The samples are then spotted, either singly or in duplicate, onto slides using a robotic GMS 417 or 427 arrayer (Affymetrix, Ca).

The boundaries of the spots on the microarray may be marked with a diamond scriber (as the spots become invisible after post-processing). The arrays are rehydrated by suspending the slides over a dish of warm particle free ddH_20 for approximately one minute (the spots will swell slightly but will not run into each other) and snap-dried on a 70-80°C inverted heating block for 3 seconds. Nucleic acid is then UV crosslinked to the slide (Stratagene, Stratalinker, 65 mJ – set display to "650" which is 650 x 100 uJ) or the array is baked at 80C for two to four hours prior to hybridization. The arrays are placed in a slide rack. An empty slide chamber is prepared and filled with the following solution: 3.0 grams of succinic anhydride (Aldrich) was dissolved in 189 ml of 1-methyl-2-pyrrolidinone (rapid addition of reagent is crucial); immediately after the last flake of succinic anhydride is dissolved, -21.0 ml of 0.2 M sodium borate is mixed in and the solution is poured into the slide chamber. The slide rack is plunged rapidly and evenly in the slide chamber and vigorously shaken up and down for a few seconds, making sure the slides never leave the solution, and then mixed on an orbital shaker for 15-20 minutes. The slide rack is then gently plunged in 95°C ddH_20 for 2 minutes, followed by plunging five times in 95% ethanol. The slides are then air dried by allowing excess ethanol to drip onto paper towels. The arrays are stored in the slide box at room temperature until use.

Numerous methods may be used for attachment of the nucleic acid members of the invention to the substrate (a process referred to as "spotting"). For example, nucleic acids are attached using the techniques of, for example U.S. Pat. No. 5,807,522, which is incorporated herein by reference, for teaching methods of polymer attachment.

Alternatively, spotting may be carried out using contact printing technology as is known in the art.

Nucleic acid Microarrays

Any combination of the nucleic acid sequences generated from any of the chondrocyte cDNA libraries are used for the construction of a microarray. In one embodiment, the microarray is chondrocyte-specific and is anticipated to encompass the entire spectrum of genes that are important in the osteoarthritis disease process. A microarray according to the invention preferably comprises between 10 and 20,000 nucleic acid members, and more preferably comprises at least 5000 nucleic acid members. The nucleic acid members are known or novel nucleic acid sequences described herein, or any combination thereof. A microarray according to the invention is used to confirm differential gene expression profiles of genes that are specifically expressed at different cartilage development and osteoarthritis disease stages.

The invention also provides for a microarray comprising genes that are differentially expressed between normal and mild osteoarthritis patients to allow for the identification of early risk factors for osteoarthritis development. The invention also provides for a microarray for osteoarthritis diagnosis comprising one or more nucleic acid sequences that are differentially expressed between a normal individual and a patient diagnosed with mild, moderate, marked or severe osteoarthritis. Such arrays also may be used for prognostic methods to monitor a patient's response to therapy. Preferably, an array for osteoarthritis diagnosis comprises 10-20,000 nucleic acid members and more preferably 50-15,000 nucleic acid members. In one embodiment, the above microarrays are used to identify a therapeutic agent that modulates the anabolic activity of a chondrocyte or changes (e.g., increases or decreases) the level of expression of at least one nucleic acid sequence that is differentially expressed in a chondrocyte derived from any of the following chondrocyte disease or developmental stages: fetal, normal, mild osteoarthritic, moderate osteoarthritic, marked osteoarthritic and severe osteoarthritic.

The probe nucleic acid samples that are hybridized to and analyzed with a microarray of the invention are preferably from human cartilage. A limitation for this procedure lies in the amount of RNA available for use as a probe nucleic acid sample. Preferably, at least 1 microgram of total RNA is obtained for use according to this invention. This is advantageous because the amount of RNA in many cartilage biopsy samples is very minimal.

GENECHIP®

GeneChip® target arrays are manufactured through a unique and robust process— a combination of photolithography and combinatorial chemistry— that results in many of the arrays' powerful capabilities. With a calculated minimum number of synthesis steps, GeneChip technology produces arrays with hundreds of thousands of different targets packed at an extremely high density. This feature enables researchers to obtain high quality, genome-wide data using small sample volumes. Manufacture is scalable because the length of the targets, not their number, determines the number of synthesis steps required. This robust and automated production process yields arrays with highly reproducible properties, which reduces user set-up time by eliminating the need for individual labs to produce and test their own arrays.

Using technologies adapted from the semiconductor industry, GeneChip manufacturing begins with a 5-inch square quartz wafer. Initially the quartz is washed to ensure uniform hydroxylation across its surface. Because quartz is naturally hydroxylated, it provides an excellent substrate for the attachment of chemicals, such as linker molecules, that are later used to position the targets on the arrays.

The wafer is placed in a bath of silane, which reacts with the hydroxyl groups of the quartz, and forms a matrix of covalently linked molecules. The distance between these silane molecules determines the targets' packing density, allowing arrays to hold over 500,000 target locations, or features, within a mere 1.28 square centimeters. Each of these features harbors millions of identical DNA molecules. The silane film provides a uniform hydroxyl density to initiate target assembly. Linker molecules, attached to the silane matrix, provide a surface that may be spatially activated by light.

Target synthesis occurs in parallel, resulting in the addition of an A, C, T, or G nucleotide to multiple growing chains simultaneously. To define which oligonucleotide chains will receive a nucleotide in each step, photolithographic masks, carrying 18 to 20 square micron windows that correspond to the dimensions of individual features, are placed over the coated wafer. The windows are distributed over the mask based on the desired sequence of each target. When ultraviolet light is shone over the mask in the first step of synthesis, the exposed linkers become deprotected and are available for nucleotide coupling. Critical to this step is the precise alignment of the mask with the wafer before each synthesis step. To ensure that this critical step is accurately completed, chrome marks on the wafer and on the mask are perfectly aligned.

Once the desired features have been activated, a solution containing a single type of deoxynucleotide with a removable protection group is flushed over the wafer's surface. The nucleotide attaches to the activated linkers, initiating the synthesis process.

Although the process is highly efficient, some activated molecules fail to attach the new nucleotide. To prevent these "outliers" from becoming target with missing nucleotides, a capping step is used to truncate them. In addition, the side chains of the nucleotides are protected to prevent the formation of branched oligonucleotides.

In the following synthesis step, another mask is placed over the wafer to allow the next round of deprotection and coupling. The process is repeated until the targets reach their full length, usually 25 nucleotides.

Although each position in the sequence of an oligonucleotide can be occupied by 1 of 4 nucleotides, resulting in an apparent need for 25 x 4, or 100, different masks per wafer, the synthesis process can be designed to significantly reduce this requirement. Algorithms that help minimize mask usage calculate how to best coordinate target growth by adjusting synthesis rates of individual targets and identifying situations when the same mask can be used multiple times.

Once the synthesis is complete, the wafers are deprotected, diced, and the resulting individual arrays are packaged in flowcell cartridges. Depending on the number of target features per array, a single wafer can yield between 49 and 400 arrays.

The manufacturing process ends with a comprehensive series of quality control tests. Additionally, a sampling of arrays from every wafer is used to test the batch by running control hybridizations. A quantitative test of hybridization is also performed using standardized control targets.

After passing these rigorous tests, GeneChip target arrays are well prepared to help pursue ambitious goals ranging from the discovery of basic biological mechanisms to the development of new disease therapies.

THE HUMAN GENOME U133 SET

The Human Genome U133 (HG-U133) Set, consisting of two GeneChip® arrays, contains almost 45,000 target sets representing more than 39,000 transcripts derived from approximately 33,000 well-substantiated human genes. This set design uses sequences selected from GenBank®, dbEST, and RefSeq.

The sequence clusters were created from the UniGene database (Build 133, April 20, 2001). They were then refined by analysis and comparison with a number of other publicly available databases including the Washington University EST trace repository and the University of California, Santa Cruz Golden Path human genome database (April 2001 release).

The HG-U133A Array includes representation of the RefSeq database sequences and target sets related to sequences previously represented on the Human Genome U95Av2 Array. The HG-U133B Array contains primarily target sets representing EST clusters.

15 K ChondroChip™ (Version 2b)

The ChondroChip™ version 2b is chondrocyte-specific microarray chip comprising 15000 novel and known EST sequences of the chondrocyte from chondrocyte-specific cDNA libraries.

Controls on the ChondroChip™

There are two types of controls used on microarrays. First, positive controls are genes whose expression level is invariant between different stages of investigation and are used to monitor:

a) target DNA binding to the slide,
b) quality of the spotting and binding processes of the target DNA onto the slide,
c) quality of the RNA samples, and
d) efficiency of the reverse transcription and fluorescent labelling of the probes.

Second, negative controls are external controls derived from an organism unrelated to and therefore unlikely to cross-hybridize with the sample of interest. These are used to monitor for:

a) variation in background fluorescence on the slide, and
b) non-specific hybridization.

There are currently 63 controls spots on the ChondroChip™ consisting of:

Type	*No.*
Positive Controls:	2
Alien DNA	12
A. thaliana DNA	10
Spotting Buffer	41

Protein arrays

Polypeptides of the invention can be immobilized on a protein array. The protein array can be used as a diagnostic tool, *e.g.*, to screen medical samples (such as biopsies, and the like) for the presence of the polypeptides encoded by one or more of the genes of a biomarker as defined herein. The protein array can also include antibodies as well as other ligands, *e.g.*, that bind to the polypeptides encoded by the genes of a biomarker.

Methods of producing polypeptide arrays are described, *e.g.*, in De Wildt *et al.* (2000) *Nature Biotech.* 18:989-994; Lueking *et al.* (1999) *Anal. Biochem.* 270:103-111; Ge (2000) *Nuc. Acids Res.* 28:e3; MacBeath and Schreiber (2000) *Science* 289:1760-1763; WO 01/40803 , WO 99/51773A1 and U.S. Patent No. 6,406,921. Polypeptides for the array can be spotted at high speed, *e.g.*, using commercially available robotic apparati, *e.g.*, from Genetic MicroSystems and Affymetrix (Santa Clara, California, USA) or BioRobotics (Cambridge, UK). The array substrate can be, for example, nitrocellulose, plastic, glass, *e.g.*, surface-modified glass. The array can also include a porous matrix, *e.g.*, acrylamide, agarose, or another polymer.

For example, the array can be an array of antibodies, *e.g.*, as described in De Wildt, *supra*. Cells that produce the polypeptide ligands can be grown on a filter in an arrayed format. Polypeptide production is induced, and the expressed antibodies are immobilized to the filter at the location of the cell. Information about the extent of binding at each address of the array can be stored as a profile, *e.g.*, in a computer database.

In another example, the array is an array of polypeptides encoded by the genes of the invention, as described herein.

RT-PCR

In one aspect, nucleic acid sequences useful as nucleic acid targets or nucleic acid target probes of the invention can be made by amplifying RNA from cartilage using reverse transcription (RT) in combination with the polymerase chain reaction (PCR). RT-PCR methods are well-known to those skilled in the art.

Total RNA, or mRNA is used as a template and a primer specific to the transcribed portion of a gene of the invention is used to initiate reverse transcription. Primer design can be accomplished utilizing commercially available software (e.g. Primer Designer 1.0, Scientific Sofware etc.). The product of the reverse transcription is subsequently used as a template for PCR.

PCR provides a method for rapidly amplifying a particular nucleic acid sequence by using multiple cycles of DNA replication catalyzed by a thermostable, DNA-dependent DNA polymerase to amplify the probe sequence of interest. PCR requires the presence of a nucleic acid to be amplified, two single-stranded oligonucleotide primers flanking the sequence to be amplified, a DNA polymerase, deoxyribonucleoside triphosphates, a buffer and salts.

The method of PCR is well known in the art. PCR, is performed as described in Mullis and Faloona, 1987, *Methods Enzymol.,* 155: 335, herein incorporated by reference.

PCR is performed using template DNA (at least 1fg; more usefully, 1-1000 ng) and at least 25 pmol of oligonucleotide primers. A typical reaction mixture includes: 2μl of DNA, 25 pmol of oligonucleotide primer, 2.5 μl of 10H PCR buffer 1 (Perkin-Elmer, Foster City, CA), 0.4

µl of 1.25 µM dNTP, 0.15 µl (or 2.5 units) of Taq DNA polymerase (Perkin Elmer, Foster City, CA) and deionized water to a total volume of 25 µl. Mineral oil is overlaid and the PCR is performed using a programmable thermal cycler.

The length and temperature of each step of a PCR cycle, as well as the number of cycles, are adjusted according to the stringency requirements in effect. Annealing temperature and timing are determined both by the efficiency with which a primer is expected to anneal to a template and the degree of mismatch that is to be tolerated. The ability to optimize the stringency of primer annealing conditions is well within the knowledge of one of moderate skill in the art. An annealing temperature of between 30°C and 72°C is used. Initial denaturation of the template molecules normally occurs at between 92°C and 99°C for 4 minutes, followed by 20-40 cycles consisting of denaturation (94-99°C for 15 seconds to 1 minute), annealing (temperature determined as discussed above; 1-2 minutes), and extension (72°C for 1 minute). The final extension step is generally carried out for 4 minutes at 72°C, and may be followed by an indefinite (0-24 hour) step at 4°C.

Quantitative Real-Time RT PCR

Several techniques for detecting PCR products quantitatively without electrophoresis may be useful according to the invention (see for example *PCR Protocols, A Guide to Methods and Applications*, Innis et al., Academic Press, Inc. N.Y., (1990)).

One of these techniques, for which there are commercially available kits such as Taqman® (Perkin Elmer, Foster City, CA), is performed with a transcript-specific antisense probe. This probe is specific for the PCR product (e.g. a nucleic acid fragment derived from a gene) and is prepared with a quencher and fluorescent reporter probe complexed to the 5' end of the oligonucleotide. Different fluorescent markers are attached to different reporters, allowing for measurement of two products in one reaction. When Taq DNA polymerase is activated, it cleaves off the fluorescent reporters of the probe bound to the template by virtue of its 5'-to-3' exonuclease activity. In the absence of the quenchers, the reporters now fluoresce. The color change in the reporters is proportional to the amount of each specific product and is measured by a fluorometer; therefore, the amount of each color is measured and the PCR product is quantified. The PCR reactions are performed in 96 well plates so that samples derived from many individuals are processed and measured simultaneously. The Taqman® system has the additional advantage of not requiring gel electrophoresis and allows for quantification when used with a standard curve.

A second technique useful for detecting PCR products quantitatively without electrophoresis, for which there is a commercially available kit such as QuantiTect™ SYBR® Green PCR (Qiagen, Valencia California) is performed using SYBR® green as a fluorescent label which is incorporated into the PCR product during the PCR stage and produces a flourescense proportional to the amount of PCR product.

Both Taqman® and QuantiTect™ SYBR® systems can be used subsequent to reverse transcription of RNA. Reverse transcription can either be performed in the same reaction mixture as the PCR step (one-step protocol) or reverse transcription can be performed first prior to amplification utilizing PCR (two-step protocol).

Kits

The invention provides for kits for performing expression assays using the arrays of the present invention. Such kits according to the subject invention will at least comprise the arrays of the invention having associated nucleic acid members and packaging means therefore. The kits may further comprise one or more additional reagents employed in the various methods, such as: 1) primers for generating test nucleic acids; 2) dNTPs and/or rNTPs (either premixed or separate), optionally with one or more uniquely labeled dNTPs and/or rNTPs (e.g., biotinylated or Cy3 or Cy5 tagged dNTPs); 3) post synthesis labeling reagents, such as chemically active derivatives of fluorescent dyes; 4) enzymes, such as reverse transcriptases, DNA polymerases, and the like; 5) various buffer mediums, e.g., hybridization and washing buffers; 6) labeled probe purification reagents and components, like spin columns, etc.; and 7) signal generation and detection reagents, e.g., streptavidin-alkaline phosphatase conjugate, chemifluorescent or chemiluminescent substrate, and the like.

Use of a Microarray

Nucleic acid arrays according to the invention can be used in high throughput techniques that can assay a large number of nucleic acids in a sample comprising one or more target nucleic acid sequences. The arrays of the subject invention find use in a variety of applications, including gene expression analysis, diagnosis of osteoarthritis and prognosis of osteoarthritis, monitoring a patient's response to therapy, drug screening, and the like.

In one aspect, the arrays of the invention are used in, among other applications, differential gene expression assays. For example, arrays are useful in the differential expression analysis of: (a) diagnosis of disease and/or disease stage; (b) developing cartilage (e.g., fetal cartilage); (c) chondrocyte responses to external or internal stimuli; (d) cartilage/chondrocyte response to treatment; (e) cartilage tissue engineering; (f) pharmacogenomics; and the like.

For example, arrays useful in the invention can include sequences which demonstrate increased or decreased expression in patient's having osteoarthritis as compared to normal individuals. More particularly, an array useful in accordance with the invention include sequences which demonstrate increased or decreased expression in patients identified as having a particular stage of progression of the disease, for example mild osteoarthritis but not demonstrating increased or decreased expression in another stage of progression of the disease, for example severe osteoarthritis.

Arrays can be made using at least one, more preferably a majority of these sequences, as a means of diagnosing osteoarthritis, or for purposes of monitoring efficacy of treatmentand of osteoarthritis.

For example an array of the invention can be used to diagnose an individual having osteoarthritis by hybridizing a sample complementary to a patient's RNA to an array comprising sequences identified as having increased or decreased expression, and comparing the level of intensity of hybridization as between this sample and a sample complementary to RNA isolated from normal individuals to a similar or identical second array.

Similarly, an array of the invention can be used to monitor the efficacy of treatment in patients who have osteoarthritis by hybridizing a sample complementary to a patient's RNA, wherein the patient has been treated so as to reduce the progression of osteoarthritis, and determining the intensity of the hybridization as compared with the intensity of hybridization of a standard sample hybridized to another array of the invention.

Additionally, an array of the invention can be utilized to identify an agent that increases or decreases the expression of a polynucleotide sequence of the invention by incubating a chondrocyte derived from a normal individual with a candidate agent, wherein said chondrocyte is isolated from a cartilage sample obtained from said normal individual less than 14 hours post-mortem; hybridizing a sample complementary to a patient's RNA to an array of the invention, and hybridizing a sample useful as a standard to another array of the invention and comparing the intensity of expression between corresponding unique positions on the arrays.

The choice of a standard sample would be well understood by a person skilled in the art, and would include a sample complementary to RNA isolated from one or more normal individuals, wherein a normal individual is an individual not suffering from osteoarthritis. A standard sample would include a sample complementary to RNA isolated from chondrocytes.

Probe Preparation

The probes for the microarrays according to the invention are preferably derived from human cartilage.

A probe nucleic acid is capable of binding to a nucleic acid target or nucleic acid member of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation.

As used herein, a "nucleic acid derived from an mRNA transcript: or a "nucleic acid corresponding to an mRNA" refers to a nucleic acid for which synthesis of the mRNA transcript or a sub-sequence thereof has ultimately served as a template. Thus, a cDNA reverse transcribed from an mRNA, an RNA transcribed from that cDNA, a DNA amplified from the cDNA, an RNA transcribed from the amplified DNA, etc., are all derived from or correspond to the mRNA transcript and detection of such derived or corresponding products is indicative of or proportional to the presence and/or abundance of the original transcript in a sample. Thus, suitable probe nucleic acid samples include, but are not limited to, mRNA transcripts of a gene or genes, cDNA reverse transcribed from the mRNA, cRNA transcribed from the cDNA, DNA amplified from a gene or genes, RNA transcribed from amplified DNA, and the like. The nucleic acid probes used herein are preferably derived from human cartilage. Preferably, the probes are nucleic acids derived from human cartilage extracts. Nucleic acids can be single- or double-stranded DNA, RNA, or DNA-RNA hybrids synthesized from human cartilage mRNA extracts using methods known in the art, for example, reverse transcription or PCR.

In the simplest embodiment, such a nucleic acid probe comprises total mRNA or a nucleic acid sample corresponding to mRNA (e.g., cDNA) isolated from cartilage samples. In another embodiment, total mRNA is isolated from a given sample using, for example, an acid guanidinium-phenol-chloroform extraction method and polyA+ mRNA is isolated by oligo dT column chromatography or by using (dT)n magnetic beads (see, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual* (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory, (1989), or Current Protocols in Molecular Biology, F. Ausubel et al., ed. Greene Publishing and Wiley-Interscience, New York (1987). In a preferred embodiment, total RNA is extracted using TRIzol® reagent (GIBCO/BRL, Invitrogen Life Technologies, Cat. No. 15596). Purity and integrity of RNA is assessed by absorbance at 260/280nm and agarose gel electrophoresis followed by inspection under ultraviolet light.

In some embodiments, it is desirable to amplify the probe nucleic acid sample prior to hybridization. One of skill in the art will appreciate that whatever amplification method is used, if a quantitative result is desired, care must be taken to use a method that maintains or controls for the relative frequencies of the amplified nucleic acids. Methods of "quantitative" amplification are well known to those of skill in the art. For example, quantitative PCR involves simultaneously co-amplifying a known quantity of a control sequence using the same primers. This provides an internal standard that may be used to calibrate the PCR reaction. The high density array may then include targets specific to the internal standard for quantification of the amplified nucleic acid. Detailed protocols for quantitative PCR are provided in *PCR Protocols, A Guide to Methods and Applications*, Innis et al., Academic Press, Inc. N.Y., (1990).

Other suitable amplification methods include, but are not limited to polymerase chain reaction (PCR) (Innis, et al., *PCR Protocols. A Guide to Methods and Application.* Academic Press, Inc. San Diego, (1990)), ligase chain reaction (LCR) (see Wu and Wallace, 1989, *Genomics*, 4:560; Landegren, et al., 1988, *Science*, 241:1077 and Barringer, et al., 1990, *Gene*, 89:117, transcription amplification (Kwoh, et al., 1989, *Proc. Natl. Acad. Sci. USA*, 86: 1173), and self-sustained sequence replication (Guatelli, et al., 1990, *Proc. Nat. Acad. Sci. USA,* 87: 1874).

In a particularly preferred embodiment, the probe nucleic acid sample mRNA is reverse transcribed with a reverse transcriptase and a primer consisting of oligo dT and a sequence encoding the phage T7 promoter to provide single-stranded DNA template. The second DNA strand is polymerized using a DNA polymerase. After synthesis of double-stranded cDNA, T7 RNA polymerase is added and RNA is transcribed from the cDNA template. Successive rounds of transcription from each single cDNA template results in amplified RNA. Methods of *in vitro* transcription are well known to those of skill in the art (see, e.g., Sambrook, *supra.*) and this particular method is described in detail by Van Gelder, et al., 1990, *Proc. Natl. Acad. Sci. USA*, 87: 1663-1667 who demonstrate that *in vitro* amplification according to this method preserves the relative frequencies of the various RNA transcripts. Moreover, Eberwine et al. *Proc. Natl. Acad. Sci. USA*, 89: 3010-3014 provide a protocol that uses two rounds of amplification via *in vitro* transcription to achieve greater than 10^6 fold amplification of the original starting material thereby permitting expression monitoring even where biological samples are limited.

Labeling of Target or Nucleic Acid Probe

Either the target or the probe can be labeled.

Any analytically detectable marker that is attached to or incorporated into a molecule may be used in the invention. An analytically detectable marker refers to any molecule, moiety or atom which is analytically detected and quantified.

Detectable labels suitable for use in the present invention include any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include biotin for staining with labeled streptavidin conjugate, magnetic beads (e.g., Dynabeads^{TM}), fluorescent dyes (e.g., fluorescein, texas red, rhodamine, green fluorescent protein, and the like), radiolabels (e.g., ^{3}H, ^{125}I, 35S, ^{14}C, or ^{32}P), enzymes (e.g., horse radish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic (e.g., polystyrene, polypropylene, latex, etc.) beads. Patents teaching the use of such labels include U.S. Pat. Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241, the entireties of which are incorporated by reference herein.

Means of detecting such labels are well known to those of skill in the art. Thus, for example, radiolabels may be detected using photographic film or scintillation counters, fluorescent markers may be detected using a photodetector to detect emitted light. Enzymatic labels are typically detected by providing the enzyme with a substrate and detecting the reaction product produced by the action of the enzyme on the substrate, and colorimetric labels are detected by simply visualizing the colored label.

The labels may be incorporated by any of a number of means well known to those of skill in the art. However, in a preferred embodiment, the label is simultaneously incorporated during the amplification step in the preparation of the sample nucleic acids. Thus, for example, polymerase chain reaction (PCR) with labeled primers or labeled nucleotides will provide a labeled amplification product. In a preferred embodiment, transcription amplification, as described above, using a labeled nucleotide (e.g. fluorescein-labeled UTP and/or CTP) incorporates a label into the transcribed nucleic acids.

Alternatively, a label may be added directly to the original nucleic acid sample (e.g., mRNA, polyA mRNA, cDNA, etc.) or to the amplification product after the amplification is completed. Means of attaching labels to nucleic acids are well known to those of skill in the art and include, for example, nick translation or end-labeling (e.g. with a labeled RNA) by kinasing of the nucleic acid and subsequent attachment (ligation) of a nucleic acid linker joining the sample nucleic acid to a label (e.g., a fluorophore).

In a preferred embodiment, the fluorescent modifications are by cyanine dyes e.g. Cy-3/Cy-5 dUTP, Cy-3/Cy-5 dCTP (Amersham Pharmacia) or alexa dyes (Khan,et al., 1998, *Cancer Res.* 58:5009-5013).

In a preferred embodiment, the two probe samples used for comparison are labeled with different fluorescent dyes which produce distinguishable detection signals, for example, probes made from normal cartilage are labeled with Cy5 and probes made from mild osteoarthritis cartilage are labeled with Cy3. The differently labeled probe samples are hybridized to the same microarray simultaneously. In a preferred embodiment, the labeled probes are purified using methods known in the art, e.g., by ethanol purification or column purification.

In a preferred embodiment, the probe will include one or more control molecules which hybridize to control targets on the microarray to normalize signals generated from the microarray. Preferably, labeled normalization probes are nucleic acid sequences that are perfectly complementary to control oligonucleotides that are spotted onto the microarray as described above. The signals obtained from the normalization controls after hybridization provide a control for variations in hybridization conditions, label intensity, "reading" efficiency and other factors that may cause the signal of a perfect hybridization to vary between arrays. In a preferred embodiment, signals (e.g., fluorescence intensity) read from all other targets in the array are divided by the signal (e.g., fluorescence intensity) from the control targets, thereby normalizing the measurements.

Preferred normalization probes are selected to reflect the average length of the other probes present in the sample, however, they are selected to cover a range of lengths. The normalization control(s) also can be selected to reflect the (average) base composition of the other targets in the array, however, in a preferred embodiment, only one or a few normalization targets are used and they are selected such that they hybridize well (i.e., have no secondary structure and do not self hybridize) and do not match any probe molecules.

Normalization targets are localized at any position in the array or at multiple positions throughout the array to control for spatial variation in hybridization efficiency. In a preferred embodiment, normalization controls are located at the corners or edges of the array as well as in the middle.

Hybridization Conditions

Nucleic acid hybridization involves providing a denatured target nucleic acid member and probe nucleic acid under conditions where the probe nucleic acid member and its complementary target can form stable hybrid duplexes through complementary base pairing. The nucleic acids that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids. Under low stringency conditions (e.g., low temperature and/or high salt) hybrid duplexes (e.g., DNA:DNA, RNA:RNA, or RNA:DNA) will form even where the annealed sequences are not perfectly complementary. Thus specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (e.g., higher temperature or lower salt) successful hybridization requires fewer mismatches.

The invention provides for hybridization conditions comprising the Dig hybridization mix (Boehringer); or formamide-based hybridization solutions, for example as described in Ausubel et al., *supra* and Sambrook et al. *supra*.

Methods of optimizing hybridization conditions are well known to those of skill in the art (see, e.g., *Laboratory Techniques in Biochemistry and Molecular Biology*, Vol. 24: *Hybridization With Nucleic acid Probes*, P. Tijssen, ed. Elsevier, N.Y., (1993)).

Following hybridization, non-hybridized labeled or unlabeled nucleic acid is removed from the support surface, conveniently by washing, thereby generating a pattern of hybridized probe nucleic acid on the substrate surface. A variety of wash solutions are known to those of skill in the art and may be used. The resultant hybridization patterns of labeled, hybridized oligonucleotides and/or nucleic acids may be visualized or detected in a variety of ways, with the particular manner of detection being chosen based on the particular label of the test nucleic acid, where representative detection means include scintillation counting, autoradiography, fluorescence measurement, calorimetric measurement, light emission measurement and the like.

Image Acquisition and Data Analysis

Following hybridization and any washing step(s) and/or subsequent treatments, as described above, the resultant hybridization pattern is detected. In detecting or visualizing the hybridization pattern, the intensity or signal value of the label will be not only be detected but quantified, by which is meant that the signal from each spot of the hybridization will be measured and compared to a unit value corresponding to the signal emitted by a known number of end labeled probe nucleic acids to obtain a count or absolute value of the copy number of each end-labeled probe that is hybridized to a particular spot on the array in the hybridization pattern.

Methods for analyzing the data collected from hybridization to arrays are well known in the art. For example, where detection of hybridization involves a fluorescent label, data analysis can include the steps of determining fluorescent intensity as a function of substrate position from the data collected, removing outliers, i.e., data deviating from a predetermined statistical distribution, and calculating the relative binding affinity of the test nucleic acids from the remaining data. The resulting data is displayed as an image with the intensity in each region varying according to the binding affinity between associated oligonucleotides and/or nucleic acids and the test nucleic acids.

The following detection protocol is used for the simultaneous analysis of two cartilage samples to be compared, where each sample is labeled with a different fluorescent dye.

Each element of the microarray is scanned for the first fluorescent color. The intensity of the fluorescence at each array element is proportional to the expression level of that gene in the sample.

The scanning operation is repeated for the second fluorescent label. The ratio of the two fluorescent intensities provides a highly accurate and quantitative measurement of the relative gene expression level in the two tissue samples.

In a preferred embodiment, fluorescence intensities of immobilized probe nucleic acid sequences were determined from images taken with a custom confocal microscope equipped with laser excitation sources and interference filters appropriate for the Cy3 and Cy5 fluors. Separate scans were taken for each fluor at a resolution of 225 μm^2 per pixel and 65,536 gray levels. Image segmentation to identify areas of hybridization, normalization of the intensities between the two fluor images, and calculation of the normalized mean fluorescent values at each probe are as described (Khan, et al., 1998, *Cancer Res.* 58:5009-5013. Chen, et al., 1997, *Biomed. Optics* 2:364-374). Normalization between the images is used to adjust for the different efficiencies in labeling and detection with the two different fluors. This is achieved by equilibrating to a value of one the signal intensity ratio of a set of internal control genes spotted on the array.

In another preferred embodiment, the array is scanned in the Cy 3 and Cy5 channels and stored as separate 16-bit TIFF images. The images are incorporated and analysed using software which includes a gridding process to capture the hybridization intensity data from each spot on the array. The fluorescence intensity and background-subtracted hybridization intensity of each spot is collected and a ratio of measured mean intensities of Cy5 to Cy3 is calculated. A liner regression approach is used for normalization and assumes that a scatter plot of the measured Cy5 versus Cy3 intensities should have a scope of one. The average of the ratios is calculated and used to rescale the data and adjust the slope to one. A post-normalization cutoff of greater than 1.0 fold up- or down-regulation is used to identify differentially expressed genes.

Following detection or visualization, the hybridization pattern is used to determine quantitative information about the genetic profile of the labeled probe nucleic acid sample that was contacted with the array to generate the hybridization pattern, as well as the physiological source from which the labeled probe nucleic acid sample was derived. By "genetic profile" is meant information regarding the types of nucleic acids present in the sample, e.g., such as the types of genes to which they are complementary, and/or the copy number of each particular nucleic acid in the sample. From this data, one can also derive information about the physiological source from which the probe nucleic acid sample was derived, such as the types of genes expressed in the tissue or cell which is the physiological source of the target, as well as the levels of expression of each gene, particularly in quantitative terms.

Diagnostic or Prognostic Tests

The invention also provides for diagnostic tests for detecting osteoarthritis. The invention also provides for prognostic tests for monitoring a patient's response to therapy.

According to the method of the invention, mild, moderate, marked or severe osteoarthritis is detected by obtaining a cartilage sample from a patient. A sample comprising nucleic acid corresponding to RNA (i.e., RNA or cDNA) is prepared from the patient cartilage sample. The sample comprising nucleic acid corresponding to RNA is hybridized to an array comprising a solid substrate and a plurality of nucleic acid members, where at least one member is differentially expressed in cartilage isolated from a patient diagnosed with mild, moderate, marked or severe osteoarthritis, as compared to a "normal individual", according to the invention. According to this diagnostic test, differential hybridization of RNA of the sample as compared to a normal control is indicative of disease.

A patient response to therapy is monitored by using a prognostic test according to the invention. In one aspect, a prognostic test according to the invention comprises obtaining a cartilage sample from a patient prior to treatment, during the course of treatment and after treatment. Preferably, the patient is treated for at least 12 hours before a sample is taken. A sample comprising nucleic acid corresponding to RNA (i.e., RNA or cDNA) is prepared from the patient cartilage samples. The samples comprising nucleic acid corresponding to RNA are hybridized to an array comprising a solid substrate and a plurality of nucleic acid members, wherein at least one member is differentially expressed in cartilage isolated from a patient diagnosed with mild, moderate, marked or severe osteoarthritis, as compared to a normal individual, according to the invention. Arrays are selected in accordance with the diagnostic state of the patient whose treatment is being monitored. According to this prognostic test, differential hybridization of the samples comprising nucleic acid corresponding to RNA isolated prior to and after treatment to one or more nucleic acid members on the array is indicative of an effective treatment. Preferably, gene expression profiles in patients being treated changes to resemble more closely gene expression profiles in patients with less severe forms of the disease or more preferably more closely resembles gene expression profiles in normal patients. The extent of change in a gene expression profile can be further correlated with various therapeutic endpoints such as a decrease in the severity and/or occurrence of one or more symptoms associated with the disease.

Therapeutic Agents

A useful therapeutic agent according to the invention can increase or decrease the anabolic and/or the catabolic activity of a chondrocyte. Preferably, a therapeutic agent can increase or decrease the anabolic and/or catabolic activity of a chondrocyte by greater than 1.0-

fold, more preferably, 1.5-5-fold, and most preferably, 5-100-fold, as compared to an untreated chondrocyte.

In one embodiment, a therapeutic agent changes (e.g., increases or decreases) the level of expression of at least one nucleic acid sequence that is differentially expressed in a chondrocyte derived from any of the following chondrocyte disease or developmental stages: fetal, normal, mild osteoarthritic, moderate osteoarthritic, marked osteoarthritic and severe osteoarthritic. Preferably, a therapeutic agent causes a change in the level of expression of a nucleic acid sequence or increase or decrease in the expression of a nucleic acid sequence that is differentially expressed in a chondrocyte derived from any of the following chondrocyte disease or developmental stages: fetal, normal, mild osteoarthritic, moderate osteoarthritic, marked osteoarthritic and severe osteoarthritic, where the change is greater than 1.0-fold, more preferably 1.5-5-fold, and most preferably 5-100-fold, more or less than the level of expression in the absence of a candidate therapeutic agent.

In another embodiment, a therapeutic agent according to the invention can ameliorate at least one of the symptoms and/or changes associated with osteoarthritis including cartilage degeneration, or pain, swelling, weakness and/or loss of functional ability in the afflicted joints, associated with cartilage degeneration.

The candidate therapeutic agent may be a synthetic compound, or a mixture of compounds, or may be a natural product (*e.g.* a plant extract or culture supernatant).

Candidate therapeutic agents or compounds from large libraries of synthetic or natural compounds can be screened. Numerous means are currently used for random and directed synthesis of saccharide, peptide, and nucleic acid-based compounds. Synthetic compound libraries are commercially available from a number of companies including Maybridge Chemical Co. (Trevillet, Cornwall, UK), Comgenex (Princeton, NJ), Brandon Associates (Merrimack, NH), and Microsource (New Milford, CT). A rare chemical library is available from Aldrich (Milwaukee, WI). Combinatorial libraries are available and are prepared. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available from e.g., Pan Laboratories (Bothell, WA) or MycoSearch (NC), or are readily produceable by methods well known in the art. Additionally, natural and synthetically produced libraries and compounds are readily modified through conventional chemical, physical, and biochemical means.

Useful compounds may be found within numerous chemical classes. Useful compounds may be organic compounds, or small organic compounds. Small organic compounds have a molecular weight of more than 50 yet less than about 2,500 daltons, preferably less than about 750, more preferably less than about 350 daltons. Exemplary classes include heterocycles, peptides, saccharides, steroids, and the like. The compounds may be modified to enhance efficacy, stability, pharmaceutical compatibility, and the like. Structural identification of an agent may be used to identify, generate, or screen additional agents. For example, where peptide agents are identified, they may be modified in a variety of ways to enhance their stability, such as using an unnatural amino acid, such as a D-amino acid, particularly D-alanine, by functionalizing the amino or carboxylic terminus, e.g. for the amino group, acylation or alkylation, and for the carboxyl group, esterification or amidification, or the like.

Monitoring Drug Efficacy

The drug efficacy can be monitored by comparing the expression profile of one or more differentially expressed genes between any two cartilage samples from one stage of osteoarthritis as compared with a different stages of osteoarthritis. Cartilage samples were taken from an individual during or after the treatment of a candidate drug as described herein above. As a comparison, cartilage samples were also taken from either the same individual prior to the treatment of the drug or from another individual not treated with the drug. Nucleic acids were extracted from the samples as described and hybridized to an array of the present invention. If one or more nucleic acid members on the array were found to be expressed at different levels in the sample taken from the treated individual compared to the sample taken from the untreated individual, it was indicative of the efficacy of the drug for the treatment of osteoarthritis. Follow-up analysis (e.g., by PCR or Western blot analysis) were then followed to verify the expression differences.

Dosage and Administration

Therapeutic agents of the invention are administered to a patient, preferably in a biologically compatible solution or a pharmaceutically acceptable delivery vehicle, by ingestion, injection, inhalation or any number of other methods routine in the art. The dosages administered will vary from patient to patient. A "therapeutically effective dose" is determined, for example, by the level of enhancement of function (e.g., increased or decreased chondrocyte anabolic activity, or an increase or decrease in the expression of at least one nucleic acid sequence that is differentially expressed in a chondrocyte derived from any of the following chondrocyte disease or developmental stages: fetal, normal, mild osteoarthritic, moderate osteoarthritic, marked osteoarthritic or severe osteoarthritic).

A therapeutic agent according to the invention is administered in a single dose. This dosage may be repeated daily, weekly, monthly, yearly, or as considered appropriate by the treating physician.

Pharmaceutical Compositions

The invention provides for compositions comprising a therapeutic agent according to the invention admixed with a physiologically compatible carrier. As used herein, "physiologically compatible carrier" refers to a physiologically acceptable diluent such as water, phosphate buffered saline, or saline, and further may include an adjuvant. Adjuvants such as incomplete Freund's adjuvant, aluminum phosphate, aluminum hydroxide, or alum are materials well known in the art.

The invention also provides for pharmaceutical compositions. In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically acceptable carrier preparations which is used pharmaceutically.

Pharmaceutical compositions for oral administration are formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for ingestion by the patient.

Pharmaceutical preparations for oral use are obtained through a combination of active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are carbohydrate or protein fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethyl cellulose; and gums including arabic and tragacanth; and proteins such as gelatin and collagen. If desired, disintegrating or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, alginic acid, or a salt thereof, such as sodium alginate.

Dragee cores are provided with suitable coatings such as concentrated sugar solutions, which may also contain gum arabic, talc, polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, i.e., dosage.

Pharmaceutical preparations which are used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with a filler or binders such as lactose or starches, lubricants such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycol with or without stabilizers.

Pharmaceutical formulations for parenteral administration include aqueous solutions of active compounds. For injection, the pharmaceutical compositions of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hank's solution, Ringer' solution, or physiologically buffered saline. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

For nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

The pharmaceutical compositions of the present invention may be manufactured in a manner known in the art, e.g. by means of conventional mixing, dissolving, granulating, dragee-making, levitating, emulsifying, encapsulating, entrapping or lyophilizing processes.

The pharmaceutical composition may be provided as a salt and are formed with many acids, including but not limited to hydrochloric, sulfuric, acetic, lactic, tartaric, malic, succinic, etc. Salts tend to be more soluble in aqueous or other protonic solvents that are the corresponding free base forms. In other cases, the preferred preparation may be a lyophilized powder in 1mM-50 mM histidine, 0.1%-2% sucrose, 2%-7% mannitol at a pH range of 4.5 to 5.5 that is combined with buffer prior to use.

After pharmaceutical compositions comprising a therapeutic agent of the invention formulated in a acceptable carrier have been prepared, they are placed in an appropriate container and labeled for treatment of an indicated condition with information including amount, frequency and method of administration.

Efficacy of Osteoarthritis Therapy Using Defined Therapeutic Agents

The efficacy of the therapy using any of the therapeutic agents according to the invention is determined by a medical practitioner. This determination may be related to alleviating osteoarthritis symptoms such as pain, swelling, weakness and loss of functional ability in the afflicted joint(s), and/or criteria for osteoarthritis diagnosis and staging described in Marshall (1996, supra).

The above disclosure generally describes the present invention. A more complete understanding can be obtained by reference to the following specific examples, which are provided herein for purposes of illustration only and are not intended to limit the scope of the invention.

Examples

The examples below are non-limiting and are merely representative of various aspects and features of the present invention

Example 1: RNA Extraction, cDNA Library Construction and EST Analysis

Normal cartilage was obtained from the donor program of Department of Orthopaedics and Rehabilitation, University of Miami. OA cartilage samples were obtained from either areas of very early cartilage degeneration (mild) or from sites of moderate, marked or severe cartilage degeneration during either arthroscopic knee surgery or total knee replacement. OA severity was graded according to the system described by Marshall (Marshall KW. J Rheumatol, 1996:23(4) 582-85). Briefly, each of the six knee articular surfaces was assigned a cartilage grade with points based on the worst lesion seen on each particular surface. Grade 0 is normal (0 points), Grade I cartilage is soft or swollen but the articular surface is intact (1 point). In Grade II lesions, the cartilage surface is not intact but the lesion does not extend down to subchondral bone (2 points). Grade III damage extends to subchondral bone but the bone is neither eroded nor eburnated (3 points). In Grade IV lesions, there is eburnation of or erosion into bone (4 points). A global OA score is calculated by summing the points from all six cartilage surfaces. If there is any associated pathology, such as meniscus tear, an extra point will be added to the global score. Based on the total score, each patient is then categorized into one of four OA groups: mild (1-6), moderate (7-12), marked (13-18), and severe (>18).

Total RNA from cartilage was extracted using TRIzol® reagent (GIBCO). cDNA libraries were constructed into λTriplEx2 vector through a PCR-based method, using SMART (Switching Mechanism At 5' end of RNA Transcript) cDNA Library Construction Kit (Clontech) as described above. Phage plaques were randomly picked and positive inserts were identified by PCR. Agarose gel electrophoresis was used to assess the presence and purity of inserts. PCR product was then subjected to automated DNA sequencing with a 5'vector-specific forward primer and sequenced by ABI PRISM 377 DNA sequencer (Perkin Elmer) and ABI PRISM 3700 DNA Analyzer (Applied Biosystems). ESTs were obtained from each of the cDNA libraries and sequenced.

Large-scale sequencing of cDNA inserts

From the amplified λ ZAP Express library, phage plaques were plated at a density of 200-500 pfu/150 mm plate onto *Escherichia coli* XL1-blue MRF' lawn with IPTG/X-gal for color selection. Plaques were picked into 75 ul suspension media buffer (100 mM NaCl, 10 mM $MgSO_4$, 1 mM Tris, pH7.5, 0.02% gelatin). Phage elutes (5 ul) were used for PCR reactions (50 ul total volume) with 125 umol/L of each dNTP (Pharmacia), 10 pmol each of modified T3 (5'-GCCAAGCTCGAAATTAACCCTCACTAAAG GG-3' (SEQ ID NO: 19)) and T7 (5'-CCAGTGAATTGTAATACGACTCACTATAGGGCG-3' (SEQ ID NO: 20)) primers, and 2 U of Taq DNA polymerase (Pharmacia). Reactions were cycled in a DNA Thermal Cycler (Perkin-Elmer) [denaturation at 95°C for 5 minutes, followed by 30 cycles of amplification (94° C, 45 seconds; 55°C, 30 seconds; 72°C, 3 minutes) and a terminal isothermal extension (72°C, 3 minutes)]. Agarose gel electrophoresis was used to assess the presence and purity of inserts. PCR products are subjected to DNA sequencing reactions using specific primers, BigDye™ Terminator Cycle Sequencing v2.0 Ready Reaction (PE Biosystems), Tris MgCl buffer and water in a thermocycler. Sequencing reactions were incubated at 94°C for 2 minutes, followed by 25 cycles of 94°C, 30 seconds; 55°C, 20 seconds; and 72°C, 1 minute; and 15 cycles of 94°C, 30 seconds; and 72°C for 1 minute; and 72°C for 5minues. Reactions were then put on hold at 4 °C until purified through methods well known in the prior art (i.e. column purification or alcohol precipitation). Automated sequencing was carried out with a PE Biosystems ABI Prism 3700 DNA Analyzer.

Sequences were manually edited or edited using Sequencher software (GeneCodes). All edited EST sequences were compared to the non-redundant Genbank/EMBL/DDBJ and dbEST databases using the BLAST algorithm (8). A minimum value of $P = 10^{-10}$ and nucleotide sequence identity >95% were required for assignments of putative identities for ESTs matching to known genes or to other ESTs. Construction of a non-redundant list of genes represented in the EST set was done with the help of Unigene, Entrez and PubMed at the National Center for Biotechnology Information (NCBI) site (Web address: www.ncbi.nlm.nih.gov/).

Example 2: Microarray Construction

Microarrays using ESTs isolated from the four cDNA libraries as described above were created.

PCR products (~40 ul) of cDNA clones from OA cartilage cDNA libraries as described above were utilized in the same 96-well tubes used for amplification, are precipitated with 4 ul (1/10 volume) of 3M sodium acetate (pH 5.2) and 100 ul (2.5 volumes) of ethanol and stored overnight at –20°C. They are then centrifuged at 3,300 rpm at 4°C for 1 hour. The obtained pellets were washed with 50 ul ice-cold 70% ethanol and centrifuged again for 30 minutes. The pellets are then air-dried and resuspended well in 50% dimethylsulfoxide (DMSO) or 20ul 3X SSC overnight. The samples are then deposited either singly or in duplicate onto Gamma Amino Propyl Silane (Corning CMT-GAPS or CMT-GAP2, Catalog No. 40003, 40004) or polylysine-coated slides (Sigma Cat. No. P0425) using a robotic GMS 417 or 427 arrayer (Affymetrix, CA). The boundaries of the DNA spots on the microarray are marked with a diamond scriber. The invention provides for arrays where 10-20,000 PCR products are spotted onto a solid support to prepare an array.

The arrays are rehydrated by suspending the slides over a dish of warm particle free ddH_20 for approximately one minute (the spots will swell slightly but not run into each other) and snap-dried on a 70-80°C inverted heating block for 3 seconds. DNA is then UV crosslinked to the slide (Stratagene, Stratalinker, 65 mJ – set display to "650" which is 650 x 100 uJ) or baked at 80C for two to four hours. The arrays are placed in a slide rack. An empty slide chamber is prepared and filled with the following solution: 3.0 grams of succinic anhydride (Aldrich) is dissolved in 189 ml of 1-methyl-2-pyrrolidinone (rapid addition of reagent is crucial); immediately after the last flake of succinic anhydride dissolved, 21.0 ml of 0.2 M sodium borate is mixed in and the solution is poured into the slide chamber. The slide rack is plunged rapidly and evenly in the slide chamber and vigorously shaken up and down for a few seconds, making sure the slides never leave the solution, and then mixed on an orbital shaker for 15-20 minutes. The slide rack is then gently plunged in 95°C ddH_20 for 2 minutes, followed by plunging five times in 95% ethanol. The slides are then air dried by allowing excess ethanol to drip onto paper towels. The arrays are then stored in the slide box at room temperature until use.

Example 3: Target Nucleic acid Preparation and Hybridization using Constructed Arrays

Preparation of Fluorescent DNA Probe from mRNA

Fluorescently labeled target nucleic acid samples are prepared for analysis with an array of the invention.

2 μg Oligo-dT primers are annealed to 2 ug of mRNA isolated from a cartilage sample from patient diagnosed with osteoarthritis as described above in a total volume of 15 ul, by heating to 70°C for 10 min, and cooled on ice. The mRNA is reverse transcribed by incubating the sample at 42°C for 1.5-2 hours in a 100 μl volume containing a final concentration of 50 mM Tris-HCl (pH 8.3), 75 mM KCl, 3 mM MgC12, 25 mM DTT, 25 mM unlabeled dNTPs, 400 units of Superscript II (200 U/uL, Gibco BRL), and 15 mM of Cy3 or Cy5 (Amersham). RNA is then degraded by addition of 15μl of 0.1N NaOH, and incubation at 70°C for 10 min. The reaction mixture is neutralized by addition of 15μl of 0.1N HCL, and the volume is brought to 500μl with TE (10mM Tris, 1mM EDTA), and 20 μg of Cot1 human DNA (Gibco-BRL) is added.

The labeled target nucleic acid sample is purified by centrifugation in a Centricon-30 micro-concentrator (Amicon). If two different target nucleic acid samples (e.g., two samples derived from different patients) are being analyzed and compared by hybridization to the same array, each target nucleic acid sample is labeled with a different fluorescent label (e.g., Cy3 and Cy5) and separately concentrated. The separately concentrated target nucleic acid samples (Cy3 and Cy5 labeled) are combined into a fresh centricon, washed with 500μl TE, and concentrated again to a volume of less than 7μl. 1μL of 10μ g/μl polyA RNA (Sigma, #P9403) and 1 μl of 10μg/ul tRNA (Gibco-BRL, #15401-011) is added and the volume is adjusted to 9.5 μl with distilled water. For final target nucleic acid preparation 2.1μl 20XSSC (1.5M NaCl, 150mM NaCitrate (pH8.0)) and 0.35μl 10%SDS is added.

Hybridization Using the ChondroChip™ Constructed Array

Labeled nucleic acid is denatured by heating for 2 min at 100°C, and incubated at 37°C for 20-30 min before being placed on a nucleic acid array under a 22mm x 22mm glass cover slip. Hybridization is carried out at 65°C for 14 to 18 hours in a custom slide chamber with humidity maintained by a small reservoir of 3XSSC. The array is washed by submersion and agitation for 2-5 min in 2X SSC with 0.1%SDS, followed by 1X SSC, and 0.1X SSC. Finally, the array is dried by centrifugation for 2 min in a slide rack in a Beckman GS-6 tabletop centrifuge in Microplus carriers at 650 RPM for 2 min.

Example 4: Target Nucleic acid Preparation and Hybridization using Affymetrix® U133A Microarray

Preparation of Biotinylated cDNA

Biotinylated DNA probes are prepared from total mRNA using the Affymetrix® Eukaryotic Target Preparation protocol.

More particularly 2 μg T7 Oligo-dT primers (5uM) are annealed to 2 ug of mRNA isolated from a cartilage sample from patient diagnosed with osteoarthritis, as described above, in a total volume of 2 ul, by heating to 70°C for 6 min, and cooled on ice. The mRNA is reverse transcribed by incubating the sample at 42°C for 1hour in a 20 μl volume containing a final concentration of 1X first stand buffer (Affymetrix®), 20 mM DTT, 1.25 mM unlabeled dNTPs, 100 units of Superscript II (200 U/uL, Gibco BRL). Second strand synthesis is performed by incubating at 16°C for 2 hours the first strand reaction in a final concentration of 1X Second Strand Reaction Buffer (Affymetrix®) 200uM dNTPs, 10U *E. Coli* DNA Ligase; 40U *E. Coli* DNA Polymerase 1 and 2U of *E. Coli* Rnase H (Affymetrix®) to a final volume of 150μl. 2μl (10U) of T4 DNA Polymerase is added and the reaction reincubated for an additional 5 minutes. Reaction is stopped with the addition of 10μl of 0.5M EDTA. cDNA is purified utilizing the Affymetrix® GeneChip Sample Cleanup Module.

cRNA is created and labelled by incubating the template cDNA with 1xHY Reaction Buffer; 1X biotin-lableled ribonucleotides, 1X DTT; 1X Rnase Inhibitor Mix and 1X T7 RNA polymerase (Affymetrix®) and the reaction incubated at 37°C for 4-5 hours.

The labeled cRNA nucleic acid sample is purified using the Affymetrix® GeneChip Sample Cleanup Module. CRNA is fragmented in accordance with the Affymetrix® protocol prior to hybridization.

Hybridization Using the Affymetrix® U133A Array

Hybridization is performed in accordance with the Affymetrix® Eukaryotic Target Preparation protocol. Following hybridization of an array with one or more labeled target nucleic acid samples, arrays are scanned immediately using a GeneChip Fluidics Station 450 and Genechip Scanner (Affymetrix®).

Example 5: Detection of OA Biomarkers (Nucleic acids) Specific for Mild OA or Severe OA.

This example demonstrates the use of the claimed invention to detect either mild OA specific or severe OA specific biomarkers utilizing the ChondroChip™ as demonstrated in Figures 1-4.

Data Analysis was performed on RNA isolated from cartilage samples of normal individuals, individuals having mild osteoarthritis, and individuals having severe osteoarthritis. OA severity was graded according to the system described by Marshall (Marshall KW. J Rheumatol, 1996:23(4) 582-85) as described herein.

Sample RNA from either normal, mild or severe OA cartilage was labelled with fluorescent dye Cy3 or Cy5, and Universal Human Reference RNA (Stratagene, Product# 740000) labelled with the remaining fluorescent dye and normalized intensities for each sample RNA determined having taken into account intensity differences as a result of the use of the different dyes. Analysis was performed using GeneSpring 4.1.5 and genes demonstrating a stage specific difference in expression intensity of greater than 2 fold when compared to either the intensity form the normal cartilage or any other stage specific cartilage RNA were identified.

Figure 1 - 4 provide those genes identified as unique to either mild or severe OA.

Example 6: Detection of OA Biomarkers Specific for Mild OA, Marked OA, Moderate OA or Severe OA

This example demonstrates the use of the claimed invention to detect stage specific OA biomarkers utilizing the ChondroChip™ or the Affymetrix® U133A as demonstrated in Figure 6 and Figure 7 respectively.

Data Analysis was performed on RNA isolated from cartilage samples of normal individuals, individuals having mild osteoarthritis, individuals having moderate osteoarthritis, individuals having marked osteoarthritis and individuals having severe osteoarthritis. OA severity was graded according to the system described by Marshall (Marshall KW. J Rheumatol, 1996:23(4) 582-85) as described herein.

Sample RNA from either normal, mild, moderate, marked or severe OA cartilage was labelled with fluorescent dye Cy3 or Cy5, and Universal Human Reference RNA (Stratagene, Product# 740000) labelled with the remaining fluorescent dye and normalized intensities for each sample RNA determined having taken into account intensity differences as a result of the use of the different dyes. Analysis was performed using GeneSpring 6.0. Each disease group was compared to the normal samples: mild/normal, moderate/normal, marked/normal and severe/normal. A cut-off p-value for statistical significance was 0.05. Statistical tests: non-parametric (Wilcoxon-Mann-Witney or Kruskal-Wallis) or parametric, variances not assumed equal (Welch ANOVA) (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002). Genes were identified as disease group associated genes from the 14, 967 genes on the 15K ChondroChip™ which demonstrated a statistically significant difference when compared with the normal control. ("OA list"). Genes wherein the expression level correlated with other parameters, such as age, gender, hybridization date and slide batch, when such parameters could be reviewed, were removed from the OA list. The OA list generated from each stage specific sample were compared and genes identified which were unique for each specific stage.

Example 8 Detection of OA Biomarkers (proteins) Specific for Mild OA or Severe OA.

This example demonstrates the use of the invention to diagnose mild or severe osteoarthritis by detecting differential gene expression in samples taken from patients with OA as compared to samples taken from healthy patients.

Cartilage samples are taken from patients who are clinically diagnosed with mild or severe osteoarthritis as defined herein. Gene expression profiles are then analyzed and compared to profiles from patients unaffected by OA. In each case, the diagnosis of osteoarthritis is corroborated by a skilled Board certified physician.

Total cellular protein from a cartilage sample taken from each patient is first isolated and labelled using the BD Clontech Protein Extraction and labelling kit (Catalogue #K1848-1 or #631786). Briefly, the Extraction Protocol consists of three main steps: mechanically disrupting the cells, solubilizing the cells, and centrifuging the extract The process may start with a cell pellet or frozen tissue and may use any method of mechanical disruption – French press, sonication, mincing, or grinding. Once disrupted, the sample is solubilized by adding the Extraction/Labeling Buffer (1:20 w/v). Because the Buffer is formulated for labeling with N-hydroxysuccinimide (NHS)-ester dyes (e.g. Cy3 and CyS dyes), it does not contain any protease inhibitors or reducing agents that would compete for reaction with the dye. After extraction, the sample is centrifuged to pellet insoluble material such as chromosomal DNA. The soluble extract is then labelled with Cy3 and Cy5 Fluorescent Dyes (monofunctional NHS-esters). The labelled proteins are then incubated with an array of monoclonal antibodies which are directed to full length polypeptides encoded by the genes described in Figures 1, 3, 6a, 7a (mild OA) or Figures 2, 4, 6d or 7b (Severe OA). Detection of specific binding to the array is then measured by scanning with a GMS Scanner 418 and processing of the experimental data with Scanalyzer software (Michael Eisen, Stanford University), followed by GeneSpring software (Silicon Genetics, CA) analysis. Differential expression of the mild OA specific of severe OA-specific genes in the samples from patients with mild and severe osteoarthritis respectively as compared to healthy patients is determined by statistical analysis using the Wilcox Mann Whitney rank sum test (Glantz SA. Primer of Biostatistics. 5th ed. New York, USA: McGraw-Hill Medical Publishing Division, 2002). Differential expression of each of the genes described in Figure 1, 3, 6a, 7a is diagnostic for mild osteoarthritis. Differential expression of each of the genes described in Figures 2, 4, 6d or 7b is diagnostic of severe OA.

Example 9. Monitoring Drug Efficacy

The drug efficacy can be monitored by comparing the expression profile of one or more differentially expressed genes between any two cartilage samples from normal and different stages of osteoarthritic. Cartilage samples are taken from an individual during or after the treatment of a candidate drug as described herein above. As a comparison, cartilage samples can also taken from either the same individual prior to the treatment of the drug or from another individual not treated with the drug. Nucleic acids are extracted from the samples as described and hybridized to an array of the present invention. If one or more nucleic acid members on the array are found to be expressed at different levels in the sample taken from the treated individual compared to the sample taken from the untreated individual, it was indicative of the efficacy of the drug for the treatment of osteoarthritis. Follow-up analysis (e.g., by PCR or Western blot analysis) can be followed to verify the expression differences.

Variations, modifications, and other implementations of what is described herein will occur to those of ordinary skill in the art without departing from the spirit and scope of the invention. The references provided below and referred to herein above are incorporated herein by reference in their entireties.

SEQUENCE LISTING

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```

CLAIMS

What is claimed is:

1. An isolated biomarker comprising 51% or more genes selected from the group consisting of the nucleic acids identified in Figures 1, 3, 5, 6a and 7a.

2. An isolated biomarker comprising two or more genes selected from the group consisting of the nucleic acids identified in Figures 1, 3, 5, 6a and 7a.

3. An isolated biomarker consisting essentially of the nucleic acids identified in Figures 1, 3, 5, 6a and 7a.

4. An isolated biomarker comprising 51% or more genes selected from the group consisting of the nucleic acids identified in Figures 6b.

5. An isolated biomarker comprising two or more genes selected from the group consisting of the nucleic acids identified in Figures 6b.

6. An isolated biomarker consisting essentially of the nucleic acids identified in Figures 6b.

7. An isolated biomarker comprising 51% or more genes selected from the group consisting of the nucleic acids identified in Figures 6c.

8. An isolated biomarker comprising two or more genes selected from the group consisting of the nucleic acids identified in Figures 6c.

9. An isolated biomarker consisting essentially of the nucleic acids identified in Figures 6c.

10. An isolated biomarker comprising 51% or more genes selected from the group consisting of the nucleic acids identified in Figures 2, 4, 5, 6d and 7b.

11. An isolated biomarker comprising two or more genes selected from the group consisting of the nucleic acids identified in Figures 2, 4, 5, 6d and 7b.

12. An isolated biomarker consisting essentially of the nucleic acids identified in Figures 2, 4, 5, 6d and 7b.

13. A method of diagnosing mild osteoarthritis in an individual, comprising determining the level of expression of a biomarker in a sample wherein said biomarker comprises one or more polynucleotide sequences selected from the group consisting of the nucleic acids identified in Figures 1, 3, 5, 6a, 7a , whereby a difference in said level of expression of said biomarker compared to a biomarker control is indicative or predictive of mild osteoarthritis.

14. The method of claim 10, wherein said polynucleotide sequences are from the 5' region of a gene selected from the group consisting of the nucleic acids identified in Figures 1, 3, 5, 6a, 7a.

15. The method of claim 10, wherein said polynucleotide sequences are from the 3' region of a gene selected from the group consisting of the nucleic acids identified in Figures 1, 3, 5, 6a, 7a.

16. The method of claim 10, wherein said polynucleotide sequences are from the internal coding region of a gene selected from the group consisting of the nucleic acids identified in Figures 1, 3, 5, 6a, 7a.

17. A method of diagnosing severe osteoarthritis in an individual, comprising determining the level of expression of a biomarker in a sample wherein said biomarker comprises one or more polynucleotide sequences selected from the group consisting of the nucleic acids identified in Figures 2, 4, 5, 6d, 7b whereby a difference in said level of expression of said biomarker compared to a biomarker control is indicative or predictive of severe osteoarthritis.

18. The method of claim 14, wherein said polynucleotide sequences are from the 5' region of a gene selected from the group consisting of the nucleic acids identified in Figures 2, 4, 5, 6d, 7b.

19. The method of claim 14, wherein said polynucleotide sequences are from the 3' region of a gene selected from the group consisting of the nucleic acids identified in Figures 2, 4, 5, 6d, 7b.

20. The method of claim 14, wherein said polynucleotide sequences are from the internal coding region of a gene selected from the group consisting of the nucleic acids identified in Figures 2, 4, 5, 6d, 7b.

21. A method of diagnosing moderate osteoarthritis in an individual, comprising determining the level of expression of a biomarker in a sample wherein said biomarker comprises one or more polynucleotide sequences selected from the group consisting of the nucleic acids identified in Figures 6b, whereby a difference in said level of expression of said biomarker compared to a biomarker control is indicative or predictive of moderate osteoarthritis.

22. The method of claim 18, wherein said polynucleotide sequences are from the 5' region of a gene selected from the group consisting of the nucleic acids identified in Figures 6b.

23. The method of claim 18, wherein said polynucleotide sequences are from the 3' region of a gene selected from the group consisting of the nucleic acids identified in Figures 6b.

24. The method of claim 18, wherein said polynucleotide sequences are from the internal coding region of a gene selected from the group consisting of the nucleic acids identified in Figures 6b.

25. A method of diagnosing marked osteoarthritis in an individual, comprising determining the level of expression of a biomarker in a sample wherein said biomarker comprises one or more polynucleotide sequences selected from the group consisting of the nucleic acids identified in Figures 6c, whereby a difference in said level of expression of said biomarker compared to a biomarker control is indicative or predictive of marked osteoarthritis.

26. The method of claim 22, wherein said polynucleotide sequences are from the 5' region of a gene selected from the group consisting of the nucleic acids identified in Figures 6c.

27. The method of claim 22, wherein said polynucleotide sequences are from the 3' region of a gene selected from the group consisting of the nucleic acids identified in Figures 6c.

28. The method of claim 22, wherein said polynucleotide sequences are from the internal coding region of a gene selected from the group consisting of the nucleic acids identified in Figures 6c.

29. A method for monitoring efficacy of a drug for treatment of mild osteoarthritis in a patient, comprising the steps of:

(a) obtaining a sample from a patient before treatment and a second sample from said patient after said treatment;

(b) detecting the level of expression of the isolated biomarker of claim 2 in said first sample and said second sample; and

(c) determining a difference in said level of expression of said biomarker in said first sample as compared with said second sample, wherein said difference is indicative of the efficacy of said drug for said treatment of mild osteoarthritis in said patient.

30. A method for monitoring efficacy of a drug for treatment of moderate osteoarthritis in a patient, comprising the steps of:

(a) obtaining a sample from a patient before treatment and a second sample from said patient after said treatment;

(b) detecting the level of expression of the isolated biomarker of claim 5 in said first sample and said second sample; and

(c) determining a difference in said level of expression of said biomarker in said first sample as compared with said second sample, wherein said difference is indicative of the efficacy of said drug for said treatment of moderate osteoarthritis in said patient.

31. A method for monitoring efficacy of a drug for treatment of marked osteoarthritis in a patient, comprising the steps of:

(a) obtaining a sample from a patient before treatment and a second sample from said patient after said treatment;

(b) detecting the level of expression of the isolated biomarker of claim 8 in said first sample and said second sample; and

determining a difference in said level of expression of said biomarker in said first sample as compared with said second sample, wherein said difference is indicative of the efficacy of said drug for said treatment of marked osteoarthritis in said patient.

32. A method for monitoring efficacy of a drug for treatment of severe osteoarthritis in a patient, comprising the steps of:

(a) obtaining a sample from a patient before treatment and a second sample from said patient after said treatment;

(b) detecting the level of expression of the isolated biomarker of claim 11 in said first sample and said second sample; and

(c) determining a difference in said level of expression of said biomarker in said first sample as compared with said second sample, wherein said difference is indicative of the efficacy of said drug for said treatment of severe osteoarthritis in said patient.

33. A method of identifying a therapeutic agent for the treatment of osteoarthritis, said method comprising:

a) providing a sample from a patient diagnosed with osteoarthrtis;

b) measuring the level of expression of a biomarker as set out in Figures 1 - 7 in the presence and the absence of said therapeutic agent; and

c) comparing said level of expression measured in the presence of said therapeutic agent to said level of expression measured in the absence of said therapeutic agent, wherein a decrease in the differential expression of said biomarker is indicative of a therapeutic agent for the treatment of osteoarthritis.

34. The methods of claims 13, 17, 21, 25, 29, 30, 31, 32 or 33 wherein said sample is human cartilage.

35. The methods of claims 13, 17, 21, 25, 29, 30, 31, 32 or 33,wherein said biomarker is immobilized to a microarray.

36. The methods of claims 13, 17, 21, 25, 29, 30, 31, 32 or 33, wherein said level of expression of said biomarker is determined by hybridization to a microarray or real time RT-PCR.

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NOTE POUR LE TOME / VOLUME NOTE:

	FIGURE 1: Down in Mild OA Only							
SEQ ID No	Description of Sequence	Gene Accession Number	Ref Accession Number	UniGene	Protein Accession Number	normal	mild	severe
1	FCR1090;Novel;					1 (0.725 to 1.275)	0.499	0.556 (0.504 to 0.608)
	MIOA2900;ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY ;P39188	BC035122.1		Hs.382273		1 (0.686 to 1.314)	0.497	1.53 (1.205 to 1.854)
	seob7176;U50' snoRNA and U50 snoRNA ;AB017710.1	AB017710.1				1 (0.837 to 1.163)	0.497	0.651 (0.572 to 0.731)
2	miob0185;DNA sequence (clone RP11-38M8 from 7q31) ;AC009275.5	AC009275.8				1.000 (0.696 to 1.304)	0.497	0.585 (0.568 to 0.601)
	seoa5479;EST(aa89a04.r1 Stratagene fetal retina 937202 clone 838446 5') ;AA457594	AA457594	NM_024843	Hs.31297	NP_079119	1 (0.977 to 1.023)	0.495	0.832 (0.561 to 1.102)
	seob3694;hypothetical protein FLJ10147 (FLJ10147)(ORF) ;NM_018010.1	NM_018010.1	NM_018010	Hs.170318	NP_060480	1 (0.927 to 1.073)	0.493	0.934 (0.808 to 1.060)
3	MIOA1763;MHC class 1 region ;AF055066	AF055066			AAC24825.	1 (0.523 to 1.477)	0.493	0.88 (0.815 to 0.945)
	ncrc1999;INTERFERON-INDUCED TRANSMEMBRANE PROTEIN 3 (INTERFERON-INDUCIBLE PROTEIN 1-8U) ;Q01628	NM_021034.1	NM_021034.1	Hs.433414	NP_066362.1	1.000 (0.529 to 1.471)	0.492	0.711 (0.638 to 0.784)
	MIOA6236;EST(qr24f06.x1 NCI_CGAP_GC6 clone IMAGE:1941827 3') ;AI203343	AI203343	NM_016586	Hs.16755	NP_057670	1 (0.716 to 1.284)	0.492	0.61 (0.567 to 0.653)

4	SEOA6643a;DNA sequence (chromosome 16 cloneRPCI-11_567P19, WORKING DRAFT SEQUENCE, 63 unordered pieces) ;AC009152.1	AC009152.7				1 (0.794 to 1.206)	0.491	0.774 (0.611 to 0.938)
5	fcrb5788;H19, imprinted maternally expressed untranslated ;Hs.334822	AF087017.1				1 (0.848 to 1.152)	0.491	1.191 (1.007 to 1.375)
	SEOA3908;elongation factor-1-gamma ;Z11531	Z11531	NM_001404	Hs.256184	NP_001395	1 (0.833 to 1.167)	0.49	0.742 (0.683 to 0.802)
	FCR6188;hypothetical protein (KIAA0121) ;D50911	D50911	XM_052386	Hs.155584		1 (0.846 to 1.154)	0.49	0.704 (0.580 to 0.827)
	MIOB2691;HRIHFB2072 (=AF115778 M.musculus short coiled coil protein SCOCO (Scoc)) ;AB015335.1	AB015335.1	NM_032547	Hs.286013	NP_115936	1 (0.686 to 1.314)	0.486	1.157 (1.108 to 1.207)
	seoa3242;EST zp96a07.r1 Stratagene muscle 937209 cDNA clone 628020 5' ;AA196423	AA196423		Hs.374621		1 (0.85 to 1.150)	0.486	0.885
	SEOA5977a;hypothetical protein (KIAA0569) ;AB011141	AB011141	NM_014795	Hs.34871	NP_055610	1.000 (0.959 to 1.041)	0.485	0.960 (0.88 to 1.041)
	ncrb7403;EST (EST390300 MAGE resequences, MAGO cDNA) ;AW978191.1	AW978191.1		Hs.117927		1 (0.831 to 1.169)	0.485	0.613 (0.61 to 0.616)

	seob6836;hXBP-1 transcription factor DNA (=TREB protein) ;L13850.1	L13850.1				1 (0.933 to 1.067)	0.485	0.616 (0.554 to 0.678)
	miob3968;gamma-aminobutyric acid (GABA) A receptor, alpha 4 (GABRA4) ;NM_000809.1	NM_000809.1	NM_000809	Hs.248112	NP_000800	1 (0.747 to 1.253)	0.484	0.926 (0.898 to 0.954)
	SEOA2970a;major histocompatibility class II antigen gamma chain ;K01144	K01144	NM_004355	Hs.84298	NP_004346	1 (0.615 to 1.385)	0.48	1.777 (1.256 to 2.297)
	SEOA9357;hypothetical protein, estradiol-induced (E2IG5), (ORF) ;NM_014367.1	NM_014367.1	NM_014367	Hs.5243	NP_055182	1 (0.783 to 1.217)	0.48	0.658 (0.528 to 0.788)
	MIOA8338;HepG2 ;D17039	D17039	NM_004048	Hs.48516	NP_004039	1 (0.525 to 1.475)	0.48	0.635 (0.529 to 0.742)
	SEOB1273;CGI-129 protein ;AF151887.1	AF151887.1	NM_016098	Hs.108725	NP_057182	1 (0.963 to 1.037)	0.474	0.909 (0.823 to 0.995)
	SEOA9433;fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA ;NM_013231.1	NM_013231.1	NM_013231	Hs.48998	NP_037363	1 (0.910 to 1.09)	0.473	0.598 (0.489 to 0.707)
	seoa1431;EST (wg57e08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 clone IMAGE:2369222 3') ;AI760043.1	AI760043.1	NM_019000	Hs.82273	NP_061873	1 (0.569 to 1.431)	0.472	0.866 (0.862 to 0.870)

	ncr0238;EST tt13f10.x1 NCI_CGAP_GC6 IMAGE:2240683 3' similar to TR:P97434 P97434 P116RIP. ;contains element A3R repetitive element ;AI655514	AI655514	NM_007032	Hs.40342	NP_619538	1 (0.639 to 1.361)	0.472	0.968 (0.778 to 1.158)
	SEOB1513;T-cell receptor alpha chain-c6.1A fusion protein (c6.1A-TCRC) gene ;S72931.1	S72931.1			AAB30469	1 (0.81 to 1.190)	0.469	0.567 (0.483 to 0.651)
	seob7039;high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha (=AB007900 KIAA0440) ;AF090989.1	AF090989.1	NM_015556	Hs.172180	NP_056371	1 (0.735 to 1.265)	0.469	0.702 (0.665 to 0.738)
	ncrc6072;testis specific ankyrin-like protein 1 (LOC51281) ;NM_016552.1	NM_016552.1	NM_016552	Hs.122275	NP_060314	1 (0.846 to 1.154)	0.463	0.846 (0.748 to 0.944)
	ncrb0045;chitinase 3-like 1(cartilage glycoprotein-39) (CHI3L1) ;NM_001276.1	NM_001276.1	NM_001276	Hs.75184	NP_001267	1 (0.764 to 1.236)	0.454	0.644 (0.608 to 0.681)
	miob4752;EST(aa17g07.r1 Soares_NhHMPu_S1 clone IMAGE:813564 5') ;AA455459.1	AA455459.1		Hs.445247		1 (0.905 to 1.095)	0.452	0.77 (0.511 to 1.029)

	seob5203;microvascular endothelial differentiation gene 1 product ;AB026908.1	AB026908.1	NM_012328	Hs.6790	NP_036460	1	0.451	0.525 (0.374 to 0.675)
	SEOB1411;KIAA0879 protein (KIAA0879) ;NM_014936.1	NM_014936.1	NM_014936	Hs.54037	NP_055751	1 (0.706 to 1.294)	0.449	0.614 (0.558 to 0.669)
	MIOA6207;EST(an41g01.s1 Gessler Wilms tumor clone IMAGE:1701264 3') ;AI174629	AI174629		Hs.6634		1 (0.537 to 1.463)	0.447	0.517 (0.467 to 0.567)
6	miob4692;dJ93K22.1 (novel protein (contains DKFZP564B116)) ;AL050333	AL050333				1 (0.315 to 1.685)	0.447	0.588 (0.426 to 0.749)
	ncrc4864;fibroblast activation protein, alpha;seprase (RefSeq aa 6e-91) ;NP_004451.1	NM_004460.2	NM_004460.2	Hs.418	NP_004451.1	1 (0.353 to 1.647)	0.446	0.738 (0.515 to 0.960)
	SEOB2750;PGK1=phosphoglycerate kinase 1 ;S75476.1	S75476.1				1 (0.994 to 1.006)	0.445	1.370 (1.174 to 1.567)
7	miob5780;DNA sequence (clone 24_A_9) ;AC007371.16	AC007371.16				1 (0.796 to 1.204)	0.443	0.522 (0.498 to 0.547)
	fcrb1731;NDUFV3 gene for mitochondrial NADH-Ubiquinone oxidoreductase ;AB038163.1	AB038163.1			BAB13732	1 (0.975 to 1.025)	0.439	1.555 (0.334 to 2.775)

	seob5880;EST zx48b06.r1 Soares_testis_NHT cDNA clone IMAGE:795443 5' similar to contains Alu repetitive element;contains element MER13 repetitive element ; ;AA454038.1	AA454038.1	NM_017925	Hs.29032	NP_060395	1 (0.676 to 1.324)	0.428	0.740 (0.646 to 0.834)
	miob2355;NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3 (12kD, B12) (NDUFB3) ;NM_002491.1	NM_002491.1	NM_002491	Hs.109760	NP_002482	1 (0.865 to 1.135)	0.428	0.739 (0.669 to 0.808)
	ncr0644;EST(AV724328 HTB cDNA clone HTBAYE08 5') ;AV724328.1	AV724328.1	NM_007111	Hs.79353	NP_009042	1 (0.664 to 1.336)	0.427	0.549 (0.546 to 0.553)
	fcrb5537;slug (chicken homolog), zinc finger protein, clone MGC:10182 IMAGE:3908245, mRNA, complete cds /cds=(152,958) /gb=BC014890 /gi=15928855 /ug=Hs.93005 /len=2010 ;Hs.93005	BC014890	NM_003068	Hs.93005	NP_003059	1 (0.329 to 1.671)	0.42	0.52 (0.482 to 0.558)

	fcrb3691;FLJ22066 fis, clone HEP10611 /cds=UNKNOWN /gb=AK025719 /gi=10438328 /ug=Hs.251664 /len=2281 ;Hs.251664	AK025719		Hs.251664		1 (0.582 to 1.418)	0.419	1.101 (0.419 to 1.783)
	MIOA4076a;ARP 2/3 COMPLEX 20 KD SUBUNIT (P20-ARC), putative ;Q18491	NM_020154.1	NM_020154.1	Hs.4245	NP_064539.1	1 (0.383 to 1.617)	0.418	2.909 (2.011 to 3.806)
8	SEOB1449;C-type lectin ;BAA95671.1	no significant match				1 (0.833 to 1.167)	0.393	0.572 (0.517 to 0.626)
	ncrb4957;WNT1 inducible signalling pathway protein 2 (WISP2) ;NM_003881.1	NM_003881.1	NM_003881	Hs.194679	NP_003872	1 (0.769 to 1.231)	0.387	0.722 (0.646 to 0.798)
	SEOB3360;dual specificity phosphatase 1 (DUSP1) ;NM_004417.2	NM_004417.2	NM_004417	Hs.171695	NP_004408	1 (0.821 to 1.179)	0.386	0.646 (0.573 to 0.719)
	seob1967;hypothetical protein (FLJ11041 fis, clone PLACE1004405) ;AK001903.1	AK001903.1		Hs.28792		1 (0.217 to 1.783)	0.384	2.451 (1.884 to 3.019)
	SEOB1385;hypothetical protein (KIAA0907) ;AB020714.1	AB020714.1	NM_014949	Hs.24656	NP_055764	1 (0.749 to 1.251)	0.377	0.601 (0.527 to 0.676)
	mioa4318;embryonic lung protein (HUEL) ;AF006621.1	AF006621.1	NM_006345	Hs.270956	NP_006336	1 (0.924 to 1.076)	0.377	0.601 (0.536 to 0.667)
	seob4726;differentiation-related gene 1 (nickel-specific induction protein) (RTP) ;NM_006096.1	NM_006096.1	NM_006096	Hs.75789	NP_006087	1 (0.637 to 1.363)	0.359	0.710 (0.479 to 0.941)
	SEOA8195a;SOX9 ;Z46629	Z46629	NM_000346	Hs.2316	NP_000337	1 (0.386 to 1.614)	0.356	0.516 (0.381 to 0.651)

	ncrc0981;EST (cDNA clone HEMBA1000915 3' HEMBA1) ;AU144114.1	AU144114.1		Hs.453087		1 (0.976 to 1.024)	0.35	1.322 (0.621 to 2.022)
	miob2375;H3 histone, family 3B (H3.3B) (H3F3B) ;NM_005324.1	NM_005324.1	NM_005324	Hs.393660	NP_005315	1 (0.850 to 1.15)	0.339	0.632 (0.580 to 0.684)
	SEOB1322;fos proto-oncogene (c-fos) ;K00650.1	K00650.1			AAA52471	1 (0.688 to 1.312)	0.289	0.643 (0.622 to 0.665)
	SEOA1079a;chitinase (HUMTCHIT) ;U58515	U58515	NM_004000	Hs.154138	NP_003991	1 (0.172 to 1.828)	0.282	2.606 (2.244 to 2.969)
	ncrc2705;EST(wr53g02.x1 NCI_CGAP_Ut1 cDNA clone IMAGE:2491442 3') ;AI973251.1	AI973251.1	NM_031461	Hs.182364	NP_113649	1 (0.261 to 1.739)	0.269	0.748 (0.252 to 1.243)
	MIOA7395a;SOD2 manganese superoxide dismutase ;X65965	X65965				1 (0.218 to 1.782)	0.232	0.595 (0.273 to 0.916)

	FIGURE 2: Down in Severe OA Only							
SEQ ID NO	**Description of Sequence**	**Gene Accession Number**	**Ref Accession Number**	**UniGene**	**Protein Accession Number**	**normal**	**mild**	**severe**
	FCR1566;EST (np83a06.s1 NCI_CGAP_Thy1 clone IMAGE:1132882 gb:L06505 60S RIBOSOMAL PROTEIN L12);AA632687	AA632687	NM_000976	Hs.378011	NP_000967	1 (0.401 to 1.599)	0.694	0.42 (0.341 to 0.499)
	fcrb1690;EST (7n15h06.x1 NCI_CGAP_Brn23 DNA clone IMAGE:3564899 3') ;BF195152.1	BF195152.1		Hs.451373		1 (0.667 to 1.333)	0.523	0.412 (0.328 to 0.497)
	ncrc3541;EST(xn38h02.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:2696019 3') ;AW195479.1	AW195479.1	NM_005398	Hs.303090	NP_005389	1 (0.943 to 1.057)	0.832	0.489 (0.489 to 0.489)
	ncrb8425;EST(601463665F1 NIH_MGC_67 cDNA clone IMAGE:3866801 5') ;BE777895.1	BE777895.1	NM_021639	Hs.169854	NP_067652	1 (0.806 to 1.194)	0.554	0.48 (0.474 to 0.485)
	ncrb8303;Hypothetical protein(cDNA FLJ11339 fis, clone PLACE1010743, weakly similar to myosin-IXb splice variant mRNA) ;AK002201.1	AK002201.1	NM_004145	Hs.159629	NP_004136	1 (0.319 to 1.681)	0.528	0.394 (0.305 to 0.482)
	ncr1204;promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds ;AF060568	AF060568			AAD03619	1	0.824	0.402 (0.324 to 0.48)

	MIOA0090;EST (wh87a08.x1 NCI_CGAP_CLL 1 clone IMAGE:2387702 3' WP:B0035.2 CE05160 DNAJ PROTEIN LIKE) ;AI760344.1	AI760344.1	NM_004125	Hs.433898	NP_004116	1 (0.606 to 1.394)	0.6	0.442 (0.425 to 0.459)
	seoa8384;EST(th76e02.x1 Soares_NhHMPu_S1 clone IMAGE:2124602 3') ;AI434978.1	AI434978.1		Hs.164315		1	NO DATA	0.424 (0.418 to 0.431)
	MIOA3760a;zinc finger transCRiption factor GKLF ;AF105036.1	AF105036.1	NM_004235	Hs.356370	NP_004226	1 (0.831 to 1.169)	NO DATA	0.384 (0.367 to 0.402)
	FCR1580;EST (zs83g12.s1 NCI_CGAP_GCB1 clone IMAGE:704134 3');AA279281	AA279281	NM_004089	Hs.75450	NP_004080	1 (0.288 to 1.712)	0.676	0.336 (0.272 to 0.399)
	miob4857;EST(DKFZp434O1572 clone DKFZp434O1572) ;AL137333.1	AL137333.1	XM_042234	Hs.194478		1 (0.918 to 1.082)	0.659	0.411 (0.391 to 0.432)
	miob6713;zinc finger protein (ZNF-U69274) ;NM_014415.1	NM_014415.1	NM_014415	Hs.301956	NP_055230	1 (0.892 to 1.108)	0.539	0.41 (0.373 to 0.447)
	seoa3815;EST(oj25g11.s1 NCI_CGAP_Kid5 clone IMAGE:1493252 3') ;AA886870	AA886870	NM_018359	Hs.107381	NP_060829	1 (0.642 to 1.358)	NO DATA	0.359 (0.345 to 0.373)

	ncrc9528;nuclear factor of kappa lightpolypeptide gene enhancer in B-cells inhibitor, alpha;Nuclear factor of kappa light chain gene enhancer inB-cells (RefSeq aa 4e-38) ;NP_065390.1	NM_020529			NP_065390.1	1 (0.458 to 1.542)	NO DATA	0.38 (0.356 to 0.403)
	ncrb8237;TSC-22-like Protein mRNA, ;AF183393.1	AF183393.1	NM_004089	Hs.75450	NP_004080	1 (0.286 to 1.714)	0.707	0.326 (0.297 to 0.355)
9	miob2933;DNA sequence PAC clone RP5-1060B11 from 7q11.23-q21.1, complete sequence ;AC006322.2	AC006322.2				1 (0.714 to 1.286)	1.088	0.388 (0.352 to 0.424)
	MIOA1025;myleoid differentiation primary response protein MyD88 ;U70451	U70451	NM_002468	Hs.82116	NP_002459	1 (0.912 to 1.088)	0.554	0.366 (0.331 to 0.401)
	miob0762;EST(tc01c04.x1 NCI_CGAP_Co16 cDNA clone IMAGE:2062566 3') ;AI343957.1	AI343957.1				1	NO DATA	0.325 (0.320 to 0.33)
	FCR6730;DNA sequence (Xq13 3' end of PAC 92E23 containing the X inactivation transcipt (XIST)) ;U80460	U80460				1 (0.331 to 1.669)	1.621	0.329 (0.320 to 0.337)
10	miob4228;DNA sequence (PAC 121G13 chromosome 6) ;Z86062.1	Z86062.1				1 (0.969 to 1.031)	NO DATA	0.398 (0.3 to 0.497)

	ncr6316;selenium binding protein 1 (RefSeq aa 8e-40) ;NP_003935.1	NM_003944.2	NM_003944.2	Hs.334841	NP_003935.1	1 (0.454 to 1.546)	0.519	0.202 (0.189 to 0.214)

FIGURE 3: Up in Mild OA Only

SEQ ID NO	Description of Sequence	Gene Accession Number	Ref Accession Number	UniGene	Protein Accession Number	normal	mild	severe
	MIOA8106;DNA sequence(HS_5573_B1_E05_SP6 RPCI-11 Male BAC Library genomic clone Plate=1149 Col=9 Row=J) ;AQ750872.1	AQ750872.1				1 (0.871 to 1.129)	3.168	1.018 (0.964 to 1.072)
	FCR4376;EST (ol15b11.s1 Soares_NFL_T_GBC_S1 clone IMAGE:1523517 3') ;AA904355	AA904355	NM_032682	Hs.274344	NP_116071	1 (0.871 to 1.129)	3.047	0.901 (0.798 to 1.005)
11	hfcr8691;No significant match;					1 (0.823 to 1.177)	2.727	1.791 (1.729 to 1.852)
	SEOA0824;alpha-tubulin ;K00557	K00557	NM_006009	Hs.433394	NP_006000	1 (0.728 to 1.272)	2.688	1.151 (1.051 to 1.252)
12	FCR6361;DNA sequence (12p13.3 BAC RPCI11-500M8 (Roswell Park Cancer Institute Human BAC Library) ;AC005832	AC005832				1 (0.977 to 1.023)	2.625	1.3 (1.254 to 1.345)
	hfcr3990;Novel;	U48696.1				1 (0.808 to 1.192)	2.614	1.784 (1.553 to 2.015)
	SEOA0114;MacMarcks ;X70326	X70326	NM_023009	Hs.75061	NP_075385	1 (0.742 to 1.258)	2.556	1.125 (0.872 to 1.378)
	ncrb4428;Ras association (RalGDS/AF-6) domain family 2 (RASSF2)(= KIAA0168) ;NM_014737.1	NM_014737.1	NM_014737	Hs.80905	NP_739580	1 (0.635 to 1.365)	2.507	1.304 (1.298 to 1.309)

	ncrb4154;glucosamine-6-phosphate ;AJ002231.1	AJ002231.1	NM_005471	Hs.278500	NP_005462	1 (0.609 to 1.391)	2.35	1.386 (0.950 to 1.823)
	ncr0679;membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA	NM_001932.2	NM_001932.2	Hs.423809	NP_001923.2	1 (0.935 to 1.065)	2.277	0.871 (0.840 to 0.901)
	fcrb1982;hypothetical protein MGC3047 (MGC3047) ;XM_027710.1	NM_032348	NM_032348	Hs.59384		1 (0.547 to 1.453)	2.272	1.714 (1.584 to 1.844)
	MIOA8952;erythrocyte membrane protein band 4.1-like 2 (EPB41L2) ;NM_001431.1	NM_001431.1	NM_001431	Hs.7857	NP_001422	1 (0.627 to 1.373)	2.268	1.793 (1.761 to 1.826)
13	bfcn0190n;Homo sapiens chromosome 15, clone CTD1-2291N1, complete sequence	AC107908.3				1 (0.987 to 1.013)	2.248	1.309 (1.124 to 1.494)
	fcr3730;EST xb22e11.x1 NCI_CGAP_Kid13 cDNA clone IMAGE:2577068 3' ;AW075553	AW075553		Hs.243278		1 (0.999 to 1.001)	2.241	1.33 (0.973 to 1.687)
	fcrb5705;kinesin-like 5 (mitotic kinesin-like protein 1) (KNSL5), mRNA /cds=(117,2687) /gb=NM_004856 /gi=13699831 /ug=Hs.270845 /len=3323 ;Hs.270845	NM_004856	NM_138555	Hs.270845	NP_612565	1 (0.911 to 1.089)	2.203	1.190 (1.054 to 1.326)
	seoa0387;matrix Gla protein (MGP) ;M55270	M55270			AAB53765	1 (0.775 to 1.225)	2.202	1.174 (0.889 to 1.458)

	hfcr0439;alpha-1-antitrypsin mRNA, complete cds ;K01396.1	K01396.1	NM_000295	Hs.297681	NP_000286	1 (0.945 to 1.055)	2.192	1.028 (0.879 to 1.178)
	miob1269;EST (an12d12.s1 Stratagene schizo brain S11 IMAGE:1685399 3') ;AI003217.1	AI003217.1				1	2.187	1.813 (1.454 to 2.173)
	miob3252;CILP gene for cartilage intermediate layer protein, complete cds ;AB022430.1	AB022430.1			BAA76692	1 (0.901 to 1.099)	2.18	0.993 (0.958 to 1.028)
	ncrb4477;Homo sapiens serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), mRNA	NM_000295.2	NM_000295.2	Hs.297681	NP_000286.2	1 (0.756 to 1.244)	2.179	1.224 (0.773 to 1.674)
14	cr0517;Homo sapiens 12 BAC RP13-820C6 (Roswell Park Cancer Institute Human BAC Library) complete sequence	AC137590.2				1	2.178	1.082 (1.035 to 1.128)
	FCR2743;EST (qa21e02.x1 NCI_CGAP_Brn23 clone IMAGE:1687418 3');AI088910	AI088910	NM_017714	Hs.88367	NP_060184	1 (0.961 to 1.039)	2.175	1.231 (1.213 to 1.249)
	fcr6308;EST df54g09.y1 Morton Fetal Cochlea cDNA clone IMAGE:2487353 5' ;AW023432	AW023432		Hs.188375		1 (0.871 to 1.129)	2.159	1.332 (1.179 to 1.486)

	ncrb4843;replication protein A1 (70kD) (RPA1) ;NM_002945.1	NM_002945.1	NM_002945	Hs.84318	NP_002936	1	2.154	1.158 (1.098 to 1.218)
15	seob4891;DNA sequence (BAC clone RP11-15J24 chromosome 2) ;AC007736.3	AC007736.3				1 (0.729 to 1.271)	2.147	1.27 (1.145 to 1.394)
16	MIOB2566;DNA sequence (chromosome 4 clone RP11-340K9 map 4, WORKING DRAFT SEQUENCE, 24 unordered pieces) ;AC012205.3	AC012205.3				1	2.145	1.082 (0.827 to 1.338)
	FCR0620;EST (oe35b11.s1 NCI_CGAP_Pr25 clone IMAGE:1410525 3');AA857238	AA857238		Hs.4248		1 (0.946 to 1.054)	2.13	0.849 (0.828 to 0.869)
	FCR6069;EST (zf01g11.s1 Soares fetal heart NbHH19W clone 375716 3') ;AA033743	AA033743	XM_087386	Hs.433452		1 (0.908 to 1.092)	2.119	1.418 (1.396 to 1.441)
17	miob4693;DNA sequence (chromosome 6 clone RP11-780P12, WORKING DRAFT SEQUENCE, 4 unordered pieces) ;AC022218.4	AC022218.5				1 (0.767 to 1.233)	2.096	1.812 (1.559 to 2.066)

	hfcr7667;EST (yr10e10.s1 Soares fetal liver spleen 1NFLS clone IMAGE:204906 3')(contains Alu repetitive element) ;H57324.1	H57324.1				1	2.087	1.585
	cr0503;EST (PM4-NN0090-230400-001-d11 NN0090) ;AW899788.1	AW899788.1				1 (0.882 to 1.118)	2.085	1.001 (0.908 to 1.093)
	FCR5665;EST (yd33h08.r1 clone 110079 5') ;T85246	T85246		Hs.452509		1 (0.880 to 1.12)	2.081	1.408 (1.393 to 1.423)
	ncr7382;protease inhibitor 1 (anti-elastase),alpha-1-antitrypsin (RefSeq aa 3e-43) ;NP_000286.1	NM_000295			NP_000286.1	1 (0.783 to 1.217)	2.076	0.893 (0.68 to 1.105)
	fcr4642;EST (integral membrane protein 2A, clone IMAGE:4149910, mRNA);BC010511	BC010511	NM_004867	Hs.17109	NP_004858	1 (0.764 to 1.236)	2.068	1.172 (1.144 to 1.200)
	SEOA4017a;retinoic acid-induced protein (RAI2) ;AF136587.1	AF136587.1			AAD33688	1 (0.882 to 1.118)	2.059	1.718 (1.634 to 1.801)
18	hfcr1438;No significant match;					1 (0.933 to 1.067)	2.052	1.294 (1.100 to 1.489)
	hfcr0263;paired basic amino acid cleaving enzyme (furin, membrane associated receptor protein) (PACE) ;NM_002569.1	NM_002569.1	NM_002569	Hs.59242	NP_002560	1 (0.975 to 1.025)	2.049	0.884 (0.882 to 0.885)

	ncr7477;cDNA sequence (cDNA sequence FLJ11736 fis, clone HEMBA1005468) ;AK021798.1	AK021798.1			BAB13899	1	2.045	1.602 (1.422 to 1.783)
	ncr2015;G protein-coupled receptor 23 (GPR23) ;NM_005296.1	NM_005296 .1	NM_005296	Hs.27812	NP_005287	1 (0.765 to 1.235)	2.044	1.973 (1.816 to 2.131)
	mioa9984;EST wm09d08.x1 NCI_CGAP_ cDNA clone IMAGE:2435439 3' similar to contains Alu repetitive element;contains element THR repetitive element ; ;AI859280	AI859280	NM_017523	Hs.139262	NP_059993	1 (0.722 to 1.278)	2.036	1.245 (1.202 to 1.287)
	FCR1427;EST (zt75e12.r1 Soares testis NHT clone 728206 5');AA393418	AA393418	NM_014335	Hs.381137	NP_055150	1 (0.958 to 1.042)	2.023	0.914 (0.852 to 0.977)
	MIOA2551;EST(vz 29h10.r1 Soares 2NbMT clone 1327939 5') (low match) ;AA915413	AA915413				1 (0.860 to 1.14)	2.022	1.988 (1.462 to 2.514)
	FCR6039;protein kinase Dyrk2 ;Y13493	Y13493	NM_006482	Hs.173135	NP_006473	1 (0.868 to 1.132)	2.02	1.177 (1.157 to 1.197)
	miob1165;DNA sequence (clone 23698) ;AF052094.1	AF052094.1	NM_001430	Hs.8136	NP_001421	1 (0.611 to 1.389)	2.013	1.761 (1.745 to 1.777)

	fcrb3863;cDNA, 3' end /clone=IMAGE:2504281 /clone_end=3' /gb=AW009305 /gi=5858083 /ug=Hs.337337 /len=456 ;Hs.337337	AW009305		Hs.337337		1 (0.941 to 1.059)	2.007	1.217 (1.002 to 1.432)
	fcrb1183;tubulin-specific chaperone d (TBCD)= AJ006417 beta-tubulin cofactor D ;NM_005993.2	NM_005993.2	NM_005993	Hs.12570	NP_005984	1	2.004	0.781
	hfcr6052;EST hi90a09.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2979544 3' ;AW665381.1	AW665381.1		Hs.445324		1 (0.889 to 1.111)	2.002	1.354 (1.19 to 1.519)

	FIGURE 4: Up in Severe OA Only							
SEQ ID NO	**Description of Sequence**	**Gene Accession Number**	**Ref Accession Number**	**UniGene**	**Protein Accession Number**	**normal**	**mild**	**severe**
	FCR1346;receptor of retinoic acid (=M73779 PML-RAR protein (PML-RAR));X06614	X06614	NM_000964	Hs.361071	NP_000955	1 (0.804 to 1.196)	1.577	2.651 (2.19 to 3.113)
	MIOA5404a;actin-like 6 (ACTL6)=AF041474 =BAF53a (BAF53a)(ORF) ;NM_004301.1	NM_004301.1	NM_178042	Hs.274350	NP_829888	1	1.011	2.975 (2.785 to 3.165)
	SEOA6743;EST(ze26h09.r1 Soares retina N2b4HR clone 360161 5') ;AA013461	AA013461		Hs.161598		1 (0.953 to 1.047)	1.442	2.349 (2.297 to 2.401)
	FCR5026;6-phosphofructo-2-kinase/fructose-2,6 bisphosphatase (PF2K) (=AB007902 KIAA0442) ;AF041832	AF041832				1 (0.944 to 1.056)	1.46	2.289 (2.269 to 2.309)
	miob4484;hypothetical protein (KIAA0584) ;AB011156.1	AB011156.1	NM_015101	Hs.106794	NP_055916	1	1.547	3.424 (2.207 to 4.641)
	seob7571;EST (qh03a05.x1 Soares_NFL_T_GBC_S1 IMAGE:1843568 3') ;AI222189.1	AI222189.1	NM_002556	Hs.24734	NP_002547	1 (0.945 to 1.055)	1.615	2.080 (2.041 to 2.12)

FIGURE 5: Down in Mild OA Up in Severe OA

SEQ ID NO	Description of Sequence	Gene Accession Number	Ref Accession Number	UniGene	Protein Accession Number	normal	mild	severe
	MIOA4076a;ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC), putative ;Q18491	NM_020154.1	NM_020154.1	Hs.4245	NP_064539.1	1 (0.383 to 1.617)	0.418	2.909 (2.011 to 3.806)
	seob1967;hypothetical protein (FLJ11041 fis, clone PLACE1004405) ;AK001903.1	AK001903.1		Hs.28792		1 (0.217 to 1.783)	0.384	2.451 (1.884 to 3.019)

FIGURE 6a: OA stage specific markers for mild OA only

Common name	Genbank	Description	RefSeq	UniGene	Rep_Prot
ncrc6905	AB007916	mRNA for KIAA0447 protein, partial cds. /cds=(234,1634) /gb=AB007916 /gi=6683704 /ug=Hs.214646 /len=5932		Hs.214646	NP_878258
seoa9924	AB007960	chromosome 1 specific transcript KIAA0491	NM_016009	Hs.136309	NP_057093
ncrc2701	AB011110	mRNA for KIAA0538 protein, partial cds	NM_006989	Hs.184367	NP_008920
seoc4468	AB014540	mRNA for KIAA0640 protein, partial cds. /cds=(1,1813) /gb=AB014540 /gi=3327093 /ug=Hs.153026 /len=4824		Hs.153026	NP_055870
seob7030	AB023420	mRNA for heat shock protein apg-2, complete cds. /cds=(279,2801) /gb=AB023420 /gi=4579908 /ug=Hs.90093 /len=2839		Hs.90093	NP_002145
seoa8696	AB037754	mRNA for KIAA1333 protein, partial cds	NM_017769	Hs.79828	NP_060239
miob8583	AB037788	mRNA for KIAA1367 protein, partial cds. /cds=(1,1741) /gb=AB037788 /gi=7243114 /ug=Hs.224961 /len=4196		Hs.224961	NP_059133
miob8583	AB037788	mRNA for KIAA1367 protein, partial cds. /cds=(1,1741) /gb=AB037788 /gi=7243114 /ug=Hs.224961 /len=4196		Hs.224961	NP_059133
seob4263	AB040894	mRNA for KIAA1461 protein, partial cds	NM_018328	Hs.94125	NP_060798
seob4263	AB040894	mRNA for KIAA1461 protein, partial cds	NM_018328	Hs.94125	NP_060798
miob2503	AB051541	mRNA for KIAA1754 protein, partial cds. /cds=(32,1816) /gb=AB051541 /gi=12698052 /ug=Hs.28501 /len=4088	NM_033397	Hs.28501	NP_203755
mioc2385	AB067500	mRNA for KIAA1913 protein, partial cds. /cds=(818,2347) /gb=AB067500 /gi=15620884 /ug=Hs.172870 /len=3512	NM_052913	Hs.172870	NP_443145
mioc7513	AF279370	DZIP3 mRNA, partial cds	NM_014648	Hs.165662	NP_055463
mioc7513	AF279370	DZIP3 mRNA, partial cds	NM_014648	Hs.165662	NP_055463
mioc7513	AF279370	DZIP3 mRNA, partial cds	NM_014648	Hs.165662	NP_055463
fcrb6309	AF324892	myosin phosphatase target subunit 2 (MYPT2) gene, exons 11 through 24, and complete cds	NM_002481; NM_032103; NM_032104; NM_032105		NP_002472; NP_115286; NP_115287; NP_115288
fcrc6564	AF474370	chemokine-like factor super family member 8 (CKLFSF8) mRNA, complete cds /cds=(295,816) /gb=AF474370 /gi=25167350 /ug=Hs.154986 /len=1185		Hs.154986	NP_849199

fcrc6564	AF474370	chemokine-like factor super family member 8 (CKLFSF8) mRNA, complete cds /cds=(295,816) /gb=AF474370 /gi=25167350 /ug=Hs.154986 /len=1185		Hs.154986	NP_849199
ncrc0075	AF545571	sulfatase SULF1 precursor, mRNA, complete cds /cds=(707,3322) /gb=AF545571 /gi=28191289 /ug=Hs.70823 /len=5699	NM_015170	Hs.70823	NP_055985
ncr1522	AJ000052	gene encoding splicing factor SF1, exons 2-8	NM_004630		NP_004621
miod7007	AJ251973	partial steerin-1 gene	NM_020443		NP_065176
miod1528	AJ420597	mRNA full length insert cDNA clone EUROIMAGE881791		Hs.34665	NP_775945
seoc5609	AK001419	cDNA FLJ10557 fis, clone NT2RP2002537	NM_014053	Hs.270594	NP_054772
ncr3785	AK001911	cDNA FLJ11049 fis, clone PLACE1004548	NM_020819	Hs.107287	NP_065870
seoc3640	AK021499	cDNA FLJ11437 fis, clone HEMBA1001226	NM_002788; NM_152132		NP_002779
miob9087	AK024433	mRNA for FLJ00023 protein, partial cds	NM_022497	Hs.23450	NP_071942
miod6848	AK026850	cDNA: FLJ23197 fis, clone REC00917	NM_005402	Hs.6906	NP_005393
mioc9655	AK055915	cDNA FLJ31353 fis, clone MESAN2000264. /gb=AK055915 /gi=16550762 /ug=Hs.352554 /len=2192		Hs.352554	NP_006440
miob8096	AK057924	cDNA FLJ25195 fis, clone REC04480, highly similar to Mus musculus exportin 4 mRNA	NM_022459	Hs.117102	NP_071904
seob1782	AK074172	mRNA for FLJ00245 protein		Hs.244343	NP_443068
seob7534	AK075026	cDNA FLJ90545 fis, clone OVARC1000410, weakly similar to angiopoietin Y1 mRNA		Hs.8025	NP_036230
seob5621	AK090874	cDNA FLJ33555 fis, clone BRAMY2009349, moderately similar to Mus musculus ubiquitin-protein ligase E3-alpha (Ubr1) mRNA		Hs.15303	NP_056070
seoc6732	AK098206	cDNA FLJ40887 fis, clone UTERU2000696, moderately similar to Endoplasmic reticulum resident protein 58		Hs.83286	NP_714916
ncrc1765	AL080156	mRNA; cDNA DKFZp434J214 (from clone DKFZp434J214); partial cds /cds=(1,1082) /gb=AL080156 /gi=5262614 /ug=Hs.12813 /len=2749		Hs.12813	NP_056323
miod7095	AL096734	mRNA; cDNA DKFZp434M011 (from clone DKFZp434M011)	NM_030980	Hs.301904	NP_112242
fcrc6486	AL110153	mRNA; cDNA DKFZp586E0524 (from clone DKFZp586E0524)	NM_000983	Hs.326249	NP_000974
mioc2507	AL137295	mRNA; cDNA DKFZp434M2216 (from clone DKFZp434M2216)	NM_004641	Hs.199429	NP_004632

seoa3357	AL162009	mRNA; cDNA DKFZp586C2117 (from clone DKFZp586C2117)		Hs.356386	NP_004628
miod2065	AL832012	mRNA; cDNA DKFZp451D084 (from clone DKFZp451D084); complete cds	NM_006827	Hs.74137	NP_006818
miob8803	AL833934	mRNA; cDNA DKFZp547F222 (from clone DKFZp547F222)	NM_022458	Hs.107537	NP_071903
ncrc7173	AL834204	mRNA; cDNA DKFZp434J1323 (from clone DKFZp434J1323)	NM_015208		NP_056023
fcrc2573	AL834255	mRNA; cDNA DKFZp586M1819 (from clone DKFZp586M1819) /cds=(1,795) /gb=AL834255 /gi=21739805 /ug=Hs.355753 /len=1723		Hs.355753	NP_848934
ncrb8113	AW182493	xj42g07.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2659932 3', mRNA sequence /clone=IMAGE:2659932 /clone_end=3' /gb=AW182493 /gi=6450953 /ug=Hs.176245 /len=432		Hs.176245	NP_060046
fcr3932	BC011767	clone IMAGE:3609644, mRNA		Hs.56828	NP_006577
ncr7284	BC013088	clone IMAGE:3452986, mRNA	NM_001894; NM_152221	Hs.79658	NP_689407
mioc8879	BC017107	clone IMAGE:3537687, mRNA		Hs.16577	NP_208385
fcrb9161	BC017973	clone MGC:24133 IMAGE:4693393, mRNA, complete cds /cds=(61,528) /gb=BC017973 /gi=22450811 /ug=Hs.288010 /len=946	NM_174896	Hs.288010	NP_777556
miod0057	BC020167	clone IMAGE:3529287, mRNA	NM_152740	Hs.284170	NP_689953
seoc4785	BC022792	Vpr-binding protein, mRNA (cDNA clone MGC:23092 IMAGE:4853730), complete cds	NM_014703	Hs.118738	NP_055518
ncrc2382	BC032405	clone IMAGE:5209850, mRNA		Hs.146428	NP_000084
seob0220	BC032437	clone IMAGE:4432159, mRNA /gb=BC032437 /gi=21595543 /ug=Hs.249247 /len=2309		Hs.249247	
mioa8580	BC032643	Similar to NS1-associated protein 1, clone MGC:45213 IMAGE:5495201, mRNA, complete cds		Hs.373499	NP_006363
fcrb8094	BC034757	Indian hedgehog (Drosophila), clone MGC:34815 IMAGE:5182642, mRNA, complete cds /cds=(74,955) /gb=BC034757 /gi=21961329 /ug=Hs.115274 /len=1760		Hs.115274	
ncrc3706	BC035312	clone MGC:21662 IMAGE:4747440, mRNA, complete cds		Hs.145010	NP_115965
ncrc3089	BC036649	Sec23 A (S. cerevisiae), clone MGC:26267 IMAGE:4821858, mRNA, complete cds	NM_006364	Hs.272927	NP_006355
miob0681	BC037306	Similar to CD47 antigen (Rh-related antigen, integrin-associated signal transducer), clone MGC:33903 IMAGE:5260986, mRNA, complete cds	NM_001777	Hs.313342	NP_001768
ncr3803	BC037492	clone IMAGE:5260578, mRNA		Hs.5518	NP_689971

fcrb4479	BC042102	Similar to RIKEN cDNA 3110032G18 gene, clone IMAGE:4472603, mRNA /gb=BC042102 /gi=27695553 /ug=Hs.432901 /len=2132		Hs.432901	NP_859060
fcrc6611	BC042998	Similar to adducin 1 (alpha), clone MGC:44427 IMAGE:5297337, mRNA, complete cds /cds=(869,2857) /gb=BC042998 /gi=28175763 /ug=Hs.183706 /len=4761	NM_001119; NM_014189; NM_014190; NM_176801	Hs.183706	NP_789771
fcr3593	BC044258	clone IMAGE:6068796, mRNA		Hs.11861	NP_005112
seoc5538	BG434947	602507208F1 NIH_MGC_79 cDNA clone IMAGE:4604760 5', mRNA sequence /clone=IMAGE:4604760 /clone_end=5' /gb=BG434947 /gi=13341453 /ug=Hs.382990 /len=677		Hs.382990	NP_060135
mioc7077	BQ649741	AGENCOURT_8493271 NIH_MGC_100 cDNA clone IMAGE:6299336 5', mRNA sequence /clone=IMAGE:6299336 /clone_end=5' /gb=BQ649741 /gi=21773913 /ug=Hs.44701 /len=993		Hs.44701	NP_055301
fcrb4351	BU536672	AGENCOURT_10227215 NIH_MGC_141 cDNA clone IMAGE:6565196 5', mRNA sequence /clone=IMAGE:6565196 /clone_end=5' /gb=BU536672 /gi=22847113 /ug=Hs.380933 /len=1275		Hs.380933	NP_000974
ncrc8884	BU627064	UI-H-FG0-bct-g-21-0-UI.s1 NCI_CGAP_EN1_2 cDNA clone UI-H-FG0-bct-g-21-0-UI 3', mRNA sequence /clone=UI-H-FG0-bct-g-21-0-UI /clone_end=3' /gb=BU627064 /gi=23293278 /ug=Hs.85999 /len=1075		Hs.85999	NP_060312
seoc4779	BU728934	UI-E-CQ1-aew-e-07-0-UI.s1 UI-E-CQ1 cDNA clone UI-E-CQ1-aew-e-07-0-UI 3', mRNA sequence /clone=UI-E-CQ1-aew-e-07-0-UI /clone_end=3' /gb=BU728934 /gi=23651308 /ug=Hs.436272 /len=1132		Hs.436272	NP_060312
seob0562	BX094256	BX094256 Soares_fetal_heart_NbHH19W cDNA clone IMAGp998B20783, mRNA sequence /clone=IMAGp998B20783_;_IMAGE:342835 /gb=BX094256 /gi=27841884 /ug=Hs.407356 /len=477		Hs.407356	NP_055301
seob6628	BX110894	BX110894 Soares fetal liver spleen 1NFLS cDNA clone IMAGp998F21129, mRNA sequence /clone=IMAGp998F21129_;_IMAGE:127124 /gb=BX110894 /gi=27836709 /ug=Hs.309257 /len=612		Hs.309257	T02670

miob0542	CA848700	ir24c06.y1 HR85 islet cDNA clone IMAGE:6546227 5', mRNA sequence /clone=IMAGE:6546227 /clone_end=5' /gb=CA848700 /gi=26999906 /ug=Hs.389121 /len=616		Hs.389121	NP_060312
seob4499	CB050438	NISC_gj17d11.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:3272108 3', mRNA sequence /clone=IMAGE:3272108 /clone_end=3' /gb=CB050438 /gi=27788725 /ug=Hs.435309 /len=534		Hs.435309	NP_060265
ncr1150	D83778	mRNA for KIAA0194 gene, partial cds. /cds=(1,4310) /gb=D83778 /gi=1228038 /ug=Hs.216958 /len=5245		Hs.216958	BAA12107
miob6124	L24123	NRF1 protein (NRF1) mRNA	NM_003204		NP_003195
ncr5649	M24095	MHC class I HLA-A10-alpha-2 chain mRNA, partial cds, clone 8/16		Hs.181244	NP_002107
seob7184	M37435	macrophage-specific colony-stimulating factor (CSF-1) mRNA, complete cds	NM_000757; NM_172210; NM_172211; NM_172212		NP_000748; NP_757349; NP_757350; NP_757351
ncrb5537	NM_000014	alpha-2-macroglobulin (A2M), mRNA /cds=(44,4468) /gb=NM_000014 /gi=6226959 /ug=Hs.74561 /len=4577	NM_000014	Hs.74561	NP_000005
mioa6969	NM_000027	aspartylglucosaminidase (AGA), mRNA /cds=(171,1211) /gb=NM_000027 /gi=4557272 /ug=Hs.207776 /len=2150	NM_000027	Hs.207776	NP_000018
miob4512	NM_000090	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), mRNA /cds=(118,4518) /gb=NM_000090 /gi=15149480 /ug=Hs.119571 /len=5489	NM_000090	Hs.119571	NP_000081
hfcr5232	NM_000095	cartilage oligomeric matrix protein (pseudoachondroplasia, epiphyseal dysplasia 1, multiple) (COMP), mRNA /cds=(26,2299) /gb=NM_000095 /gi=4557482 /ug=Hs.1584 /len=2439	NM_000095	Hs.1584	NP_000086
fcr0796	NM_000146	ferritin, light polypeptide (FTL), mRNA /cds=(189,716) /gb=NM_000146 /gi=20149497 /ug=Hs.430150 /len=878	NM_000146	Hs.430150	NP_000137
mioa7241	NM_000147	fucosidase, alpha-L- 1, tissue (FUCA1), mRNA /cds=(19,1404) /gb=NM_000147 /gi=24475878 /ug=Hs.576 /len=2035	NM_000147	Hs.576	NP_000138
fcrb2137	NM_000184	hemoglobin, gamma G (HBG2), mRNA /cds=(54,497) /gb=NM_000184 /gi=28302132 /ug=Hs.386655 /len=583	NM_000184	Hs.386655	NP_000175
ncrc3092	NM_000216	Kallmann syndrome 1 sequence (KAL1), mRNA /cds=(151,2193) /gb=NM_000216 /gi=4557682 /ug=Hs.89591 /len=6314	NM_000216	Hs.89591	NP_000207

fcrc2254	NM_000234	ligase I, DNA, ATP-dependent (LIG1), mRNA /cds=(121,2880) /gb=NM_000234 /gi=4557718 /ug=Hs.1770 /len=3083	NM_000234	Hs.1770	NP_000225
hfcr0439	NM_000295	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), mRNA /cds=(233,1489) /gb=NM_000295 /gi=21361197 /ug=Hs.297681 /len=1584	NM_000295	Hs.297681	NP_000286
mioa1277	NM_000313	protein S (alpha) (PROS1), mRNA /cds=(147,2177) /gb=NM_000313 /gi=4506116 /ug=Hs.64016 /len=3309	NM_000313	Hs.64016	NP_000304
fcrc4935	NM_000337	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) (SGCD), transcript variant 1, mRNA /cds=(333,1205) /gb=NM_000337 /gi=27477099 /ug=Hs.151899 /len=1440	NM_000337; NM_172244	Hs.151899	NP_758447
ncrc3604	NM_000393	collagen, type V, alpha 2 (COL5A2), mRNA /cds=(158,4648) /gb=NM_000393 /gi=16554580 /ug=Hs.82985 /len=6217	NM_000393	Hs.82985	NP_000384
fcrb4616	NM_000426	laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA /cds=(50,9382) /gb=NM_000426 /gi=4557708 /ug=Hs.75279 /len=9534	NM_000426	Hs.75279	NP_000417
ncrc4376	NM_000454	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult)) (SOD1), mRNA /cds=(1,465) /gb=NM_000454 /gi=4507148 /ug=Hs.75428 /len=560	NM_000454	Hs.75428	NP_000445
mioa0577	NM_000574	decay accelerating factor for complement (CD55, Cromer blood group system) (DAF), mRNA /cds=(66,1211) /gb=NM_000574 /gi=10835142 /ug=Hs.1369 /len=2102	NM_000574	Hs.1369	NP_000565
seoa8501	NM_000579	chemokine (C-C motif) receptor 5 (CCR5), mRNA /cds=(358,1416) /gb=NM_000579 /gi=4502638 /ug=Hs.54443 /len=3655	NM_000579	Hs.54443	NP_000570
miob7319	NM_000611	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344) (CD59), mRNA /cds=(50,436) /gb=NM_000611 /gi=20127410 /ug=Hs.278573 /len=1946	NM_000611	Hs.278573	NP_000602
ncr9165	NM_000636	superoxide dismutase 2, mitochondrial (SOD2), mRNA /cds=(5,673) /gb=NM_000636 /gi=10835186 /ug=Hs.372783 /len=1026	NM_000636	Hs.372783	NP_000627
miob3618	NM_000693	aldehyde dehydrogenase 1 family, member A3 (ALDH1A3), mRNA /cds=(53,1591) /gb=NM_000693 /gi=4502040 /ug=Hs.75746 /len=3442	NM_000693	Hs.75746	NP_000684
ncr2954	NM_000791	dihydrofolate reductase (DHFR), mRNA /cds=(480,1043) /gb=NM_000791 /gi=7262376 /ug=Hs.83765 /len=3900	NM_000791	Hs.83765	NP_000782

seob1879	NM_000861	histamine receptor H1 (HRH1), mRNA /cds=(179,1642) /gb=NM_000861 /gi=13435403 /ug=Hs.1570 /len=3870	NM_000861	Hs.1570	NP_000852
seoa9883	NM_000925	pyruvate dehydrogenase (lipoamide) beta (PDHB), mRNA /cds=(19,1098) /gb=NM_000925 /gi=4505686 /ug=Hs.979 /len=1501	NM_000925	Hs.979	NP_000916
mioa3598	NM_000933	phospholipase C, beta 4 (PLCB4), mRNA /cds=(231,3299) /gb=NM_000933 /gi=4505866 /ug=Hs.283006 /len=3707	NM_000933	Hs.283006	NP_877949
seob7392	NM_000937	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa (POLR2A), mRNA /cds=(387,6299) /gb=NM_000937 /gi=14589948 /ug=Hs.171880 /len=6732	NM_000937	Hs.171880	NP_000928
fcrc4319	NM_000941	P450 (cytochrome) oxidoreductase (POR), nuclear gene encoding mitochondrial protein, mRNA /cds=(16,2058) /gb=NM_000941 /gi=24307876 /ug=Hs.167246 /len=2446	NM_000941	Hs.167246	NP_000932
seob8082	NM_000944	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA /cds=(407,1972) /gb=NM_000944 /gi=19923130 /ug=Hs.272458 /len=4425	NM_000944	Hs.272458	NP_000935
seoa1117	NM_000944	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA /cds=(407,1972) /gb=NM_000944 /gi=19923130 /ug=Hs.272458 /len=4425	NM_000944	Hs.272458	NP_000935
mioc8016	NM_000944	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha) (PPP3CA), mRNA /cds=(407,1972) /gb=NM_000944 /gi=19923130 /ug=Hs.272458 /len=4425	NM_000944	Hs.272458	NP_000935
ncr3037	NM_000975	ribosomal protein L11 (RPL11), mRNA /cds=(21,557) /gb=NM_000975 /gi=15431289 /ug=Hs.388664 /len=609	NM_000975	Hs.388664	NP_000966
seob8311	NM_000985	ribosomal protein L17 (RPL17), mRNA /cds=(287,841) /gb=NM_000985 /gi=14591906 /ug=Hs.82202 /len=898	NM_000985	Hs.82202	NP_000976
seob3513	NM_001003	ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003 /gi=16905511 /ug=Hs.424299 /len=512	NM_001003	Hs.424299	NP_000994
fcr6708	NM_001003	ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003 /gi=16905511 /ug=Hs.424299 /len=512	NM_001003	Hs.424299	NP_000994
miob9652	NM_001003	ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003 /gi=16905511 /ug=Hs.424299 /len=512	NM_001003	Hs.424299	NP_000994
seob3326	NM_001004	ribosomal protein, large P2 (RPLP2), mRNA	NM_001004	Hs.297753	NP_000995
seob4140	NM_001004	ribosomal protein, large P2 (RPLP2), mRNA	NM_001004	Hs.297753	NP_000995

fcr4212	NM_001008	ribosomal protein S4, Y-linked (RPS4Y), mRNA /cds=(13,804) /gb=NM_001008 /gi=17981706 /ug=Hs.180911 /len=931	NM_001008	Hs.180911	NP_000999
seob4689	NM_001154	annexin A5 (ANXA5), mRNA /cds=(193,1155) /gb=NM_001154 /gi=4809273 /ug=Hs.300711 /len=1630	NM_001154	Hs.300711	NP_001145
seob5894	NM_001177	ADP-ribosylation factor-like 1 (ARL1), mRNA /cds=(105,650) /gb=NM_001177 /gi=4755126 /ug=Hs.242894 /len=968	NM_001177	Hs.242894	NP_001168
ncrb2458	NM_001202	bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA /cds=(478,1704) /gb=NM_001202 /gi=19528648 /ug=Hs.68879 /len=1999	NM_001202; NM_130850; NM_130851	Hs.68879	NP_570912
hfcr6384	NM_001211	BUB1 budding uninhibited by benzimidazoles 1 beta (yeast) (BUB1B), mRNA /cds=(135,3287) /gb=NM_001211 /gi=20149508 /ug=Hs.36708 /len=3702	NM_001211	Hs.36708	NP_001202
ncrc0696	NM_001280	cold inducible RNA binding protein (CIRBP), mRNA /cds=(81,599) /gb=NM_001280 /gi=4502846 /ug=Hs.119475 /len=1322	NM_001280	Hs.119475	NP_001271
seob5645	NM_001344	defender against cell death 1 (DAD1), mRNA /cds=(67,408) /gb=NM_001344 /gi=4503252 /ug=Hs.82890 /len=699	NM_001344	Hs.82890	NP_001335
seob3464	NM_001378	dynein, cytoplasmic, intermediate polypeptide 2 (DNCI2), mRNA /cds=(166,2082) /gb=NM_001378 /gi=24307878 /ug=Hs.66881 /len=2602	NM_001378	Hs.66881	NP_001369
mioc3490	NM_001378	dynein, cytoplasmic, intermediate polypeptide 2 (DNCI2), mRNA /cds=(166,2082) /gb=NM_001378 /gi=24307878 /ug=Hs.66881 /len=2602	NM_001378	Hs.66881	NP_001369
seoa0743	NM_001387	dihydropyrimidinase-like 3 (DPYSL3), mRNA /cds=(111,1823) /gb=NM_001387 /gi=4503378 /ug=Hs.74566 /len=5047	NM_001387	Hs.74566	NP_001378
ncr3040	NM_001402	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
fcrb0386	NM_001402	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
fcrb1741	NM_001416	eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1), mRNA /cds=(17,1237) /gb=NM_001416 /gi=4503528 /ug=Hs.129673 /len=1383	NM_001416	Hs.129673	NP_001407
mioa7361	NM_001431	erythrocyte membrane protein band 4.1-like 2 (EPB41L2), mRNA /cds=(45,3062) /gb=NM_001431 /gi=4503578 /ug=Hs.7857 /len=4336	NM_001431	Hs.7857	NP_001422

fcrc2710	NM_001541	heat shock 27kDa protein 2 (HSPB2), mRNA /cds=(70,618) /gb=NM_001541 /gi=4504518 /ug=Hs.78846 /len=874	NM_001541	Hs.78846	NP_001532
miob9529	NM_001689	ATP synthase, H transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3 (ATP5G3), mRNA /cds=(255,683) /gb=NM_001689 /gi=4502300 /ug=Hs.429 /len=826	NM_001689	Hs.429	NP_001680
seob5767	NM_001690	ATPase, H transporting, lysosomal 70kDa, V1 subunit A, isoform 1 (ATP6V1A1), mRNA /cds=(67,1920) /gb=NM_001690 /gi=19913423 /ug=Hs.281866 /len=4567	NM_001690	Hs.281866	NP_001681
seoc4161	NM_001690	ATPase, H transporting, lysosomal 70kDa, V1 subunit A, isoform 1 (ATP6V1A1), mRNA /cds=(67,1920) /gb=NM_001690 /gi=19913423 /ug=Hs.281866 /len=4567	NM_001690	Hs.281866	NP_001681
seoa2134	NM_001801	cysteine dioxygenase, type I (CDO1), mRNA /cds=(255,857) /gb=NM_001801 /gi=4502754 /ug=Hs.3229 /len=1556	NM_001801	Hs.3229	NP_001792
fcrb1867	NM_001916	cytochrome c-1 (CYC1), mRNA /cds=(5,982) /gb=NM_001916 /gi=21359866 /ug=Hs.289271 /len=1273	NM_001916	Hs.289271	NP_001907
hfcr1646	NM_001930	deoxyhypusine synthase (DHPS), transcript variant 1, mRNA /cds=(98,1207) /gb=NM_001930 /gi=7108341 /ug=Hs.79064 /len=1351	NM_001930; NM_013406; NM_013407	Hs.79064	NP_037539
fcrb2318	NM_002023	fibromodulin (FMOD), mRNA /cds=(21,1151) /gb=NM_002023 /gi=5016093 /ug=Hs.230 /len=2863	NM_002023	Hs.230	NP_002014
mioa0597	NM_002048	growth arrest-specific 1 (GAS1), mRNA /cds=(411,1448) /gb=NM_002048 /gi=4503918 /ug=Hs.65029 /len=2828	NM_002048	Hs.65029	NP_002039
fcrb1689	NM_002128	high-mobility group box 1 (HMGB1), mRNA /cds=(77,724) /gb=NM_002128 /gi=20149538 /ug=Hs.6727 /len=1207	NM_002128	Hs.6727	NP_002119
fcrb6464	NM_002135	nuclear receptor subfamily 4, group A, member 1 (NR4A1), transcript variant 1, mRNA /cds=(315,2111) /gb=NM_002135 /gi=27894342 /ug=Hs.1119 /len=2699	NM_002135; NM_173157; NM_173158	Hs.1119	NP_775181
seoa8776	NM_002157	heat shock 10kDa protein 1 (chaperonin 10) (HSPE1), mRNA /cds=(42,350) /gb=NM_002157 /gi=4504522 /ug=Hs.1197 /len=538	NM_002157	Hs.1197	NP_002148
miod3302	NM_002160	tenascin C (hexabrachion) (TNC), mRNA /cds=(314,6919) /gb=NM_002160 /gi=4504548 /ug=Hs.289114 /len=7560	NM_002160	Hs.289114	NP_002151
fcrc0727	NM_002165	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein (ID1), mRNA /cds=(36,500) /gb=NM_002165 /gi=4504568 /ug=Hs.75424 /len=926	NM_002165	Hs.75424	NP_851998

ncrb5595	NM_002318	lysyl oxidase-like 2 (LOXL2), mRNA /cds=(248,2572) /gb=NM_002318 /gi=4505010 /ug=Hs.83354 /len=3432	NM_002318	Hs.83354	NP_002309
fcrc4408	NM_002337	low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1) (LRPAP1), mRNA /cds=(14,1087) /gb=NM_002337 /gi=4505020 /ug=Hs.75140 /len=1493	NM_002337	Hs.75140	NP_002328
mioc0760	NM_002355	mannose-6-phosphate receptor (cation dependent) (M6PR), mRNA /cds=(171,1004) /gb=NM_002355 /gi=10947032 /ug=Hs.134084 /len=2454	NM_002355	Hs.134084	NP_002346
hfcr4462	NM_002388	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) (MCM3), mRNA /cds=(45,2471) /gb=NM_002388 /gi=6631094 /ug=Hs.179565 /len=3061	NM_002388	Hs.179565	NP_002379
fcrb6917	NM_002455	metaxin 1 (MTX1), mRNA /cds=(1,954) /gb=NM_002455 /gi=4505280 /ug=Hs.247551 /len=1065	NM_002455	Hs.247551	NP_002446
seob3670	NM_002488	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa (NDUFA2), mRNA /cds=(57,356) /gb=NM_002488 /gi=4505354 /ug=Hs.163867 /len=590	NM_002488	Hs.163867	NP_002479
ncr0851	NM_002537	ornithine decarboxylase antizyme 2 (OAZ2), mRNA /gb=NM_002537 /gi=9845506 /ug=Hs.74563 /len=1906	NM_002537	Hs.74563	NP_002528
seoc1023	NM_002546	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B), mRNA /cds=(252,1457) /gb=NM_002546 /gi=22547122 /ug=Hs.81791 /len=2291	NM_002546	Hs.81791	NP_002537
miob3315	NM_002634	prohibitin (PHB), mRNA /cds=(74,892) /gb=NM_002634 /gi=6031190 /ug=Hs.75323 /len=1826	NM_002634	Hs.75323	NP_002625
fcrb2051	NM_002635	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 (SLC25A3), nuclear gene encoding mitochondrial protein, transcript variant 1b, mRNA /cds=(49,1134) /gb=NM_002635 /gi=4505774 /ug=Hs.78713 /len=1330	NM_002635; NM_005888	Hs.78713	NP_005879
seoa0003	NM_002775	protease, serine, 11 (IGF binding) (PRSS11), mRNA /cds=(49,1491) /gb=NM_002775 /gi=21327712 /ug=Hs.75111 /len=2039	NM_002775	Hs.75111	NP_002766
mioa3857	NM_002797	proteasome (prosome, macropain) subunit, beta type, 5 (PSMB5), mRNA /cds=(20,811) /gb=NM_002797 /gi=22538468 /ug=Hs.261927 /len=1050	NM_002797	Hs.261927	NP_002788
miod6835	NM_002802	proteasome (prosome, macropain) 26S subunit, ATPase, 1 (PSMC1), mRNA /cds=(49,1371) /gb=NM_002802 /gi=24430150 /ug=Hs.4745 /len=1586	NM_002802	Hs.4745	NP_002793

seob7465	NM_002819	polypyrimidine tract binding protein 1 (PTBP1), transcript variant 1, mRNA /cds=(89,1762) /gb=NM_002819 /gi=14165462 /ug=Hs.172550 /len=3322	NM_002819; NM_031990; NM_031991; NM_175847	Hs.172550	NP_787041
ncrc4633	NM_002835	protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA /cds=(30,2372) /gb=NM_002835 /gi=18375651 /ug=Hs.62 /len=3161	NM_002835	Hs.62	NP_002826
fcrb0354	NM_002852	pentaxin-related gene, rapidly induced by IL-1 beta (PTX3), mRNA /cds=(68,1213) /gb=NM_002852 /gi=4506332 /ug=Hs.2050 /len=1837	NM_002852	Hs.2050	NP_002843
fcrb2344	NM_002869	RAB6A, member RAS oncogene family (RAB6A), mRNA /cds=(427,1053) /gb=NM_002869 /gi=19923230 /ug=Hs.5636 /len=3079	NM_002869	Hs.5636	NP_002860
fcrb2756	NM_002904	RD RNA binding protein (RDBP), mRNA /cds=(109,1251) /gb=NM_002904 /gi=20631983 /ug=Hs.106061 /len=1464	NM_002904	Hs.106061	NP_002895
fcrb9633	NM_002913	replication factor C (activator 1) 1, 145kDa (RFC1), mRNA /cds=(429,3875) /gb=NM_002913 /gi=15011930 /ug=Hs.166563 /len=5185	NM_002913	Hs.166563	NP_002904
miob3809	NM_002948	ribosomal protein L15 (RPL15), mRNA /cds=(37,651) /gb=NM_002948 /gi=15431292 /ug=Hs.74267 /len=2018	NM_002948	Hs.74267	NP_002939
fcrb2321	NM_002952	ribosomal protein S2 (RPS2), mRNA /cds=(12,893) /gb=NM_002952 /gi=15055538 /ug=Hs.356360 /len=978	NM_002952	Hs.356360	NP_002943
seoc5858	NM_002964	S100 calcium binding protein A8 (calgranulin A) (S100A8), mRNA /cds=(56,337) /gb=NM_002964 /gi=21614543 /ug=Hs.416073 /len=428	NM_002964	Hs.416073	NP_002955
fcrb8485	NM_003016	splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(156,821) /gb=NM_003016 /gi=4506898 /ug=Hs.73965 /len=1879	NM_003016	Hs.73965	NP_003007
hfcr3183	NM_003016	splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(156,821) /gb=NM_003016 /gi=4506898 /ug=Hs.73965 /len=1879	NM_003016	Hs.73965	NP_003007
fcr7705	NM_003017	splicing factor, arginine/serine-rich 3 (SFRS3), mRNA /cds=(106,600) /gb=NM_003017 /gi=24025684 /ug=Hs.388623 /len=1403	NM_003017	Hs.388623	NP_003008
fcrb8668	NM_003029	SHC (Src 2 domain containing) transforming protein 1 (SHC1), mRNA /cds=(195,1946) /gb=NM_003029 /gi=10835030 /ug=Hs.81972 /len=3664	NM_003029	Hs.81972	NP_892113

fcrb6436	NM_003075	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2 (SMARCC2), transcript variant 1, mRNA /cds=(33,3677) /gb=NM_003075 /gi=21237804 /ug=Hs.236030 /len=4039	NM_003075; NM_139067	Hs.236030	NP_620706
seoa4289	NM_003101	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1 (SOAT1), transcript variant 688113, mRNA /cds=(64,1716) /gb=NM_003101 /gi=24431944 /ug=Hs.14553 /len=3407	NM_003101	Hs.14553	NP_003092
seob2958	NM_003104	sorbitol dehydrogenase (SORD), mRNA /cds=(140,1213) /gb=NM_003104 /gi=21314633 /ug=Hs.878 /len=2637	NM_003104	Hs.878	NP_003095
seoa7408	NM_003136	signal recognition particle 54kDa (SRP54), mRNA /cds=(225,1739) /gb=NM_003136 /gi=20149548 /ug=Hs.49346 /len=2164	NM_003136	Hs.49346	NP_003127
ncrb7211	NM_003155	stanniocalcin 1 (STC1), mRNA /cds=(285,1028) /gb=NM_003155 /gi=4507264 /ug=Hs.25590 /len=3901	NM_003155	Hs.25590	NP_003146
miod3600	NM_003157	NIMA (never in mitosis gene a)-related kinase 4 (NEK4), mRNA /cds=(179,2704) /gb=NM_003157 /gi=4507276 /ug=Hs.1087 /len=3698	NM_003157	Hs.1087	NP_003148
seob4127	NM_003187	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa (TAF9), transcript variant 1, mRNA /cds=(159,953) /gb=NM_003187 /gi=21166375 /ug=Hs.60679 /len=1153	NM_003187; NM_016283	Hs.60679	NP_057367
seoa3296	NM_003239	transforming growth factor, beta 3 (TGFB3), mRNA	NM_003239	Hs.2025	NP_003230
seob4804	NM_003291	tripeptidyl peptidase II (TPP2), mRNA /cds=(24,3773) /gb=NM_003291 /gi=4507656 /ug=Hs.1117 /len=4626	NM_003291	Hs.1117	NP_003282
mioa0059	NM_003297	nuclear receptor subfamily 2, group C, member 1 (NR2C1), mRNA /cds=(57,1868) /gb=NM_003297 /gi=4507672 /ug=Hs.108301 /len=2202	NM_003297	Hs.108301	NP_003288
seob3517	NM_003314	tetratricopeptide repeat domain 1 (TTC1), mRNA /cds=(51,929) /gb=NM_003314 /gi=4507710 /ug=Hs.7733 /len=1407	NM_003314	Hs.7733	NP_003305
miob4803	NM_003316	tetratricopeptide repeat domain 3 (TTC3), mRNA /cds=(1470,7547) /gb=NM_003316 /gi=21359840 /ug=Hs.118174 /len=9078	NM_003316	Hs.118174	NP_003307
seob6751	NM_003321	Tu translation elongation factor, mitochondrial (TUFM), mRNA /cds=(72,1430) /gb=NM_003321 /gi=21359836 /ug=Hs.12084 /len=1636	NM_003321	Hs.12084	NP_003312
miob2533	NM_003374	voltage-dependent anion channel 1 (VDAC1), mRNA /cds=(100,951) /gb=NM_003374 /gi=4507878 /ug=Hs.149155 /len=1806	NM_003374	Hs.149155	NP_003365

seob3197	NM_003374	voltage-dependent anion channel 1 (VDAC1), mRNA /cds=(100,951) /gb=NM_003374 /gi=4507878 /ug=Hs.149155 /len=1806	NM_003374	Hs.149155	NP_003365
seob1848	NM_003440	zinc finger protein 140 (clone pHZ-39) (ZNF140), mRNA /cds=(273,1646) /gb=NM_003440 /gi=4507990 /ug=Hs.154205 /len=2407	NM_003440	Hs.154205	NP_003431
fcrb4360	NM_003479	protein tyrosine phosphatase type IVA, member 2 (PTP4A2), transcript variant 1, mRNA /cds=(1011,1514) /gb=NM_003479 /gi=18104974 /ug=Hs.82911 /len=3925	NM_003479; NM_080391; NM_080392	Hs.82911	NP_536317
mioa0497	NM_003569	syntaxin 7 (STX7), mRNA /cds=(80,865) /gb=NM_003569 /gi=4507294 /ug=Hs.8906 /len=1614	NM_003569	Hs.8906	NP_003560
seoa0792	NM_003676	degenerative spermatocyte lipid desaturase (Drosophila) (DEGS), transcript variant 1, mRNA /cds=(112,1083) /gb=NM_003676 /gi=21614503 /ug=Hs.185973 /len=2058	NM_003676; NM_144780	Hs.185973	NP_659004
fcrb8393	NM_003732	eukaryotic translation initiation factor 4E binding protein 3 (EIF4EBP3), mRNA /cds=(73,375) /gb=NM_003732 /gi=4503536 /ug=Hs.375012 /len=698	NM_003732	Hs.375012	NP_003723
hfcr2850	NM_003769	splicing factor, arginine/serine-rich 9 (SFRS9), mRNA /cds=(53,718) /gb=NM_003769 /gi=4506902 /ug=Hs.77608 /len=1069	NM_003769	Hs.77608	NP_003760
ncr7967	NM_003796	chromosome 19 open reading frame 2 (C19orf2), transcript variant 1, mRNA /cds=(31,1638) /gb=NM_003796 /gi=19924158 /ug=Hs.7943 /len=2295	NM_003796; NM_134447	Hs.7943	NP_604431
ncr1494	NM_003880	WNT1 inducible signaling pathway protein 3 (WISP3), transcript variant 1, mRNA /cds=(111,1175) /gb=NM_003880 /gi=18491002 /ug=Hs.194678 /len=1307	NM_003880; NM_130396	Hs.194678	NP_569080
mioc6878	NM_003887	development and differentiation enhancing factor 2 (DDEF2), mRNA /cds=(341,3361) /gb=NM_003887 /gi=4502248 /ug=Hs.12802 /len=5711	NM_003887	Hs.12802	NP_003878
fcrc2613	NM_003921	B-cell CLL/lymphoma 10 (BCL10), mRNA /cds=(706,1407) /gb=NM_003921 /gi=20336470 /ug=Hs.193516 /len=2809	NM_003921	Hs.193516	NP_003912
seob2987	NM_003928	CAAX box 1 (CXX1), mRNA /cds=(335,964) /gb=NM_003928 /gi=4503180 /ug=Hs.250708 /len=1209	NM_003928	Hs.250708	NP_003919
seoc6666	NM_003953	myelin protein zero-like 1 (MPZL1), mRNA /cds=(160,969) /gb=NM_003953 /gi=20070164 /ug=Hs.287832 /len=1805	NM_003953	Hs.287832	NP_003944
mioa2213	NM_003973	ribosomal protein L14 (RPL14), mRNA /cds=(38,688) /gb=NM_003973 /gi=16753224 /ug=Hs.235422 /len=843	NM_003973	Hs.235422	NP_003964

mioa1353	NM_003983	solute carrier family 7 (cationic amino acid transporter, y system), member 6 (SLC7A6), mRNA /cds=(262,1809) /gb=NM_003983 /gi=4507052 /ug=Hs.10315 /len=6296	NM_003983	Hs.10315	NP_003974
seoa9377	NM_004036	adenylate cyclase 3 (ADCY3), mRNA /cds=(148,3582) /gb=NM_004036 /gi=10947058 /ug=Hs.8402 /len=4342	NM_004036	Hs.8402	NP_004027
ncrc3415	NM_004075	cryptochrome 1 (photolyase-like) (CRY1), mRNA /cds=(587,2347) /gb=NM_004075 /gi=19923246 /ug=Hs.151573 /len=2999	NM_004075	Hs.151573	NP_004066
miod7011	NM_004083	DNA-damage-inducible transcript 3 (DDIT3), mRNA /cds=(191,700) /gb=NM_004083 /gi=21361117 /ug=Hs.400353 /len=965	NM_004083	Hs.400353	NP_004074
mioc7152	NM_004120	guanylate binding protein 2, interferon-inducible (GBP2), mRNA /cds=(157,1932) /gb=NM_004120 /gi=6996011 /ug=Hs.171862 /len=2107	NM_004120	Hs.171862	NP_004111
hfcr2984	NM_004175	small nuclear ribonucleoprotein D3 polypeptide 18kDa (SNRPD3), mRNA /cds=(88,468) /gb=NM_004175 /gi=4759159 /ug=Hs.1575 /len=626	NM_004175	Hs.1575	NP_004166
ncrc4189	NM_004199	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II (P4HA2), mRNA /cds=(188,1795) /gb=NM_004199 /gi=4758867 /ug=Hs.3622 /len=2194	NM_004199	Hs.3622	NP_004190
seoc7762	NM_004242	high mobility group nucleosomal binding domain 3 (HMGN3), transcript variant 1, mRNA /cds=(179,478) /gb=NM_004242 /gi=23238229 /ug=Hs.77558 /len=935	NM_004242; NM_138730	Hs.77558	NP_620058
hfcr2892	NM_004272	homer 1 (Drosophila) (HOMER1), mRNA /cds=(278,1342) /gb=NM_004272 /gi=20127465 /ug=Hs.337737 /len=1445	NM_004272	Hs.337737	NP_004263
mioa1410	NM_004290	ring finger protein 14 (RNF14), mRNA /cds=(237,1661) /gb=NM_004290 /gi=19923285 /ug=Hs.215857 /len=3056	NM_004290	Hs.215857	NP_004281
fcr2089	NM_004404	neural precursor cell expressed, developmentally down-regulated 5 (NEDD5), mRNA /cds=(259,1344) /gb=NM_004404 /gi=4758157 /ug=Hs.155595 /len=3433	NM_004404	Hs.155595	NP_004395
miob9393	NM_004404	neural precursor cell expressed, developmentally down-regulated 5 (NEDD5), mRNA /cds=(259,1344) /gb=NM_004404 /gi=4758157 /ug=Hs.155595 /len=3433	NM_004404	Hs.155595	NP_004395
fcrb8020	NM_004413	dipeptidase 1 (renal) (DPEP1), mRNA /cds=(296,1531) /gb=NM_004413 /gi=4758189 /ug=Hs.109 /len=1738	NM_004413	Hs.109	NP_004404

seoa0023	NM_004487	golgi autoantigen, golgin subfamily b, macrogolgin (with transmembrane signal), 1 (GOLGB1), mRNA /cds=(127,9906) /gb=NM_004487 /gi=4758453 /ug=Hs.7844 /len=10300	NM_004487	Hs.7844	NP_004478
fcrb6220	NM_004555	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 (NFATC3), transcript variant 2, mRNA /cds=(211,3417) /gb=NM_004555 /gi=27886542 /ug=Hs.172674 /len=4005	NM_004555; NM_173163; NM_173164; NM_173165	Hs.172674	NP_775188
ncrc4231	NM_004563	phosphoenolpyruvate carboxykinase 2 (mitochondrial) (PCK2), mRNA /cds=(67,1989) /gb=NM_004563 /gi=4758885 /ug=Hs.75812 /len=2165	NM_004563	Hs.75812	NP_004554
mioc2872	NM_004577	phosphoserine phosphatase (PSPH), mRNA /cds=(20,697) /gb=NM_004577 /gi=21614545 /ug=Hs.56407 /len=1432	NM_004577	Hs.56407	NP_004568
fcr1791	NM_004607	tubulin-specific chaperone a (TBCA), mRNA /cds=(50,376) /gb=NM_004607 /gi=4759211 /ug=Hs.433254 /len=574	NM_004607	Hs.433254	NP_004598
ncr5065	NM_004652	ubiquitin specific protease 9, X chromosome (fat facets-like Drosophila) (USP9X), transcript variant 1, mRNA /cds=(60,7751) /gb=NM_004652 /gi=11641424 /ug=Hs.77578 /len=8171	NM_004652; NM_021906	Hs.77578	NP_068706
seob6028	NM_004859	clathrin, heavy polypeptide (Hc) (CLTC), mRNA /cds=(173,5200) /gb=NM_004859 /gi=4758011 /ug=Hs.178710 /len=6111	NM_004859	Hs.178710	NP_004850
mioc7561	NM_004878	prostaglandin E synthase (PTGES), mRNA /cds=(36,494) /gb=NM_004878 /gi=19923282 /ug=Hs.146688 /len=1846	NM_004878	Hs.146688	NP_004869
seoa7897	NM_004891	mitochondrial ribosomal protein L33 (MRPL33), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA /cds=(60,257) /gb=NM_004891 /gi=21735607 /ug=Hs.14454 /len=541	NM_004891; NM_145330	Hs.14454	NP_663303
hfcr2544	NM_004911	protein disulfide isomerase related protein (calcium-binding protein, intestinal-related) (ERP70), mRNA /cds=(243,2180) /gb=NM_004911 /gi=21624646 /ug=Hs.93659 /len=2930	NM_004911	Hs.93659	NP_004902
ncrc8851	NM_004926	zinc finger protein 36, C3H type-like 1 (ZFP36L1), mRNA /cds=(131,1147) /gb=NM_004926 /gi=15812179 /ug=Hs.85155 /len=3022	NM_004926	Hs.85155	NP_004917
ncrc2730	NM_004944	deoxyribonuclease I-like 3 (DNASE1L3), mRNA /cds=(71,988) /gb=NM_004944 /gi=4826697 /ug=Hs.88646 /len=1079	NM_004944	Hs.88646	NP_004935
seoa4174	NM_004987	LIM and senescent cell antigen-like domains 1 (LIMS1), mRNA	NM_004987	Hs.112378	NP_004978

miod7270	NM_004999	myosin VI (MYO6), mRNA /cds=(140,3997) /gb=NM_004999 /gi=4826845 /ug=Hs.118483 /len=5212	NM_004999	Hs.118483	NP_004990
ncrc5608	NM_005013	nucleobindin 2 (NUCB2), mRNA /cds=(220,1482) /gb=NM_005013 /gi=4826869 /ug=Hs.3164 /len=1586	NM_005013	Hs.3164	NP_005004
fcrc1654	NM_005016	poly(rC) binding protein 2 (PCBP2), transcript variant 1, mRNA /cds=(89,1189) /gb=NM_005016 /gi=14141167 /ug=Hs.63525 /len=1362	NM_005016; NM_031989	Hs.63525	NP_114366
seob0031	NM_005034	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa (POLR2K), mRNA /cds=(67,243) /gb=NM_005034 /gi=14589955 /ug=Hs.351475 /len=540	NM_005034	Hs.351475	NP_005025
seoa2209	NM_005087	fragile X mental retardation, autosomal 1 (FXR1), mRNA /cds=(13,1878) /gb=NM_005087 /gi=4826735 /ug=Hs.82712 /len=2132	NM_005087	Hs.82712	NP_005078
seob5147	NM_005146	squamous cell carcinoma antigen recognised by T cells (SART1), mRNA /cds=(43,2445) /gb=NM_005146 /gi=21327688 /ug=Hs.288319 /len=2536	NM_005146	Hs.288319	NP_005137
seoa1056	NM_005190	cyclin C (CCNC), mRNA /cds=(29,940) /gb=NM_005190 /gi=7382485 /ug=Hs.118442 /len=1508	NM_005190	Hs.118442	NP_005181
miod1200	NM_005218	defensin, beta 1 (DEFB1), mRNA /cds=(72,278) /gb=NM_005218 /gi=13124884 /ug=Hs.32949 /len=366	NM_005218	Hs.32949	NP_005209
seoa5743	NM_005218	defensin, beta 1 (DEFB1), mRNA /cds=(72,278) /gb=NM_005218 /gi=13124884 /ug=Hs.32949 /len=366	NM_005218	Hs.32949	NP_005209
fcrc2306	NM_005259	growth differentiation factor 8 (GDF8), mRNA /cds=(134,1261) /gb=NM_005259 /gi=4885258 /ug=Hs.41565 /len=2823	NM_005259	Hs.41565	NP_005250
mioc1205	NM_005311	growth factor receptor-bound protein 10 (GRB10), mRNA /cds=(782,2548) /gb=NM_005311 /gi=19923302 /ug=Hs.81875 /len=5431	NM_005311	Hs.81875	NP_005302
fcrb6650	NM_005348	heat shock 90kDa protein 1, alpha (HSPCA), mRNA /cds=(61,2259) /gb=NM_005348 /gi=13129149 /ug=Hs.356531 /len=2259	NM_005348	Hs.356531	NP_005339
hfcr6509	NM_005397	podocalyxin-like (PODXL), mRNA /cds=(251,1837) /gb=NM_005397 /gi=4885556 /ug=Hs.16426 /len=5869	NM_005397	Hs.16426	NP_005388
mioc6261	NM_005478	insulin-like 5 (INSL5), mRNA /cds=(48,455) /gb=NM_005478 /gi=5729885 /ug=Hs.251380 /len=726	NM_005478	Hs.251380	NP_005469
fcrc6551	NM_005606	legumain (LGMN), mRNA /cds=(142,1443) /gb=NM_005606 /gi=21914880 /ug=Hs.18069 /len=1981	NM_005606	Hs.18069	NP_005597

ncrc0292	NM_005687	phenylalanyl-tRNA synthetase beta-subunit (FRSB), mRNA /cds=(14,1783) /gb=NM_005687 /gi=19923332 /ug=Hs.9081 /len=3118	NM_005687	Hs.9081	NP_005678
fcrc4738	NM_005689	ATP-binding cassette, sub-family B (MDR/TAP), member 6 (ABCB6), nuclear gene encoding mitochondrial protein, mRNA /cds=(278,2806) /gb=NM_005689 /gi=9955962 /ug=Hs.107911 /len=2993	NM_005689	Hs.107911	NP_005680
ncr3434	NM_005699	interleukin 18 binding protein (IL18BP), transcript variant C, mRNA /cds=(929,1522) /gb=NM_005699 /gi=27502394 /ug=Hs.325978 /len=3630	NM_005699; NM_173042; NM_173043; NM_173044	Hs.325978	NP_766632
mioc6902	NM_005745	accessory protein BAP31 (DXS1357E), mRNA /cds=(137,877) /gb=NM_005745 /gi=10047078 /ug=Hs.291904 /len=1314	NM_005745	Hs.291904	NP_005736
seoa2652	NM_005780	lipoma HMGIC fusion partner (LHFP), mRNA /cds=(357,959) /gb=NM_005780 /gi=5031864 /ug=Hs.93765 /len=2012	NM_005780	Hs.93765	NP_005771
seoa2734	NM_005783	ATP binding protein associated with cell differentiation (APACD), mRNA /cds=(130,810) /gb=NM_005783 /gi=18104958 /ug=Hs.153884 /len=1494	NM_005783	Hs.153884	NP_005774
seoa1460	NM_005843	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2 (STAM2), mRNA /cds=(351,1928) /gb=NM_005843 /gi=21265030 /ug=Hs.17200 /len=3928	NM_005843	Hs.17200	NP_005834
fcrc0730	NM_005860	follistatin-like 3 (secreted glycoprotein) (FSTL3), mRNA /cds=(8,799) /gb=NM_005860 /gi=5031700 /ug=Hs.433827 /len=2500	NM_005860	Hs.433827	NP_005851
mioc4145	NM_005903	MAD, mothers against decapentaplegic 5 (Drosophila) (MADH5), mRNA /cds=(193,1590) /gb=NM_005903 /gi=20070216 /ug=Hs.37501 /len=2049	NM_005903	Hs.37501	NP_005894
seoc2589	NM_005904	MAD, mothers against decapentaplegic 7 (Drosophila) (MADH7), mRNA /cds=(296,1576) /gb=NM_005904 /gi=5174516 /ug=Hs.100602 /len=3111	NM_005904	Hs.100602	NP_005895
seoa5721	NM_005973	papillary renal cell carcinoma (translocation-associated) (PRCC), mRNA /cds=(219,1694) /gb=NM_005973 /gi=20070217 /ug=Hs.9629 /len=2075	NM_005973	Hs.9629	NP_005964
ncrb8056	NM_006013	ribosomal protein L10 (RPL10), mRNA /cds=(42,686) /gb=NM_006013 /gi=15718685 /ug=Hs.412900 /len=2188	NM_006013	Hs.412900	NP_006004

seoc2030	NM_006015	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily f, member 1 (SMARCF1), transcript variant 1, mRNA /cds=(371,7228) /gb=NM_006015 /gi=21264564 /ug=Hs.123090 /len=8595	NM_006015; NM_018450; NM_139135	Hs.123090	NP_624361
ncr3843	NM_006094	deleted in liver cancer 1 (DLC1), mRNA /cds=(296,3571) /gb=NM_006094 /gi=6633799 /ug=Hs.8700 /len=3821	NM_006094	Hs.8700	NP_872584
seob0885	NM_006098	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 (GNB2L1), mRNA /cds=(96,1049) /gb=NM_006098 /gi=24475893 /ug=Hs.5662 /len=1093	NM_006098	Hs.5662	NP_006089
fcr3599	NM_006198	Purkinje cell protein 4 (PCP4), mRNA /cds=(59,247) /gb=NM_006198 /gi=5453857 /ug=Hs.80296 /len=540	NM_006198	Hs.80296	NP_006189
seob3163	NM_006207	platelet-derived growth factor receptor-like (PDGFRL), mRNA /cds=(62,1189) /gb=NM_006207 /gi=5453871 /ug=Hs.170040 /len=1502	NM_006207	Hs.170040	NP_006198
fcr1068	NM_006265	RAD21 (S. pombe) (RAD21), mRNA /cds=(185,2080) /gb=NM_006265 /gi=5453993 /ug=Hs.81848 /len=3647	NM_006265	Hs.81848	NP_006256
seob3378	NM_006356	ATP synthase, H transporting, mitochondrial F0 complex, subunit d (ATP5H), mRNA /cds=(46,531) /gb=NM_006356 /gi=5453558 /ug=Hs.49018 /len=628	NM_006356	Hs.49018	NP_006347
seoa0099	NM_006357	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 yeast) (UBE2E3), mRNA /cds=(120,743) /gb=NM_006357 /gi=5454145 /ug=Hs.4890 /len=1294	NM_006357	Hs.4890	NP_872619
seoa0860	NM_006472	thioredoxin interacting protein (TXNIP), mRNA /cds=(222,1397) /gb=NM_006472 /gi=5454161 /ug=Hs.179526 /len=2704	NM_006472	Hs.179526	NP_006463
fcrc7102	NM_006472	thioredoxin interacting protein (TXNIP), mRNA /cds=(222,1397) /gb=NM_006472 /gi=5454161 /ug=Hs.179526 /len=2704	NM_006472	Hs.179526	NP_006463
miod4686	NM_006472	thioredoxin interacting protein (TXNIP), mRNA /cds=(222,1397) /gb=NM_006472 /gi=5454161 /ug=Hs.179526 /len=2704	NM_006472	Hs.179526	NP_006463
seob8204	NM_006475	osteoblast specific factor 2 (fasciclin I-like) (OSF-2), mRNA /cds=(12,2522) /gb=NM_006475 /gi=5453833 /ug=Hs.136348 /len=3213	NM_006475	Hs.136348	NP_006466
fcrb2306	NM_006533	melanoma inhibitory activity (MIA), mRNA /cds=(72,467) /gb=NM_006533 /gi=5729924 /ug=Hs.279651 /len=538	NM_006533	Hs.279651	NP_006524
hfcr0618	NM_006571	likely ortholog of mouse dynactin 6 (DCTN6), mRNA /cds=(88,660) /gb=NM_006571 /gi=18426895 /ug=Hs.39913 /len=1044	NM_006571	Hs.39913	NP_006562

mioa9179	NM_006585	chaperonin containing TCP1, subunit 8 (theta) (CCT8), mRNA /cds=(29,1675) /gb=NM_006585 /gi=6005726 /ug=Hs.15071 /len=1821	NM_006585	Hs.15071	NP_006576
fcrb3001	NM_006603	stromal antigen 2 (STAG2), mRNA /cds=(405,3893) /gb=NM_006603 /gi=27552767 /ug=Hs.8217 /len=4197	NM_006603	Hs.8217	NP_006594
fcr2182	NM_006659	tubulin, gamma complex associated protein 2 (TUBGCP2), mRNA /cds=(64,2772) /gb=NM_006659 /gi=5729839 /ug=Hs.13386 /len=2846	NM_006659	Hs.13386	NP_006650
mioa1603	NM_006701	similar to S. pombe dim1 (DIM1), mRNA /cds=(141,569) /gb=NM_006701 /gi=20070233 /ug=Hs.433683 /len=1415	NM_006701	Hs.433683	NP_006692
ncr7952	NM_006734	immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA /cds=(16,7518) /gb=NM_006734 /gi=19923373 /ug=Hs.75063 /len=9175	NM_006734	Hs.75063	NP_006725
miob3456	NM_006748	Src-like-adaptor (SLA), mRNA /cds=(42,872) /gb=NM_006748 /gi=5803170 /ug=Hs.75367 /len=2665	NM_006748	Hs.75367	NP_006739
ncrc2839	NM_006793	peroxiredoxin 3 (PRDX3), nuclear gene encoding mitochondrial protein, mRNA /cds=(7,777) /gb=NM_006793 /gi=5802973 /ug=Hs.75454 /len=1542	NM_006793	Hs.75454	NP_054817
seob9145	NM_006813	proline rich 2 (PROL2), mRNA /cds=(114,1097) /gb=NM_006813 /gi=5802981 /ug=Hs.75969 /len=2061	NM_006813	Hs.75969	NP_006804
mioa7239	NM_006815	coated vesicle membrane protein (RNP24), mRNA /cds=(24,629) /gb=NM_006815 /gi=21314646 /ug=Hs.75914 /len=2060	NM_006815	Hs.75914	NP_006806
ncrc6981	NM_006815	coated vesicle membrane protein (RNP24), mRNA /cds=(24,629) /gb=NM_006815 /gi=21314646 /ug=Hs.75914 /len=2060	NM_006815	Hs.75914	NP_006806
seob6279	NM_006818	ALL1-fused gene from chromosome 1q (AF1Q), mRNA /cds=(353,625) /gb=NM_006818 /gi=21626459 /ug=Hs.75823 /len=1653	NM_006818	Hs.75823	NP_006809
hfcr0594	NM_006839	inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA /cds=(93,2369) /gb=NM_006839 /gi=5803114 /ug=Hs.78504 /len=2697	NM_006839	Hs.78504	NP_006830
mioc5772	NM_006873	stoned B-like factor (SBLF), mRNA /cds=(11,2218) /gb=NM_006873 /gi=26787992 /ug=Hs.54961 /len=5822	NM_006873	Hs.54961	NP_006864
ncrb6357	NM_006885	AT-binding transcription factor 1 (ATBF1), mRNA /cds=(674,11785) /gb=NM_006885 /gi=19923286 /ug=Hs.101842 /len=11893	NM_006885	Hs.101842	NP_008816

seob0133	NM_006886	ATP synthase, H transporting, mitochondrial F1 complex, epsilon subunit (ATP5E), nuclear gene encoding mitochondrial protein, mRNA /cds=(95,250) /gb=NM_006886 /gi=21327678 /ug=Hs.177530 /len=417	NM_006886	Hs.177530	NP_008817
seob1423	NM_006924	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor) (SFRS1), mRNA /cds=(36,782) /gb=NM_006924 /gi=19923382 /ug=Hs.73737 /len=2708	NM_006924	Hs.73737	NP_008855
seob0221	NM_006936	SMT3 suppressor of mif two 3 1 (yeast) (SMT3H1), mRNA /cds=(95,406) /gb=NM_006936 /gi=5902095 /ug=Hs.85119 /len=1733	NM_006936	Hs.85119	NP_008867
fcrc7338	NM_006979	HLA class II region expressed gene KE4 (HKE4), mRNA /cds=(327,1616) /gb=NM_006979 /gi=5901935 /ug=Hs.278721 /len=2358	NM_006979	Hs.278721	NP_008910
fcrb2040	NM_006986	melanoma antigen, family D, 1 (MAGED1), mRNA /cds=(143,2479) /gb=NM_006986 /gi=14195633 /ug=Hs.5258 /len=2713	NM_006986	Hs.5258	NP_008917
fcrb3895	NM_007002	adhesion regulating molecule 1 (ADRM1), transcript variant 1, mRNA /cds=(81,1304) /gb=NM_007002 /gi=28373191 /ug=Hs.90107 /len=1410	NM_007002; NM_175573	Hs.90107	NP_783163
ncr0238	NM_007021	decidual protein induced by progesterone (DEPP), mRNA /cds=(219,857) /gb=NM_007021 /gi=5901937 /ug=Hs.93675 /len=2114	NM_007021	Hs.93675	NP_008952
miob8630	NM_007032	Tara-like protein (HRIHFB2122), transcript variant 1, mRNA /cds=(176,1957) /gb=NM_007032 /gi=20336765 /ug=Hs.40342 /len=2687	NM_007032; NM_138632	Hs.40342	NP_619538
fcrb1428	NM_007063	vascular Rab-GAP/TBC-containing (VRP), mRNA /cds=(1118,3811) /gb=NM_007063 /gi=5902153 /ug=Hs.164170 /len=4404	NM_007063	Hs.164170	NP_008994
fcr4695	NM_007104	ribosomal protein L10a (RPL10A), mRNA	NM_007104	Hs.425293	NP_009035
ncr8867	NM_007108	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B) (TCEB2), mRNA /cds=(1,357) /gb=NM_007108 /gi=6005889 /ug=Hs.172772 /len=357	NM_007108	Hs.172772	NP_009039
seoa6038	NM_007145	zinc finger protein 146 (ZNF146), mRNA /cds=(857,1735) /gb=NM_007145 /gi=6005965 /ug=Hs.301819 /len=3186	NM_007145	Hs.301819	NP_009076
mioc6898	NM_007194	CHK2 checkpoint (S. pombe) (CHEK2), transcript variant 1, mRNA /cds=(762,2393) /gb=NM_007194 /gi=22209010 /ug=Hs.146329 /len=2547	NM_007194; NM_145862	Hs.146329	NP_665861

fcrb3515	NM_007245	ataxin 2 related protein (A2LP), transcript variant A, mRNA /cds=(169,3396) /gb=NM_007245 /gi=27262646 /ug=Hs.43509 /len=4386	NM_007245; NM_017492; NM_145714; NM_148414; NM_148415; NM_148416	Hs.43509	NP_680782
miob7276	NM_007247	AP1 gamma subunit binding protein 1 (AP1GBP1), transcript variant 1, mRNA /cds=(44,2113) /gb=NM_007247 /gi=18105003 /ug=Hs.15384 /len=5115	NM_007247; NM_080550; NM_080551	Hs.15384	NP_542118
fcr3163	NM_007250	Kruppel-like factor 8 (KLF8), mRNA /cds=(439,1518) /gb=NM_007250 /gi=28376642 /ug=Hs.320861 /len=2208	NM_007250	Hs.320861	NP_009181
mioa4532	NM_007332	ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA /cds=(175,3534) /gb=NM_007332 /gi=6601589 /ug=Hs.137674 /len=5190	NM_007332	Hs.137674	NP_015628
fcrb5948	NM_007370	replication factor C (activator 1) 5, 36.5kDa (RFC5), mRNA /cds=(102,1124) /gb=NM_007370 /gi=19923788 /ug=Hs.171075 /len=2097	NM_007370	Hs.171075	NP_853556
seob3191	NM_012090	microtubule-actin crosslinking factor 1 (MACF1), transcript variant 1, mRNA /cds=(52,16344) /gb=NM_012090 /gi=15011903 /ug=Hs.108258 /len=17532	NM_012090; NM_033024; NM_033044	Hs.108258	NP_149033
ncrb5704	NM_012115	CASP8 associated protein 2 (CASP8AP2), mRNA /cds=(197,6145) /gb=NM_012115 /gi=16306505 /ug=Hs.122843 /len=6782	NM_012115	Hs.122843	NP_036247
fcrb7785	NM_012154	eukaryotic translation initiation factor 2C, 2 (EIF2C2), mRNA /cds=(111,1868) /gb=NM_012154 /gi=24307940 /ug=Hs.193053 /len=2815	NM_012154	Hs.193053	NP_036286
ncrc0457	NM_012201	golgi apparatus protein 1 (GLG1), mRNA /cds=(27,3560) /gb=NM_012201 /gi=6912389 /ug=Hs.78979 /len=3909	NM_012201	Hs.78979	NP_036333
mioc7662	NM_012218	interleukin enhancer binding factor 3, 90kDa (ILF3), transcript variant 1, mRNA /cds=(267,2951) /gb=NM_012218 /gi=24234749 /ug=Hs.256583 /len=6058	NM_004516; NM_012218; NM_153464	Hs.256583	NP_703194
fcr5211	NM_012286	mortality factor 4 like 2 (MORF4L2), mRNA /cds=(306,1172) /gb=NM_012286 /gi=6912447 /ug=Hs.173714 /len=1826	NM_012286	Hs.173714	NP_036418
seob1001	NM_012334	myosin X (MYO10), mRNA /cds=(223,6399) /gb=NM_012334 /gi=11037056 /ug=Hs.61638 /len=7787	NM_012334	Hs.61638	NP_036466

fcrb8239	NM_012369	olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA /cds=(1,954) /gb=NM_012369 /gi=6912557 /ug=Hs.159898 /len=954	NM_012369	Hs.159898	NP_036501
ncrb7844	NM_012421	rearranged L-myc fusion sequence (RLF), mRNA /cds=(13,5757) /gb=NM_012421 /gi=6912631 /ug=Hs.13321 /len=6229	NM_012421	Hs.13321	NP_036553
ncr3815	NM_012423	ribosomal protein L13a (RPL13A), mRNA /cds=(23,634) /gb=NM_012423 /gi=14591905 /ug=Hs.389335 /len=1142	NM_012423	Hs.389335	NP_036555
fcrc5604	NM_012423	ribosomal protein L13a (RPL13A), mRNA /cds=(23,634) /gb=NM_012423 /gi=14591905 /ug=Hs.389335 /len=1142	NM_012423	Hs.389335	NP_036555
fcrb4470	NM_012423	ribosomal protein L13a (RPL13A), mRNA /cds=(23,634) /gb=NM_012423 /gi=14591905 /ug=Hs.389335 /len=1142	NM_012423	Hs.389335	NP_036555
seoa4571	NM_013252	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 5 (CLECSF5), mRNA /cds=(198,764) /gb=NM_013252 /gi=10281668 /ug=Hs.126355 /len=3510	NM_013252	Hs.126355	NP_037384
mioa8261	NM_013263	bromodomain containing 7 (BRD7), mRNA /cds=(6,1964) /gb=NM_013263 /gi=7019344 /ug=Hs.279762 /len=2137	NM_013263	Hs.279762	NP_037395
fcrc4067	NM_013265	chromosome 11 open reading frame2 (C11orf2), mRNA	NM_013265	Hs.5258	NP_037397
fcrb1969	NM_013292	myosin light chain 2 (HUMMLC2B), mRNA /cds=(60,569) /gb=NM_013292 /gi=28372498 /ug=Hs.50889 /len=687	NM_013292	Hs.50889	NP_037424
seob0976	NM_013293	transformer-2 alpha (htra-2 alpha) (HSU53209), mRNA /cds=(158,1006) /gb=NM_013293 /gi=9558732 /ug=Hs.130829 /len=1563	NM_013293	Hs.130829	NP_037425
seob5213	NM_013338	Alg5, S. cerevisiae, of (ALG5), mRNA /cds=(28,1002) /gb=NM_013338 /gi=9665250 /ug=Hs.227933 /len=1125	NM_013338	Hs.227933	NP_037470
fcrc4151	NM_013403	striatin, calmodulin binding protein 4 (STRN4), mRNA /cds=(1,2262) /gb=NM_013403 /gi=7019572 /ug=Hs.108665 /len=3188	NM_013403	Hs.108665	NP_037535
fcrb8697	NM_013417	isoleucine-tRNA synthetase (IARS), transcript variant long, mRNA /cds=(256,4044) /gb=NM_013417 /gi=7770071 /ug=Hs.172801 /len=4508	NM_002161; NM_013417	Hs.172801	NP_038203
seob9485	NM_014016	SAC1 suppressor of actin mutations 1-like (yeast) (SACM1L), mRNA /cds=(70,1833) /gb=NM_014016 /gi=7662337 /ug=Hs.5867 /len=3572	NM_014016	Hs.5867	NP_054735
miob8425	NM_014018	mitochondrial ribosomal protein S28 (MRPS28), nuclear gene encoding mitochondrial protein, mRNA /cds=(24,587) /gb=NM_014018 /gi=16579882 /ug=Hs.55097 /len=724	NM_014018	Hs.55097	NP_054737

seoc3469	NM_014034	anti-silencing function 1A (DKFZP547E2110), mRNA /cds=(193,807) /gb=NM_014034 /gi=7661591 /ug=Hs.108110 /len=2367	NM_014034	Hs.108110	NP_054753
ncrc6047	NM_014056	likely ortholog of mouse hypoxia induced gene 1 (HIG1), mRNA /cds=(93,374) /gb=NM_014056 /gi=7661619 /ug=Hs.7917 /len=1362	NM_014056	Hs.7917	NP_054775
miob9671	NM_014129	PRO0478 protein (PRO0478), mRNA	NM_014129	Hs.279558	NP_054848
miod4063	NM_014145	chromosome 20 open reading frame 30 (C20orf30), mRNA /cds=(114,476) /gb=NM_014145 /gi=15559214 /ug=Hs.3576 /len=1440	NM_014145	Hs.3576	NP_054864
ncrb3317	NM_014166	HSPC126 protein (HSPC126), mRNA /cds=(26,838) /gb=NM_014166 /gi=7661787 /ug=Hs.181112 /len=1424	NM_014166	Hs.181112	NP_054885
fcr2102	NM_014300	signal peptidase complex (18kD) (SPC18), mRNA /cds=(78,617) /gb=NM_014300 /gi=7657608 /ug=Hs.9534 /len=1105	NM_014300	Hs.9534	NP_055115
mioa3888	NM_014305	dTDP-D-glucose 4,6-dehydratase (TDPGD), mRNA /cds=(94,1146) /gb=NM_014305 /gi=7657640 /ug=Hs.12393 /len=1889	NM_014305	Hs.12393	NP_055120
seoa0486	NM_014313	small membrane protein 1 (SMP1), mRNA /cds=(151,624) /gb=NM_014313 /gi=20357549 /ug=Hs.107979 /len=2284	NM_014313	Hs.107979	NP_055128
mioa2343	NM_014342	mitochondrial carrier 2 (MTCH2), nuclear gene encoding mitochondrial protein, mRNA /cds=(49,960) /gb=NM_014342 /gi=7657346 /ug=Hs.279609 /len=1104	NM_014342	Hs.279609	NP_055157
fcr5895	NM_014362	3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA /cds=(64,1209) /gb=NM_014362 /gi=7657159 /ug=Hs.236642 /len=1311	NM_014362	Hs.236642	NP_055177
seoc2595	NM_014386	polycystic kidney disease 2-like 2 (PKD2L2), mRNA /cds=(24,1853) /gb=NM_014386 /gi=7657458 /ug=Hs.272418 /len=2205	NM_014386	Hs.272418	NP_055201
miob4760	NM_014412	Siah-interacting protein (SIP), mRNA /cds=(118,804) /gb=NM_014412 /gi=7656951 /ug=Hs.27258 /len=2435	NM_014412	Hs.27258	NP_055227
ncr3284	NM_014454	p53 regulated PA26 nuclear protein (PA26), mRNA /cds=(12,1667) /gb=NM_014454 /gi=7657436 /ug=Hs.14125 /len=2785	NM_014454	Hs.14125	NP_055269
miod1613	NM_014462	Lsm1 protein (LSM1), mRNA /cds=(189,590) /gb=NM_014462 /gi=7657312 /ug=Hs.425311 /len=935	NM_014462	Hs.425311	NP_055277
fcrb3135	NM_014473	putative dimethyladenosine transferase (HSA9761), mRNA /cds=(79,1020) /gb=NM_014473 /gi=7657197 /ug=Hs.125819 /len=1505	NM_014473	Hs.125819	NP_055288

miod4895	NM_014584	ERO1-like (S. cerevisiae) (ERO1L), mRNA /cds=(227,1633) /gb=NM_014584 /gi=7657068 /ug=Hs.25740 /len=3334	NM_014584	Hs.25740	NP_055399
seob3322	NM_014585	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3 (SLC11A3), mRNA /cds=(315,2030) /gb=NM_014585 /gi=19923794 /ug=Hs.5944 /len=3333	NM_014585	Hs.5944	NP_055400
miob1126	NM_014629	Rho guanine nucleotide exchange factor (GEF) 10 (ARHGEF10), mRNA /cds=(3732,7097) /gb=NM_014629 /gi=7662041 /ug=Hs.20695 /len=8467	NM_014629	Hs.20695	NP_055444
ncr1550	NM_014672	KIAA0391 gene product (KIAA0391), mRNA /cds=(360,2063) /gb=NM_014672 /gi=7662093 /ug=Hs.154668 /len=5677	NM_014672	Hs.154668	NP_055487
ncr4590	NM_014733	endosome-associated FYVE-domain protein (ENDOFIN), mRNA /cds=(249,4868) /gb=NM_014733 /gi=7662047 /ug=Hs.83790 /len=6632	NM_014733	Hs.83790	NP_055548
mioa3367	NM_014751	KIAA0429 gene product (KIAA0429), mRNA /cds=(2374,3444) /gb=NM_014751 /gi=7662113 /ug=Hs.77694 /len=5645	NM_014751	Hs.77694	NP_055566
seoa1992	NM_014814	KIAA0107 gene product (P44S10), mRNA /cds=(26,1195) /gb=NM_014814 /gi=7661913 /ug=Hs.23488 /len=1308	NM_014814	Hs.23488	NP_055629
seob2994	NM_014819	KIAA0438 gene product (KIAA0438), mRNA /cds=(118,2244) /gb=NM_014819 /gi=7662123 /ug=Hs.279849 /len=4765	NM_014819	Hs.279849	NP_055634
seoa0029	NM_014888	family with sequence similarity 3, member C (FAM3C), mRNA /cds=(168,851) /gb=NM_014888 /gi=7661713 /ug=Hs.29882 /len=2475	NM_014888	Hs.29882	NP_055703
seoc0034	NM_014899	Rho-related BTB domain containing 3 (RHOBTB3), mRNA /cds=(336,2171) /gb=NM_014899 /gi=7662355 /ug=Hs.10432 /len=4099	NM_014899	Hs.10432	NP_055714
mioa2073	NM_014915	KIAA1074 protein (KIAA1074), mRNA /cds=(151,5280) /gb=NM_014915 /gi=7662473 /ug=Hs.129218 /len=5360	NM_014915	Hs.129218	NP_055730
seoa9160	NM_015049	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 3 (ALS2CR3), mRNA /cds=(382,3126) /gb=NM_015049 /gi=13027379 /ug=Hs.154248 /len=6470	NM_015049	Hs.154248	NP_055864
hfcr3011	NM_015079	KIAA1055 protein (KIAA1055), mRNA /cds=(428,1675) /gb=NM_015079 /gi=24307996 /ug=Hs.126084 /len=4863	NM_015079	Hs.126084	NP_055894
mioc6055	NM_015149	RalGDS-like gene (RGL), mRNA /cds=(450,2861) /gb=NM_015149 /gi=20127535 /ug=Hs.79219 /len=5111	NM_015149	Hs.79219	NP_055964
ncr7292	NM_015208	KIAA0874 protein (KIAA0874), mRNA /cds=(1,6189) /gb=NM_015208 /gi=14140237 /ug=Hs.27973 /len=6189	NM_015208	Hs.27973	NP_056023

seoa4647	NM_015216	KIAA0433 protein (KIAA0433), mRNA /cds=(510,4241) /gb=NM_015216 /gi=7662117 /ug=Hs.26179 /len=5814	NM_015216	Hs.26179	NP_056031
mioa6442	NM_015254	kinesin family member 13B (KIF13B), mRNA /cds=(38,5518) /gb=NM_015254 /gi=13194196 /ug=Hs.15711 /len=8743	NM_015254	Hs.15711	NP_056069
mioc2928	NM_015254	kinesin family member 13B (KIF13B), mRNA /cds=(38,5518) /gb=NM_015254 /gi=13194196 /ug=Hs.15711 /len=8743	NM_015254	Hs.15711	NP_056069
mioc4232	NM_015271	tripartite motif-containing 2 (TRIM2), mRNA /cds=(147,2381) /gb=NM_015271 /gi=15011942 /ug=Hs.12372 /len=6734	NM_015271	Hs.12372	NP_056086
fcrb6160	NM_015278	KIAA0790 protein (KIAA0790), mRNA /cds=(10,3204) /gb=NM_015278 /gi=24308024 /ug=Hs.12002 /len=3711	NM_015278	Hs.12002	NP_056093
fcrb8257	NM_015319	tensin like C1 domain-containing phosphatase (TENC1), transcript variant 2, mRNA /cds=(196,4455) /gb=NM_015319 /gi=23943863 /ug=Hs.6147 /len=4944	NM_015319; NM_170754	Hs.6147	NP_736610
fcrb5720	NM_015385	sorbin and SH3 domain containing 1 (SORBS1), mRNA /cds=(191,2641) /gb=NM_015385 /gi=7661699 /ug=Hs.108924 /len=5943	NM_006434; NM_015385	Hs.108924	NP_056200
seoc2518	NM_015397	KIAA1892 protein (KIAA1892), mRNA /cds=(308,1669) /gb=NM_015397 /gi=22218618 /ug=Hs.102669 /len=3636	NM_015397	Hs.102669	NP_056212
mioc5546	NM_015434	DKFZP434B168 protein (DKFZP434B168), mRNA /cds=(106,2994) /gb=NM_015434 /gi=7661565 /ug=Hs.48604 /len=3463	NM_015434	Hs.48604	NP_056249
seoc1425	NM_015440	DKFZP586G1517 protein (DKFZP586G1517), mRNA /cds=(127,2328) /gb=NM_015440 /gi=24308062 /ug=Hs.44155 /len=2749	NM_015440	Hs.44155	NP_056255
seoc1876	NM_015461	early hematopoietic zinc finger (EHZF), mRNA /cds=(150,4085) /gb=NM_015461 /gi=24308068 /ug=Hs.26799 /len=4869	NM_015461	Hs.26799	NP_056276
fcrb1962	NM_015466	protein tyrosine phosphatase, non-receptor type 23 (PTPN23), mRNA /cds=(62,4972) /gb=NM_015466 /gi=24308072 /ug=Hs.25524 /len=5248	NM_015466	Hs.25524	NP_056281
fcrb8674	NM_015466	protein tyrosine phosphatase, non-receptor type 23 (PTPN23), mRNA /cds=(62,4972) /gb=NM_015466 /gi=24308072 /ug=Hs.25524 /len=5248	NM_015466	Hs.25524	NP_056281
fcrb2697	NM_015497	DKFZP564G2022 protein (DKFZP564G2022), mRNA /cds=(43,1710) /gb=NM_015497 /gi=13794264 /ug=Hs.16492 /len=2286	NM_015497	Hs.16492	NP_056312
fcr5679	NM_015559	SET binding protein 1 (SETBP1), mRNA /cds=(6,4634) /gb=NM_015559 /gi=7662121 /ug=Hs.151717 /len=5744	NM_015559	Hs.151717	NP_056374

ncrc4815	NM_015642	zinc finger protein 288 (ZNF288), mRNA /cds=(489,2495) /gb=NM_015642 /gi=7661651 /ug=Hs.159456 /len=2829	NM_015642	Hs.159456	NP_056457
seoa8754	NM_015710	glioma tumor suppressor candidate region gene 2 (GLTSCR2), mRNA /cds=(53,1489) /gb=NM_015710 /gi=21359905 /ug=Hs.421907 /len=1610	NM_015710	Hs.421907	NP_056525
mioc2019	NM_015710	glioma tumor suppressor candidate region gene 2 (GLTSCR2), mRNA /cds=(53,1489) /gb=NM_015710 /gi=21359905 /ug=Hs.421907 /len=1610	NM_015710	Hs.421907	NP_056525
miob5491	NM_015938	CGI-07 protein (CGI-07), mRNA /cds=(124,1635) /gb=NM_015938 /gi=19923795 /ug=Hs.181022 /len=2762	NM_015938	Hs.181022	NP_057022
hfcr0370	NM_015966	serologically defined breast cancer antigen 84 (SDBCAG84), mRNA /cds=(28,1179) /gb=NM_015966 /gi=7706277 /ug=Hs.169992 /len=1337	NM_015966	Hs.169992	NP_057050
miod3946	NM_015969	mitochondrial ribosomal protein S17 (MRPS17), nuclear gene encoding mitochondrial protein, mRNA /cds=(31,423) /gb=NM_015969 /gi=16554613 /ug=Hs.44298 /len=600	NM_015969	Hs.44298	NP_057053
ncrb8649	NM_016060	CGI-125 protein (CGI-125), mRNA /cds=(79,474) /gb=NM_016060 /gi=7705591 /ug=Hs.27289 /len=1196	NM_016060	Hs.27289	NP_057144
seoa3392	NM_016081	palladin (KIAA0992), mRNA /cds=(212,3532) /gb=NM_016081 /gi=21361584 /ug=Hs.194431 /len=5773	NM_016081	Hs.194431	NP_057165
mioc4331	NM_016105	FK506 binding protein 7 (FKBP7), mRNA /cds=(96,875) /gb=NM_016105 /gi=23618828 /ug=Hs.344379 /len=1067	NM_016105	Hs.344379	NP_851939
ncr9487	NM_016125	PTD016 protein (LOC51136), mRNA /cds=(183,809) /gb=NM_016125 /gi=21361528 /ug=Hs.30154 /len=1917	NM_016125	Hs.30154	NP_057209
hfcr6265	NM_016162	inhibitor of growth family, member 4 (ING4), mRNA /cds=(18,767) /gb=NM_016162 /gi=7705860 /ug=Hs.108183 /len=1377	NM_016162	Hs.108183	NP_057246
seob0321	NM_016167	retinoic acid repressible protein (RARG-1), mRNA /cds=(33,806) /gb=NM_016167 /gi=15743546 /ug=Hs.106346 /len=896	NM_016167	Hs.106346	NP_057251
ncrc0185	NM_016245	retinal short-chain dehydrogenase/reductase 2 (RetSDR2), mRNA /cds=(189,1091) /gb=NM_016245 /gi=7705904 /ug=Hs.12150 /len=1760	NM_016245	Hs.12150	NP_057329
ncrb5940	NM_016252	baculoviral IAP repeat-containing 6 (apollon) (BIRC6), mRNA /cds=(1,14490) /gb=NM_016252 /gi=10442821 /ug=Hs.250646 /len=14490	NM_016252	Hs.250646	NP_057336
mioc6391	NM_016271	STRIN protein (STRIN), mRNA /cds=(100,837) /gb=NM_016271 /gi=21361538 /ug=Hs.180403 /len=3226	NM_016271	Hs.180403	NP_057355

mioc4842	NM_016277	RAB23, member RAS oncogene family (RAB23), mRNA /cds=(151,864) /gb=NM_016277 /gi=19923480 /ug=Hs.94769 /len=2588	NM_016277	Hs.94769	NP_057361
ncrc4132	NM_016315	CED-6 protein (CED-6), mRNA /cds=(429,1343) /gb=NM_016315 /gi=7705317 /ug=Hs.107056 /len=3277	NM_016315	Hs.107056	NP_057399
mioc8694	NM_016316	REV1-like (yeast) (REV1L), mRNA /cds=(213,3968) /gb=NM_016316 /gi=7706680 /ug=Hs.110347 /len=4276	NM_016316	Hs.110347	NP_057400
fcrc6174	NM_016397	TH1-like (Drosophila) (TH1L), mRNA /cds=(8,1429) /gb=NM_016397 /gi=7705462 /ug=Hs.5184 /len=2130	NM_016397	Hs.5184	NP_057481
seoa4163	NM_016399	hypothetical protein HSPC132 (HSPC132), mRNA /cds=(4,234) /gb=NM_016399 /gi=7705466 /ug=Hs.69499 /len=1171	NM_016399	Hs.69499	NP_057483
mioc2116	NM_016400	Huntingtin interacting protein K (HYPK), mRNA /cds=(177,566) /gb=NM_016400 /gi=21361540 /ug=Hs.300954 /len=1349	NM_016400	Hs.300954	NP_057484
ncrb3226	NM_016468	chromosome 14 open reading frame 112 (C14orf112), mRNA /cds=(119,439) /gb=NM_016468 /gi=21361531 /ug=Hs.433630 /len=933	NM_016468	Hs.433630	NP_057552
seob5886	NM_016530	RAB-8b protein (LOC51762), mRNA /cds=(92,715) /gb=NM_016530 /gi=7706562 /ug=Hs.321245 /len=1265	NM_016530	Hs.321245	NP_057614
ncrb0074	NM_016547	calcium binding protein Cab45 precursor (Cab45), mRNA /cds=(294,1340) /gb=NM_016547 /gi=7706572 /ug=Hs.42806 /len=2092	NM_016176; NM_016547	Hs.42806	NP_057631
miod6292	NM_016618	hypothetical protein LOC51315 (LOC51315), mRNA /cds=(395,1174) /gb=NM_016618 /gi=7706155 /ug=Hs.5721 /len=1774	NM_016618	Hs.5721	NP_057702
seoc7811	NM_016623	hypothetical protein BM-009 (BM-009), mRNA /cds=(386,1048) /gb=NM_016623 /gi=7705303 /ug=Hs.92918 /len=1919	NM_016623	Hs.92918	NP_057707
seob5193	NM_016645	mesenchymal stem cell protein DSC92 (NEUGRIN), mRNA /cds=(632,1291) /gb=NM_016645 /gi=7706195 /ug=Hs.323467 /len=1729	NM_016645	Hs.323467	NP_057729
hfcr2693	NM_016733	LIM domain kinase 2 (LIMK2), transcript variant 2b, mRNA /cds=(316,2169) /gb=NM_016733 /gi=8051617 /ug=Hs.278027 /len=3806	NM_005569; NM_016733	Hs.278027	NP_057952
seob1783	NM_017423	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNT7), mRNA /cds=(33,2006) /gb=NM_017423 /gi=8393408 /ug=Hs.246315 /len=4266	NM_017423	Hs.246315	NP_059119

seoc1009	NM_017664	ankyrin repeat domain 10 (ANKRD10), mRNA /cds=(136,1398) /gb=NM_017664 /gi=8923103 /ug=Hs.172572 /len=2509	NM_017664	Hs.172572	NP_060134
mioc6251	NM_017845	hypothetical protein FLJ20502 (FLJ20502), mRNA /cds=(29,580) /gb=NM_017845 /gi=8923457 /ug=Hs.23956 /len=1373	NM_017845	Hs.23956	NP_060315
miod0080	NM_017850	hypothetical protein FLJ20508 (FLJ20508), mRNA /cds=(191,802) /gb=NM_017850 /gi=8923468 /ug=Hs.272673 /len=2376	NM_017850	Hs.272673	NP_060320
ncrc0304	NM_017869	BTG3 associated nuclear protein (BANP), transcript variant 1, mRNA /cds=(153,1562) /gb=NM_017869 /gi=17986265 /ug=Hs.352397 /len=2136	NM_017869; NM_079837	Hs.352397	NP_524576
ncrc0324	NM_017903	hypothetical protein FLJ20618 (FLJ20618), mRNA /cds=(319,726) /gb=NM_017903 /gi=8923570 /ug=Hs.52184 /len=2213	NM_017903	Hs.52184	NP_060373
fcrc6010	NM_017931	hypothetical protein FLJ20699 (FLJ20699), mRNA /cds=(33,1043) /gb=NM_017931 /gi=8923627 /ug=Hs.15125 /len=2594	NM_017931	Hs.15125	NP_060401
miod4507	NM_017953	hypothetical protein FLJ20729 (FLJ20729), mRNA /cds=(135,1547) /gb=NM_017953 /gi=20149642 /ug=Hs.5111 /len=2821	NM_017953	Hs.5111	NP_060423
ncrc9187	NM_018004	hypothetical protein FLJ10134 (FLJ10134), mRNA /cds=(314,1141) /gb=NM_018004 /gi=8922242 /ug=Hs.104800 /len=1564	NM_018004	Hs.104800	NP_060474
mioc4077	NM_018013	hypothetical protein FLJ10159 (FLJ10159), mRNA /cds=(1,807) /gb=NM_018013 /gi=8922262 /ug=Hs.22505 /len=2070	NM_018013	Hs.22505	NP_060483
fcrb3808	NM_018090	hypothetical protein FLJ10420 (FLJ10420), mRNA /cds=(34,825) /gb=NM_018090 /gi=20127581 /ug=Hs.289087 /len=2046	NM_018090	Hs.289087	NP_060560
ncr1221	NM_018121	chromosome 10 open reading frame 6 (C10orf6), mRNA /cds=(543,4064) /gb=NM_018121 /gi=27532981 /ug=Hs.93581 /len=7284	NM_018121; NM_144592	Hs.93581	NP_653193
mioc2459	NM_018149	hypothetical protein FLJ10587 (FLJ10587), mRNA /cds=(16,2991) /gb=NM_018149 /gi=21361713 /ug=Hs.7296 /len=3256	NM_018149	Hs.7296	NP_060619
miod4066	NM_018247	hypothetical protein FLJ10856 (FLJ10856), mRNA /cds=(148,1233) /gb=NM_018247 /gi=8922719 /ug=Hs.108530 /len=3720	NM_018247	Hs.108530	NP_060717
seob4676	NM_018845	stromal cell protein (LOC55974), mRNA /cds=(61,726) /gb=NM_018845 /gi=10047123 /ug=Hs.292154 /len=1316	NM_018845	Hs.292154	NP_061333
mioa8919	NM_018947	cytochrome c, somatic (CYCS), mRNA /cds=(61,378) /gb=NM_018947 /gi=21361707 /ug=Hs.169248 /len=3990	NM_018947	Hs.169248	NP_061820
ncr9956	NM_018997	mitochondrial ribosomal protein S21 (MRPS21), transcript variant 2, nuclear gene encoding mitochondrial protein, mRNA /cds=(519,782) /gb=NM_018997 /gi=16950592 /ug=Hs.81281 /len=939	NM_018997; NM_031901	Hs.81281	NP_114107

miob0171	NM_019014	similar to DNA-directed RNA polymerase I (135 kDa) (Rpo1-2), mRNA /cds=(53,1063) /gb=NM_019014 /gi=9506618 /ug=Hs.86337 /len=4684	NM_019014; NM_032212	Hs.86337	NP_061887
mioc4112	NM_019026	putative membrane protein (LOC54499), mRNA /cds=(139,705) /gb=NM_019026 /gi=24308132 /ug=Hs.93832 /len=1186	NM_019026	Hs.93832	NP_061899
fcrc5164	NM_019035	protocadherin 18 (PCDH18), mRNA /cds=(388,3795) /gb=NM_019035 /gi=14589928 /ug=Hs.97266 /len=5157	NM_019035	Hs.97266	NP_061908
miob5012	NM_019842	potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), mRNA /cds=(84,2882) /gb=NM_019842 /gi=28373064 /ug=Hs.283644 /len=3325	NM_019842	Hs.283644	NP_062816
seob4002	NM_020159	likely ortholog of mouse enhancer trap locus 1 (ETL1), mRNA /cds=(79,3159) /gb=NM_020159 /gi=14149729 /ug=Hs.21356 /len=4935	NM_020159	Hs.21356	NP_064544
ncr4332	NM_020186	DC11 protein (DC11), mRNA /cds=(21,398) /gb=NM_020186 /gi=9910179 /ug=Hs.42785 /len=957	NM_020186	Hs.42785	NP_064571
ncr1545	NM_020313	hypothetical protein LOC57019 (LOC57019), mRNA /gb=NM_020313 /gi=10092672 /ug=Hs.4900 /len=2105	NM_020313	Hs.4900	NP_064709
seob4539	NM_020365	eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa (EIF2B3), mRNA /cds=(103,1461) /gb=NM_020365 /gi=9966778 /ug=Hs.283627 /len=1602	NM_020365	Hs.283627	NP_065098
seob6853	NM_020414	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 24 (DDX24), mRNA /cds=(100,2679) /gb=NM_020414 /gi=14251213 /ug=Hs.155986 /len=2967	NM_020414	Hs.155986	NP_065147
seob9406	NM_020432	hypothetical protein DKFZp564F013 (DKFZP564F013), mRNA /cds=(107,2194) /gb=NM_020432 /gi=24308192 /ug=Hs.128653 /len=4572	NM_020432	Hs.128653	NP_065165
fcrb5389	NM_020532	reticulon 4 (RTN4), mRNA /cds=(245,3823) /gb=NM_020532 /gi=24638438 /ug=Hs.65450 /len=4166	NM_007008; NM_020532; NM_153828	Hs.65450	NP_722550
ncrc6756	NM_020548	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein) (DBI), mRNA /cds=(20,334) /gb=NM_020548 /gi=24475624 /ug=Hs.78888 /len=556	NM_020548	Hs.78888	NP_065438
seob8031	NM_020548	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein) (DBI), mRNA /cds=(20,334) /gb=NM_020548 /gi=24475624 /ug=Hs.78888 /len=556	NM_020548	Hs.78888	NP_065438

ncr9572	NM_020674	cytochrome P450 monooxygenase (CYP-M), mRNA /cds=(88,1395) /gb=NM_020674 /gi=10257438 /ug=Hs.352566 /len=1755	NM_020674; NM_177538	Hs.352566	NP_803882
miob3986	NM_020749	AT2 receptor-interacting protein 1 (ATIP1), mRNA /cds=(1,1311) /gb=NM_020749 /gi=21361871 /ug=Hs.7946 /len=3455	NM_020749	Hs.7946	NP_065800
ncr4020	NM_020824	Rho-GTPase activating protein 10 (ARHGAP10), mRNA /cds=(438,6311) /gb=NM_020824 /gi=20977540 /ug=Hs.11611 /len=7130	NM_020824	Hs.11611	NP_065875
fcrb8855	NM_020839	WD repeat endosomal protein (KIAA1449), mRNA /cds=(11,2044) /gb=NM_020839 /gi=21314694 /ug=Hs.109778 /len=3705	NM_020839	Hs.109778	NP_065890
ncrb8319	NM_021005	nuclear receptor subfamily 2, group F, member 2 (NR2F2), mRNA /cds=(343,1587) /gb=NM_021005 /gi=14149745 /ug=Hs.347991 /len=1740	NM_021005	Hs.347991	NP_066285
ncrc1999	NM_021034	interferon induced transmembrane protein 3 (1-8U) (IFITM3), mRNA /cds=(238,639) /gb=NM_021034 /gi=11995467 /ug=Hs.381234 /len=808	NM_021034	Hs.381234	NP_066362
mioc5603	NM_021122	fatty-acid-Coenzyme A ligase, long-chain 2 (FACL2), mRNA /cds=(14,2110) /gb=NM_021122 /gi=12669906 /ug=Hs.154890 /len=3635	NM_021122	Hs.154890	NP_066945
seob0046	NM_021145	cyclin D binding myb-like transcription factor 1 (DMTF1), mRNA /cds=(276,2558) /gb=NM_021145 /gi=10863946 /ug=Hs.5671 /len=3767	NM_021145	Hs.5671	NP_066968
fcrb1580	NM_021145	cyclin D binding myb-like transcription factor 1 (DMTF1), mRNA /cds=(276,2558) /gb=NM_021145 /gi=10863946 /ug=Hs.5671 /len=3767	NM_021145	Hs.5671	NP_066968
ncrc5760	NM_021222	TcD37 (HTCD37), mRNA /cds=(137,1498) /gb=NM_021222 /gi=24308262 /ug=Hs.78524 /len=2995	NM_021222	Hs.78524	NP_067045
ncrc3161	NM_021626	likely of rat and mouse retinoid-inducible serine carboxypeptidase (RISC), mRNA /cds=(33,1391) /gb=NM_021626 /gi=11055991 /ug=Hs.106747 /len=1921	NM_021626	Hs.106747	NP_067639
mioc0690	NM_021639	hypothetical protein SP192 (SP192), mRNA /cds=(445,1869) /gb=NM_021639 /gi=21314695 /ug=Hs.169854 /len=2728	NM_021639	Hs.169854	NP_067652
miob8146	NM_021818	WW45 protein (WW45), mRNA /cds=(339,1490) /gb=NM_021818 /gi=18860913 /ug=Hs.288906 /len=3031	NM_021818	Hs.288906	NP_068590
mioa5594	NM_021914	cofilin 2 (muscle) (CFL2), mRNA	NM_021914	Hs.180141	NP_619579
fcrb1525	NM_021941	chromosome 21 open reading frame 97 (C21orf97), mRNA /cds=(665,1351) /gb=NM_021941 /gi=11345479 /ug=Hs.4746 /len=1819	NM_021941	Hs.4746	NP_068760

fcrc6826	NM_022073	egl nine 3 (C. elegans) (EGLN3), mRNA /cds=(327,1046) /gb=NM_022073 /gi=11545786 /ug=Hs.18878 /len=2770	NM_022073; NM_033344	Hs.18878	NP_071356
fcrb5709	NM_022130	golgi phosphoprotein 3 (coat-protein) (GOLPH3), mRNA /cds=(241,1137) /gb=NM_022130 /gi=20149665 /ug=Hs.18271 /len=2655	NM_022130	Hs.18271	NP_071413
ncrb8142	NM_022130	golgi phosphoprotein 3 (coat-protein) (GOLPH3), mRNA /cds=(241,1137) /gb=NM_022130 /gi=20149665 /ug=Hs.18271 /len=2655	NM_022130	Hs.18271	NP_071413
fcrb5687	NM_022464	endoplasmic reticulum chaperone SIL1, of yeast (SIL1), mRNA /cds=(97,1482) /gb=NM_022464 /gi=11968008 /ug=Hs.297875 /len=1702	NM_022464	Hs.297875	NP_071909
miod1792	NM_022495	hypothetical protein FLJ12799 (FLJ12799), mRNA /cds=(485,1324) /gb=NM_022495 /gi=22095362 /ug=Hs.22549 /len=1926	NM_022495	Hs.22549	NP_071940
ncrc2531	NM_022662	anaphase-promoting complex 1 (meiotic checkpoint regulator) (ANAPC1), mRNA /cds=(263,6097) /gb=NM_022662 /gi=12056970 /ug=Hs.40137 /len=6282	NM_022662	Hs.40137	NP_073153
ncrb8343	NM_022748	tumor endothelial marker 6 (TEM6), mRNA /cds=(93,3710) /gb=NM_022748 /gi=17511208 /ug=Hs.12210 /len=6702	NM_022748	Hs.12210	NP_073585
ncrb6818	NM_022830	hypothetical protein FLJ22347 (FLJ22347), mRNA /cds=(60,2684) /gb=NM_022830 /gi=12383073 /ug=Hs.106004 /len=2747	NM_022830	Hs.106004	NP_073741
seoc8306	NM_022917	nucleolar protein family 6 (RNA-associated) (NOL6), transcript variant alpha, mRNA /cds=(61,3501) /gb=NM_022917 /gi=22212928 /ug=Hs.183253 /len=4854	NM_022917; NM_130793; NM_139235	Hs.183253	NP_631981
fcrb7207	NM_023109	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome) (FGFR1), transcript variant 7, mRNA /cds=(727,2715) /gb=NM_023109 /gi=13186244 /ug=Hs.748 /len=4066	NM_000604; NM_015850; NM_023105; NM_023106; NM_023107; NM_023108; NM_023109; NM_023110; NM_023111	Hs.748	NP_075599

fcrc0076	NM_024047	nudix (nucleoside diphosphate linked moiety X)-type motif 9 (NUDT9), mRNA /cds=(326,1378) /gb=NM_024047 /gi=20127621 /ug=Hs.301789 /len=1718	NM_024047	Hs.301789	NP_076952
seob7224	NM_024077	SECIS binding protein 2 (SBP2), mRNA /cds=(58,2622) /gb=NM_024077 /gi=21359954 /ug=Hs.288141 /len=3457	NM_024077	Hs.288141	NP_076982
ncrb5227	NM_024292	ubiquitin-like 5 (UBL5), mRNA /cds=(66,287) /gb=NM_024292 /gi=13236509 /ug=Hs.13836 /len=413	NM_024292	Hs.13836	NP_077268
seob4213	NM_024420	phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA /cds=(139,2388) /gb=NM_024420 /gi=23943919 /ug=Hs.211587 /len=2875	NM_024420	Hs.211587	NP_077734
seoa7249	NM_024430	proline-serine-threonine phosphatase interacting protein 2 (PSTPIP2), mRNA	NM_024430	Hs.69149	NP_077748
miod1820	NM_024570	hypothetical protein FLJ11712 (FLJ11712), mRNA /cds=(287,1225) /gb=NM_024570 /gi=13375741 /ug=Hs.14920 /len=1515	NM_024570	Hs.14920	NP_078846
mioc4769	NM_024635	hypothetical protein FLJ22643 (FLJ22643), mRNA /cds=(15,650) /gb=NM_024635 /gi=13375865 /ug=Hs.43579 /len=997	NM_024635	Hs.43579	NP_078911
mioc3904	NM_024683	hypothetical protein FLJ22729 (FLJ22729), mRNA /cds=(603,1079) /gb=NM_024683 /gi=13375953 /ug=Hs.94891 /len=1278	NM_024683	Hs.94891	NP_078959
miob9901	NM_024697	hypothetical protein FLJ22419 (FLJ22419), mRNA /cds=(409,1596) /gb=NM_024697 /gi=13375980 /ug=Hs.99256 /len=1674	NM_024697	Hs.99256	NP_078973
seob8641	NM_024715	hypothetical protein FLJ22625 (FLJ22625), mRNA /cds=(694,1776) /gb=NM_024715 /gi=21362011 /ug=Hs.106534 /len=2747	NM_024715	Hs.106534	NP_078991
miob9714	NM_024769	hypothetical protein FLJ22415 (FLJ22415), mRNA /cds=(342,1463) /gb=NM_024769 /gi=13376114 /ug=Hs.135121 /len=2627	NM_024769	Hs.135121	NP_079045
fcrb2330	NM_024899	hypothetical protein FLJ12542 (FLJ12542), mRNA /cds=(157,2136) /gb=NM_024899 /gi=21314727 /ug=Hs.236940 /len=2884	NM_024899	Hs.236940	NP_079175
fcr7667	NM_025133	F-box only protein 11 (FBXO11), mRNA /cds=(319,2748) /gb=NM_025133 /gi=28316723 /ug=Hs.284289 /len=3960	NM_012167; NM_018693; NM_025133	Hs.284289	NP_079409
miod3341	NM_025137	hypothetical protein FLJ21439 (FLJ21439), mRNA /cds=(207,1484) /gb=NM_025137 /gi=13376718 /ug=Hs.288872 /len=2010	NM_025137	Hs.288872	NP_079413
mioc3565	NM_025191	chromosome 1 open reading frame 22 (C1orf22), mRNA /cds=(54,2723) /gb=NM_025191 /gi=19923618 /ug=Hs.279951 /len=6298	NM_025191	Hs.279951	NP_079467
mioc1596	NM_025202	likely ortholog of neuronally expressed calcium binding protein (FLJ13612), mRNA /cds=(101,820) /gb=NM_025202 /gi=20149495 /ug=Hs.24391 /len=1898	NM_025202	Hs.24391	NP_079478

miod1942	NM_030921	hypothetical protein DC42 (DC42), mRNA /cds=(463,771) /gb=NM_030921 /gi=24475707 /ug=Hs.72805 /len=1632	NM_030921	Hs.72805	NP_112183
ncrc1140	NM_031284	hypothetical protein DKFZp434B195 (DKFZP434B195), mRNA /cds=(514,1290) /gb=NM_031284 /gi=21361960 /ug=Hs.10748 /len=2262	NM_031284	Hs.10748	NP_112574
ncr5149	NM_031305	hypothetical protein DKFZp564B1162 (DKFZP564B1162), mRNA /cds=(661,2628) /gb=NM_031305 /gi=13775229 /ug=Hs.93589 /len=4593	NM_031305	Hs.93589	NP_112595
ncrc9060	NM_031370	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa) (HNRPD), transcript variant 1, mRNA /cds=(286,1353) /gb=NM_031370 /gi=14110419 /ug=Hs.406404 /len=2197	NM_002138; NM_031369; NM_031370	Hs.406404	NP_112738
mioc5636	NM_031458	B aggressive lymphoma gene (BAL), mRNA /cds=(229,2793) /gb=NM_031458 /gi=13899296 /ug=Hs.47783 /len=3243	NM_031458	Hs.47783	NP_113646
fcrb1560	NM_031484	hypothetical protein MGC4415 (MGC4415), mRNA /cds=(154,675) /gb=NM_031484 /gi=13899343 /ug=Hs.209614 /len=3243	NM_031484	Hs.209614	NP_113672
fcrb3848	NM_031484	hypothetical protein MGC4415 (MGC4415), mRNA /cds=(154,675) /gb=NM_031484 /gi=13899343 /ug=Hs.209614 /len=3243	NM_031484	Hs.209614	NP_113672
hfcr3160	NM_031492	hypothetical protein similar to RNA-binding protein lark (MGC10871), mRNA /cds=(54,1133) /gb=NM_031492 /gi=13899353 /ug=Hs.49994 /len=1821	NM_031492	Hs.49994	NP_113680
hfcr2722	NM_031902	mitochondrial ribosomal protein S5 (MRPS5), nuclear gene encoding mitochondrial protein, mRNA /cds=(219,1511) /gb=NM_031902 /gi=16554614 /ug=Hs.433117 /len=1678	NM_031902	Hs.433117	NP_114108
miob0670	NM_032042	hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA /cds=(22,1272) /gb=NM_032042 /gi=21362017 /ug=Hs.25307 /len=4204	NM_032042	Hs.25307	NP_114431
ncr3971	NM_032102	Splicing factor, arginine/serine-rich, 46kD (SRP46), mRNA /cds=(283,1131) /gb=NM_032102 /gi=15055542 /ug=Hs.155160 /len=2186	NM_032102	Hs.155160	NP_115285
mioc0214	NM_032151	dimerization cofactor of hepatocyte nuclear factor 1 (HNF1) from muscle (DCOHM), mRNA /cds=(21,413) /gb=NM_032151 /gi=14149824 /ug=Hs.150186 /len=5641	NM_032151	Hs.150186	NP_115527
seoa0488	NM_032236	FLJ23277 protein (FLJ23277), mRNA /cds=(141,3089) /gb=NM_032236 /gi=18860906 /ug=Hs.334477 /len=3911	NM_032236	Hs.334477	NP_115612
ncrb4101	NM_032297	hypothetical protein DKFZp761D112 (DKFZp761D112), mRNA /cds=(60,464) /gb=NM_032297 /gi=14150051 /ug=Hs.103849 /len=2573	NM_032297	Hs.103849	NP_115673

ncrc1884	NM_032348	hypothetical protein MGC3047 (MGC3047), mRNA /cds=(41,1369) /gb=NM_032348 /gi=14150144 /ug=Hs.59384 /len=2299	NM_032348	Hs.59384	NP_115724
fcrb5588	NM_032548	ankyrin repeat and BTB (POZ) domain containing 1 (ABTB1), transcript variant 1, mRNA /cds=(526,1536) /gb=NM_032548 /gi=25777622 /ug=Hs.107812 /len=2020	NM_032548; NM_172027; NM_172028	Hs.107812	NP_742025
seob0418	NM_032557	HP43.8KD protein (HP43.8KD), mRNA /cds=(507,3635) /gb=NM_032557 /gi=27545312 /ug=Hs.332841 /len=4684	NM_032557	Hs.332841	NP_115946
ncr8111	NM_032601	methylmalonyl CoA epimerase (MCEE), mRNA /cds=(11,541) /gb=NM_032601 /gi=21314761 /ug=Hs.94949 /len=850	NM_032601	Hs.94949	NP_115990
fcrb1539	NM_032704	tubulin alpha 6 (TUBA6), mRNA /cds=(1,1350) /gb=NM_032704 /gi=14389308 /ug=Hs.406578 /len=1350	NM_032704	Hs.406578	NP_116093
ncr2507	NM_032772	hypothetical protein MGC2555 (MGC2555), mRNA /cds=(258,2198) /gb=NM_032772 /gi=24432031 /ug=Hs.158210 /len=2807	NM_032772	Hs.158210	NP_116161
fcrb1697	NM_032801	junctional adhesion molecule 3 (JAM3), mRNA /cds=(25,1092) /gb=NM_032801 /gi=21704285 /ug=Hs.334703 /len=3675	NM_032801	Hs.334703	NP_116190
fcrb4921	NM_032836	hypothetical protein FLJ14768 (FLJ14768), mRNA /cds=(91,1581) /gb=NM_032836 /gi=14249547 /ug=Hs.129888 /len=2651	NM_032836	Hs.129888	NP_116225
seob1219	NM_032936	DC32 (DC32), mRNA /cds=(229,630) /gb=NM_032936 /gi=24475725 /ug=Hs.19025 /len=883	NM_032936	Hs.19025	NP_116325
mioc0940	NM_032936	DC32 (DC32), mRNA /cds=(229,630) /gb=NM_032936 /gi=24475725 /ug=Hs.19025 /len=883	NM_032936	Hs.19025	NP_116325
ncrc6455	NM_032961	protocadherin 10 (PCDH10), transcript variant 1, mRNA /cds=(827,3949) /gb=NM_032961 /gi=14589915 /ug=Hs.146858 /len=5384	NM_020815; NM_032961	Hs.146858	NP_116586
ncr5890	NM_052860	kruppel-like zinc finger protein (ZNF300), mRNA /cds=(268,2082) /gb=NM_052860 /gi=16604251 /ug=Hs.288928 /len=3104	NM_052860	Hs.288928	NP_443092
mioa2620	NM_054027	ankylosis, progressive (mouse) (ANKH), transcript variant 2, mRNA /cds=(265,1743) /gb=NM_054027 /gi=21536394 /ug=Hs.168640 /len=4031	NM_019847; NM_054027	Hs.168640	NP_473368
seoa0799	NM_057180	vacuolar protein sorting 29 (yeast) (VPS29) transcript variant 2, mRNA /cds=(61,621) /gb=NM_057180 /gi=17402911 /ug=Hs.69192 /len=1107	NM_016226; NM_057180	Hs.69192	NP_476528

mioa0908	NM_080425	GNAS complex locus (GNAS), transcript variant 3, mRNA /cds=(1,2730) /gb=NM_080425 /gi=18426897 /ug=Hs.374523 /len=3091	NM_000516; NM_016592; NM_080425; NM_080426	Hs.374523	NP_536351
miob8191	NM_080597	oxysterol binding protein-like 1A (OSBPL1A), transcript variant OSBPL1B, mRNA /cds=(175,3027) /gb=NM_080597 /gi=19718740 /ug=Hs.252716 /len=4165	NM_018030; NM_080597; NM_133268	Hs.252716	NP_579802
miod4938	NM_080737	synaptotagmin-like 4 (granuphilin-a) (SYTL4), mRNA /cds=(333,2348) /gb=NM_080737 /gi=18152766 /ug=Hs.247525 /len=3914	NM_080737	Hs.247525	NP_542775
ncrc5536	NM_080748	chromosome 20 open reading frame 52 (C20orf52), mRNA /cds=(164,403) /gb=NM_080748 /gi=18152784 /ug=Hs.401703 /len=602	NM_080748	Hs.401703	NP_542786
mioc4910	NM_080792	protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1), mRNA /cds=(28,1542) /gb=NM_080792 /gi=18426910 /ug=Hs.156114 /len=3872	NM_080792	Hs.156114	NP_542970
fcrb2460	NM_100264	WW domain-containing adapter with a coiled-coil region (WAC), transcript variant 2, mRNA /cds=(332,2140) /gb=NM_100264 /gi=18379329 /ug=Hs.70333 /len=3088	NM_016628; NM_100264; NM_100486	Hs.70333	NP_567823
fcrc4734	NM_133502	zinc finger protein 274 (ZNF274), transcript variant ZNF274c, mRNA /cds=(460,2421) /gb=NM_133502 /gi=19743800 /ug=Hs.83761 /len=2839	NM_016324; NM_016325; NM_133502	Hs.83761	NP_598009
mioc5179	NM_134442	cAMP responsive element binding protein 1 (CREB1), transcript variant B, mRNA /cds=(182,1207) /gb=NM_134442 /gi=22219460 /ug=Hs.79194 /len=3006	NM_004379; NM_134442	Hs.79194	NP_604391
seoc0317	NM_138459	hypothetical protein, MGC:7199 (LOC116150), mRNA /cds=(174,1055) /gb=NM_138459 /gi=20270242 /ug=Hs.289008 /len=2645	NM_138459	Hs.289008	NP_612468
fcr4699	NM_139276	signal transducer and activator of transcription 3 (acute-phase response factor) (STAT3), transcript variant 1, mRNA /cds=(241,2553) /gb=NM_139276 /gi=21618339 /ug=Hs.321677 /len=3455	NM_003150; NM_139276	Hs.321677	NP_644805
fcrb9684	NM_144582	hypothetical protein MGC32043 (MGC32043), mRNA /cds=(8,457) /gb=NM_144582 /gi=21389354 /ug=Hs.226138 /len=3131	NM_144582	Hs.226138	NP_653183

miod1863	NM_144583	ATPase, H transporting, lysosomal 42kDa, V1 subunit C isoform 2 (ATP6V1C2), mRNA /cds=(21,1166) /gb=NM_144583 /gi=21389364 /ug=Hs.372429 /len=3033	NM_144583	Hs.372429	NP_653184
seob9772	NM_144629	hypothetical protein FLJ30574 (FLJ30574), mRNA /cds=(403,1908) /gb=NM_144629 /gi=21389456 /ug=Hs.350388 /len=3113	NM_144629	Hs.350388	NP_653230
mioc7352	NM_144664	hypothetical protein MGC33371 (MGC33371), mRNA /cds=(318,1019) /gb=NM_144664 /gi=21389552 /ug=Hs.288304 /len=1399	NM_144664	Hs.288304	NP_653265
miod6947	NM_144721	hypothetical protein MGC30052 (MGC30052), mRNA /cds=(35,703) /gb=NM_144721 /gi=21389506 /ug=Hs.143692 /len=2260	NM_144721	Hs.143692	NP_653322
fcrb6676	NM_145056	thymus expressed gene 3-like (MGC15476), mRNA /cds=(441,1655) /gb=NM_145056 /gi=21450823 /ug=Hs.134185 /len=2544	NM_145056	Hs.134185	NP_659493
seob0409	NM_145241	similar to spermatid WD-repeat protein (LOC114987), mRNA /cds=(238,1338) /gb=NM_145241 /gi=21687047 /ug=Hs.133331 /len=3121	NM_145241	Hs.133331	NP_660284
mioa0582	NM_145297	similar to DNA-binding protein; zinc finger protein 253 (LOC199777), mRNA /cds=(130,408) /gb=NM_145297 /gi=21699081 /ug=Hs.334568 /len=647	NM_145297	Hs.334568	NP_660340
ncr3163	NM_145645	Williams-Beuren Syndrome critical region protein 20 copy B (WBSCR20B), mRNA /cds=(984,1448) /gb=NM_145645 /gi=21717802 /ug=Hs.406306 /len=1634	NM_145645	Hs.406306	NP_663620
mioa0891	NM_145693	lipin 1 (LPIN1), mRNA /cds=(68,2740) /gb=NM_145693 /gi=22027647 /ug=Hs.81412 /len=5363	NM_145693	Hs.81412	NP_663731
seoa7943	NM_145728	desmuslin (DMN), transcript variant A, mRNA /cds=(121,4818) /gb=NM_145728 /gi=22027637 /ug=Hs.10587 /len=7343	NM_015286; NM_145728	Hs.10587	NP_663780
miob6113	NM_145791	microsomal glutathione S-transferase 1 (MGST1), transcript variant 1c, mRNA /cds=(144,611) /gb=NM_145791 /gi=22035635 /ug=Hs.389700 /len=987	NM_020300; NM_145764; NM_145791; NM_145792	Hs.389700	NP_665735
mioa3239	NM_145859	programmed cell death 10 (PDCD10), transcript variant 2, mRNA	NM_007217; NM_145859; NM_145860	Hs.28866	NP_665859

seob2717	NM_147166	A kinase (PRKA) anchor protein (yotiao) 9 (AKAP9), transcript variant 4, mRNA /cds=(223,5190) /gb=NM_147166 /gi=22538388 /ug=Hs.58103 /len=6058	NM_005751; NM_147166; NM_147171; NM_147185	Hs.58103	NP_671714
seoa4802	NM_148571	mitochondrial ribosomal protein L27 (MRPL27), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA /cds=(32,316) /gb=NM_148571 /gi=22547130 /ug=Hs.7736 /len=2472	NM_016504; NM_148570; NM_148571	Hs.7736	NP_683412
fcr6635	NM_152253	choline kinase-like (CHKL), transcript variant 2, mRNA /cds=(185,568) /gb=NM_152253 /gi=23238260 /ug=Hs.154886 /len=4914	NM_005198; NM_152253	Hs.154886	NP_689466
fcrb3776	NM_152282	hypothetical protein FLJ23751 (FLJ23751), mRNA /cds=(121,1563) /gb=NM_152282 /gi=22748648 /ug=Hs.37443 /len=2994	NM_152282	Hs.37443	NP_689495
seoc5833	NM_152380	T-box 15 (TBX15), mRNA /cds=(230,1093) /gb=NM_152380 /gi=23943887 /ug=Hs.164680 /len=2782	NM_152380	Hs.164680	NP_689593
fcr6748	NM_152436	hypothetical protein MGC39497 (MGC39497), mRNA /cds=(9,770) /gb=NM_152436 /gi=22748922 /ug=Hs.406728 /len=1745	NM_152436	Hs.406728	NP_689649
ncr3944	NM_152586	hypothetical protein FLJ37318 (FLJ37318), mRNA /cds=(226,2025) /gb=NM_152586 /gi=22749206 /ug=Hs.130184 /len=3114	NM_152586	Hs.130184	NP_689799
mioc7974	NM_152594	sprouty-related, EVH1 domain containing 1 (SPRED1), mRNA /cds=(106,1440) /gb=NM_152594 /gi=22749220 /ug=Hs.302718 /len=3816	NM_152594	Hs.302718	NP_689807
ncr4545	NM_152608	hypothetical protein FLJ35382 (FLJ35382), mRNA /cds=(165,1235) /gb=NM_152608 /gi=22749244 /ug=Hs.99210 /len=1349	NM_152608	Hs.99210	NP_689821
ncrb7600	NM_152609	hypothetical protein FLJ32001 (FLJ32001), mRNA /cds=(212,2389) /gb=NM_152609 /gi=22749246 /ug=Hs.288742 /len=3608	NM_152609	Hs.288742	NP_689822
seob5859	NM_152731	hypothetical protein FLJ30162 (FLJ30162), mRNA /cds=(272,841) /gb=NM_152731 /gi=22749448 /ug=Hs.311163 /len=2278	NM_152731	Hs.311163	NP_689944
mioc0734	NM_152912	mitochondrial translational initiation factor 3 (MTIF3), mRNA /cds=(237,1073) /gb=NM_152912 /gi=24432096 /ug=Hs.406591 /len=1693	NM_152912	Hs.406591	NP_690876
seob0547	NM_152989	SRY (sex determining region Y)-box 5 (SOX5), transcript variant B, mRNA /cds=(373,2625) /gb=NM_152989 /gi=23308714 /ug=Hs.87224 /len=4492	NM_006940; NM_152989; NM_178010	Hs.87224	NP_821078

ncr8995	NM_153366	hypothetical protein FLJ90754 (FLJ90754), mRNA /cds=(677,5170) /gb=NM_153366 /gi=23503304 /ug=Hs.8963 /len=5421	NM_153366	Hs.8963	NP_699197
ncr6637	NM_153607	adult retina protein (LOC153222), mRNA /cds=(305,2224) /gb=NM_153607 /gi=23957697 /ug=Hs.163725 /len=5446	NM_153607	Hs.163725	NP_705835
fcrb2483	NM_153649	tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=NM_153649 /gi=24119202 /ug=Hs.85844 /len=2089	NM_152263; NM_153649	Hs.85844	NP_705935
fcr3575	NM_153822	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4 (PSMD4), transcript variant 2, mRNA /cds=(63,869) /gb=NM_153822 /gi=25121957 /ug=Hs.148495 /len=1508	NM_002810; NM_153822	Hs.148495	NP_722544
seoc7373	NM_170601	cytosolic sialic acid 9-O-acetylesterase (CSE-C), mRNA	NM_018978; NM_170601		NP_733746
seob7402	NM_170665	ATPase, Ca transporting, cardiac muscle, slow twitch 2 (ATP2A2), transcript variant 1, mRNA /cds=(164,3292) /gb=NM_170665 /gi=27886537 /ug=Hs.1526 /len=4205	NM_001681; NM_170665	Hs.1526	NP_733765
ncr0377	NM_170695	TGFB-induced factor (TALE family homeobox) (TGIF), transcript variant 1, mRNA /cds=(388,1593) /gb=NM_170695 /gi=28178842 /ug=Hs.90077 /len=2076	NM_003244; NM_170695; NM_173207; NM_173208; NM_173209; NM_173210; NM_173211; NM_174886	Hs.90077	NP_777480
mioa1015	NM_172178	mitochondrial ribosomal protein L42 (MRPL42), transcript variant 3, nuclear gene encoding mitochondrial protein, mRNA /cds=(179,607) /gb=NM_172178 /gi=26667173 /ug=Hs.112110 /len=2093	NM_014050; NM_172177; NM_172178	Hs.112110	NP_751918
miob0746	NM_173639	hypothetical protein FLJ35976 (FLJ35976), mRNA /cds=(59,601) /gb=NM_173639 /gi=27735030 /ug=Hs.131810 /len=1838	NM_173639	Hs.131810	NP_775910
seob3840	NM_173824	hypothetical protein MGC26717 (MGC26717), mRNA /cds=(107,1090) /gb=NM_173824 /gi=28376661 /ug=Hs.406060 /len=1387	NM_173824	Hs.406060	NP_776185
fcr1994	NM_174856	isocitrate dehydrogenase 3 (NAD) beta (IDH3B), transcript variant 3, nuclear gene encoding mitochondrial protein, mRNA /cds=(572,1273) /gb=NM_174856 /gi=28178818 /ug=Hs.155410 /len=1645	NM_006899; NM_174855; NM_174856	Hs.155410	NP_777281

seoc2232	NM_174928	hypothetical protein LOC221143 (LOC221143), mRNA /cds=(82,726) /gb=NM_174928 /gi=28372546 /ug=Hs.32450 /len=890	NM_174928	Hs.32450	NP_777588
seoc7006	U79258	clone 23732 mRNA, partial cds	NM_018997; NM_031901		NP_061870
seoa4670	U93051	putative protein tyrosine phosphatase (PTEN) mRNA, complete cds /cds=(1,1212) /gb=U93051 /gi=1916351 /ug=Hs.356062 /len=1212	NM_000314	Hs.356062	NP_000305
fcr7508	X56932	23 kD highly basic protein	NM_012423	Hs.389335	NP_036555
seob9187	X60459	IFNAR gene for interferon alpha/beta receptor			CAA42992
fcr4214	X63224	ubiquinone oxidoreductase complex CI-PDSW	NM_175818	Bt.70	NP_787012
mioc2561	XM_040708	KIAA1377 protein (KIAA1377), mRNA			XP_040708
ncrc4016	XM_046097	LOC92606 (LOC92606), mRNA			XP_046097
seob2938	XM_046827	nuclear factor I/A (NFIA), mRNA			NP_005586
ncrc5491	XM_046853	LOC92719 (LOC92719), mRNA			XP_046853
seoc0416	XM_058647	similar to mitochondrial ribosomal protein L52 CG1577-PA (LOC122704), mRNA			NP_851824
hfcr0412	XM_084654	LOC143914 (LOC143914), mRNA			XP_084654
seob3462	XM_088391	similar to Tropomyosin alpha 4 chain (Tropomyosin 4) (TM30p1) (LOC157784), mRNA			XP_088391
fcrb1763	XM_209913	similar to ring finger protein 5 (LOC286140), mRNA			NP_872402

FIGURE 6b: OA stage specific markers for moderate OA only

Clone Name	Genbank	Description	RefSeq	UniGene	Rep_prot
fcrb0131	NM_000018	acyl-Coenzyme A dehydrogenase, very long chain (ACADVL), nuclear gene encoding mitochondrial protein, mRNA /cds=(86,2053) /gb=NM_000018 /gi=4557234 /ug=Hs.82208 /len=2219	NM_000018	Hs.82208	NP_000009
seoa0045	NM_000060	biotinidase (BTD), mRNA /cds=(36,1667) /gb=NM_000060 /gi=4557372 /ug=Hs.78885 /len=2016	NM_000060	Hs.78885	NP_000051
ncrc0644	NM_000063	complement component 2 (C2), mRNA /cds=(37,2295) /gb=NM_000063 /gi=20631970 /ug=Hs.2253 /len=2609	NM_000063	Hs.2253	NP_000054
ncrb6394	NM_000088	collagen, type I, alpha 1 (COL1A1), mRNA /cds=(120,4514) /gb=NM_000088 /gi=14719826 /ug=Hs.172928 /len=5921	NM_000088	Hs.172928	NP_000079
seoa0032	NM_000089	collagen, type I, alpha 2 (COL1A2), mRNA /cds=(138,4238) /gb=NM_000089 /gi=21536289 /ug=Hs.179573 /len=5084	NM_000089	Hs.179573	NP_000080
mioa1097	NM_000089	collagen, type I, alpha 2 (COL1A2), mRNA /cds=(138,4238) /gb=NM_000089 /gi=21536289 /ug=Hs.179573 /len=5084	NM_000089	Hs.179573	NP_000080

miob4221	NM_000130	coagulation factor V (proaccelerin, labile factor) (F5), mRNA /cds=(98,6772) /gb=NM_000130 /gi=10518500 /ug=Hs.30054 /len=6914	NM_000130	Hs.30054	NP_000121
seob0370	NM_000137	fumarylacetoacetate hydrolase (fumarylacetoacetase) (FAH), mRNA /cds=(57,1316) /gb=NM_000137 /gi=4557586 /ug=Hs.73875 /len=1447	NM_000137	Hs.73875	NP_000128
seob0200	NM_000186	H factor 1 (complement) (HF1), mRNA /cds=(74,3769) /gb=NM_000186 /gi=4504374 /ug=Hs.250651 /len=3926	NM_000186	Hs.250651	NP_000177
miob4975	NM_000204	I factor (complement) (IF), mRNA /cds=(15,1766) /gb=NM_000204 /gi=4504578 /ug=Hs.36602 /len=1963	NM_000204	Hs.36602	NP_000195
mioa1445	NM_000255	methylmalonyl Coenzyme A mutase (MUT), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,2329) /gb=NM_000255 /gi=4557766 /ug=Hs.155212 /len=2798	NM_000255	Hs.155212	NP_000246

miod0592	NM_000255	methylmalonyl Coenzyme A mutase (MUT), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,2329) /gb=NM_000255 /gi=4557766 /ug=Hs.155212 /len=2798	NM_000255	Hs.155212	NP_000246
seoa0054	NM_000269	non-metastatic cells 1, protein (NM23A) expressed in (NME1), mRNA /cds=(85,543) /gb=NM_000269 /gi=4557796 /ug=Hs.118638 /len=732	NM_000269	Hs.118638	NP_000260
seoa8348	NM_000274	ornithine aminotransferase (gyrate atrophy) (OAT), nuclear gene encoding mitochondrial protein, mRNA /cds=(55,1374) /gb=NM_000274 /gi=4557808 /ug=Hs.75485 /len=2013	NM_000274	Hs.75485	NP_000265
ncrb8539	NM_000319	peroxisome receptor 1 (PXR1), mRNA /cds=(52,1947) /gb=NM_000319 /gi=21361203 /ug=Hs.158084 /len=3227	NM_000319	Hs.158084	NP_000310
seob3307	NM_000358	transforming growth factor, beta-induced, 68kDa (TGFBI), mRNA /cds=(48,2099) /gb=NM_000358 /gi=4507466 /ug=Hs.118787 /len=2691	NM_000358	Hs.118787	NP_000349

miob9124	NM_000358	transforming growth factor, beta-induced, 68kDa (TGFBI), mRNA /cds=(48,2099) /gb=NM_000358 /gi=4507466 /ug=Hs.118787 /len=2691	NM_000358	Hs.118787	NP_000349
seob4925	NM_000385	aquaporin 1 (channel-forming integral protein, 28kDa) (AQP1), mRNA /cds=(39,848) /gb=NM_000385 /gi=4755121 /ug=Hs.76152 /len=1662	NM_000385	Hs.76152	NP_000376
seoa4518	NM_000390	choroideremia (Rab escort protein 1) (CHM), transcript variant 2950156, mRNA /cds=(31,1992) /gb=NM_000390 /gi=9966760 /ug=Hs.2010 /len=2115	NM_000390	Hs.2010	NP_000381
seoa4158	NM_000391	ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease) (CLN2), mRNA /cds=(30,1721) /gb=NM_000391 /gi=5597012 /ug=Hs.20478 /len=3502	NM_000391	Hs.20478	NP_000382
seoc4960	NM_000405	GM2 ganglioside activator protein (GM2A), mRNA /cds=(96,677) /gb=NM_000405 /gi=16507969 /ug=Hs.289082 /len=2478	NM_000405	Hs.289082	NP_000396

seoa8399	NM_000414	hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA /cds=(49,2259) /gb=NM_000414 /gi=4504504 /ug=Hs.75441 /len=2593	NM_000414	Hs.75441	NP_000405
fcr4129	NM_000466	peroxisome biogenesis factor 1 (PEX1), mRNA /cds=(61,3912) /gb=NM_000466 /gi=4505724 /ug=Hs.99847 /len=4343	NM_000466	Hs.99847	NP_000457
fcrb4266	NM_000500	cytochrome P450, family 21, subfamily A, polypeptide 2 (CYP21A2), mRNA /cds=(119,1606) /gb=NM_000500 /gi=20522237 /ug=Hs.278430 /len=2112	NM_000500	Hs.278430	NP_000491
fcrb3298	NM_000581	glutathione peroxidase 1 (GPX1), mRNA /cds=(319,924) /gb=NM_000581 /gi=10834975 /ug=Hs.76686 /len=1134	NM_000581	Hs.76686	NP_000572
miob2093	NM_000593	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) (TAP1), mRNA /cds=(165,2591) /gb=NM_000593 /gi=24797159 /ug=Hs.352018 /len=2960	NM_000593	Hs.352018	NP_000584
miob9285	NM_000596	insulin-like growth factor binding protein 1 (IGFBP1), mRNA /cds=(166,945) /gb=NM_000596 /gi=4504614 /ug=Hs.102122 /len=1514	NM_000596	Hs.102122	NP_000587

ncr0212	NM_000599	insulin-like growth factor binding protein 5 (IGFBP5), mRNA /cds=(752,1570) /gb=NM_000599 /gi=10834981 /ug=Hs.380833 /len=1722	NM_000599	Hs.380833	NP_000590
ncr0429	NM_000624	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5 (SERPINA5), mRNA /cds=(140,1360) /gb=NM_000624 /gi=21361194 /ug=Hs.76353 /len=2254	NM_000624	Hs.76353	NP_000615
miob3320	NM_000627	latent transforming growth factor beta binding protein 1 (LTBP1), mRNA /cds=(91,4275) /gb=NM_000627 /gi=4557730 /ug=Hs.241257 /len=5075	NM_000627	Hs.241257	NP_000618
fcr6054	NM_000646	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) (AGL), transcript variant 6, mRNA	NM_000028; NM_000642; NM_000643; NM_000644; NM_000645; NM_000646	Hs.904	NP_000637
ncrb6462	NM_000689	aldehyde dehydrogenase 1 family, member A1 (ALDH1A1), mRNA /cds=(54,1559) /gb=NM_000689 /gi=25777722 /ug=Hs.76392 /len=2116	NM_000689	Hs.76392	NP_000680

seoa4739	NM_000690	aldehyde dehydrogenase 2 family (mitochondrial) (ALDH2), nuclear gene encoding mitochondrial protein, mRNA /cds=(442,1995) /gb=NM_000690 /gi=25777731 /ug=Hs.195432 /len=2445	NM_000690	Hs.195432	NP_000681
fcrc1311	NM_000696	aldehyde dehydrogenase 9 family, member A1 (ALDH9A1), mRNA /cds=(378,1862) /gb=NM_000696 /gi=25777738 /ug=Hs.2533 /len=2713	NM_000696	Hs.2533	NP_000687
miob3968	NM_000809	gamma-aminobutyric acid (GABA) A receptor, alpha 4 (GABRA4), mRNA /cds=(39,1703) /gb=NM_000809 /gi=4557604 /ug=Hs.248112 /len=1703	NM_000809	Hs.248112	NP_000800
seoa9777	NM_000849	glutathione S-transferase M3 (brain) (GSTM3), mRNA /cds=(311,988) /gb=NM_000849 /gi=23065551 /ug=Hs.2006 /len=1572	NM_000849	Hs.2006	NP_000840
seoa9582	NM_000877	interleukin 1 receptor, type I (IL1R1), mRNA /cds=(83,1792) /gb=NM_000877 /gi=27894331 /ug=Hs.82112 /len=4909	NM_000877	Hs.82112	NP_000868

ncrc6012	NM_000938	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa (POLR2B), mRNA /cds=(44,3568) /gb=NM_000938 /gi=4505940 /ug=Hs.296014 /len=3748	NM_000938	Hs.296014	NP_000929
fcrb4985	NM_000967	ribosomal protein L3 (RPL3), mRNA /cds=(27,1238) /gb=NM_000967 /gi=16507968 /ug=Hs.119598 /len=1311	NM_000967	Hs.119598	NP_000958
mioc8766	NM_000969	ribosomal protein L5 (RPL5), mRNA /cds=(63,956) /gb=NM_000969 /gi=14591908 /ug=Hs.180946 /len=1033	NM_000969	Hs.180946	NP_000960
mioa8076	NM_000982	ribosomal protein L21 (RPL21), mRNA /cds=(30,512) /gb=NM_000982 /gi=18104947 /ug=Hs.431927 /len=568	NM_000982	Hs.431927	NP_000973
seob9869	NM_000982	ribosomal protein L21 (RPL21), mRNA /cds=(30,512) /gb=NM_000982 /gi=18104947 /ug=Hs.431927 /len=568	NM_000982	Hs.431927	NP_000973
ncrc9749	BC032295	clone IMAGE:3921971, mRNA, partial cds		Hs.326249	NP_000974
seoa0429	NM_000984	ribosomal protein L23a (RPL23A), mRNA /cds=(22,492) /gb=NM_000984 /gi=17105393 /ug=Hs.419463 /len=546	NM_000984	Hs.419463	NP_000975

fcrb5472	NM_000991	ribosomal protein L28 (RPL28), mRNA /cds=(43,456) /gb=NM_000991 /gi=13904865 /ug=Hs.356371 /len=500	NM_000991	Hs.356371	NP_000982
fcrb3181	NM_000991	ribosomal protein L28 (RPL28), mRNA /cds=(43,456) /gb=NM_000991 /gi=13904865 /ug=Hs.356371 /len=500	NM_000991	Hs.356371	NP_000982
ncr3339	NM_000996	ribosomal protein L35a (RPL35A), mRNA /cds=(74,406) /gb=NM_000996 /gi=16117790 /ug=Hs.288544 /len=511	NM_000996	Hs.288544	NP_000987
seoa4202	NM_001001	ribosomal protein L36a-like (RPL36AL), mRNA /cds=(95,415) /gb=NM_001001 /gi=16306559 /ug=Hs.419465 /len=537	NM_001001	Hs.419465	NP_000992
ncrb8802	NM_001010	ribosomal protein S6 (RPS6), mRNA /cds=(43,792) /gb=NM_001010 /gi=17158043 /ug=Hs.380843 /len=829	NM_001010	Hs.380843	NP_001001
mioa2156	NM_001010	ribosomal protein S6 (RPS6), mRNA /cds=(43,792) /gb=NM_001010 /gi=17158043 /ug=Hs.380843 /len=829	NM_001010	Hs.380843	NP_001001
fcrb3841	NM_001012	ribosomal protein S8 (RPS8), mRNA /cds=(24,650) /gb=NM_001012 /gi=4506742 /ug=Hs.399720 /len=705	NM_001012	Hs.399720	NP_001003

ncr2926	NM_001015	ribosomal protein S11 (RPS11), mRNA /cds=(34,510) /gb=NM_001015 /gi=14277698 /ug=Hs.182740 /len=594	NM_001015	Hs.182740	NP_001006
mioa3693	NM_001019	ribosomal protein S15a (RPS15A), mRNA /cds=(84,476) /gb=NM_001019 /gi=14165468 /ug=Hs.433406 /len=541	NM_001019	Hs.433406	NP_001010
seob4303	NM_001028	ribosomal protein S25 (RPS25), mRNA /cds=(64,441) /gb=NM_001028 /gi=14591916 /ug=Hs.409158 /len=514	NM_001028	Hs.409158	NP_001019
mioa9792	NM_001067	topoisomerase (DNA) II alpha 170kDa (TOP2A), mRNA /cds=(127,4722) /gb=NM_001067 /gi=19913405 /ug=Hs.156346 /len=5698	NM_001067	Hs.156346	NP_001058
fcrb6740	NM_001084	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3 (PLOD3), mRNA /cds=(323,2539) /gb=NM_001084 /gi=21361165 /ug=Hs.153357 /len=2852	NM_001084	Hs.153357	NP_001075
hfcr2832	NM_001101	actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793	NM_001101	Hs.426930	NP_001092
ncrc9637	NM_001101	actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793	NM_001101	Hs.426930	NP_001092

mioc4888	NM_001101	actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793	NM_001101	Hs.426930	NP_001092
hfcr5970	NM_001103	actinin, alpha 2 (ACTN2), mRNA /cds=(174,2858) /gb=NM_001103 /gi=4501892 /ug=Hs.83672 /len=4181	NM_001103	Hs.83672	NP_001094
ncr3442	NM_001124	adrenomedullin (ADM), mRNA /cds=(157,714) /gb=NM_001124 /gi=4501944 /ug=Hs.394 /len=1449	NM_001124	Hs.394	NP_001115
ncrc4780	NM_001124	adrenomedullin (ADM), mRNA /cds=(157,714) /gb=NM_001124 /gi=4501944 /ug=Hs.394 /len=1449	NM_001124	Hs.394	NP_001115
seoa4608	NM_001159	aldehyde oxidase 1 (AOX1), mRNA /cds=(299,4315) /gb=NM_001159 /gi=6598319 /ug=Hs.406238 /len=5125	NM_001159	Hs.406238	NP_001150
ncrb4351	NM_001206	basic transcription element binding protein 1 (BTEB1), mRNA /cds=(1265,1999) /gb=NM_001206 /gi=4557374 /ug=Hs.150557 /len=4859	NM_001206	Hs.150557	NP_001197
mioc3671	NM_001239	cyclin H (CCNH), mRNA /cds=(233,1204) /gb=NM_001239 /gi=17738313 /ug=Hs.514 /len=1398	NM_001239	Hs.514	NP_001230

ncr6745	NM_001240	cyclin T1 (CCNT1), mRNA /cds=(324,2504) /gb=NM_001240 /gi=17978465 /ug=Hs.279906 /len=2568	NM_001240	Hs.279906	NP_001231
miod6488	NM_001253	CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA /cds=(260,2668) /gb=NM_001253 /gi=16357499 /ug=Hs.155174 /len=3012	NM_001253	Hs.155174	NP_001244
seoc2205	NM_001271	chromodomain helicase DNA binding protein 2 (CHD2), mRNA /cds=(708,5927) /gb=NM_001271 /gi=4557448 /ug=Hs.36787 /len=7764	NM_001271	Hs.36787	NP_001262
mioa4818	NM_001310	cAMP responsive element binding protein like 2 (CREBL2), mRNA /cds=(277,639) /gb=NM_001310 /gi=21536277 /ug=Hs.13313 /len=3748	NM_001310	Hs.13313	NP_001301
mioc1580	NM_001354	aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III) (AKR1C2), mRNA /cds=(23,994) /gb=NM_001354 /gi=24497581 /ug=Hs.201967 /len=1290	NM_001354	Hs.201967	NP_001345

mioc3571	NM_001354	aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III) (AKR1C2), mRNA /cds=(23,994) /gb=NM_001354 /gi=24497581 /ug=Hs.201967 /len=1290	NM_001354	Hs.201967	NP_001345
seob4972	NM_001386	dihydropyrimidinase-like 2 (DPYSL2), mRNA /cds=(275,1993) /gb=NM_001386 /gi=19923654 /ug=Hs.173381 /len=4459	NM_001386	Hs.173381	NP_001377
fcr0781	NM_001398	enoyl Coenzyme A hydratase 1, peroxisomal (ECH1), mRNA /cds=(28,1014) /gb=NM_001398 /gi=4503446 /ug=Hs.196176 /len=1196	NM_001398	Hs.196176	NP_001389
fcrb2346	NM_001402	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
fcrc1115	NM_001402	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393

ncrb4025	NM_001439	exostoses (multiple)-like 2 (EXTL2), mRNA /cds=(288,1280) /gb=NM_001439 /gi=14149608 /ug=Hs.61152 /len=2833	NM_001439	Hs.61152	NP_001430
miob6338	NM_001449	four and a half LIM domains 1 (FHL1), mRNA /cds=(218,1060) /gb=NM_001449 /gi=21361121 /ug=Hs.239069 /len=2407	NM_001449	Hs.239069	NP_001440
mioc3648	BC028089	Similar to filamin A, alpha (actin binding protein 280), clone IMAGE:4156935, mRNA		Hs.195464	NP_001447
mioc4472	NM_001461	flavin containing monooxygenase 5 (FMO5), mRNA /cds=(82,1683) /gb=NM_001461 /gi=4503760 /ug=Hs.14286 /len=2326	NM_001461	Hs.14286	NP_001452
ncrc4940	NM_001463	frizzled-related protein (FRZB), mRNA /cds=(209,1186) /gb=NM_001463 /gi=4503788 /ug=Hs.153684 /len=1476	NM_001463	Hs.153684	NP_001454
mioa1165	NM_001514	general transcription factor IIB (GTF2B), mRNA /cds=(39,989) /gb=NM_001514 /gi=13435384 /ug=Hs.258561 /len=1268	NM_001514	Hs.258561	NP_001505
seoc2192	NM_001514	general transcription factor IIB (GTF2B), mRNA /cds=(39,989) /gb=NM_001514 /gi=13435384 /ug=Hs.258561 /len=1268	NM_001514	Hs.258561	NP_001505

ncrc6848	NM_001521	general transcription factor IIIC, polypeptide 2, beta 110kDa (GTF3C2), mRNA /cds=(40,2775) /gb=NM_001521 /gi=4504204 /ug=Hs.75782 /len=3594	NM_001521	Hs.75782	NP_001512
seob6492	NM_001540	heat shock 27kDa protein 1 (HSPB1), mRNA /cds=(108,725) /gb=NM_001540 /gi=4996892 /ug=Hs.76067 /len=865	NM_001540	Hs.76067	NP_001531
seob6268	AB007935	mRNA for KIAA0466 protein, partial cds	NM_001542	Hs.81234	NP_001533
seoa6175	NM_001545	immature colon carcinoma transcript 1 (ICT1), mRNA /cds=(3,623) /gb=NM_001545 /gi=4557656 /ug=Hs.9078 /len=888	NM_001545	Hs.9078	NP_001536
seob4945	NM_001560	interleukin 13 receptor, alpha 1 (IL13RA1), mRNA /cds=(44,1327) /gb=NM_001560 /gi=26787975 /ug=Hs.285115 /len=4006	NM_001560	Hs.285115	NP_001551
ncrc1871	NM_001568	eukaryotic translation initiation factor 3, subunit 6 48kDa (EIF3S6), mRNA /cds=(23,1360) /gb=NM_001568 /gi=4503520 /ug=Hs.106673 /len=1510	NM_001568	Hs.106673	NP_001559
ncrb3585	NM_001613	actin, alpha 2, smooth muscle, aorta (ACTA2), mRNA /cds=(48,1181) /gb=NM_001613 /gi=4501882 /ug=Hs.195851 /len=1330	NM_001613	Hs.195851	NP_001604

seob7906	NM_001642	amyloid beta (A4) precursor-like protein 2 (APLP2), mRNA /cds=(73,2364) /gb=NM_001642 /gi=4502146 /ug=Hs.279518 /len=3727	NM_001642	Hs.279518	NP_001633
miob6615	NM_001685	ATP synthase, H transporting, mitochondrial F0 complex, subunit F6 (ATP5J), nuclear gene encoding mitochondrial protein, mRNA /cds=(693,1019) /gb=NM_001685 /gi=19913429 /ug=Hs.73851 /len=1178	NM_001685	Hs.73851	NP_001676
fcr4166	BC016512	Similar to ATP synthase, H transporting, mitochondrial F1 complex, beta polypeptide, clone MGC:5231 IMAGE:2900336, mRNA, complete cds	NM_001686	Hs.406510	NP_001677
fcrc0591	NM_001686	ATP synthase, H transporting, mitochondrial F1 complex, beta polypeptide (ATP5B), nuclear gene encoding mitochondrial protein, mRNA /cds=(46,1665) /gb=NM_001686 /gi=4502294 /ug=Hs.406510 /len=1807	NM_001686	Hs.406510	NP_001677

mioc4534	NM_001686	ATP synthase, H transporting, mitochondrial F1 complex, beta polypeptide (ATP5B), nuclear gene encoding mitochondrial protein, mRNA /cds=(46,1665) /gb=NM_001686 /gi=4502294 /ug=Hs.406510 /len=1807	NM_001686	Hs.406510	NP_001677
seob6758	NM_001688	ATP synthase, H transporting, mitochondrial F0 complex, subunit b, isoform 1 (ATP5F1), mRNA /cds=(98,868) /gb=NM_001688 /gi=21361564 /ug=Hs.81634 /len=1230	NM_001688	Hs.81634	NP_001679
ncrc7127	NM_001688	ATP synthase, H transporting, mitochondrial F0 complex, subunit b, isoform 1 (ATP5F1), mRNA /cds=(98,868) /gb=NM_001688 /gi=21361564 /ug=Hs.81634 /len=1230	NM_001688	Hs.81634	NP_001679
fcrc6228	NM_001731	B-cell translocation gene 1, anti-proliferative (BTG1), mRNA /cds=(309,824) /gb=NM_001731 /gi=4502472 /ug=Hs.77054 /len=1783	NM_001731	Hs.77054	NP_001722
ncr3165	NM_001743	calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA /cds=(69,518) /gb=NM_001743 /gi=20428653 /ug=Hs.425808 /len=1128	NM_001743	Hs.425808	NP_001734

ncr0496	NM_001748	calpain 2, (m/II) large subunit (CAPN2), mRNA /cds=(143,2245) /gb=NM_001748 /gi=12408645 /ug=Hs.76288 /len=3419	NM_001748	Hs.76288	NP_001739
seoa9627	NM_001762	chaperonin containing TCP1, subunit 6A (zeta 1) (CCT6A), mRNA /cds=(56,1651) /gb=NM_001762 /gi=22095341 /ug=Hs.82916 /len=2562	NM_001762	Hs.82916	NP_001753
mioa4667	NM_001799	cyclin-dependent kinase 7 (MO15 Xenopus laevis, cdk-activating kinase) (CDK7), mRNA /cds=(89,1129) /gb=NM_001799 /gi=16950659 /ug=Hs.184298 /len=1427	NM_001799	Hs.184298	NP_001790
seoa2004	NM_001826	CDC28 protein kinase regulatory subunit 1B (CKS1B), mRNA /cds=(10,249) /gb=NM_001826 /gi=4502856 /ug=Hs.348669 /len=717	NM_001826	Hs.348669	NP_001817
fcrb7535	NM_001846	collagen, type IV, alpha 2 (COL4A2), mRNA /cds=(289,5427) /gb=NM_001846 /gi=17986276 /ug=Hs.75617 /len=6276	NM_001846	Hs.75617	NP_001837

seoc2218	NM_001863	cytochrome c oxidase subunit VIb (COX6B), nuclear gene encoding mitochondrial protein, mRNA /cds=(163,423) /gb=NM_001863 /gi=17999530 /ug=Hs.431668 /len=578	NM_001863	Hs.431668	NP_001854
seoa4708	NM_001865	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) (COX7A2), nuclear gene encoding mitochondrial protein, mRNA /cds=(76,327) /gb=NM_001865 /gi=18105035 /ug=Hs.70312 /len=470	NM_001865	Hs.70312	NP_001856
seob0876	NM_001865	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) (COX7A2), nuclear gene encoding mitochondrial protein, mRNA /cds=(76,327) /gb=NM_001865 /gi=18105035 /ug=Hs.70312 /len=470	NM_001865	Hs.70312	NP_001856
miod1714	NM_001892	casein kinase 1, alpha 1 (CSNK1A1), mRNA /cds=(140,1153) /gb=NM_001892 /gi=19923745 /ug=Hs.283738 /len=2080	NM_001892	Hs.283738	NP_001883
ncr0679	NM_001932	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA /cds=(337,2094) /gb=NM_001932 /gi=21536463 /ug=Hs.423809 /len=3012	NM_001932	Hs.423809	NP_001923

ncrc4219	BC033736	dermatopontin, clone MGC:45278 IMAGE:5176855, mRNA, complete cds		Hs.80552	NP_001928
mioa2290	NM_001937	dermatopontin (DPT), mRNA /cds=(7,612) /gb=NM_001937 /gi=4755134 /ug=Hs.80552 /len=717	NM_001937	Hs.80552	NP_001928
miod1108	NM_001949	E2F transcription factor 3 (E2F3) mRNA, complete cds /cds=(67,1464) /gb=NM_001949 /gi=12669913 /ug=Hs.1189 /len=4744	NM_001949	Hs.1189	NP_001940
seob6041	NM_001949	E2F transcription factor 3 (E2F3) mRNA, complete cds /cds=(67,1464) /gb=NM_001949 /gi=12669913 /ug=Hs.1189 /len=4744	NM_001949	Hs.1189	NP_001940
fcrb2979	NM_001961	eukaryotic translation elongation factor 2 (EEF2), mRNA /cds=(69,2645) /gb=NM_001961 /gi=25453476 /ug=Hs.75309 /len=3148	NM_001961	Hs.75309	NP_001952
fcrb8215	NM_001964	early growth response 1 (EGR1), mRNA /cds=(271,1902) /gb=NM_001964 /gi=4503492 /ug=Hs.326035 /len=3132	NM_001964	Hs.326035	NP_001955
seoa6155	NM_002027	farnesyltransferase, CAAX box, alpha (FNTA), mRNA /cds=(7,1146) /gb=NM_002027 /gi=4503770 /ug=Hs.356463 /len=1644	NM_002027	Hs.356463	NP_002018

fcrb1329	NM_002032	ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(92,664) /gb=NM_002032 /gi=4503794 /ug=Hs.418650 /len=801	NM_002032	Hs.418650	NP_002023
seob8333	NM_002032	ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(92,664) /gb=NM_002032 /gi=4503794 /ug=Hs.418650 /len=801	NM_002032	Hs.418650	NP_002023
fcr1772	NM_002046	glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA /cds=(76,1083) /gb=NM_002046 /gi=7669491 /ug=Hs.169476 /len=1283	NM_002046	Hs.169476	NP_002037
seob3131	NM_002056	glutamine-fructose-6-phosphate transaminase 1 (GFPT1), mRNA /cds=(123,2168) /gb=NM_002056 /gi=4503980 /ug=Hs.1674 /len=3082	NM_002056	Hs.1674	NP_002047
mioc1135	BC017742	clone IMAGE:4391536, mRNA	NM_002076	Hs.334534	NP_002067
fcr1404	NM_002087	granulin (GRN), mRNA	NM_002087	Hs.180577	NP_002078
seob9946	NM_002113	H factor (complement)-like 1 (HFL1), mRNA /cds=(78,1070) /gb=NM_002113 /gi=11321586 /ug=Hs.278568 /len=1266	NM_002113	Hs.278568	NP_002104
seob3370	NM_002124	major histocompatibility complex, class II, DR beta 1 (HLA-DRB1), mRNA /cds=(63,863) /gb=NM_002124 /gi=4504410 /ug=Hs.375570 /len=1182	NM_002124	Hs.375570	NP_002115

fcrb8915	NM_002129	high-mobility group box 2 (HMGB2), mRNA /cds=(191,820) /gb=NM_002129 /gi=14141173 /ug=Hs.80684 /len=1277	NM_002129	Hs.80684	NP_002120
ncrc5738	NM_002157	heat shock 10kDa protein 1 (chaperonin 10) (HSPE1), mRNA /cds=(42,350) /gb=NM_002157 /gi=4504522 /ug=Hs.1197 /len=538	NM_002157	Hs.1197	NP_002148
miob2087	NM_002157	heat shock 10kDa protein 1 (chaperonin 10) (HSPE1), mRNA /cds=(42,350) /gb=NM_002157 /gi=4504522 /ug=Hs.1197 /len=538	NM_002157	Hs.1197	NP_002148
seoa5366	NM_002160	tenascin C (hexabrachion) (TNC), mRNA	NM_002160	Hs.289114	NP_002151
mioa0485	NM_002213	integrin, beta 5 (ITGB5), mRNA /cds=(307,2706) /gb=NM_002213 /gi=20127445 /ug=Hs.149846 /len=3401	NM_002213	Hs.149846	NP_002204
seob4669	NM_002265	karyopherin (importin) beta 1 (KPNB1), mRNA /cds=(337,2967) /gb=NM_002265 /gi=24797084 /ug=Hs.180446 /len=4205	NM_002265	Hs.180446	NP_002256
hfcr1716	NM_002290	laminin, alpha 4 (LAMA4), mRNA /cds=(284,5734) /gb=NM_002290 /gi=9845494 /ug=Hs.78672 /len=6297	NM_002290	Hs.78672	NP_002281

ncrc5091	NM_002381	matrilin 3 (MATN3) precursor, mRNA /cds=(64,1524) /gb=NM_002381 /gi=13518040 /ug=Hs.278461 /len=2599	NM_002381	Hs.278461	NP_002372
miob8992	NM_002414	CD99 antigen (CD99), mRNA /cds=(184,741) /gb=NM_002414 /gi=20149541 /ug=Hs.433387 /len=1264	NM_002414	Hs.433387	NP_002405
fcr2861	NM_002415	macrophage migration inhibitory factor (glycosylation-inhibiting factor) (MIF), mRNA /cds=(98,445) /gb=NM_002415 /gi=4505184 /ug=Hs.407995 /len=561	NM_002415	Hs.407995	NP_002406
miob6562	NM_002416	chemokine (C-X-C motif) ligand 9 (CXCL9), mRNA /cds=(40,417) /gb=NM_002416 /gi=4505186 /ug=Hs.77367 /len=2545	NM_002416	Hs.77367	NP_002407
seob6696	NM_002431	menage a trois 1 (CAK assembly factor) (MNAT1), mRNA /cds=(35,964) /gb=NM_002431 /gi=4505224 /ug=Hs.433410 /len=1281	NM_002431	Hs.433410	NP_002422
ncr6878	NM_002439	mutS 3 (E. coli) (MSH3), mRNA /cds=(17,3403) /gb=NM_002439 /gi=4505248 /ug=Hs.42674 /len=4374	NM_002439	Hs.42674	NP_002430

seoc2447	NM_002473	myosin, heavy polypeptide 9, non-muscle (MYH9), mRNA /cds=(1,5883) /gb=NM_002473 /gi=22507396 /ug=Hs.146550 /len=7274	NM_002473	Hs.146550	NP_002464
fcrb8605	NM_002488	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa (NDUFA2), mRNA /cds=(57,356) /gb=NM_002488 /gi=4505354 /ug=Hs.163867 /len=590	NM_002488	Hs.163867	NP_002479
seoa8543	NM_002495	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), mRNA /cds=(9,536) /gb=NM_002495 /gi=4505368 /ug=Hs.10758 /len=668	NM_002495	Hs.10758	NP_002486
mioc1991	NM_002495	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), mRNA /cds=(9,536) /gb=NM_002495 /gi=4505368 /ug=Hs.10758 /len=668	NM_002495	Hs.10758	NP_002486
fcrb4294	NM_002496	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase) (NDUFS8), mRNA /cds=(93,725) /gb=NM_002496 /gi=4505370 /ug=Hs.90443 /len=779	NM_002496	Hs.90443	NP_002487

seoa5578	NM_002520	nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), mRNA /cds=(100,984) /gb=NM_002520 /gi=20070168 /ug=Hs.355719 /len=1347	NM_002520	Hs.355719	NP_002511
ncrc9039	NM_002520	nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), mRNA /cds=(100,984) /gb=NM_002520 /gi=20070168 /ug=Hs.355719 /len=1347	NM_002520	Hs.355719	NP_002511
fcrb6301	NM_002520	nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1), mRNA /cds=(100,984) /gb=NM_002520 /gi=20070168 /ug=Hs.355719 /len=1347	NM_002520	Hs.355719	NP_002511
miod4332	BC039158	Similar to pyruvate dehydrogenase kinase, isoenzyme 1, clone MGC:24867 IMAGE:4778360, mRNA, complete cds	NM_002610	Hs.61712	NP_002601
ncrc1633	NM_002687	pinin, desmosome associated protein (PNN), mRNA /cds=(31,2262) /gb=NM_002687 /gi=4505922 /ug=Hs.44499 /len=2617	NM_002687	Hs.44499	NP_002678
seoa8432	NM_002696	polymerase (RNA) II (DNA directed) polypeptide G (POLR2G), mRNA /cds=(107,625) /gb=NM_002696 /gi=4505946 /ug=Hs.14839 /len=828	NM_002696	Hs.14839	NP_002687

ncr3705	NM_002764	phosphoribosyl pyrophosphate synthetase 1 (PRPS1), mRNA /cds=(101,1057) /gb=NM_002764 /gi=19923737 /ug=Hs.56 /len=2078	NM_002764	Hs.56	NP_002755
mioa1513	NM_002778	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), mRNA /cds=(39,1613) /gb=NM_002778 /gi=11386146 /ug=Hs.406455 /len=2767	NM_002778	Hs.406455	NP_002769
ncrc6875	NM_002793	proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1), mRNA /cds=(48,773) /gb=NM_002793 /gi=22538462 /ug=Hs.407981 /len=872	NM_002793	Hs.407981	NP_002784
seoc1203	NM_002794	proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA /cds=(111,716) /gb=NM_002794 /gi=22538463 /ug=Hs.432607 /len=850	NM_002794	Hs.432607	NP_002785
seob2077	NM_002795	proteasome (prosome, macropain) subunit, beta type, 3 (PSMB3), mRNA /cds=(79,696) /gb=NM_002795 /gi=22538464 /ug=Hs.82793 /len=784	NM_002795	Hs.82793	NP_002786

ncrc0427	NM_002805	proteasome (prosome, macropain) 26S subunit, ATPase, 5 (PSMC5), mRNA /cds=(42,1262) /gb=NM_002805 /gi=24497434 /ug=Hs.79387 /len=1332	NM_002805	Hs.79387	NP_002796
ncrc3030	NM_002806	proteasome (prosome, macropain) 26S subunit, ATPase, 6 (PSMC6), mRNA /cds=(21,1190) /gb=NM_002806 /gi=24430159 /ug=Hs.79357 /len=1590	NM_002806	Hs.79357	NP_002797
fcrb3702	NM_002823	prothymosin, alpha (gene sequence 28) (PTMA), mRNA /cds=(182,514) /gb=NM_002823 /gi=21359859 /ug=Hs.250655 /len=1233	NM_002823	Hs.250655	NP_002814
mioc7225	NM_002851	protein tyrosine phosphatase, receptor-type, Z polypeptide 1 (PTPRZ1), mRNA /cds=(148,7092) /gb=NM_002851 /gi=4506328 /ug=Hs.78867 /len=7941	NM_002851	Hs.78867	NP_002842
ncr0223	NM_002865	RAB2, member RAS oncogene family (RAB2), mRNA /cds=(209,847) /gb=NM_002865 /gi=4506364 /ug=Hs.78305 /len=1148	NM_002865	Hs.78305	NP_002856
ncrc4773	NM_002901	reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA /cds=(53,1048) /gb=NM_002901 /gi=4506454 /ug=Hs.167791 /len=2104	NM_002901	Hs.167791	NP_002892

mioa1632	NM_002947	replication protein A3, 14kDa (RPA3), mRNA /cds=(1182,1547) /gb=NM_002947 /gi=19923751 /ug=Hs.1608 /len=1622	NM_002947	Hs.1608	NP_002938
fcr7659	NM_002952	ribosomal protein S2 (RPS2), mRNA /cds=(12,893) /gb=NM_002952 /gi=15055538 /ug=Hs.356360 /len=978	NM_002952	Hs.356360	NP_002943
mioc6212	NM_002958	RYK receptor-like tyrosine kinase (RYK), mRNA /cds=(104,1918) /gb=NM_002958 /gi=11863158 /ug=Hs.79350 /len=3031	NM_002958	Hs.79350	NP_002949
ncrc9944	NM_002970	spermidine/spermine N1-acetyltransferase (SAT), mRNA /cds=(166,681) /gb=NM_002970 /gi=4506788 /ug=Hs.28491 /len=1060	NM_002970	Hs.28491	NP_002961
hfcr4645	NM_003012	secreted frizzled-related protein 1 (SFRP1), mRNA /cds=(303,1244) /gb=NM_003012 /gi=8400731 /ug=Hs.7306 /len=4469	NM_003012	Hs.7306	NP_003003
seoa1065	NM_003017	splicing factor, arginine/serine-rich 3 (SFRS3), mRNA /cds=(106,600) /gb=NM_003017 /gi=24025684 /ug=Hs.388623 /len=1403	NM_003017	Hs.388623	NP_003008
mioa4771	AF114488	intersectin short isoform (ITSN) mRNA, complete cds	NM_003024	Hs.66392	NP_003015

fcrc2089	NM_003040	solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1) (SLC4A2), mRNA /cds=(175,3900) /gb=NM_003040 /gi=21361550 /ug=Hs.79410 /len=4078	NM_003040	Hs.79410	NP_003031
seob4160	NM_003068	snail 2 (Drosophila) (SNAI2), mRNA /cds=(165,971) /gb=NM_003068 /gi=24497625 /ug=Hs.93005 /len=2101	NM_003068	Hs.93005	NP_003059
seoa8486	NM_003096	small nuclear ribonucleoprotein polypeptide G (SNRPG), mRNA /cds=(89,319) /gb=NM_003096 /gi=21359839 /ug=Hs.77496 /len=606	NM_003096	Hs.77496	NP_003087
seob5081	NM_003133	signal recognition particle 9kDa (SRP9), mRNA /cds=(107,367) /gb=NM_003133 /gi=4507216 /ug=Hs.75975 /len=1466	NM_003133	Hs.75975	NP_003124
seoa3852	NM_003144	signal sequence receptor, alpha (translocon-associated protein alpha) (SSR1), mRNA /cds=(112,972) /gb=NM_003144 /gi=6552340 /ug=Hs.250773 /len=3285	NM_003144	Hs.250773	NP_003135

seoa5258	NM_003203	chromosome 2 open reading frame 3 (C2orf3), mRNA /cds=(69,2414) /gb=NM_003203 /gi=7108364 /ug=Hs.184175 /len=2661	NM_003203	Hs.184175	NP_003194
ncrc1631	NM_003217	testis enhanced gene transcript (TEGT), mRNA /cds=(41,754) /gb=NM_003217 /gi=4507432 /ug=Hs.74637 /len=2600	NM_003217	Hs.74637	NP_003208
miob3329	NM_003248	thrombospondin 4 (THBS4), mRNA /cds=(28,2913) /gb=NM_003248 /gi=4507488 /ug=Hs.75774 /len=3074	NM_003248	Hs.75774	NP_003239
fcr4503	NM_003258	thymidine kinase 1, soluble (TK1), mRNA /cds=(58,762) /gb=NM_003258 /gi=4507518 /ug=Hs.105097 /len=1421	NM_003258	Hs.105097	NP_003249
ncrc5162	NM_003270	transmembrane 4 superfamily member 6 (TM4SF6), mRNA /cds=(104,841) /gb=NM_003270 /gi=21265115 /ug=Hs.121068 /len=2069	NM_003270	Hs.121068	NP_003261
fcrc6389	NM_003279	troponin C2, fast (TNNC2), mRNA /cds=(65,547) /gb=NM_003279 /gi=4507616 /ug=Hs.182421 /len=677	NM_003279	Hs.182421	NP_003270
hfcr5905	NM_003286	topoisomerase (DNA) I (TOP1), mRNA /cds=(247,2544) /gb=NM_003286 /gi=19913404 /ug=Hs.317 /len=3734	NM_003286	Hs.317	NP_003277

seoa0044	NM_003295	tumor protein, translationally-controlled 1 (TPT1), mRNA /cds=(95,613) /gb=NM_003295 /gi=4507668 /ug=Hs.401448 /len=830	NM_003295	Hs.401448	NP_003286
seob7500	NM_003295	tumor protein, translationally-controlled 1 (TPT1), mRNA /cds=(95,613) /gb=NM_003295 /gi=4507668 /ug=Hs.401448 /len=830	NM_003295	Hs.401448	NP_003286
fcrb3795	NM_003302	thyroid hormone receptor interactor 6 (TRIP6), mRNA /cds=(76,1506) /gb=NM_003302 /gi=23308730 /ug=Hs.380230 /len=1695	NM_003302	Hs.380230	NP_003293
seob7022	NM_003350	ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA /cds=(22,459) /gb=NM_003350 /gi=12025664 /ug=Hs.79300 /len=1535	NM_003350	Hs.79300	NP_003341
mioc0206	NM_003350	ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA /cds=(22,459) /gb=NM_003350 /gi=12025664 /ug=Hs.79300 /len=1535	NM_003350	Hs.79300	NP_003341
miod3079	NM_003377	vascular endothelial growth factor B (VEGFB), mRNA /cds=(50,673) /gb=NM_003377 /gi=20070172 /ug=Hs.78781 /len=1181	NM_003377	Hs.78781	NP_003368

seoa0396	NM_003383	very low density lipoprotein receptor (VLDLR), mRNA /cds=(86,2707) /gb=NM_003383 /gi=4507900 /ug=Hs.73729 /len=3355	NM_003383	Hs.73729	NP_003374
ncr9337	NM_003407	zinc finger protein 36, C3H type, (mouse) (ZFP36), mRNA /cds=(60,1040) /gb=NM_003407 /gi=4507960 /ug=Hs.343586 /len=1746	NM_003407	Hs.343586	NP_003398
fcrb9843	NM_003407	zinc finger protein 36, C3H type, (mouse) (ZFP36), mRNA /cds=(60,1040) /gb=NM_003407 /gi=4507960 /ug=Hs.343586 /len=1746	NM_003407	Hs.343586	NP_003398
seoa1749	NM_003418	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein) (ZNF9), mRNA /cds=(103,636) /gb=NM_003418 /gi=4827070 /ug=Hs.2110 /len=1500	NM_003418	Hs.2110	NP_003409
fcrb1311	NM_003442	zinc finger protein 143 (clone pHZ-1) (ZNF143), mRNA /cds=(155,2035) /gb=NM_003442 /gi=24475652 /ug=Hs.374355 /len=2641	NM_003442	Hs.374355	NP_003433
ncrc6871	NM_003455	zinc finger protein 202 (ZNF202), mRNA /cds=(11,1957) /gb=NM_003455 /gi=10835040 /ug=Hs.9443 /len=4053	NM_003455	Hs.9443	NP_003446

ncr8337	NM_003470	ubiquitin specific protease 7 (herpes virus-associated) (USP7), mRNA /cds=(200,3508) /gb=NM_003470 /gi=4507856 /ug=Hs.78683 /len=4022	NM_003470	Hs.78683	NP_003461
fcrc5138	NM_003504	CDC45 cell division cycle 45-like (S. cerevisiae) (CDC45L), mRNA /cds=(71,1771) /gb=NM_003504 /gi=16357475 /ug=Hs.114311 /len=1932	NM_003504	Hs.114311	NP_003495
ncrc5327	NM_003563	speckle-type POZ protein (SPOP), mRNA /cds=(158,1282) /gb=NM_003563 /gi=4507182 /ug=Hs.129951 /len=1642	NM_003563	Hs.129951	NP_003554
ncrc4302	NM_003576	serine/threonine kinase 24 (STE20 yeast) (STK24), mRNA /cds=(146,1477) /gb=NM_003576 /gi=20070157 /ug=Hs.168913 /len=2505	NM_003576	Hs.168913	NP_003567
mioa7544	NM_003580	neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), mRNA /cds=(13,2766) /gb=NM_003580 /gi=4505464 /ug=Hs.78687 /len=3380	NM_003580	Hs.78687	NP_003571
mioa5540	NM_003596	tyrosylprotein sulfotransferase 1 (TPST1), mRNA /cds=(328,1440) /gb=NM_003596 /gi=21361092 /ug=Hs.421194 /len=2033	NM_003596	Hs.421194	NP_003587

seoa2620	NM_003615	solute carrier family 4, sodium bicarbonate cotransporter, member 7 (SLC4A7), mRNA /cds=(72,3716) /gb=NM_003615 /gi=19923175 /ug=Hs.132904 /len=7785	NM_003615	Hs.132904	NP_003606
mioa1149	NM_003642	histone acetyltransferase 1 (HAT1), mRNA /cds=(37,1296) /gb=NM_003642 /gi=4504340 /ug=Hs.13340 /len=1568	NM_003642	Hs.13340	NP_003633
miod4867	NM_003663	CGG triplet repeat binding protein 1 (CGGBP1), mRNA /cds=(357,863) /gb=NM_003663 /gi=21361098 /ug=Hs.86041 /len=4279	NM_003663	Hs.86041	NP_003654
seoa8638	NM_003670	basic helix-loop-helix domain containing, class B, 2 (BHLHB2), mRNA /cds=(197,1435) /gb=NM_003670 /gi=4503298 /ug=Hs.171825 /len=2922	NM_003670	Hs.171825	NP_003661
mioa3514	NM_003690	protein kinase, interferon-inducible double stranded RNA dependent activator (PRKRA), mRNA /cds=(108,1049) /gb=NM_003690 /gi=20149526 /ug=Hs.18571 /len=1843	NM_003690	Hs.18571	NP_003681

mioc2681	NM_003739	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II) (AKR1C3), mRNA /cds=(70,1041) /gb=NM_003739 /gi=24497582 /ug=Hs.78183 /len=1224	NM_003739	Hs.78183	NP_003730
miob8663	BC031264	clone MGC:39731 IMAGE:5275603, mRNA, complete cds		Hs.6651	NP_003753
seoa3989	NM_003798	catenin (cadherin-associated protein), alpha-like 1 (CTNNAL1), mRNA /cds=(44,2248) /gb=NM_003798 /gi=4503128 /ug=Hs.58488 /len=2446	NM_003798	Hs.58488	NP_003789
seoa6223	NM_003800	RNA guanylyltransferase and 5'-phosphatase (RNGTT), mRNA /cds=(289,2082) /gb=NM_003800 /gi=4506562 /ug=Hs.27345 /len=4546	NM_003800	Hs.27345	NP_003791
seoa0070	NM_003850	succinate-CoA ligase, ADP-forming, beta subunit (SUCLA2), mRNA /cds=(58,1449) /gb=NM_003850 /gi=11321582 /ug=Hs.182217 /len=2178	NM_003850	Hs.182217	NP_003841
ncr1235	NM_003859	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit (DPM1), mRNA /cds=(1,783) /gb=NM_003859 /gi=4503362 /ug=Hs.5085 /len=1047	NM_003859	Hs.5085	NP_003850

ncrc0829	NM_003870	IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA /cds=(468,5441) /gb=NM_003870 /gi=4506786 /ug=Hs.1742 /len=7573	NM_003870	Hs.1742	NP_003861
fcrb2160	NM_003878	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase) (GGH), mRNA /cds=(60,1016) /gb=NM_003878 /gi=4503986 /ug=Hs.78619 /len=1280	NM_003878	Hs.78619	NP_003869
ncrc8903	NM_003879	CASP8 and FADD-like apoptosis regulator (CFLAR), mRNA /cds=(482,1924) /gb=NM_003879 /gi=21361768 /ug=Hs.195175 /len=2243	NM_003879	Hs.195175	NP_003870
hfcr0045	NM_003932	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein) (ST13), mRNA /cds=(144,1253) /gb=NM_003932 /gi=21237722 /ug=Hs.119222 /len=3214	NM_003932	Hs.119222	NP_003923
ncr0721	NM_003945	ATPase, H transporting, lysosomal 9kDa, V0 subunit e (ATP6V0E), mRNA /cds=(76,321) /gb=NM_003945 /gi=19913435 /ug=Hs.415629 /len=849	NM_003945	Hs.415629	NP_003936

seoa8960	NM_003945	ATPase, H transporting, lysosomal 9kDa, V0 subunit e (ATP6V0E), mRNA /cds=(76,321) /gb=NM_003945 /gi=19913435 /ug=Hs.415629 /len=849	NM_003945	Hs.415629	NP_003936
mioa9891	NM_003972	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (Mot1 S. cerevisiae) (BTAF1), mRNA /cds=(118,5667) /gb=NM_003972 /gi=27477069 /ug=Hs.180930 /len=6345	NM_003972	Hs.180930	NP_003963
ncr0733	NM_004048	beta-2-microglobulin (B2M), mRNA /cds=(14,373) /gb=NM_004048 /gi=4757825 /ug=Hs.48516 /len=925	NM_004048	Hs.48516	NP_004039
ncrc1687	NM_004064	cyclin-dependent kinase inhibitor 1B (p27, Kip1) (CDKN1B), mRNA /cds=(466,1062) /gb=NM_004064 /gi=17978497 /ug=Hs.238990 /len=2422	NM_004064	Hs.238990	NP_004055
miob8639	NM_004064	cyclin-dependent kinase inhibitor 1B (p27, Kip1) (CDKN1B), mRNA /cds=(466,1062) /gb=NM_004064 /gi=17978497 /ug=Hs.238990 /len=2422	NM_004064	Hs.238990	NP_004055

ncrc0672	NM_004065	cerebellar degeneration-related protein 1, 34kDa (CDR1), mRNA /cds=(61,732) /gb=NM_004065 /gi=4757963 /ug=Hs.278427 /len=1165	NM_004065	Hs.278427	NP_004056
ncrc2693	NM_004065	cerebellar degeneration-related protein 1, 34kDa (CDR1), mRNA /cds=(61,732) /gb=NM_004065 /gi=4757963 /ug=Hs.278427 /len=1165	NM_004065	Hs.278427	NP_004056
ncrb8237	BC018148	delta sleep inducing peptide, immunoreactor, clone MGC:9719 IMAGE:3851403, mRNA, complete cds	NM_004089	Hs.75450	NP_004080
hfcr6515	NM_004102	fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor) (FABP3), mRNA /cds=(46,447) /gb=NM_004102 /gi=10938020 /ug=Hs.49881 /len=679	NM_004102	Hs.49881	NP_004093
miod3591	NM_004117	FK506 binding protein 5 (FKBP5), mRNA /cds=(154,1527) /gb=NM_004117 /gi=17149847 /ug=Hs.7557 /len=3781	NM_004117	Hs.7557	NP_004108
mioc0090	NM_004117	FK506 binding protein 5 (FKBP5), mRNA /cds=(154,1527) /gb=NM_004117 /gi=17149847 /ug=Hs.7557 /len=3781	NM_004117	Hs.7557	NP_004108

seoa6364	NM_004124	glia maturation factor, beta (GMFB), mRNA /cds=(98,526) /gb=NM_004124 /gi=4758441 /ug=Hs.151413 /len=4131	NM_004124	Hs.151413	NP_004115
seob6415	NM_004134	heat shock 70kDa protein 9B (mortalin-2) (HSPA9B), nuclear gene encoding mitochondrial protein, mRNA /cds=(94,2133) /gb=NM_004134 /gi=24234687 /ug=Hs.3069 /len=2852	NM_004134	Hs.3069	NP_004125
fcrb5259	NM_004147	developmentally regulated GTP binding protein 1 (DRG1), mRNA /cds=(66,1169) /gb=NM_004147 /gi=4758795 /ug=Hs.115242 /len=1383	NM_004147	Hs.115242	NP_004138
seob6601	AK055927	cDNA FLJ31365 fis, clone NB9N41000135, highly similar to RAS-RELATED PROTEIN RAB-1A	NM_004161	Hs.227327	NP_004152
miod4518	NM_004215	estrogen receptor binding site associated, antigen, 9 (EBAG9), mRNA /cds=(362,1003) /gb=NM_004215 /gi=14577926 /ug=Hs.9222 /len=1182	NM_004215	Hs.9222	NP_004206
ncrc5553	NM_004251	RAB9A, member RAS oncogene family (RAB9A), mRNA /cds=(192,797) /gb=NM_004251 /gi=20070189 /ug=Hs.330994 /len=1106	NM_004251	Hs.330994	NP_004242

mioc1416	NM_004268	cofactor required for Sp1 transcriptional activation, subunit 6, 77kDa (CRSP6), mRNA /cds=(196,2151) /gb=NM_004268 /gi=10835074 /ug=Hs.22630 /len=2546	NM_004268	Hs.22630	NP_004259
mioa3361	NM_004309	Rho GDP dissociation inhibitor (GDI) alpha (ARHGDIA), mRNA /cds=(102,716) /gb=NM_004309 /gi=20149550 /ug=Hs.159161 /len=1921	NM_004309	Hs.159161	NP_004300
seob5454	NM_004311	ADP-ribosylation factor-like 3 (ARL3), mRNA /cds=(16,564) /gb=NM_004311 /gi=4757773 /ug=Hs.182215 /len=900	NM_004311	Hs.182215	NP_004302
seob5021	NM_004313	arrestin, beta 2 (ARRB2), mRNA /cds=(234,1463) /gb=NM_004313 /gi=21626464 /ug=Hs.18142 /len=1941	NM_004313	Hs.18142	NP_004304
mioa0466	NM_004323	BCL2-associated athanogene (BAG1), mRNA /cds=(66,1103) /gb=NM_004323 /gi=7549801 /ug=Hs.41714 /len=1311	NM_004323	Hs.41714	NP_004314
fcrc1957	NM_004338	chromosome 18 open reading frame 1 (C18orf1), mRNA /cds=(243,989) /gb=NM_004338 /gi=4757883 /ug=Hs.153498 /len=8093	NM_004338	Hs.153498	NP_004329

hfcr2930	NM_004356	CD81 antigen (target of antiproliferative antibody 1) (CD81), mRNA /cds=(41,751) /gb=NM_004356 /gi=21237760 /ug=Hs.54457 /len=1332	NM_004356	Hs.54457	NP_004347
seoa9874	NM_004373	cytochrome c oxidase subunit VIa polypeptide 1 (COX6A1), nuclear gene encoding mitochondrial protein, mRNA /cds=(27,356) /gb=NM_004373 /gi=17999527 /ug=Hs.180714 /len=548	NM_004373	Hs.180714	NP_004364
mioc2039	NM_004375	COX11 cytochrome c oxidase assembly protein (yeast) (COX11), nuclear gene encoding mitochondrial protein, mRNA /cds=(48,878) /gb=NM_004375 /gi=17921983 /ug=Hs.241515 /len=2717	NM_004375	Hs.241515	NP_004366
mioc3220	NM_004385	chondroitin sulfate proteoglycan 2 (versican) (CSPG2), mRNA /cds=(267,10457) /gb=NM_004385 /gi=21361115 /ug=Hs.81800 /len=11185	NM_004385	Hs.81800	NP_004376
ncr0265	NM_004414	Down syndrome critical region gene 1 (DSCR1), mRNA /cds=(66,659) /gb=NM_004414 /gi=20149552 /ug=Hs.184222 /len=2289	NM_004414	Hs.184222	NP_004405

ncrc0439	NM_004508	isopentenyl-diphosphate delta isomerase (IDI1), mRNA /cds=(51,737) /gb=NM_004508 /gi=4758583 /ug=Hs.76038 /len=1807	NM_004508	Hs.76038	NP_004499
mioa9821	NM_004566	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3), mRNA /cds=(115,1677) /gb=NM_004566 /gi=4758899 /ug=Hs.195471 /len=4322	NM_004566	Hs.195471	NP_004557
miob2656	NM_004568	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 (SERPINB6), mRNA /cds=(75,1205) /gb=NM_004568 /gi=28077084 /ug=Hs.41072 /len=1361	NM_004568	Hs.41072	NP_004559
ncr0018	NM_004568	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6 (SERPINB6), mRNA /cds=(75,1205) /gb=NM_004568 /gi=28077084 /ug=Hs.41072 /len=1361	NM_004568	Hs.41072	NP_004559
seoa9712	NM_004582	Rab geranylgeranyltransferase, beta subunit (RABGGTB), mRNA /cds=(72,1067) /gb=NM_004582 /gi=21359853 /ug=Hs.78948 /len=1526	NM_004582	Hs.78948	NP_004573

hfcr2250	NM_004629	Fanconi anemia, complementation group G (FANCG), mRNA /cds=(493,2361) /gb=NM_004629 /gi=4759335 /ug=Hs.8047 /len=2649	NM_004629	Hs.8047	NP_004620
mioa8028	AL137295	mRNA; cDNA DKFZp434M2216 (from clone DKFZp434M2216)	NM_004641	Hs.199429	NP_004632
miob3695	NM_004674	ash2 (absent, small, or homeotic)-like (Drosophila) (ASH2L), mRNA /cds=(5,1891) /gb=NM_004674 /gi=4757789 /ug=Hs.6856 /len=2381	NM_004674	Hs.6856	NP_004665
mioa6102	NM_004713	serologically defined colon cancer antigen 1 (SDCCAG1), mRNA /cds=(183,1271) /gb=NM_004713 /gi=4759077 /ug=Hs.388584 /len=2078	NM_004713	Hs.388584	NP_004704
seoa0729	NM_004718	cytochrome c oxidase subunit VIIa polypeptide 2 like (COX7A2L), nuclear gene encoding mitochondrial protein, mRNA /cds=(56,400) /gb=NM_004718 /gi=18105036 /ug=Hs.30888 /len=1145	NM_004718	Hs.30888	NP_004709
mioc3593	NM_004728	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21 (DDX21), mRNA /cds=(266,2413) /gb=NM_004728 /gi=13787208 /ug=Hs.169531 /len=3319	NM_004728	Hs.169531	NP_004719

fcrb2849	NM_004730	eukaryotic translation termination factor 1 (ETF1), mRNA /cds=(136,1449) /gb=NM_004730 /gi=4759033 /ug=Hs.77324 /len=3653	NM_004730	Hs.77324	NP_004721
seob9092	NM_004779	CCR4-NOT transcription complex, subunit 8 (CNOT8), mRNA /cds=(245,1123) /gb=NM_004779 /gi=24496777 /ug=Hs.26703 /len=2489	NM_004779	Hs.26703	NP_004770
seob3139	NM_004832	glutathione-S-transferase like; glutathione transferase omega (GSTTLp28), mRNA /cds=(10,735) /gb=NM_004832 /gi=4758483 /ug=Hs.11465 /len=793	NM_004832	Hs.11465	NP_004823
seoa1083	NM_004836	eukaryotic translation initiation factor 2-alpha kinase 3 (EIF2AK3), mRNA /cds=(303,3650) /gb=NM_004836 /gi=21361154 /ug=Hs.102506 /len=4662	NM_004836	Hs.102506	NP_004827
seob6856	NM_004850	Rho-associated, coiled-coil containing protein kinase 2 (ROCK2), mRNA /cds=(455,4621) /gb=NM_004850 /gi=6633807 /ug=Hs.58617 /len=6409	NM_004850	Hs.58617	NP_004841
fcrb1787	NM_004859	clathrin, heavy polypeptide (Hc) (CLTC), mRNA /cds=(173,5200) /gb=NM_004859 /gi=4758011 /ug=Hs.178710 /len=6111	NM_004859	Hs.178710	NP_004850

seob3904	NM_004862	LPS-induced TNF-alpha factor (PIG7), mRNA /cds=(234,920) /gb=NM_004862 /gi=4758913 /ug=Hs.76507 /len=1773	NM_004862	Hs.76507	NP_004853
seoa4717	NM_004872	chromosome 1 open reading frame 8 (C1orf8), mRNA /cds=(251,1222) /gb=NM_004872 /gi=27545320 /ug=Hs.416495 /len=1709	NM_004872	Hs.416495	NP_004863
seob3189	NM_004894	chromosome 14 open reading frame 2 (C14orf2), mRNA /cds=(61,237) /gb=NM_004894 /gi=4758939 /ug=Hs.109052 /len=627	NM_004894	Hs.109052	NP_004885
seob3226	NM_004896	vacuolar protein sorting 26 (yeast) (VPS26), mRNA /cds=(80,1063) /gb=NM_004896 /gi=17978518 /ug=Hs.67052 /len=2652	NM_004896	Hs.67052	NP_004887
seob6015	NM_004902	RNA-binding region (RNP1, RRM) containing 2 (RNPC2), mRNA /cds=(150,1724) /gb=NM_004902 /gi=4757925 /ug=Hs.145696 /len=2595	NM_004902	Hs.145696	NP_004893
mioc3867	NM_004902	RNA-binding region (RNP1, RRM) containing 2 (RNPC2), mRNA /cds=(150,1724) /gb=NM_004902 /gi=4757925 /ug=Hs.145696 /len=2595	NM_004902	Hs.145696	NP_004893

mioc4190	NM_004912	cerebral cavernous malformations 1 (CCM1), mRNA /cds=(26,1615) /gb=NM_004912 /gi=4758657 /ug=Hs.93810 /len=2004	NM_004912	Hs.93810	NP_004903
fcrb6939	NM_004926	zinc finger protein 36, C3H type-like 1 (ZFP36L1), mRNA /cds=(131,1147) /gb=NM_004926 /gi=15812179 /ug=Hs.85155 /len=3022	NM_004926	Hs.85155	NP_004917
ncr1122	NM_004958	FK506 binding protein 12-rapamycin associated protein 1 (FRAP1), mRNA /cds=(80,7729) /gb=NM_004958 /gi=19924298 /ug=Hs.338207 /len=8680	NM_004958	Hs.338207	NP_004949
ncr0491	NM_004967	integrin-binding sialoprotein (bone sialoprotein, bone sialoprotein II) (IBSP), mRNA /cds=(143,1096) /gb=NM_004967 /gi=13259536 /ug=Hs.49215 /len=1108	NM_004967	Hs.49215	NP_004958
mioa5511	NM_004992	methyl CpG binding protein 2 (Rett syndrome) (MECP2), mRNA /cds=(168,1628) /gb=NM_004992 /gi=7710148 /ug=Hs.3239 /len=10182	NM_004992	Hs.3239	NP_004983
seob4363	AJ401610	mRNA for 3'5' cyclic nucleotide phosphodiesterase (PDE1A5 gene)		Hs.41717	NP_005010

miob6688	NM_005025	serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1 (SERPINI1), mRNA /cds=(82,1314) /gb=NM_005025 /gi=4826903 /ug=Hs.78589 /len=1559	NM_005025	Hs.78589	NP_005016
fcrc5233	NM_005047	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5 (PSMD5), mRNA /cds=(20,1534) /gb=NM_005047 /gi=25777613 /ug=Hs.193725 /len=3411	NM_005047	Hs.193725	NP_005038
ncr9125	NM_005077	transducin-like enhancer of split 1 (E(sp1) Drosophila) (TLE1), mRNA /cds=(451,2763) /gb=NM_005077 /gi=21541823 /ug=Hs.28935 /len=3292	NM_005077	Hs.28935	NP_005068
ncr2391	NM_005086	sarcospan (Kras oncogene-associated gene) (SSPN), mRNA /cds=(85,816) /gb=NM_005086 /gi=16933560 /ug=Hs.183428 /len=2707	NM_005086	Hs.183428	NP_005077
ncr9881	BC045613	nuclear receptor subfamily 1, group D, member 2, clone MGC:33914 IMAGE:5274113, mRNA, complete cds		Hs.37288	NP_005117

mioa0707	NM_005175	ATP synthase, H transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1 (ATP5G1), mRNA /cds=(120,530) /gb=NM_005175 /gi=4885080 /ug=Hs.80986 /len=631	NM_005175	Hs.80986	NP_005166
ncrc4994	NM_005175	ATP synthase, H transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1 (ATP5G1), mRNA /cds=(120,530) /gb=NM_005175 /gi=4885080 /ug=Hs.80986 /len=631	NM_005175	Hs.80986	NP_005166
seoa4436	NM_005194	CCAAT/enhancer binding protein (C/EBP), beta (CEBPB), mRNA	NM_005194	Hs.99029	NP_005185
mioa8857	NM_005245	FAT tumor suppressor 1 (Drosophila) (FAT), mRNA /cds=(187,13959) /gb=NM_005245 /gi=4885228 /ug=Hs.166994 /len=14756	NM_005245	Hs.166994	NP_005236
ncr4009	NM_005313	glucose regulated protein, 58kDa (GRP58), mRNA /cds=(90,1607) /gb=NM_005313 /gi=21361656 /ug=Hs.13751 /len=2074	NM_005313	Hs.13751	NP_005304
fcr3181	NM_005318	H1 histone family, member 0 (H1F0), mRNA	NM_005318	Hs.226117	NP_005309

miob2375	NM_005324	H3 histone, family 3B (H3.3B) (H3F3B), mRNA /cds=(118,528) /gb=NM_005324 /gi=21264598 /ug=Hs.180877 /len=1662	NM_005324	Hs.180877	NP_005315
fcrb2926	NM_005324	H3 histone, family 3B (H3.3B) (H3F3B), mRNA /cds=(118,528) /gb=NM_005324 /gi=21264598 /ug=Hs.180877 /len=1662	NM_005324	Hs.180877	NP_005315
ncr6137	NM_005340	histidine triad nucleotide binding protein 1 (HINT1), mRNA /cds=(108,488) /gb=NM_005340 /gi=4885412 /ug=Hs.256697 /len=641	NM_005340	Hs.256697	NP_005331
seoa5429	NM_005347	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) (HSPA5), mRNA /cds=(205,2169) /gb=NM_005347 /gi=21361242 /ug=Hs.75410 /len=3925	NM_005347	Hs.75410	NP_005338
seob1191	NM_005347	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) (HSPA5), mRNA /cds=(205,2169) /gb=NM_005347 /gi=21361242 /ug=Hs.75410 /len=3925	NM_005347	Hs.75410	NP_005338

fcrb4788	NM_005347	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) (HSPA5), mRNA /cds=(205,2169) /gb=NM_005347 /gi=21361242 /ug=Hs.75410 /len=3925	NM_005347	Hs.75410	NP_005338
ncrc9729	NM_005360	v-maf musculoaponeurotic fibrosarcoma oncogene (avian) (MAF), mRNA /cds=(808,2019) /gb=NM_005360 /gi=5453735 /ug=Hs.30250 /len=2145	NM_005360	Hs.30250	NP_005351
mioa0311	NM_005398	protein phosphatase 1, regulatory (inhibitor) subunit 3C (PPP1R3C), mRNA /cds=(58,1011) /gb=NM_005398 /gi=21314622 /ug=Hs.303090 /len=2524	NM_005398	Hs.303090	NP_005389
miod2007	NM_005398	protein phosphatase 1, regulatory (inhibitor) subunit 3C (PPP1R3C), mRNA /cds=(58,1011) /gb=NM_005398 /gi=21314622 /ug=Hs.303090 /len=2524	NM_005398	Hs.303090	NP_005389
ncrc3541	NM_005398	protein phosphatase 1, regulatory (inhibitor) subunit 3C (PPP1R3C), mRNA /cds=(58,1011) /gb=NM_005398 /gi=21314622 /ug=Hs.303090 /len=2524	NM_005398	Hs.303090	NP_005389

ncr6881	NM_005445	chondroitin sulfate proteoglycan 6 (bamacan) (CSPG6), mRNA /cds=(92,3745) /gb=NM_005445 /gi=24475891 /ug=Hs.24485 /len=4096	NM_005445	Hs.24485	NP_005436
mioc2219	NM_005455	zinc finger protein 265 (ZNF265), mRNA /gb=NM_005455 /gi=19923317 /ug=Hs.194718 /len=2837	NM_005455	Hs.194718	NP_005446
mioa7069	NM_005484	ADP-ribosyltransferase (NAD ; poly(ADP-ribose) polymerase)-like 2 (ADPRTL2), mRNA /cds=(150,1754) /gb=NM_005484 /gi=11496991 /ug=Hs.24284 /len=1887	NM_005484	Hs.24284	NP_005475
fcrc2775	NM_005537	inhibitor of growth family, member 1 (ING1), mRNA /cds=(433,1701) /gb=NM_005537 /gi=19923770 /ug=Hs.46700 /len=2886	NM_005537	Hs.46700	NP_005528
fcrb2218	NM_005594	nascent-polypeptide-associated complex alpha polypeptide (NACA), mRNA /cds=(26,673) /gb=NM_005594 /gi=5031930 /ug=Hs.32916 /len=797	NM_005594	Hs.32916	NP_005585
ncrc0408	AK024964	cDNA: FLJ21311 fis, clone COL02167. /gb=AK024964 /gi=10437390 /ug=Hs.173933 /len=3216		Hs.173933	NP_005586

ncr5975	NM_005603	ATPase, Class I, type 8B, member 1 (ATP8B1), mRNA /cds=(1,3756) /gb=NM_005603 /gi=5031696 /ug=Hs.406187 /len=3756	NM_005603	Hs.406187	NP_005594
seob8483	NM_005605	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) (PPP3CC), mRNA /cds=(337,1875) /gb=NM_005605 /gi=21361289 /ug=Hs.75206 /len=2230	NM_005605	Hs.75206	NP_005596
seob1538	NM_005611	retinoblastoma-like 2 (p130) (RBL2), mRNA /cds=(70,3489) /gb=NM_005611 /gi=21361291 /ug=Hs.79362 /len=4853	NM_005611	Hs.79362	NP_005602
ncrc0907	NM_005623	chemokine (C-C motif) ligand 8 (CCL8), mRNA /cds=(456,755) /gb=NM_005623 /gi=22538815 /ug=Hs.271387 /len=1351	NM_005623	Hs.271387	NP_005614
mioc3045	NM_005627	serum/glucocorticoid regulated kinase (SGK), mRNA /cds=(58,1353) /gb=NM_005627 /gi=25168262 /ug=Hs.296323 /len=2386	NM_005627	Hs.296323	NP_005618

miob6290	NM_005642	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa (TAF7), mRNA /cds=(741,1790) /gb=NM_005642 /gi=14717406 /ug=Hs.155188 /len=2310	NM_005642	Hs.155188	NP_005633
miod4084	NM_005642	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa (TAF7), mRNA /cds=(741,1790) /gb=NM_005642 /gi=14717406 /ug=Hs.155188 /len=2310	NM_005642	Hs.155188	NP_005633
ncrb3329	NM_005655	TGFB inducible early growth response (TIEG), mRNA /cds=(124,1566) /gb=NM_005655 /gi=5032176 /ug=Hs.82173 /len=2899	NM_005655	Hs.82173	NP_005646
mioc4204	NM_005655	TGFB inducible early growth response (TIEG), mRNA /cds=(124,1566) /gb=NM_005655 /gi=5032176 /ug=Hs.82173 /len=2899	NM_005655	Hs.82173	NP_005646
miod1044	NM_005724	tetraspan 3 (TSPAN-3), mRNA /cds=(218,979) /gb=NM_005724 /gi=21264581 /ug=Hs.100090 /len=1842	NM_005724	Hs.100090	NP_005715

seoc1034	T66132	yc77a06.s1 Soares infant brain 1NIB cDNA clone IMAGE:21844 3', mRNA sequence /clone=IMAGE:21844 /clone_end=3' /gb=T66132 /gi=675177 /ug=Hs.332583 /len=246		Hs.332583	NP_005728
seob9818	NM_005738	ADP-ribosylation factor-like 4 (ARL4), mRNA /cds=(154,756) /gb=NM_005738 /gi=5031602 /ug=Hs.245540 /len=1077	NM_005738	Hs.245540	NP_005729
seob5726	NM_005749	transducer of ERBB2, 1 (TOB1), mRNA /cds=(36,1073) /gb=NM_005749 /gi=22035666 /ug=Hs.178137 /len=1830	NM_005749	Hs.178137	NP_005740
seoc6745	NM_005752	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 1 (cartilage-derived) (CLECSF1), mRNA /cds=(80,673) /gb=NM_005752 /gi=5031636 /ug=Hs.287364 /len=673	NM_005752	Hs.287364	NP_005743
ncr0791	NM_005759	abl-interactor 2 (ABI-2), mRNA /cds=(35,1462) /gb=NM_005759 /gi=20127476 /ug=Hs.343575 /len=1735	NM_005759	Hs.343575	NP_005750
seob6291	NM_005760	CCAAT-box-binding transcription factor (CBF2), mRNA /cds=(12,3008) /gb=NM_005760 /gi=5031624 /ug=Hs.184760 /len=3216	NM_005760	Hs.184760	NP_005751

fcr0707	NM_005770	small EDRK-rich factor 2 (SERF2), mRNA /cds=(1023,1319) /gb=NM_005770 /gi=21361286 /ug=Hs.380718 /len=1408	NM_005770	Hs.380718	NP_005761
miob6029	NM_005770	small EDRK-rich factor 2 (SERF2), mRNA /cds=(1023,1319) /gb=NM_005770 /gi=21361286 /ug=Hs.380718 /len=1408	NM_005770	Hs.380718	NP_005761
ncrc1537	NM_005783	ATP binding protein associated with cell differentiation (APACD), mRNA /cds=(130,810) /gb=NM_005783 /gi=18104958 /ug=Hs.153884 /len=1494	NM_005783	Hs.153884	NP_005774
mioa1343	AK056862	cDNA FLJ32300 fis, clone PROST2002227, highly similar to M-PHASE PHOSPHOPROTEIN 10. /gb=AK056862 /gi=16552379 /ug=Hs.201676 /len=2334		Hs.201676	NP_005782
seob8627	X91648	mRNA for pur alpha extended 3'untranslated region		Hs.29117	NP_005850
ncrb8396	NM_005863	neuroepithelial cell transforming gene 1 (NET1), mRNA /cds=(147,1775) /gb=NM_005863 /gi=19923326 /ug=Hs.25155 /len=3236	NM_005863	Hs.25155	NP_005854

ncrc9004	NM_005863	neuroepithelial cell transforming gene 1 (NET1), mRNA /cds=(147,1775) /gb=NM_005863 /gi=19923326 /ug=Hs.25155 /len=3236	NM_005863	Hs.25155	NP_005854
seoc1218	NM_005892	formin-like (FMNL), mRNA /cds=(635,2026) /gb=NM_005892 /gi=21735573 /ug=Hs.100217 /len=2384	NM_005892	Hs.100217	NP_005883
seoa9931	NM_005981	sarcoma amplified sequence (SAS), mRNA /cds=(155,787) /gb=NM_005981 /gi=21264346 /ug=Hs.50984 /len=1809	NM_005981	Hs.50984	NP_005972
seob3090	NM_006002	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) (UCHL3), mRNA /cds=(43,735) /gb=NM_006002 /gi=20149578 /ug=Hs.77917 /len=911	NM_006002	Hs.77917	NP_005993
seoa4395	NM_006004	ubiquinol-cytochrome c reductase hinge protein (UQCRH), mRNA /cds=(37,312) /gb=NM_006004 /gi=5174744 /ug=Hs.73818 /len=515	NM_006004	Hs.73818	NP_005995
fcrb4252	NM_006009	tubulin, alpha 3 (TUBA3), mRNA /cds=(100,1455) /gb=NM_006009 /gi=17986282 /ug=Hs.433394 /len=1677	NM_006009	Hs.433394	NP_006000

ncrc9709	NM_006013	ribosomal protein L10 (RPL10), mRNA /cds=(42,686) /gb=NM_006013 /gi=15718685 /ug=Hs.412900 /len=2188	NM_006013	Hs.412900	NP_006004
ncr0634	NM_006029	paraneoplastic antigen MA1 (PNMA1), mRNA /cds=(665,1726) /gb=NM_006029 /gi=14719429 /ug=Hs.194709 /len=2530	NM_006029	Hs.194709	NP_006020
seob1617	NM_006055	LanC lantibiotic synthetase component C-like 1 (bacterial) (LANCL1), mRNA /cds=(105,1304) /gb=NM_006055 /gi=5174444 /ug=Hs.13351 /len=4544	NM_006055	Hs.13351	NP_006046
fcrb1618	NM_006082	tubulin, alpha, ubiquitous (K-ALPHA-1), mRNA /cds=(68,1423) /gb=NM_006082 /gi=5174476 /ug=Hs.334842 /len=1596	NM_006082	Hs.334842	NP_006073
seob4726	NM_006096	N-myc downstream regulated gene 1 (NDRG1), mRNA /cds=(111,1295) /gb=NM_006096 /gi=5174656 /ug=Hs.75789 /len=3020	NM_006096	Hs.75789	NP_006087
miob9902	NM_000202	iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 1, mRNA /cds=(332,1984) /gb=NM_000202 /gi=5360215 /ug=Hs.172458 /len=2504	NM_000202; NM_006123	Hs.172458	NP_006114

mioa4674	NM_006134	chromosome 21 open reading frame 4 (C21orf4), mRNA /cds=(159,635) /gb=NM_006134 /gi=8659558 /ug=Hs.284142 /len=750	NM_006134	Hs.284142	NP_006125
seoa5784	NM_006148	LIM and SH3 protein 1 (LASP1), mRNA /cds=(76,861) /gb=NM_006148 /gi=5453709 /ug=Hs.334851 /len=3846	NM_006148	Hs.334851	NP_006139
seoa4587	NM_006153	NCK adaptor protein 1 (NCK1), mRNA /cds=(117,1250) /gb=NM_006153 /gi=20070226 /ug=Hs.54589 /len=1947	NM_006153	Hs.54589	NP_006144
mioc7559	NM_006166	nuclear transcription factor Y, beta (NFYB), mRNA /cds=(101,724) /gb=NM_006166 /gi=11496976 /ug=Hs.84928 /len=734	NM_006166	Hs.84928	NP_006157
fcrb0265	NM_006196	poly(rC) binding protein 1 (PCBP1), mRNA /cds=(178,1248) /gb=NM_006196 /gi=14141164 /ug=Hs.2853 /len=1634	NM_006196	Hs.2853	NP_006187
seob7082	NM_006196	poly(rC) binding protein 1 (PCBP1), mRNA /cds=(178,1248) /gb=NM_006196 /gi=14141164 /ug=Hs.2853 /len=1634	NM_006196	Hs.2853	NP_006187

ncrc9910	NM_006206	platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), mRNA /cds=(395,3664) /gb=NM_006206 /gi=15451787 /ug=Hs.74615 /len=6633	NM_006206	Hs.74615	NP_006197
ncr4793	D30036	mRNA for phosphatidylinositol transfer protein (PI-TPalpha), complete cds	NM_006224	Hs.433429	NP_006215
seoc1906	NM_006241	protein phosphatase 1, regulatory (inhibitor) subunit 2 (PPP1R2), mRNA /cds=(235,852) /gb=NM_006241 /gi=19923357 /ug=Hs.267819 /len=3355	NM_006241	Hs.267819	NP_006232
ncr0766	NM_006286	transcription factor Dp-2 (E2F dimerization partner 2) (TFDP2), mRNA /cds=(141,1301) /gb=NM_006286 /gi=5454111 /ug=Hs.379018 /len=2320	NM_006286	Hs.379018	NP_006277
seoa1132	NM_006294	ubiquinol-cytochrome c reductase binding protein (UQCRB), mRNA /cds=(54,389) /gb=NM_006294 /gi=20070231 /ug=Hs.131255 /len=965	NM_006294	Hs.131255	NP_006285
seob6535	NM_006317	brain abundant, membrane attached signal protein 1 (BASP1), mRNA /cds=(53,736) /gb=NM_006317 /gi=5453749 /ug=Hs.79516 /len=1486	NM_006317	Hs.79516	NP_006308

fcrc4669	NM_006317	brain abundant, membrane attached signal protein 1 (BASP1), mRNA /cds=(53,736) /gb=NM_006317 /gi=5453749 /ug=Hs.79516 /len=1486	NM_006317	Hs.79516	NP_006308
miob4238	NM_006335	translocase of inner mitochondrial membrane 17 A (yeast) (TIMM17A), mRNA /cds=(8,523) /gb=NM_006335 /gi=5454119 /ug=Hs.20716 /len=1645	NM_006335	Hs.20716	NP_006326
seoc2504	NM_006335	translocase of inner mitochondrial membrane 17 A (yeast) (TIMM17A), mRNA /cds=(8,523) /gb=NM_006335 /gi=5454119 /ug=Hs.20716 /len=1645	NM_006335	Hs.20716	NP_006326
ncrc0327	NM_006356	ATP synthase, H transporting, mitochondrial F0 complex, subunit d (ATP5H), mRNA /cds=(46,531) /gb=NM_006356 /gi=5453558 /ug=Hs.49018 /len=628	NM_006356	Hs.49018	NP_006347
seoa5986	NM_006367	adenylyl cyclase-associated protein (CAP), mRNA /cds=(63,1490) /gb=NM_006367 /gi=10938021 /ug=Hs.104125 /len=2614	NM_006367	Hs.104125	NP_006358
seob1420	NM_006369	MUF1 protein (MUF1), mRNA /cds=(1,1854) /gb=NM_006369 /gi=5453747 /ug=Hs.172210 /len=2165	NM_006369	Hs.172210	NP_006360

fcr4128	NM_006371	cartilage associated protein (CRTAP), mRNA /cds=(12,1217) /gb=NM_006371 /gi=21536278 /ug=Hs.155481 /len=2307	NM_006371	Hs.155481	NP_006362
miod2696	NM_006380	amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2), mRNA /cds=(289,2046) /gb=NM_006380 /gi=18104961 /ug=Hs.84084 /len=6468	NM_006380	Hs.84084	NP_006371
seob4036	NM_006394	regulated in glioma (RIG), mRNA /cds=(26,358) /gb=NM_006394 /gi=5454007 /ug=Hs.278503 /len=2569	NM_006394	Hs.278503	NP_006385
mioa3945	NM_006402	hepatitis B virus x interacting protein (HBXIP), mRNA /cds=(56,331) /gb=NM_006402 /gi=5454169 /ug=Hs.433355 /len=605	NM_006402	Hs.433355	NP_006393
mioc4174	NM_006404	protein C receptor, endothelial (EPCR) (PROCR), mRNA /cds=(83,799) /gb=NM_006404 /gi=21361313 /ug=Hs.82353 /len=1381	NM_006404	Hs.82353	NP_006395
ncrc6712	NM_006407	vitamin A responsive; cytoskeleton related (JWA), mRNA /cds=(90,656) /gb=NM_006407 /gi=7669496 /ug=Hs.92384 /len=2088	NM_006407	Hs.92384	NP_006398

miob4322	NM_006449	CDC42 effector protein (Rho GTPase binding) 3 (CDC42EP3), mRNA /cds=(969,1733) /gb=NM_006449 /gi=19923355 /ug=Hs.260024 /len=2768	NM_006449	Hs.260024	NP_006440
fcrc2099	NM_006449	CDC42 effector protein (Rho GTPase binding) 3 (CDC42EP3), mRNA /cds=(969,1733) /gb=NM_006449 /gi=19923355 /ug=Hs.260024 /len=2768	NM_006449	Hs.260024	NP_006440
ncr8420	NM_006449	CDC42 effector protein (Rho GTPase binding) 3 (CDC42EP3), mRNA /cds=(969,1733) /gb=NM_006449 /gi=19923355 /ug=Hs.260024 /len=2768	NM_006449	Hs.260024	NP_006440
fcr6039	NM_006482	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 2, mRNA	NM_003583; NM_006482	Hs.173135	NP_006473
seoc4132	NM_006515	SET domain and mariner transposase fusion gene (SETMAR), mRNA	NM_006515	Hs.265855	NP_006506
miob0178	NM_006519	t-complex-associated-testis-expressed 1-like 1 (TCTEL1), mRNA /cds=(1,342) /gb=NM_006519 /gi=5730084 /ug=Hs.266940 /len=713	NM_006519	Hs.266940	NP_006510
fcr3322	NM_006533	melanoma inhibitory activity (MIA), mRNA /cds=(72,467) /gb=NM_006533 /gi=5729924 /ug=Hs.279651 /len=538	NM_006533	Hs.279651	NP_006524

fcrb1633	NM_006559	KH domain containing, RNA binding, signal transduction associated 1 (KHDRBS1), mRNA /cds=(107,1438) /gb=NM_006559 /gi=5730026 /ug=Hs.119537 /len=2685	NM_006559	Hs.119537	NP_006550
mioa6734	NM_006590	SnRNP assembly defective 1 (SAD1), mRNA /cds=(493,1467) /gb=NM_006590 /gi=5730024 /ug=Hs.12820 /len=2166	NM_006590	Hs.12820	NP_006581
seob3303	NM_006603	stromal antigen 2 (STAG2), mRNA /cds=(405,3893) /gb=NM_006603 /gi=27552767 /ug=Hs.8217 /len=4197	NM_006603	Hs.8217	NP_006594
mioc6925	NM_006603	stromal antigen 2 (STAG2), mRNA /cds=(405,3893) /gb=NM_006603 /gi=27552767 /ug=Hs.8217 /len=4197	NM_006603	Hs.8217	NP_006594
mioa5085	NM_006620	HBS1-like (S. cerevisiae) (HBS1L), mRNA /cds=(194,2248) /gb=NM_006620 /gi=24431963 /ug=Hs.221040 /len=7163	NM_006620	Hs.221040	NP_006611
miob9228	NM_006621	hydrolase-like 1 (AHCYL1), mRNA /cds=(369,1961) /gb=NM_006621 /gi=21361646 /ug=Hs.4113 /len=2677	NM_006621	Hs.4113	NP_006612

seoa3514	NM_006628	cyclic AMP phosphoprotein, 19 kD (ARPP-19), mRNA /cds=(125,463) /gb=NM_006628 /gi=19923363 /ug=Hs.7351 /len=5171	NM_006628	Hs.7351	NP_006619
seoa9709	NM_006636	methylene tetrahydrofolate dehydrogenase (NAD dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,1111) /gb=NM_006636 /gi=13699869 /ug=Hs.154672 /len=2154	NM_006636	Hs.154672	NP_006627
mioc3011	NM_006646	WAS protein family, member 3 (WASF3), mRNA /cds=(179,1687) /gb=NM_006646 /gi=21237780 /ug=Hs.82318 /len=4768	NM_006646	Hs.82318	NP_006637
fcrc2619	NM_006649	serologically defined colon cancer antigen 16 (SDCCAG16), mRNA /cds=(29,2344) /gb=NM_006649 /gi=21361347 /ug=Hs.271926 /len=2509	NM_006649	Hs.271926	NP_006640
fcrc2090	NM_006700	FLN29 gene product (FLN29), mRNA /cds=(55,1803) /gb=NM_006700 /gi=5729827 /ug=Hs.5148 /len=2618	NM_006700	Hs.5148	NP_006691

seob1586	NM_006718	pleiomorphic adenoma gene-like 1 (PLAGL1), transcript variant 2, mRNA /cds=(2242,3633) /gb=NM_006718 /gi=27894292 /ug=Hs.75825 /len=4816	NM_002656; NM_006718	Hs.75825	NP_006709
seob7015	NM_006734	immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA /cds=(16,7518) /gb=NM_006734 /gi=19923373 /ug=Hs.75063 /len=9175	NM_006734	Hs.75063	NP_006725
ncr7792	NM_006744	retinol binding protein 4, plasma (RBP4), mRNA /cds=(89,688) /gb=NM_006744 /gi=8400727 /ug=Hs.418083 /len=919	NM_006744	Hs.418083	NP_006735
fcr2607	NM_006758	U2(RNU2) small nuclear RNA auxillary factor 1 (U2AF1), mRNA /cds=(39,761) /gb=NM_006758 /gi=5803206 /ug=Hs.271687 /len=904	NM_006758	Hs.271687	NP_006749
fcrb8901	NM_006758	U2(RNU2) small nuclear RNA auxillary factor 1 (U2AF1), mRNA /cds=(39,761) /gb=NM_006758 /gi=5803206 /ug=Hs.271687 /len=904	NM_006758	Hs.271687	NP_006749
fcrb7528	NM_006796	AFG3 ATPase family gene 3-like 2 (yeast) (AFG3L2), nuclear gene encoding mitochondrial protein, mRNA /cds=(114,2507) /gb=NM_006796 /gi=5802969 /ug=Hs.29385 /len=2963	NM_006796	Hs.29385	NP_006787

seoc2221	NM_006806	BTG family, member 3 (BTG3), mRNA /cds=(155,1045) /gb=NM_006806 /gi=21361363 /ug=Hs.77311 /len=1511	NM_006806	Hs.77311	NP_006797
miob6087	NM_006810	for protein disulfide isomerase-related (PDIR), mRNA /cds=(57,1616) /gb=NM_006810 /gi=5803120 /ug=Hs.76901 /len=1693	NM_006810	Hs.76901	NP_006801
ncrc5877	NM_006822	RAB40B, member RAS oncogene family (RAB40B), mRNA /cds=(46,882) /gb=NM_006822 /gi=5803162 /ug=Hs.302498 /len=1673	NM_006822	Hs.302498	NP_006813
hfcr6370	NM_006825	cytoskeleton-associated protein 4 (CKAP4), mRNA /cds=(85,1893) /gb=NM_006825 /gi=19920316 /ug=Hs.74368 /len=2913	NM_006825	Hs.74368	NP_006816
seoa5520	NM_006826	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide (YWHAQ), mRNA /cds=(120,857) /gb=NM_006826 /gi=21464103 /ug=Hs.74405 /len=2166	NM_006826	Hs.74405	NP_006817
seoa2819	NM_006827	transmembrane trafficking protein (TMP21), mRNA	NM_006827	Hs.74137	NP_006818
mioa3668	NM_006828	RNA helicase family (RNAH), mRNA /cds=(39,6647) /gb=NM_006828 /gi=24307916 /ug=Hs.48295 /len=7315	NM_006828	Hs.48295	NP_006819

seoa6732	Z24725	mitogen inducible gene mig-2, complete CDS. /cds=(1,2165) /gb=Z24725 /gi=505032 /ug=Hs.75260 /len=3270	NM_006832	Hs.75260	NP_006823
ncr0144	NM_006860	RAB, member of RAS oncogene family-like 4 (RABL4), mRNA /cds=(364,921) /gb=NM_006860 /gi=9257237 /ug=Hs.50267 /len=1021	NM_006860	Hs.50267	NP_006851
mioa0192	NM_006870	destrin (actin depolymerizing factor) (DSTN), mRNA /cds=(73,570) /gb=NM_006870 /gi=6466447 /ug=Hs.408576 /len=1439	NM_006870	Hs.408576	NP_006861
seoa9016	NM_006918	sterol-C5-desaturase (ERG3 delta-5-desaturase fungal)-like (SC5DL), mRNA /cds=(49,948) /gb=NM_006918 /gi=10800413 /ug=Hs.288031 /len=2092	NM_006918	Hs.288031	NP_008849
ncrc9428	NM_006925	splicing factor, arginine/serine-rich 5 (SFRS5), mRNA /cds=(219,542) /gb=NM_006925 /gi=5902077 /ug=Hs.166975 /len=1865	NM_006925	Hs.166975	NP_008856
hfcr1964	NM_006985	nuclear pore complex interacting protein (NPIP), mRNA /cds=(1,1053) /gb=NM_006985 /gi=5902013 /ug=Hs.251928 /len=1070	NM_006985	Hs.251928	NP_008916

hfcr0292	NM_007015	chondromodulin I precursor (CHM-I), mRNA /cds=(1,1005) /gb=NM_007015 /gi=5901931 /ug=Hs.97932 /len=1328	NM_007015	Hs.97932	NP_008946
ncr4194	NM_007043	HIV-1 rev binding protein 2 (HRB2), mRNA /cds=(30,1175) /gb=NM_007043 /gi=21359979 /ug=Hs.154762 /len=1527	NM_007043	Hs.154762	NP_008974
hfcr3615	NM_007097	clathrin, light polypeptide (Lcb) (CLTB), transcript variant brain, mRNA /cds=(173,862) /gb=NM_007097 /gi=6005994 /ug=Hs.380749 /len=1134	NM_001834; NM_007097	Hs.380749	NP_009028
seob7622	NM_007100	ATP synthase, H transporting, mitochondrial F0 complex, subunit e (ATP5I), mRNA /cds=(64,273) /gb=NM_007100 /gi=6005716 /ug=Hs.85539 /len=336	NM_007100	Hs.85539	NP_009031
ncrc4047	NM_007106	ubiquitin-like 3 (UBL3), mRNA /cds=(110,463) /gb=NM_007106 /gi=6005927 /ug=Hs.173091 /len=3323	NM_007106	Hs.173091	NP_009037
seoc2696	NM_007111	transcription factor Dp-1 (TFDP1), mRNA /cds=(222,1454) /gb=NM_007111 /gi=21361419 /ug=Hs.79353 /len=2394	NM_007111	Hs.79353	NP_009042

miob6103	AK022561	cDNA FLJ12499 fis, clone NT2RM2001671, highly similar to Oryctolagus cuniculus sarcolemmal associated protein (SLAP1) mRNA	NM_007159	Hs.4007	NP_009090
mioc1122	NM_007266	XPA binding protein 1; putative ATP(GTP)-binding protein (NTPBP), mRNA /cds=(25,1149) /gb=NM_007266 /gi=14149628 /ug=Hs.18259 /len=1829	NM_007266	Hs.18259	NP_009197
seoa7212	NM_007270	FK506 binding protein 9, 63 kDa (FKBP9), mRNA /cds=(457,885) /gb=NM_007270 /gi=24307926 /ug=Hs.302749 /len=2517	NM_007270	Hs.302749	NP_009201
seoc0056	NM_007270	FK506 binding protein 9, 63 kDa (FKBP9), mRNA /cds=(457,885) /gb=NM_007270 /gi=24307926 /ug=Hs.302749 /len=2517	NM_007270	Hs.302749	NP_009201
fcrc2457	NM_007270	FK506 binding protein 9, 63 kDa (FKBP9), mRNA /cds=(457,885) /gb=NM_007270 /gi=24307926 /ug=Hs.302749 /len=2517	NM_007270	Hs.302749	NP_009201
seob2081	NM_007278	GABA(A) receptor-associated protein (GABARAP), mRNA /cds=(105,458) /gb=NM_007278 /gi=6005763 /ug=Hs.7719 /len=924	NM_007278	Hs.7719	NP_009209

mioa9648	NM_000345	synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant NACP140, mRNA /cds=(47,469) /gb=NM_000345 /gi=6806896 /ug=Hs.76930 /len=1543	NM_000345; NM_007308	Hs.76930	NP_009292
ncrc1653	NM_004799	MAD, mothers against decapentaplegic (Drosophila) interacting protein, receptor activation anchor (MADHIP), transcript variant 3, mRNA /cds=(439,4410) /gb=NM_004799 /gi=4759059 /ug=Hs.194716 /len=4839	NM_004799; NM_007323; NM_007324	Hs.194716	NP_015563
mioa3572	NM_007361	nidogen 2 (osteonidogen) (NID2), mRNA /cds=(1,4131) /gb=NM_007361 /gi=6679055 /ug=Hs.82733 /len=4829	NM_007361	Hs.82733	NP_031387
seoa8993	NM_007362	nuclear cap binding protein subunit 2, 20kDa (NCBP2), mRNA /cds=(27,497) /gb=NM_007362 /gi=19923386 /ug=Hs.240770 /len=2120	NM_007362	Hs.240770	NP_031388
ncrb6261	NM_007366	phospholipase A2 receptor 1, 180kDa (PLA2R1), mRNA /cds=(207,4604) /gb=NM_007366 /gi=19923388 /ug=Hs.171945 /len=5633	NM_007366	Hs.171945	NP_031392
miod1707	J04806	Mus musculus osteopontin precursor, mRNA, complete cds	NM_009263	Mm.260317	NP_033289

seob5431	NM_009405	Mus musculus troponin I, skeletal, fast 2 (Tnni2), mRNA	NM_009405	Mm.39469	NP_033431
miob4574	NM_012086	general transcription factor IIIC, polypeptide 3, 102kDa (GTF3C3), mRNA /cds=(94,2754) /gb=NM_012086 /gi=6912397 /ug=Hs.90847 /len=2961	NM_012086	Hs.90847	NP_036218
seob6064	NM_012096	adaptor protein containing pH domain, PTB domain and leucine zipper motif (APPL), mRNA /cds=(59,2188) /gb=NM_012096 /gi=6912241 /ug=Hs.27413 /len=5970	NM_012096	Hs.27413	NP_036228
seob5223	NM_012098	angiopoietin-like 2 (ANGPTL2), mRNA /cds=(22,1503) /gb=NM_012098 /gi=6912235 /ug=Hs.8025 /len=1518	NM_012098	Hs.8025	NP_036230
miod0992	NM_012124	cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1 (CHORDC1), mRNA /cds=(85,1083) /gb=NM_012124 /gi=6912303 /ug=Hs.22857 /len=2058	NM_012124	Hs.22857	NP_036256
miob3591	NM_012141	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26 (DDX26), mRNA /cds=(477,3140) /gb=NM_012141 /gi=11024693 /ug=Hs.58570 /len=3690	NM_012141	Hs.58570	NP_036273

fcrb2622	NM_012158	F-box and leucine-rich repeat protein 3A (FBXL3A), mRNA /cds=(298,1584) /gb=NM_012158 /gi=16306583 /ug=Hs.7540 /len=3489	NM_012158	Hs.7540	NP_036290
ncr8538	NM_012158	F-box and leucine-rich repeat protein 3A (FBXL3A), mRNA /cds=(298,1584) /gb=NM_012158 /gi=16306583 /ug=Hs.7540 /len=3489	NM_012158	Hs.7540	NP_036290
ncrc9959	AF307332	meningioma-expressed antigen 5s splice variant mRNA, complete cds	NM_012215	Hs.5734	NP_036347
fcrc6631	NM_012245	SKI-interacting protein (SNW1), mRNA /cds=(28,1638) /gb=NM_012245 /gi=18860912 /ug=Hs.79008 /len=2146	NM_012245	Hs.79008	NP_036377
fcr0706	NM_012268	phospholipase D3 (PLD3), mRNA /cds=(488,1801) /gb=NM_012268 /gi=7110640 /ug=Hs.74573 /len=2131	NM_012268	Hs.74573	NP_036400
mioc2868	AB023204	mRNA for KIAA0987 protein, partial cds	NM_012307	Hs.103839	NP_036439
miob8341	NM_012308	F-box and leucine-rich repeat protein 11 (FBXL11), mRNA /cds=(107,3595) /gb=NM_012308 /gi=16306579 /ug=Hs.219614 /len=6210	NM_012308	Hs.219614	NP_036440
mioa6583	NM_012322	U6 snRNA-associated Sm-like protein (LSM5), mRNA /cds=(1,276) /gb=NM_012322 /gi=6912487 /ug=Hs.227280 /len=749	NM_012322	Hs.227280	NP_036454

seoa4246	NM_012341	G protein-binding protein CRFG (CRFG), mRNA /cds=(24,1925) /gb=NM_012341 /gi=6912531 /ug=Hs.215766 /len=2414	NM_012341	Hs.215766	NP_036473
mioa3092	NM_012414	rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), mRNA /cds=(74,4255) /gb=NM_012414 /gi=19923789 /ug=Hs.197289 /len=5129	NM_012414	Hs.197289	NP_036546
ncrc6817	NM_013285	nucleolar GTPase (HUMAUANTIG), mRNA /cds=(80,2275) /gb=NM_013285 /gi=7019418 /ug=Hs.75528 /len=2331	NM_013285	Hs.75528	NP_037417
mioa8380	NM_013330	NME7 (NME7), mRNA /cds=(93,1223) /gb=NM_013330 /gi=7242158 /ug=Hs.274479 /len=1475	NM_013330	Hs.274479	NP_037462
miob9336	NM_013386	hypothetical protein DKFZp586G0123 (DKFZp586G0123), mRNA /cds=(25,315) /gb=NM_013386 /gi=9558726 /ug=Hs.24713 /len=1294	NM_013386	Hs.24713	NP_037518
ncrc3049	NM_013989	deiodinase, iodothyronine, type II (DIO2), transcript variant 1, mRNA /cds=(707,1528) /gb=NM_013989 /gi=7549802 /ug=Hs.154424 /len=6735	NM_000793; NM_013989	Hs.154424	NP_054644

seob1268	NM_013989	deiodinase, iodothyronine, type II (DIO2), transcript variant 1, mRNA /cds=(707,1528) /gb=NM_013989 /gi=7549802 /ug=Hs.154424 /len=6735	NM_000793; NM_013989	Hs.154424	NP_054644
seoa3164	NM_014028	HSPC019 protein (HSPC019), mRNA /cds=(58,444) /gb=NM_014028 /gi=7661737 /ug=Hs.163724 /len=2411	NM_014028	Hs.163724	NP_054747
ncrc0838	NM_014033	DKFZP586A0522 protein (DKFZP586A0522), mRNA /cds=(21,755) /gb=NM_014033 /gi=13378140 /ug=Hs.288771 /len=1705	NM_014033	Hs.288771	NP_054752
seob5528	NM_014056	likely ortholog of mouse hypoxia induced gene 1 (HIG1), mRNA /cds=(93,374) /gb=NM_014056 /gi=7661619 /ug=Hs.7917 /len=1362	NM_014056	Hs.7917	NP_054775
seoa7223	NM_014065	HT001 protein (HT001), mRNA /cds=(242,1204) /gb=NM_014065 /gi=7661837 /ug=Hs.279040 /len=1402	NM_014065	Hs.279040	NP_054784
seoa9997	NM_014071	nuclear receptor coactivator 6 (NCOA6), mRNA /cds=(2755,8760) /gb=NM_014071 /gi=7661975 /ug=Hs.159613 /len=9301	NM_014071	Hs.159613	NP_054790

seob4057	NM_014112	trichorhinophalangeal syndrome I (TRPS1), mRNA /cds=(639,4484) /gb=NM_014112 /gi=7657658 /ug=Hs.26102 /len=10011	NM_014112	Hs.26102	NP_054831
seob2148	NM_014153	zinc-finger protein AY163807 (HSPC055), mRNA /cds=(199,3114) /gb=NM_014153 /gi=27414496 /ug=Hs.179898 /len=3859	NM_014153	Hs.179898	NP_054872
seob6386	NM_014168	HSPC133 protein (HSPC133), mRNA /cds=(83,481) /gb=NM_014168 /gi=7661791 /ug=Hs.273063 /len=963	NM_014168	Hs.273063	NP_054887
ncr3751	NM_014206	chromosome 11 open reading frame 10 (C11orf10), mRNA /cds=(56,295) /gb=NM_014206 /gi=7656933 /ug=Hs.90918 /len=418	NM_014206	Hs.90918	NP_055021
miod3500	NM_014206	chromosome 11 open reading frame 10 (C11orf10), mRNA /cds=(56,295) /gb=NM_014206 /gi=7656933 /ug=Hs.90918 /len=418	NM_014206	Hs.90918	NP_055021
fcrb3963	NM_014220	transmembrane 4 superfamily member 1 (TM4SF1), mRNA /cds=(102,710) /gb=NM_014220 /gi=21265100 /ug=Hs.351316 /len=1583	NM_014220	Hs.351316	NP_055035

fcr2601	NM_014220	transmembrane 4 superfamily member 1 (TM4SF1), mRNA /cds=(102,710) /gb=NM_014220 /gi=21265100 /ug=Hs.351316 /len=1583	NM_014220	Hs.351316	NP_055035
mioa0461	NM_014251	solute carrier family 25, member 13 (citrin) (SLC25A13), mRNA /cds=(138,2165) /gb=NM_014251 /gi=7657580 /ug=Hs.9599 /len=3150	NM_014251	Hs.9599	NP_055066
seob1187	NM_014280	DnaJ (Hsp40) subfamily C, member 8 (DNAJC8), mRNA /cds=(8,802) /gb=NM_014280 /gi=7657610 /ug=Hs.433540 /len=1525	NM_014280	Hs.433540	NP_055095
mioa2478	NM_014300	signal peptidase complex (18kD) (SPC18), mRNA /cds=(78,617) /gb=NM_014300 /gi=7657608 /ug=Hs.9534 /len=1105	NM_014300	Hs.9534	NP_055115
seoa1844	NM_014302	Sec61 gamma (SEC61G), mRNA /cds=(91,297) /gb=NM_014302 /gi=14591933 /ug=Hs.9950 /len=482	NM_014302	Hs.9950	NP_055117
seob5054	NM_014306	hypothetical protein (HSPC117), mRNA /cds=(76,1593) /gb=NM_014306 /gi=7657014 /ug=Hs.10729 /len=2005	NM_014306	Hs.10729	NP_055121
seob5562	NM_014315	kelch domain containing 2 (KLHDC2), mRNA /cds=(317,1537) /gb=NM_014315 /gi=7657300 /ug=Hs.20597 /len=1721	NM_014315	Hs.20597	NP_055130

ncr3404	NM_014319	integral inner nuclear membrane protein (MAN1), mRNA /cds=(7,2742) /gb=NM_014319 /gi=7706606 /ug=Hs.7256 /len=4703	NM_014319	Hs.7256	NP_055134
seoa6620	NM_014325	coronin, actin binding protein, 1C (CORO1C), mRNA /cds=(97,1521) /gb=NM_014325 /gi=27477119 /ug=Hs.17377 /len=3828	NM_014325	Hs.17377	NP_055140
ncr0340	NM_014325	coronin, actin binding protein, 1C (CORO1C), mRNA /cds=(97,1521) /gb=NM_014325 /gi=27477119 /ug=Hs.17377 /len=3828	NM_014325	Hs.17377	NP_055140
miod6781	NM_014367	hypothetical protein, estradiol-induced (E2IG5), mRNA /cds=(71,643) /gb=NM_014367 /gi=21361426 /ug=Hs.5243 /len=1215	NM_014367	Hs.5243	NP_055182
miob3953	NM_014372	ring finger protein 11 (RNF11), mRNA /cds=(128,592) /gb=NM_014372 /gi=7657519 /ug=Hs.96334 /len=2529	NM_014372	Hs.96334	NP_055187
miob6713	NM_014415	zinc finger protein (ZNF-U69274), mRNA /cds=(162,3323) /gb=NM_014415 /gi=7657702 /ug=Hs.301956 /len=5052	NM_014415	Hs.301956	NP_055230

seob1008	NM_014445	stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4 (SERP1), mRNA /cds=(316,516) /gb=NM_014445 /gi=19923408 /ug=Hs.76698 /len=2488	NM_014445	Hs.76698	NP_055260
hfcr2378	AK093929	cDNA FLJ36610 fis, clone TRACH2015987		Hs.76698	NP_055260
seob4145	NM_014497	NP220 nuclear protein (NP220), mRNA /cds=(315,6251) /gb=NM_014497 /gi=21626467 /ug=Hs.169984 /len=6570	NM_014497	Hs.169984	NP_055312
ncr2035	NM_014497	NP220 nuclear protein (NP220), mRNA /cds=(315,6251) /gb=NM_014497 /gi=21626467 /ug=Hs.169984 /len=6570	NM_014497	Hs.169984	NP_055312
seoc0535	AL137543	mRNA; cDNA DKFZp434P2119 (from clone DKFZp434P2119); partial cds	NM_014547	Hs.22826	NP_055362
ncrc3313	NM_014572	LATS, large tumor suppressor, 2 (Drosophila) (LATS2), mRNA /cds=(375,3641) /gb=NM_014572 /gi=18959199 /ug=Hs.432314 /len=4098	NM_014572	Hs.432314	NP_055387
ncrc3011	NM_014585	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3 (SLC11A3), mRNA /cds=(315,2030) /gb=NM_014585 /gi=19923794 /ug=Hs.5944 /len=3333	NM_014585	Hs.5944	NP_055400

ncr1712	NM_014606	hect domain and RLD 3 (HERC3), mRNA /cds=(167,3319) /gb=NM_014606 /gi=7657151 /ug=Hs.35804 /len=4894	NM_014606	Hs.35804	NP_055421
ncrc5149	NM_014670	basic leucine zipper and W2 domains 1 (BZW1), mRNA /cds=(81,1340) /gb=NM_014670 /gi=7661849 /ug=Hs.155291 /len=2998	NM_014670	Hs.155291	NP_055485
ncrc4597	NM_014685	endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 (HERPUD1), mRNA /cds=(96,1271) /gb=NM_014685 /gi=7661869 /ug=Hs.146393 /len=1884	NM_014685	Hs.146393	NP_055500
hfcr6501	NM_014718	calsyntenin 3 (CLSTN3), mRNA /cds=(539,3445) /gb=NM_014718 /gi=7662267 /ug=Hs.107809 /len=4300	NM_014718	Hs.107809	NP_055533
fcrc0857	NM_014726	ProSAPiP2 protein (ProSAPiP2), mRNA /cds=(850,2697) /gb=NM_014726 /gi=7662301 /ug=Hs.94790 /len=4121	NM_014726	Hs.94790	NP_055541
seoa1857	NM_014739	KIAA0164 gene product (KIAA0164), mRNA /cds=(254,3016) /gb=NM_014739 /gi=7661957 /ug=Hs.80338 /len=5538	NM_014739	Hs.80338	NP_055554

mioa4552	NM_014752	KIAA0102 gene product (KIAA0102), mRNA /cds=(308,679) /gb=NM_014752 /gi=7661907 /ug=Hs.77665 /len=1370	NM_014752	Hs.77665	NP_055567
fcr0609	NM_014758	KIAA0254 gene product (KIAA0254), mRNA /cds=(529,3507) /gb=NM_014758 /gi=7662025 /ug=Hs.76906 /len=6049	NM_014758	Hs.76906	NP_055573
seoa7078	NM_014765	translocase of outer mitochondrial membrane 20 (yeast) (KIAA0016), mRNA /cds=(102,539) /gb=NM_014765 /gi=7657256 /ug=Hs.75187 /len=3259	NM_014765	Hs.75187	NP_055580
fcrb1714	NM_014765	translocase of outer mitochondrial membrane 20 (yeast) (KIAA0016), mRNA /cds=(102,539) /gb=NM_014765 /gi=7657256 /ug=Hs.75187 /len=3259	NM_014765	Hs.75187	NP_055580
seoa1080	NM_014797	KIAA0441 gene product (KIAA0441), mRNA /cds=(169,2262) /gb=NM_014797 /gi=7662127 /ug=Hs.32511 /len=5597	NM_014797	Hs.32511	NP_055612
ncrc5072	NM_014820	translocase of outer mitochondrial membrane 70 A (yeast) (TOMM70A), mRNA /cds=(92,1918) /gb=NM_014820 /gi=7662672 /ug=Hs.21198 /len=4017	NM_014820	Hs.21198	NP_055635

ncr0046	NM_014820	translocase of outer mitochondrial membrane 70 A (yeast) (TOMM70A), mRNA /cds=(92,1918) /gb=NM_014820 /gi=7662672 /ug=Hs.21198 /len=4017	NM_014820	Hs.21198	NP_055635
seob8660	NM_014886	hypothetical protein YR-29 (YR-29), mRNA /cds=(85,867) /gb=NM_014886 /gi=21359901 /ug=Hs.8170 /len=1105	NM_014886	Hs.8170	NP_055701
ncrc6382	NM_014929	KIAA0971 protein (KIAA0971), mRNA /cds=(59,2005) /gb=NM_014929 /gi=7662421 /ug=Hs.84429 /len=4999	NM_014929	Hs.84429	NP_055744
ncr1640	NM_014944	calsyntenin 1 (CLSTN1), mRNA /cds=(794,3739) /gb=NM_014944 /gi=7662373 /ug=Hs.29665 /len=5219	NM_014944	Hs.29665	NP_055759
seob1385	NM_014949	KIAA0907 protein (KIAA0907), mRNA /cds=(27,1721) /gb=NM_014949 /gi=7662371 /ug=Hs.24656 /len=4500	NM_014949	Hs.24656	NP_055764
mioc7444	NM_014992	dishevelled associated activator of morphogenesis 1 (DAAM1), mRNA /cds=(126,3362) /gb=NM_014992 /gi=21071076 /ug=Hs.197751 /len=4256	NM_014992	Hs.197751	NP_055807

ncr3237	NM_015001	SMART/HDAC1 associated repressor protein (SHARP), mRNA /cds=(205,11199) /gb=NM_015001 /gi=14790189 /ug=Hs.184245 /len=12227	NM_015001	Hs.184245	NP_055816
ncr2484	NM_015017	pVHL-interacting deubiquitinating enzyme 1 (VDU1), mRNA /cds=(262,2997) /gb=NM_015017 /gi=21489974 /ug=Hs.173694 /len=4323	NM_015017	Hs.173694	NP_055832
mioc2529	H09059	yl96f11.s1 Soares infant brain 1NIB cDNA clone IMAGE:45943 3' similar to contains Alu repetitive element;, mRNA sequence /clone=IMAGE:45943 /clone_end=3' /gb=H09059 /gi=873881 /ug=Hs.438854 /len=494		Hs.438854	NP_055833
seob8501	NM_015023	KIAA1037 protein (KIAA1037), mRNA /cds=(399,2429) /gb=NM_015023 /gi=22095348 /ug=Hs.172825 /len=4305	NM_015023	Hs.172825	NP_055838
ncrb4439	AB014540	mRNA for KIAA0640 protein, partial cds. /cds=(1,1813) /gb=AB014540 /gi=3327093 /ug=Hs.153026 /len=4824		Hs.153026	NP_055870
fcrc3760	AB020671	mRNA for KIAA0864 protein, partial cds. /cds=(1,4210) /gb=AB020671 /gi=20521679 /ug=Hs.433523 /len=4872		Hs.433523	NP_055949

miod7225	NM_015153	PHD finger protein 3 (PHF3), mRNA /cds=(28,6147) /gb=NM_015153 /gi=7662017 /ug=Hs.78893 /len=6948	NM_015153	Hs.78893	NP_055968
seoc2506	AF545571	sulfatase SULF1 precursor, mRNA, complete cds /cds=(707,3322) /gb=AF545571 /gi=28191289 /ug=Hs.70823 /len=5699	NM_015170	Hs.70823	NP_055985
miob2947	NM_015208	KIAA0874 protein (KIAA0874), mRNA /cds=(1,6189) /gb=NM_015208 /gi=14140237 /ug=Hs.27973 /len=6189	NM_015208	Hs.27973	NP_056023
ncrc2472	NM_015216	KIAA0433 protein (KIAA0433), mRNA /cds=(510,4241) /gb=NM_015216 /gi=7662117 /ug=Hs.26179 /len=5814	NM_015216	Hs.26179	NP_056031
miob0589	NM_015254	kinesin family member 13B (KIF13B), mRNA /cds=(38,5518) /gb=NM_015254 /gi=13194196 /ug=Hs.15711 /len=8743	NM_015254	Hs.15711	NP_056069
miod5505	NM_015310	ADP-ribosylation factor guanine nucleotide factor 6 (EFA6R), mRNA /cds=(53,1657) /gb=NM_015310 /gi=7662395 /ug=Hs.6763 /len=6722	NM_015310	Hs.6763	NP_056125
seoa1483	NM_015355	joined to JAZF1 (JJAZ1), mRNA /cds=(195,2414) /gb=NM_015355 /gi=15149469 /ug=Hs.197803 /len=4441	NM_015355	Hs.197803	NP_056170

miod3254	NM_015383	hypothetical protein DJ328E19.C1.1 (DJ328E19.C1.1), mRNA /cds=(18,2783) /gb=NM_015383 /gi=7657016 /ug=Hs.218329 /len=3689	NM_015383	Hs.218329	NP_056198
ncrb6680	NM_015387	preimplantation protein 3 (PREI3), mRNA /cds=(14,598) /gb=NM_015387 /gi=7661623 /ug=Hs.107942 /len=2686	NM_015387	Hs.107942	NP_056202
miod7478	AB058721	mRNA for KIAA1818 protein, partial cds	NM_015409	Hs.306094	NP_056224
mioc6320	NM_015436	zinc finger protein 363 (ZNF363), mRNA /cds=(27,812) /gb=NM_015436 /gi=24308060 /ug=Hs.48297 /len=1543	NM_015436	Hs.48297	NP_056251
seob4545	NM_015470	KIAA0857 protein (KIAA0857), mRNA /cds=(241,2202) /gb=NM_015470 /gi=24308074 /ug=Hs.24557 /len=4340	NM_015470	Hs.24557	NP_056285
miob2968	NM_015497	DKFZP564G2022 protein (DKFZP564G2022), mRNA /cds=(43,1710) /gb=NM_015497 /gi=13794264 /ug=Hs.16492 /len=2286	NM_015497	Hs.16492	NP_056312
fcrb1575	NM_015507	EGF-like-domain, multiple 6 (EGFL6), mRNA /cds=(241,1902) /gb=NM_015507 /gi=13124887 /ug=Hs.12844 /len=2398	NM_015507	Hs.12844	NP_056322

miob6485	NM_015555	coactivator for steroid receptors (COASTER), mRNA /cds=(226,3267) /gb=NM_015555 /gi=20127147 /ug=Hs.172329 /len=4999	NM_015555	Hs.172329	NP_056370
seob7039	NM_015556	signal-induced proliferation-associated 1 like 1 (KIAA0440), mRNA /cds=(349,5763) /gb=NM_015556 /gi=7662125 /ug=Hs.172180 /len=6028	NM_015556	Hs.172180	NP_056371
seob5319	NM_015577	retinoic acid induced 14 (RAI14), mRNA /cds=(112,3054) /gb=NM_015577 /gi=13470085 /ug=Hs.15165 /len=4925	NM_015577	Hs.15165	NP_056392
miod5894	NM_015578	DKFZP434D1335 protein (DKFZP434D1335), mRNA /cds=(78,1469) /gb=NM_015578 /gi=24308092 /ug=Hs.8258 /len=3389	NM_015578	Hs.8258	NP_056393
fcrb7234	AL117478	mRNA; cDNA DKFZp727I051 (from clone DKFZp727I051); partial cds /cds=(1,2099) /gb=AL117478 /gi=5911952 /ug=Hs.239370 /len=2480	NM_015597	Hs.239370	NP_056412
fcrb6382	AL117478	mRNA; cDNA DKFZp727I051 (from clone DKFZp727I051); partial cds /cds=(1,2099) /gb=AL117478 /gi=5911952 /ug=Hs.239370 /len=2480	NM_015597	Hs.239370	NP_056412

mioa8192	NM_015602	DKFZP586G011 protein (LAP1B), mRNA /cds=(56,1444) /gb=NM_015602 /gi=24308098 /ug=Hs.234265 /len=3275	NM_015602	Hs.234265	NP_056417
seob7419	BC028715	erythroid differentiation-related factor 1, mRNA (cDNA clone IMAGE:4838997), partial cds		Hs.227209	NP_056423
seoa9792	AB036063	p53R2 mRNA for ribonucleotide reductase, complete cds. /cds=(245,1300) /gb=AB036063 /gi=7229085 /ug=Hs.94262 /len=4955		Hs.94262	NP_056528
seoa3108	NM_015933	hypothetical protein (HSPC016), mRNA /cds=(39,233) /gb=NM_015933 /gi=7705430 /ug=Hs.397853 /len=384	NM_015933	Hs.397853	NP_057017
miob8825	NM_015933	hypothetical protein (HSPC016), mRNA /cds=(39,233) /gb=NM_015933 /gi=7705430 /ug=Hs.397853 /len=384	NM_015933	Hs.397853	NP_057017
mioc8917	NM_015934	nucleolar protein NOP5/NOP58 (NOP5/NOP58), mRNA /cds=(1,1590) /gb=NM_015934 /gi=7706253 /ug=Hs.119908 /len=1590	NM_015934	Hs.119908	NP_057018
ncrc0336	NM_015938	CGI-07 protein (CGI-07), mRNA /cds=(124,1635) /gb=NM_015938 /gi=19923795 /ug=Hs.181022 /len=2762	NM_015938	Hs.181022	NP_057022

fcrb8225	AK023560	cDNA FLJ13498 fis, clone PLACE1004550, highly similar to CGI-20 protein mRNA	NM_015949	Hs.107387	NP_057033
seoa5685	NM_015952	PTD013 protein (PTD013), mRNA /cds=(87,812) /gb=NM_015952 /gi=7706269 /ug=Hs.22679 /len=982	NM_015952	Hs.22679	NP_057036
seoc1402	NM_015960	CGI-32 protein (CGI-32), mRNA /cds=(103,924) /gb=NM_015960 /gi=7705727 /ug=Hs.16606 /len=1323	NM_015960	Hs.16606	NP_057044
ncrc2484	NM_015966	serologically defined breast cancer antigen 84 (SDBCAG84), mRNA /cds=(28,1179) /gb=NM_015966 /gi=7706277 /ug=Hs.169992 /len=1337	NM_015966	Hs.169992	NP_057050
ncrb8063	NM_015966	serologically defined breast cancer antigen 84 (SDBCAG84), mRNA /cds=(28,1179) /gb=NM_015966 /gi=7706277 /ug=Hs.169992 /len=1337	NM_015966	Hs.169992	NP_057050
ncrc2600	NM_004830	cofactor required for Sp1 transcriptional activation, subunit 3, 130kDa (CRSP3), mRNA /cds=(120,4226) /gb=NM_004830 /gi=7019352 /ug=Hs.29679 /len=5176	NM_004830; NM_015979	Hs.29679	NP_057063

mioa6739	NM_015984	ubiquitin carboxyl-terminal hydrolase L5 (UCHL5), mRNA /cds=(132,1121) /gb=NM_015984 /gi=7706752 /ug=Hs.171581 /len=1728	NM_015984	Hs.171581	NP_057068
hfcr2708	NM_016001	CGI-48 protein (CGI-48), mRNA /cds=(108,1673) /gb=NM_016001 /gi=7705764 /ug=Hs.6153 /len=1873	NM_016001	Hs.6153	NP_057085
seob1526	NM_016019	CGI-74 protein (CGI-59), mRNA /cds=(1,1209) /gb=NM_016019 /gi=7706309 /ug=Hs.7194 /len=2296	NM_016019	Hs.7194	NP_057103
seoa3847	NM_016026	retinol dehydrogenase 11 (all-trans and 9-cis) (RDH11), mRNA /cds=(41,997) /gb=NM_016026 /gi=20070271 /ug=Hs.179817 /len=2538	NM_016026	Hs.179817	NP_057110
hfcr4007	NM_016041	CGI-101 protein (F-LAN-1), mRNA /cds=(7,636) /gb=NM_016041 /gi=7705603 /ug=Hs.286131 /len=1123	NM_016041	Hs.286131	NP_057125
seoa6226	NM_016045	chromosome 20 open reading frame 45 (C20orf45), mRNA /cds=(85,720) /gb=NM_016045 /gi=7705609 /ug=Hs.3945 /len=2535	NM_016045	Hs.3945	NP_057129
miod5080	NM_016076	CGI-146 protein (PNAS-4), mRNA /cds=(59,640) /gb=NM_016076 /gi=7705641 /ug=Hs.42409 /len=1108	NM_016076	Hs.42409	NP_057160

miod2996	NM_016077	CGI-147 protein (CGI-147), mRNA /cds=(128,667) /gb=NM_016077 /gi=7706350 /ug=Hs.12677 /len=806	NM_016077	Hs.12677	NP_057161
mioc8153	NM_016077	CGI-147 protein (CGI-147), mRNA /cds=(128,667) /gb=NM_016077 /gi=7706350 /ug=Hs.12677 /len=806	NM_016077	Hs.12677	NP_057161
mioa6580	NM_016078	CGI-148 protein (CGI-148), mRNA /cds=(300,845) /gb=NM_016078 /gi=7705643 /ug=Hs.87295 /len=2070	NM_016078	Hs.87295	NP_057162
ncr9044	AF125100	HSPC039 protein mRNA, complete cds /cds=(81,329) /gb=AF125100 /gi=5106995 /ug=Hs.406542 /len=1583	NM_016097	Hs.406542	NP_057181
ncrc9159	NM_016098	brain protein 44-like (BRP44L), mRNA /cds=(123,452) /gb=NM_016098 /gi=7706368 /ug=Hs.108725 /len=988	NM_016098	Hs.108725	NP_057182
miob6228	NM_016123	interleukin-1 receptor-associated kinase 4 (IRAK4), mRNA /cds=(50,1432) /gb=NM_016123 /gi=7705840 /ug=Hs.142295 /len=2817	NM_016123	Hs.142295	NP_057207
ncrc1623	AF527632	INSIG-2 membrane protein mRNA, complete cds	NM_016133	Hs.7089	NP_057217

seob6872	NM_016147	protein phosphatase methylesterase-1 (PME-1), mRNA /cds=(100,1260) /gb=NM_016147 /gi=7706644 /ug=Hs.63304 /len=2484	NM_016147	Hs.63304	NP_057231
ncr5760	NM_016183	chromosome 1 open reading frame 33 (C1orf33), mRNA /cds=(32,751) /gb=NM_016183 /gi=18490986 /ug=Hs.274201 /len=1185	NM_016183	Hs.274201	NP_057267
fcr2860	NM_016207	cleavage and polyadenylation specific factor 3, 73kDa (CPSF3), mRNA /cds=(36,2090) /gb=NM_016207 /gi=21314666 /ug=Hs.16251 /len=2286	NM_016207	Hs.16251	NP_057291
ncr0438	NM_014933	yeast Sec31p (KIAA0905), mRNA /cds=(54,3716) /gb=NM_014933 /gi=7662369 /ug=Hs.70266 /len=4129	NM_014933; NM_016211	Hs.70266	NP_057295
seob6000	NM_016217	hHDC for of Drosophila headcase (HDCL), mRNA /cds=(286,1917) /gb=NM_016217 /gi=7706434 /ug=Hs.6679 /len=5634	NM_016217	Hs.6679	NP_057301
ncr9061	NM_016224	sorting nexin 9 (SNX9), mRNA /cds=(174,1961) /gb=NM_016224 /gi=23111056 /ug=Hs.7905 /len=4200	NM_016224	Hs.7905	NP_057308

ncrb2053	NM_016227	chromosome 1 open reading frame 9 (C1orf9), mRNA /cds=(125,4342) /gb=NM_016227 /gi=7705321 /ug=Hs.108636 /len=5919	NM_014283; NM_016227	Hs.108636	NP_057311
fcrc3826	NM_016274	CK2 interacting protein 1; HQ0024c protein (CKIP-1), mRNA /cds=(285,1514) /gb=NM_016274 /gi=21361610 /ug=Hs.173380 /len=1633	NM_016274	Hs.173380	NP_057358
seoa5121	NM_016304	chromosome 15 open reading frame 15 (C15orf15), mRNA /cds=(144,635) /gb=NM_016304 /gi=18491027 /ug=Hs.284162 /len=1487	NM_016304	Hs.284162	NP_057388
mioc6997	NM_016306	DnaJ (Hsp40) subfamily B, member 11 (DNAJB11), mRNA /cds=(160,1236) /gb=NM_016306 /gi=25014110 /ug=Hs.278605 /len=1621	NM_016306	Hs.278605	NP_057390
miob4333	NM_016316	REV1-like (yeast) (REV1L), mRNA /cds=(213,3968) /gb=NM_016316 /gi=7706680 /ug=Hs.110347 /len=4276	NM_016316	Hs.110347	NP_057400
seob0096	NM_016322	RAB14, member RAS oncogene family (RAB14), mRNA /cds=(184,831) /gb=NM_016322 /gi=19923482 /ug=Hs.5807 /len=4106	NM_016322	Hs.5807	NP_057406

fcrb1457	NM_016322	RAB14, member RAS oncogene family (RAB14), mRNA /cds=(184,831) /gb=NM_016322 /gi=19923482 /ug=Hs.5807 /len=4106	NM_016322	Hs.5807	NP_057406
ncrc2172	AW292456	UI-H-BI2-agp-f-12-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2725031 3', mRNA sequence /clone=IMAGE:2725031 /clone_end=3' /gb=AW292456 /gi=6699092 /ug=Hs.437793 /len=745		Hs.437793	NP_057446
miod4184	NM_016403	hypothetical protein HSPC148 (HSPC148), mRNA /cds=(64,753) /gb=NM_016403 /gi=7705474 /ug=Hs.42743 /len=1046	NM_016403	Hs.42743	NP_057487
seob4928	NM_016441	cysteine-rich motor neuron 1 (CRIM1), mRNA /cds=(40,3150) /gb=NM_016441 /gi=10092638 /ug=Hs.19280 /len=5601	NM_016441	Hs.19280	NP_057525
miod1377	NM_016441	cysteine-rich motor neuron 1 (CRIM1), mRNA /cds=(40,3150) /gb=NM_016441 /gi=10092638 /ug=Hs.19280 /len=5601	NM_016441	Hs.19280	NP_057525
miob0167	NM_016474	hypothetical protein LOC51244 (LOC51244), mRNA /cds=(340,1233) /gb=NM_016474 /gi=24475969 /ug=Hs.158006 /len=1614	NM_016474	Hs.158006	NP_057558

miod7486	BC025306	clone IMAGE:4893383, mRNA, partial cds	NM_016488	Hs.281428	NP_057572
ncr3968	NM_016505	putative S1 RNA binding domain protein (PS1D), mRNA /cds=(137,862) /gb=NM_016505 /gi=21361575 /ug=Hs.54971 /len=1602	NM_016505	Hs.54971	NP_057589
hfcr5220	NM_016581	ECSIT (LOC51295), mRNA /cds=(78,1373) /gb=NM_016581 /gi=20149632 /ug=Hs.22199 /len=1668	NM_016581	Hs.22199	NP_057665
seoa9729	NM_016587	chromobox 3 (HP1 gamma Drosophila) (CBX3), transcript variant 2, mRNA /cds=(152,703) /gb=NM_016587 /gi=20544150 /ug=Hs.406384 /len=1851	NM_007276; NM_016587	Hs.406384	NP_057671
fcrb7340	NM_016594	FK506 binding protein 11, 19 kDa (FKBP11), mRNA /cds=(73,678) /gb=NM_016594 /gi=7706130 /ug=Hs.24048 /len=727	NM_016594	Hs.24048	NP_057678
miob1134	NM_016608	ALEX1 protein (ALEX1), mRNA /cds=(372,1733) /gb=NM_016608 /gi=7706142 /ug=Hs.9728 /len=2141	NM_016608	Hs.9728	NP_057692
ncrc6332	NM_016618	hypothetical protein LOC51315 (LOC51315), mRNA /cds=(395,1174) /gb=NM_016618 /gi=7706155 /ug=Hs.5721 /len=1774	NM_016618	Hs.5721	NP_057702

miob3354	NM_016618	hypothetical protein LOC51315 (LOC51315), mRNA /cds=(395,1174) /gb=NM_016618 /gi=7706155 /ug=Hs.5721 /len=1774	NM_016618	Hs.5721	NP_057702
miod1323	NM_016627	hypothetical protein LOC51321 (LOC51321), mRNA /cds=(635,1195) /gb=NM_016627 /gi=7706167 /ug=Hs.268122 /len=1304	NM_016627	Hs.268122	NP_057711
ncr3148	NM_016632	ARF protein (LOC51326), mRNA /cds=(88,489) /gb=NM_016632 /gi=7706177 /ug=Hs.264509 /len=826	NM_016632	Hs.264509	NP_057716
seoa9724	NM_016640	mitochondrial ribosomal protein S30 (MRPS30), mRNA /cds=(39,1358) /gb=NM_016640 /gi=16950598 /ug=Hs.28555 /len=1482	NM_016640	Hs.28555	NP_057724
ncrc8873	NM_006855	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (KDELR3), transcript variant 1, mRNA /cds=(157,801) /gb=NM_006855 /gi=8051612 /ug=Hs.250696 /len=1705	NM_006855; NM_016657	Hs.250696	NP_057839
ncrb4022	NM_017444	chromatin accessibility complex 1 (CHRAC1), mRNA /cds=(196,591) /gb=NM_017444 /gi=24432041 /ug=Hs.279704 /len=2496	NM_017444	Hs.279704	NP_059140
fcr5316	NM_017510	gp25L2 protein (HSGP25L2G), mRNA	NM_017510	Hs.279929	NP_059980

ncrb2085	NM_017548	hypothetical protein H41 (H41), mRNA /cds=(324,1100) /gb=NM_017548 /gi=24475997 /ug=Hs.283690 /len=3346	NM_017548	Hs.283690	NP_060018
miod4614	NM_017599	transmembrane protein vezatin (VEZATIN), mRNA /cds=(177,1886) /gb=NM_017599 /gi=19923537 /ug=Hs.24135 /len=3949	NM_017599	Hs.24135	NP_060069
mioc5198	NM_017606	hypothetical protein DKFZp434K1210 (DKFZp434K1210), mRNA /cds=(191,580) /gb=NM_017606 /gi=8922146 /ug=Hs.32352 /len=2133	NM_017606	Hs.32352	NP_060076
mioc5210	NM_017615	hypothetical protein FLJ20003 (FLJ20003), mRNA /cds=(31,1188) /gb=NM_017615 /gi=8923008 /ug=Hs.258798 /len=1387	NM_017615	Hs.258798	NP_060085
miob9370	AF246705	putative serine-rich protein mRNA, partial cds	NM_017632	Hs.32922	NP_060102
ncrb4435	NM_017691	hypothetical protein FLJ20156 (FLJ20156), mRNA /cds=(248,2305) /gb=NM_017691 /gi=8923153 /ug=Hs.12692 /len=2780	NM_017691	Hs.12692	NP_060161
miod4629	NM_017755	hypothetical protein FLJ20303 (FLJ20303), mRNA /cds=(86,1681) /gb=NM_017755 /gi=8923284 /ug=Hs.17138 /len=2427	NM_017755	Hs.17138	NP_060225

ncrc0217	NM_017761	hypothetical protein FLJ20312 (FLJ20312), mRNA /cds=(384,803) /gb=NM_017761 /gi=20127576 /ug=Hs.7862 /len=2382	NM_017761	Hs.7862	NP_060231
ncrb2272	NM_017791	chromosome 14 open reading frame 58 (C14orf58), mRNA /cds=(325,1905) /gb=NM_017791 /gi=8923349 /ug=Hs.267566 /len=3614	NM_017791	Hs.267566	NP_060261
ncrc4373	NM_017830	ovarian carcinoma immunoreactive antigen (OCIA), mRNA /cds=(168,905) /gb=NM_017830 /gi=8923426 /ug=Hs.132071 /len=1434	NM_017830	Hs.132071	NP_060300
seoa4167	NM_017849	hypothetical protein FLJ20507 (FLJ20507), mRNA /cds=(258,974) /gb=NM_017849 /gi=8923465 /ug=Hs.202955 /len=4223	NM_017849	Hs.202955	NP_060319
seoc0957	NM_017910	hypothetical protein FLJ20628 (FLJ20628), mRNA /cds=(23,1456) /gb=NM_017910 /gi=13435382 /ug=Hs.32356 /len=1846	NM_017910	Hs.32356	NP_060380
miod3325	NM_017913	Hsp90-associating relative of Cdc37 (HARC), mRNA /cds=(100,1113) /gb=NM_017913 /gi=8923591 /ug=Hs.128646 /len=1542	NM_017913	Hs.128646	NP_060383
seob5880	AL834521	mRNA; cDNA DKFZp667F0310 (from clone DKFZp667F0310)	NM_017925	Hs.29032	NP_060395

mioc4782	NM_017943	F-box only protein 34 (FBXO34), mRNA /cds=(7,924) /gb=NM_017943 /gi=8923650 /ug=Hs.15467 /len=2006	NM_017943	Hs.15467	NP_060413
miob8286	AL832991	mRNA; cDNA DKFZp666K033 (from clone DKFZp666K033)	NM_017944	Hs.300700	NP_060414
miod1030	NM_017971	mitochondrial ribosomal protein L20 (MRPL20), nuclear gene encoding mitochondrial protein, mRNA /cds=(65,514) /gb=NM_017971 /gi=26638656 /ug=Hs.182698 /len=705	NM_017971	Hs.182698	NP_060441
ncrc0178	BC043393	Similar to hypothetical protein LOC208146, clone IMAGE:5498791, mRNA		Hs.318127	NP_060493
ncrc4402	NM_018032	LUC7-like (S. cerevisiae) (LUC7L), mRNA /cds=(89,1066) /gb=NM_018032 /gi=21359922 /ug=Hs.16803 /len=1542	NM_018032	Hs.16803	NP_060502
ncrc7169	NM_018047	hypothetical protein FLJ10290 (FLJ10290), mRNA /cds=(78,1340) /gb=NM_018047 /gi=8922327 /ug=Hs.25516 /len=2297	NM_018047	Hs.25516	NP_060517
fcrb4270	NM_018049	likely ortholog of mouse guanine nucleotide releasing protein x (GNRPX), mRNA /cds=(82,531) /gb=NM_018049 /gi=8922332 /ug=Hs.173739 /len=1215	NM_018049	Hs.173739	NP_060519

seob7682	NM_018058	cartilage acidic protein 1 (CRTAC1), mRNA /cds=(319,1575) /gb=NM_018058 /gi=8922351 /ug=Hs.326444 /len=2178	NM_018058	Hs.326444	NP_060528
seoa3761	NM_018061	hypothetical protein FLJ10330 (FLJ10330), mRNA /cds=(77,1717) /gb=NM_018061 /gi=8922357 /ug=Hs.342307 /len=3239	NM_018061	Hs.342307	NP_060531
fcrb8465	NM_018077	hypothetical protein FLJ10377 (FLJ10377), mRNA /cds=(116,2395) /gb=NM_018077 /gi=8922387 /ug=Hs.274263 /len=2809	NM_018077	Hs.274263	NP_060547
mioc8471	NM_018115	hypothetical protein FLJ10498 (FLJ10498), mRNA /cds=(37,1920) /gb=NM_018115 /gi=8922466 /ug=Hs.109045 /len=2755	NM_018115	Hs.109045	NP_060585
fcrb3896	NM_018184	hypothetical protein FLJ10702 (FLJ10702), mRNA /cds=(175,735) /gb=NM_018184 /gi=8922600 /ug=Hs.104222 /len=2944	NM_018184	Hs.104222	NP_060654
mioc3079	NM_018255	elongator protein 2 (ELP2), mRNA /cds=(11,2491) /gb=NM_018255 /gi=8922734 /ug=Hs.8739 /len=2494	NM_018255	Hs.8739	NP_060725

ncr2908	NM_018259	hypothetical protein FLJ10890 (FLJ10890), mRNA /cds=(29,3454) /gb=NM_018259 /gi=21361786 /ug=Hs.17283 /len=3533	NM_018259	Hs.17283	NP_060729
mioc3139	NM_018285	chromosome 15 open reading frame 12 (C15orf12), nuclear gene encoding mitochondrial protein, mRNA /cds=(48,602) /gb=NM_018285 /gi=8922793 /ug=Hs.6118 /len=1115	NM_018285	Hs.6118	NP_060755
miob7267	AB067490	mRNA for KIAA1903 protein, partial cds	NM_018353	Hs.89278	NP_060823
ncrb0364	NM_018382	hypothetical protein FLJ11292 (FLJ11292), mRNA /cds=(151,615) /gb=NM_018382 /gi=8922980 /ug=Hs.272246 /len=1948	NM_018382	Hs.272246	NP_060852
fcrb9959	NM_018462	uncharacterized hematopoietic stem/progenitor cells protein MDS027 (MDS027), mRNA /cds=(21,248) /gb=NM_018462 /gi=27544938 /ug=Hs.421654 /len=888	NM_018462	Hs.421654	NP_060932
miod0807	NM_018464	uncharacterized hematopoietic stem/progenitor cells protein MDS029 (MDS029), mRNA /cds=(112,438) /gb=NM_018464 /gi=8923929 /ug=Hs.43549 /len=636	NM_018464	Hs.43549	NP_060934

miob3308	NM_018471	uncharacterized hypothalamus protein HT010 (HT010), mRNA /cds=(227,1420) /gb=NM_018471 /gi=8923807 /ug=Hs.6375 /len=2140	NM_018471	Hs.6375	NP_060941
ncr2695	NM_018480	uncharacterized hypothalamus protein HT007 (HT007), mRNA /cds=(228,887) /gb=NM_018480 /gi=8923801 /ug=Hs.24371 /len=1172	NM_018480	Hs.24371	NP_060950
ncrb4182	NM_018590	chondroitin sulfate GalNAcT-2 (GALNACT-2), mRNA /cds=(336,1964) /gb=NM_018590 /gi=24429591 /ug=Hs.180758 /len=3745	NM_018590	Hs.180758	NP_061060
mioc2290	NM_018638	ethanolamine kinase (EKI1), mRNA /cds=(90,1448) /gb=NM_018638 /gi=21071078 /ug=Hs.120439 /len=2221	NM_018638	Hs.120439	NP_061108
seob3220	AB033073	mRNA for KIAA1247 protein, partial cds. /cds=(286,2943) /gb=AB033073 /gi=14133244 /ug=Hs.43857 /len=4397	NM_018837	Hs.43857	NP_061325
seoc1318	BC005940	Similar to G-protein gamma-12 subunit, clone MGC:14561 IMAGE:4049838, mRNA, complete cds		Hs.8107	NP_061329

mioa5409	NM_004105	EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), transcript variant 1, mRNA /cds=(150,1631) /gb=NM_004105 /gi=9665261 /ug=Hs.76224 /len=2742	NM_004105; NM_018894	Hs.76224	NP_061489
mioa0626	NM_018948	Gene 33/Mig-6 (MIG-6), mRNA /cds=(213,1601) /gb=NM_018948 /gi=21314673 /ug=Hs.11169 /len=3099	NM_018948	Hs.11169	NP_061821
mioa6811	NM_018948	Gene 33/Mig-6 (MIG-6), mRNA /cds=(213,1601) /gb=NM_018948 /gi=21314673 /ug=Hs.11169 /len=3099	NM_018948	Hs.11169	NP_061821
miob7831	NM_018948	Gene 33/Mig-6 (MIG-6), mRNA /cds=(213,1601) /gb=NM_018948 /gi=21314673 /ug=Hs.11169 /len=3099	NM_018948	Hs.11169	NP_061821
mioc5197	NM_018948	Gene 33/Mig-6 (MIG-6), mRNA /cds=(213,1601) /gb=NM_018948 /gi=21314673 /ug=Hs.11169 /len=3099	NM_018948	Hs.11169	NP_061821
mioc7372	NM_018948	Gene 33/Mig-6 (MIG-6), mRNA /cds=(213,1601) /gb=NM_018948 /gi=21314673 /ug=Hs.11169 /len=3099	NM_018948	Hs.11169	NP_061821
miob4933	NM_018976	solute carrier family 38, member 2 (SLC38A2), mRNA /cds=(352,1872) /gb=NM_018976 /gi=21361601 /ug=Hs.298275 /len=4795	NM_018976	Hs.298275	NP_061849

seob4766	NM_018976	solute carrier family 38, member 2 (SLC38A2), mRNA /cds=(352,1872) /gb=NM_018976 /gi=21361601 /ug=Hs.298275 /len=4795	NM_018976	Hs.298275	NP_061849
seoc2050	NM_018976	solute carrier family 38, member 2 (SLC38A2), mRNA /cds=(352,1872) /gb=NM_018976 /gi=21361601 /ug=Hs.298275 /len=4795	NM_018976	Hs.298275	NP_061849
mioc1425	NM_018976	solute carrier family 38, member 2 (SLC38A2), mRNA /cds=(352,1872) /gb=NM_018976 /gi=21361601 /ug=Hs.298275 /len=4795	NM_018976	Hs.298275	NP_061849
ncr3604	BC013629	clone IMAGE:3445410, mRNA, partial cds		Hs.432900	NP_061852
miob7155	AB002342	mRNA for KIAA0344 gene, partial cds	NM_018979	Hs.432900	NP_061852
seoc0775	BC034698	Similar to RAB5 interacting protein 2, clone IMAGE:4508733, mRNA		Hs.62349	NP_061866
mioa0791	BC034698	Similar to RAB5 interacting protein 2, clone IMAGE:4508733, mRNA		Hs.62349	NP_061866
ncrb4000	XM_033181	strand-exchange protein 1 (SEP1), mRNA			NP_061874
mioa0535	NM_019026	putative membrane protein (LOC54499), mRNA /cds=(139,705) /gb=NM_019026 /gi=24308132 /ug=Hs.93832 /len=1186	NM_019026	Hs.93832	NP_061899

ncrc4247	NM_019043	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein (APBB1IP), mRNA /cds=(88,2085) /gb=NM_019043 /gi=26665876 /ug=Hs.98874 /len=2423	NM_019043	Hs.98874	NP_061916
mioa4177	NM_019059	of Tom7 (S. cerevisiae) (TOM7), mRNA /cds=(94,261) /gb=NM_019059 /gi=9506858 /ug=Hs.112318 /len=487	NM_019059	Hs.112318	NP_061932
mioc2255	AK001149	cDNA FLJ10287 fis, clone HEMBB1001387	NM_019083	Hs.40337	NP_061956
miob2671	NM_019088	hypothetical protein F23149_1 (PD2), mRNA /cds=(229,1824) /gb=NM_019088 /gi=9506582 /ug=Hs.152894 /len=1966	NM_019088	Hs.152894	NP_061961
ncrc9469	NM_002961	S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental (S100A4), transcript variant 1, mRNA /cds=(70,375) /gb=NM_002961 /gi=9845514 /ug=Hs.81256 /len=512	NM_002961; NM_019554	Hs.81256	NP_062427
mioc2961	NM_019591	zinc finger protein 26 (KOX 20) (ZNF26), mRNA /cds=(699,1298) /gb=NM_019591 /gi=11034838 /ug=Hs.26432 /len=2385	NM_019591	Hs.26432	NP_062537
miod5008	BC000819	Similar to CG6950 gene product, clone MGC:5114 IMAGE:3453829, mRNA, complete cds		Hs.180378	NP_062556

seoc4093	NM_020123	SM-11044 binding protein (SMBP), mRNA /cds=(20,1780) /gb=NM_020123 /gi=10047129 /ug=Hs.8203 /len=3389	NM_020123	Hs.8203	NP_064508
ncrb6453	NM_020133	lysophosphatidic acid acyltransferase-delta (LPAAT-delta), mRNA /cds=(158,1294) /gb=NM_020133 /gi=9910391 /ug=Hs.353175 /len=1774	NM_020133	Hs.353175	NP_064518
ncrb8224	NM_020153	hypothetical protein FLJ21827 (FLJ21827), mRNA /cds=(379,1446) /gb=NM_020153 /gi=21361819 /ug=Hs.334360 /len=1834	NM_020153	Hs.334360	NP_064538
fcr4433	NM_020154	chromosome 11 hypothetical protein ORF3 (LOC56851), mRNA /cds=(14,742) /gb=NM_020154 /gi=9910345 /ug=Hs.4245 /len=1072	NM_020154	Hs.4245	NP_064539
ncrc3856	NM_020192	GK003 protein (GK003), mRNA /cds=(10,690) /gb=NM_020192 /gi=21281666 /ug=Hs.83313 /len=901	NM_020192	Hs.83313	NP_064577
seob6229	NM_020192	GK003 protein (GK003), mRNA /cds=(10,690) /gb=NM_020192 /gi=21281666 /ug=Hs.83313 /len=901	NM_020192	Hs.83313	NP_064577
ncr6344	NM_020199	HTGN29 protein (HTGN29), mRNA /cds=(205,1002) /gb=NM_020199 /gi=9910277 /ug=Hs.283437 /len=2371	NM_020199	Hs.283437	NP_064584

ncrb3424	NM_020213	hypothetical protein from EUROIMAGE 1977056 (LOC56965), mRNA /cds=(609,1358) /gb=NM_020213 /gi=9910373 /ug=Hs.8694 /len=2359	NM_020213; NM_020214	Hs.8694	NP_064599
seoc2923	NM_020215	hypothetical protein DKFZp761F2014 (DKFZp761F2014), mRNA /cds=(117,638) /gb=NM_020215 /gi=9910205 /ug=Hs.6434 /len=3477	NM_020215	Hs.6434	NP_064600
ncr3397	NM_020232	hepatocellular carcinoma susceptibility protein (HCCA3), mRNA /cds=(53,847) /gb=NM_020232 /gi=22726188 /ug=Hs.3726 /len=1073	NM_020232	Hs.3726	NP_064617
ncrc9591	NM_020234	x 009 protein (MDS009), mRNA /cds=(127,534) /gb=NM_020234 /gi=9910425 /ug=Hs.64641 /len=1133	NM_020234	Hs.64641	NP_064619
miob7274	NM_020250	MOST2 protein (MOST2), mRNA /cds=(3461,3952) /gb=NM_020250 /gi=9910449 /ug=Hs.193920 /len=4750	NM_020250	Hs.193920	NP_064635
ncr3587	NM_020345	I-kappa-B-interacting Ras-like protein 1 (KBRAS1), mRNA /cds=(1,579) /gb=NM_020345 /gi=9966808 /ug=Hs.173202 /len=579	NM_020345	Hs.173202	NP_065078

miod0956	BC012145	Similar to I-kappa-B-interacting Ras-like protein 1, clone MGC:20358 IMAGE:4549097, mRNA, complete cds		Hs.173202	NP_065078
miob5873	AF165191	BPAG1n3 (BPAG1) mRNA, partial cds	NM_001723; NM_015548; NM_020388	Hs.198689	NP_065121
mioc5308	AF165191	BPAG1n3 (BPAG1) mRNA, partial cds	NM_001723; NM_015548; NM_020388	Hs.198689	NP_065121
miod6773	NM_020405	tumor endothelial marker 7 precursor (TEM7), mRNA /cds=(83,1585) /gb=NM_020405 /gi=21361852 /ug=Hs.125036 /len=6140	NM_020405	Hs.125036	NP_065138
ncr5971	NM_020422	hypothetical protein from clone 24796 (LOC57146), mRNA /cds=(113,598) /gb=NM_020422 /gi=21361853 /ug=Hs.27191 /len=1683	NM_020422	Hs.27191	NP_065155
fcrb4974	BC040556	CTL2 gene, clone MGC:41799 IMAGE:5268313, mRNA, complete cds	NM_020428	Hs.105509	NP_065161
fcrc0106	AL133060	mRNA; cDNA DKFZp434M2315 (from clone DKFZp434M2315) (=BC012766.1)		Hs.180428	NP_065195
ncrb3445	NM_020466	hypothetical protein dJ122O8.2 (DJ122O8.2), mRNA /cds=(34,300) /gb=NM_020466 /gi=20070310 /ug=Hs.268115 /len=902	NM_020466	Hs.268115	NP_065199

ncrc3995	NM_020474	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1) (GALNT1), mRNA /cds=(32,1711) /gb=NM_020474 /gi=13124890 /ug=Hs.80120 /len=3778	NM_020474	Hs.80120	NP_065207
mioc3042	NM_020529	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), mRNA /cds=(95,1048) /gb=NM_020529 /gi=10092618 /ug=Hs.81328 /len=1550	NM_020529	Hs.81328	NP_065390
seoa6654	NM_020648	twisted gastrulation 1 (Drosophila) (TWSG1), mRNA /cds=(106,777) /gb=NM_020648 /gi=21314788 /ug=Hs.247302 /len=3693	NM_020648	Hs.247302	NP_065699
mioc6341	NM_020665	kidney-specific membrane protein (NX17), mRNA /cds=(261,929) /gb=NM_020665 /gi=21361864 /ug=Hs.129614 /len=1605	NM_020665	Hs.129614	NP_065716
fcrb6167	NM_020680	SCY1-like 1 (S. cerevisiae) (SCYL1), mRNA /cds=(40,2400) /gb=NM_020680 /gi=19923565 /ug=Hs.238839 /len=2580	NM_020680	Hs.238839	NP_065731
seob4734	NM_020685	HT021 (HT021), mRNA /cds=(145,531) /gb=NM_020685 /gi=10190735 /ug=Hs.47166 /len=797	NM_020685	Hs.47166	NP_065736

seoc5815	NM_020749	AT2 receptor-interacting protein 1 (ATIP1), mRNA /cds=(1,1311) /gb=NM_020749 /gi=21361871 /ug=Hs.7946 /len=3455	NM_020749	Hs.7946	NP_065800
miob2941	NM_020755	likely ortholog of mouse tumor differentially expressed 1, like (TDE1L), mRNA /cds=(76,1437) /gb=NM_020755 /gi=24308212 /ug=Hs.146668 /len=3149	NM_020755	Hs.146668	NP_065806
miod5775	AK023639	cDNA FLJ13577 fis, clone PLACE1008748		Hs.107287	NP_065870
mioa9709	NM_020843	zinc finger protein 291 (ZNF291), mRNA /cds=(38,4237) /gb=NM_020843 /gi=16507197 /ug=Hs.285848 /len=4703	NM_020843	Hs.285848	NP_065894
seoa3701	NM_020904	pleckstrin domain containing, family A (phosphoinositide binding specific) member 4 (PLEKHA4), mRNA /cds=(526,2865) /gb=NM_020904 /gi=10190743 /ug=Hs.9469 /len=3056	NM_020904	Hs.9469	NP_065955
fcrb1328	AB046829	mRNA for KIAA1609 protein, partial cds. /cds=(1,1423) /gb=AB046829 /gi=15425661 /ug=Hs.14449 /len=4683		Hs.14449	NP_065998
ncrc2827	NM_020948	mesoderm induction early response 1 (MI-ER1), mRNA /cds=(234,1844) /gb=NM_020948 /gi=24308260 /ug=Hs.222746 /len=4972	NM_020948	Hs.222746	NP_065999

ncrc3596	NM_021009	ubiquitin C (UBC), mRNA /cds=(136,2193) /gb=NM_021009 /gi=20149305 /ug=Hs.183704 /len=2309	NM_021009	Hs.183704	NP_066289
fcrb1731	NM_021075	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa (NDUFV3), mRNA /cds=(575,1945) /gb=NM_021075 /gi=21361323 /ug=Hs.59745 /len=2023	NM_021075	Hs.59745	NP_066553
fcrb4409	NM_021102	serine protease inhibitor, Kunitz type, 2 (SPINT2), mRNA /cds=(301,1059) /gb=NM_021102 /gi=10863908 /ug=Hs.31439 /len=1544	NM_021102	Hs.31439	NP_066925
ncr2700	BC035161	clone IMAGE:5265444, mRNA /gb=BC035161 /gi=23242943 /ug=Hs.7278 /len=4402		Hs.7278	NP_066940
seob7649	NM_001959	eukaryotic translation elongation factor 1 beta 2 (EEF1B2), transcript variant 1, mRNA /cds=(236,913) /gb=NM_001959 /gi=16519564 /ug=Hs.421608 /len=961	NM_001959; NM_021121	Hs.421608	NP_066944
hfcr1189	NM_001959	eukaryotic translation elongation factor 1 beta 2 (EEF1B2), transcript variant 1, mRNA /cds=(236,913) /gb=NM_001959 /gi=16519564 /ug=Hs.421608 /len=961	NM_001959; NM_021121	Hs.421608	NP_066944

seob4076	NM_021129	pyrophosphatase (inorganic) (PP), nuclear gene encoding mitochondrial protein, mRNA /cds=(78,947) /gb=NM_021129 /gi=11056043 /ug=Hs.184011 /len=1282	NM_021129	Hs.184011	NP_066952
ncrc1421	NM_021130	peptidylprolyl isomerase A (cyclophilin A) (PPIA), mRNA /cds=(45,542) /gb=NM_021130 /gi=10863926 /ug=Hs.401787 /len=753	NM_021130	Hs.401787	NP_066953
miob0636	NM_021132	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta) (PPP3CB), mRNA /cds=(117,1691) /gb=NM_021132 /gi=11036639 /ug=Hs.151531 /len=3079	NM_021132	Hs.151531	NP_066955
ncrc1203	NM_021137	tumor necrosis factor, alpha-induced protein 1 (endothelial) (TNFAIP1), mRNA /cds=(212,1162) /gb=NM_021137 /gi=26051238 /ug=Hs.76090 /len=3571	NM_021137	Hs.76090	NP_066960
ncrc6774	NM_021188	likely ortholog of mouse another partner for ARF 1 (APA1), mRNA /cds=(183,1619) /gb=NM_021188 /gi=10863994 /ug=Hs.405945 /len=2207	NM_021188	Hs.405945	NP_067011

miod3743	NM_021215	chromosome 20 open reading frame 77 (C20orf77), mRNA /cds=(298,1278) /gb=NM_021215 /gi=22507393 /ug=Hs.27192 /len=4219	NM_021215	Hs.27192	NP_067038
fcrb5964	NM_021227	DC2 protein (DC2), mRNA /cds=(60,509) /gb=NM_021227 /gi=24308270 /ug=Hs.103180 /len=1090	NM_021227	Hs.103180	NP_067050
mioa9649	NM_021645	KIAA0266 gene product (KIAA0266), mRNA /cds=(734,3034) /gb=NM_021645 /gi=11063982 /ug=Hs.127376 /len=5585	NM_021645	Hs.127376	NP_067677
seoc2477	AB014526	mRNA for KIAA0626 protein, complete cds	NM_021647	Hs.178121	NP_067679
fcrb1733	NM_021809	TGFB-induced factor 2 (TALE family homeobox) (TGIF2), mRNA /cds=(170,883) /gb=NM_021809 /gi=19923576 /ug=Hs.94785 /len=3433	NM_021809	Hs.94785	NP_068581
seob1197	NM_021814	of yeast long chain polyunsaturated fatty acid elongation enzyme 2 (HELO1), mRNA /cds=(345,1244) /gb=NM_021814 /gi=21361903 /ug=Hs.250175 /len=3011	NM_021814	Hs.250175	NP_068586
ncrb8203	NM_021826	hypothetical protein FLJ13149 (FLJ13149), mRNA /cds=(291,2585) /gb=NM_021826 /gi=11141902 /ug=Hs.112188 /len=2836	NM_021826	Hs.112188	NP_068598

seob7739	NM_021831	hypothetical protein FLJ21839 (FLJ21839), mRNA /cds=(445,2619) /gb=NM_021831 /gi=19923577 /ug=Hs.433334 /len=3252	NM_021831	Hs.433334	NP_068603
seob9285	NM_021831	hypothetical protein FLJ21839 (FLJ21839), mRNA /cds=(445,2619) /gb=NM_021831 /gi=19923577 /ug=Hs.433334 /len=3252	NM_021831	Hs.433334	NP_068603
fcrb4383	NM_021939	FK506 binding protein 10, 65 kDa (FKBP10), mRNA /cds=(87,1835) /gb=NM_021939 /gi=21361894 /ug=Hs.3849 /len=2641	NM_021939	Hs.3849	NP_068758
seoa2679	NM_021945	hypothetical protein FLJ22174 (FLJ22174), mRNA /cds=(1712,2173) /gb=NM_021945 /gi=24431990 /ug=Hs.7734 /len=3326	NM_021945	Hs.7734	NP_068764
mioc0567	NM_021967	small EDRK-rich factor 1A (telomeric) (SERF1A), mRNA /cds=(184,516) /gb=NM_021967 /gi=11415045 /ug=Hs.32567 /len=1912	NM_021967	Hs.32567	NP_068802
miod6058	NM_021970	mitogen-activated protein kinase kinase 1 interacting protein 1 (MAP2K1IP1), mRNA /cds=(250,624) /gb=NM_021970 /gi=21614526 /ug=Hs.6361 /len=1416	NM_021970	Hs.6361	NP_068805

ncrc0632	NM_021999	integral membrane protein 2B (ITM2B), mRNA /cds=(171,971) /gb=NM_021999 /gi=11527401 /ug=Hs.239625 /len=1843	NM_021999	Hs.239625	NP_068839
fcrb9802	AJ310543	mRNA for EGLN1 protein	NM_022051	Hs.6523	NP_071334
seob0569	NM_022333	TIA1 cytotoxic granule-associated RNA binding protein-like 1 (TIAL1), transcript variant 2, mRNA /cds=(158,955) /gb=NM_022333 /gi=13435393 /ug=Hs.182741 /len=1760	NM_003252; NM_022333	Hs.182741	NP_071728
fcrb1320	NM_022333	TIA1 cytotoxic granule-associated RNA binding protein-like 1 (TIAL1), transcript variant 2, mRNA /cds=(158,955) /gb=NM_022333 /gi=13435393 /ug=Hs.182741 /len=1760	NM_003252; NM_022333	Hs.182741	NP_071728
seob6198	NM_003349	ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1), transcript variant 2, mRNA /cds=(70,735) /gb=NM_003349 /gi=15718757 /ug=Hs.75875 /len=2394	NM_003349; NM_021988; NM_022442	Hs.75875	NP_071887
seob3313	NM_003349	ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1), transcript variant 2, mRNA /cds=(70,735) /gb=NM_003349 /gi=15718757 /ug=Hs.75875 /len=2394	NM_003349; NM_021988; NM_022442	Hs.75875	NP_071887

mioc7763	NM_022488	autophagy Apg3p/Aut1p-like (APG3), mRNA /cds=(120,1064) /gb=NM_022488 /gi=19526772 /ug=Hs.26367 /len=1381	NM_022488	Hs.26367	NP_071933
seob5044	NM_022551	ribosomal protein S18 (RPS18), mRNA /cds=(46,504) /gb=NM_022551 /gi=14165467 /ug=Hs.275865 /len=549	NM_022551	Hs.275865	NP_072045
fcrc6570	NM_002890	RAS p21 protein activator (GTPase activating protein) 1 (RASA1), transcript variant 1, mRNA /cds=(119,3262) /gb=NM_002890 /gi=4506430 /ug=Hs.758 /len=4307	NM_002890; NM_022650	Hs.758	NP_072179
miod0355	NM_022735	golgi complex associated protein 1, 60kDa (GOCAP1), mRNA /cds=(56,1642) /gb=NM_022735 /gi=15826851 /ug=Hs.6831 /len=3598	NM_022735	Hs.6831	NP_073572
fcrb1729	NM_022735	golgi complex associated protein 1, 60kDa (GOCAP1), mRNA /cds=(56,1642) /gb=NM_022735 /gi=15826851 /ug=Hs.6831 /len=3598	NM_022735	Hs.6831	NP_073572
seob1955	AK091247	cDNA FLJ33928 fis, clone CTONG2017444		Hs.16603	NP_073592
fcrb9909	NM_022757	hypothetical protein FLJ12892 (FLJ12892), mRNA /cds=(145,1929) /gb=NM_022757 /gi=24308284 /ug=Hs.17731 /len=2987	NM_022757	Hs.17731	NP_073594

ncrc4267	NM_022763	FAD104 (FAD104), mRNA /cds=(58,3672) /gb=NM_022763 /gi=27477058 /ug=Hs.299883 /len=6894	NM_022763	Hs.299883	NP_073600
fcrc5134	NM_017411	survival of motor neuron 2, centromeric (SMN2), transcript variant d, mRNA /cds=(164,1048) /gb=NM_017411 /gi=13259525 /ug=Hs.367729 /len=1623	NM_017411; NM_022875; NM_022876; NM_022877	Hs.367729	NP_075015
seoa0114	X70326	MacMarcks mRNA	NM_023009	Hs.75061	NP_075385
fcrc5169	NM_023012	hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4 (FLJ11021), mRNA /cds=(767,1375) /gb=NM_023012 /gi=20127619 /ug=Hs.81648 /len=1878	NM_023012	Hs.81648	NP_075388
ncrb8607	NM_023080	hypothetical protein FLJ20989 (FLJ20989), mRNA /cds=(53,742) /gb=NM_023080 /gi=12751496 /ug=Hs.169615 /len=2643	NM_023080	Hs.169615	NP_075568
ncrb8239	NM_023928	hypothetical protein FLJ12389 similar to acetoacetyl-CoA synthetase (FLJ12389), mRNA /cds=(149,2167) /gb=NM_023928 /gi=12965198 /ug=Hs.239758 /len=3253	NM_023928	Hs.239758	NP_076417

miob7156	NM_001356	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3 (DDX3), transcript variant 2, mRNA /cds=(857,2845) /gb=NM_001356 /gi=13514812 /ug=Hs.380774 /len=5322	NM_001356; NM_024005	Hs.380774	NP_076829
mioa1473	NM_024010	methyltransferase reductase (MTRR), transcript variant 2, mRNA /cds=(31,2208) /gb=NM_024010 /gi=13325067 /ug=Hs.153792 /len=3291	NM_002454; NM_024010	Hs.153792	NP_076915
fcrc0835	NM_024038	hypothetical protein MGC2803 (MGC2803), mRNA /cds=(68,598) /gb=NM_024038 /gi=13128991 /ug=Hs.239894 /len=954	NM_024038	Hs.239894	NP_076943
mioc3206	NM_024041	hypothetical protein MGC3180 (MGC3180), mRNA /cds=(76,768) /gb=NM_024041 /gi=13128997 /ug=Hs.250570 /len=846	NM_024041	Hs.250570	NP_076946
mioc3316	NM_024045	nucleolar protein GU2 (GU2), mRNA /cds=(108,2321) /gb=NM_024045 /gi=13129005 /ug=Hs.7392 /len=2575	NM_024045	Hs.7392	NP_076950
seoc0619	NM_022902	solute carrier family 30 (zinc transporter), member 5 (SLC30A5), mRNA /cds=(202,2499) /gb=NM_022902 /gi=20070322 /ug=Hs.129445 /len=2952	NM_022902; NM_024055	Hs.129445	NP_076960

mioa9033	NM_024292	ubiquitin-like 5 (UBL5), mRNA /cds=(66,287) /gb=NM_024292 /gi=13236509 /ug=Hs.13836 /len=413	NM_024292	Hs.13836	NP_077268
seoc7547	BC042615	Similar to v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian), clone IMAGE:4470615, mRNA, partial cds		Hs.7041	NP_077288
seob1513	NM_024332	c6.1A (C6.1A), mRNA /cds=(3,953) /gb=NM_024332 /gi=13236582 /ug=Hs.301927 /len=2846	NM_024332	Hs.301927	NP_077308
mioa0890	AK097314	cDNA FLJ39995 fis, clone STOMA2002141		Hs.102548	NP_077318
seoa7517	NM_024408	Notch 2 (Drosophila) (NOTCH2), mRNA /cds=(257,7672) /gb=NM_024408 /gi=24041034 /ug=Hs.8121 /len=11433	NM_024408	Hs.8121	NP_077719
seoa3245	NM_024491	p10-binding protein (BITE), mRNA /cds=(149,1942) /gb=NM_024491 /gi=13346499 /ug=Hs.42315 /len=2628	NM_024491	Hs.42315	NP_077817
ncrc4757	AB058768	mRNA for KIAA1865 protein, partial cds. /cds=(622,2793) /gb=AB058768 /gi=14017946 /ug=Hs.179260 /len=3641		Hs.179260	NP_078772
seoc0778	NM_024511	hypothetical protein MGC4701 (MGC4701), mRNA /cds=(149,1585) /gb=NM_024511 /gi=24308290 /ug=Hs.421054 /len=1686	NM_024511	Hs.421054	NP_078787

mioc2828	NM_024524	hypothetical protein FLJ20986 (FLJ20986), mRNA /cds=(1758,3863) /gb=NM_024524 /gi=21362055 /ug=Hs.324507 /len=5226	NM_024524	Hs.324507	NP_078800
fcrb3258	NM_024536	hypothetical protein FLJ22678 (FLJ22678), mRNA /cds=(188,2515) /gb=NM_024536 /gi=27545322 /ug=Hs.7718 /len=2965	NM_024536	Hs.7718	NP_078812
ncr6426	AK074267	cDNA FLJ23687 fis, clone HEP10109		Hs.13222	NP_078836
ncrc5054	NM_024592	hypothetical protein FLJ13352 (FLJ13352), mRNA /cds=(97,1053) /gb=NM_024592 /gi=13375784 /ug=Hs.22972 /len=2271	NM_024592	Hs.22972	NP_078868
ncrc6825	NM_024635	hypothetical protein FLJ22643 (FLJ22643), mRNA /cds=(15,650) /gb=NM_024635 /gi=13375865 /ug=Hs.43579 /len=997	NM_024635	Hs.43579	NP_078911
fcrb6715	NM_024656	hypothetical protein FLJ22329 (FLJ22329), mRNA /cds=(36,767) /gb=NM_024656 /gi=13375904 /ug=Hs.367653 /len=2501	NM_024656	Hs.367653	NP_078932
seoa9494	NM_024713	hypothetical protein FLJ22557 (FLJ22557), mRNA /cds=(87,1001) /gb=NM_024713 /gi=13376012 /ug=Hs.106101 /len=2676	NM_024713	Hs.106101	NP_078989

mioa8275	NM_024793	KIAA0643 protein (KIAA0643), mRNA /cds=(80,823) /gb=NM_024793 /gi=13435144 /ug=Hs.155995 /len=2221	NM_024793	Hs.155995	NP_079069
mioc1226	NM_024818	hypothetical protein FLJ23251 (FLJ23251), mRNA /cds=(235,1449) /gb=NM_024818 /gi=13376211 /ug=Hs.170737 /len=2132	NM_024818	Hs.170737	NP_079094
seoc1175	NM_024829	hypothetical protein FLJ22662 (FLJ22662), mRNA /cds=(66,1586) /gb=NM_024829 /gi=13376231 /ug=Hs.178470 /len=1707	NM_024829	Hs.178470	NP_079105
ncrc7151	NM_024843	duodenal cytochrome b (FLJ23462), mRNA /cds=(74,934) /gb=NM_024843 /gi=19923602 /ug=Hs.31297 /len=4254	NM_024843	Hs.31297	NP_079119
seoc0212	NM_025027	hypothetical protein FLJ14260 (FLJ14260), mRNA /cds=(431,1219) /gb=NM_025027 /gi=13430885 /ug=Hs.287629 /len=2441	NM_025027	Hs.287629	NP_079303
seoc2201	AB002306	mRNA for KIAA0308 gene, partial cds	NM_025134	Hs.8182	NP_079410
seoc0369	NM_025146	likely ortholog of mouse Mak3p (S. cerevisiae) (MAK3P), mRNA /cds=(301,810) /gb=NM_025146 /gi=13376734 /ug=Hs.288932 /len=3576	NM_025146	Hs.288932	NP_079422

miob7518	NM_025180	hypothetical protein FLJ13386 (FLJ13386), mRNA /cds=(428,2539) /gb=NM_025180 /gi=22095366 /ug=Hs.300876 /len=2770	NM_025180	Hs.300876	NP_079456
ncrc0747	NM_025184	hypothetical protein FLJ22843 (FLJ22843), mRNA /cds=(532,1287) /gb=NM_025184 /gi=13376775 /ug=Hs.301143 /len=2291	NM_025184	Hs.301143	NP_079460
seoc0577	AL832422	mRNA; cDNA DKFZp762K012 (from clone DKFZp762K012)		Hs.301651	NP_079465
ncrc9517	NM_025190	KIAA1641 protein (KIAA1641), mRNA /cds=(41,454) /gb=NM_025190 /gi=13449272 /ug=Hs.44566 /len=2418	NM_025190	Hs.44566	NP_079466
seoc4078	NM_025198	transcription termination factor-like protein (LOC80298), mRNA /cds=(341,1498) /gb=NM_025198 /gi=21314735 /ug=Hs.5009 /len=1792	NM_025198	Hs.5009	NP_079474
fcrb9018	NM_025222	hypothetical protein PRO2730 (PRO2730), mRNA /cds=(1346,1759) /gb=NM_025222 /gi=21361950 /ug=Hs.194110 /len=2990	NM_025222	Hs.194110	NP_079498
ncrc4663	NM_025234	recombination protein REC14 (REC14), mRNA /cds=(77,994) /gb=NM_025234 /gi=13376839 /ug=Hs.296242 /len=1205	NM_025234	Hs.296242	NP_079510

seoa2428	NM_001357	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase II; leukophysin) (DDX9), transcript variant 1, mRNA /cds=(81,3920) /gb=NM_001357 /gi=13514819 /ug=Hs.74578 /len=4199	NM_001357; NM_030588	Hs.74578	NP_085077
seoa6432	AB051481	mRNA for KIAA1694 protein, partial cds. /cds=(1,2275) /gb=AB051481 /gi=12697932 /ug=Hs.19597 /len=4235	NM_030629	Hs.19597	NP_085132
fcr1020	NM_030662	mitogen-activated protein kinase kinase 2 (MAP2K2), mRNA /cds=(255,1457) /gb=NM_030662 /gi=21614527 /ug=Hs.72241 /len=1759	NM_030662	Hs.72241	NP_109587
seob0949	NM_030752	t-complex 1 (TCP1), mRNA /cds=(22,1692) /gb=NM_030752 /gi=13540472 /ug=Hs.4112 /len=2019	NM_030752	Hs.4112	NP_110379
fcrb4413	NM_030755	thioredoxin domain-containing (TXNDC), mRNA /cds=(118,960) /gb=NM_030755 /gi=13559515 /ug=Hs.24766 /len=1112	NM_030755	Hs.24766	NP_110382
miob4684	NM_030762	basic helix-loop-helix domain containing, class B, 3 (BHLHB3), mRNA /cds=(135,1583) /gb=NM_030762 /gi=13540520 /ug=Hs.33829 /len=3641	NM_030762	Hs.33829	NP_110389

ncrb4385	AW298400	UI-H-BW0-ajj-h-09-0-UI.s1 NCI_CGAP_Sub6 cDNA clone IMAGE:2732033 3', mRNA sequence /clone=IMAGE:2732033 /clone_end=3' /gb=AW298400 /gi=6704960 /ug=Hs.438172 /len=635		Hs.438172	NP_110435
ncrc9877	NM_030917	hypothetical protein DKFZp586K0717 (DKFZP586K0717), mRNA /cds=(168,1730) /gb=NM_030917 /gi=13569873 /ug=Hs.334812 /len=1914	NM_030917	Hs.334812	NP_112179
miob8080	NM_030920	leucine-rich acidic nuclear protein like (LANPL), mRNA /cds=(332,1138) /gb=NM_030920 /gi=23463320 /ug=Hs.71331 /len=3273	NM_030920	Hs.71331	NP_112182
seoa2135	NM_030971	similar to rat tricarboxylate carrier-like protein (BA108L7.2), mRNA /cds=(75,1040) /gb=NM_030971 /gi=13569945 /ug=Hs.283844 /len=2735	NM_030971	Hs.283844	NP_112233
fcrb4271	NM_030981	RAB1B, member RAS oncogene family (RAB1B), mRNA /cds=(48,653) /gb=NM_030981 /gi=13569961 /ug=Hs.300816 /len=1985	NM_030981	Hs.300816	NP_112243

hfcr2390	NM_005968	heterogeneous nuclear ribonucleoprotein M (HNRPM), transcript variant 1, mRNA /cds=(231,2423) /gb=NM_005968 /gi=14141151 /ug=Hs.79024 /len=2703	NM_005968; NM_031203	Hs.79024	NP_112480
mioa3018	NM_031210	hypothetical protein DC50 (DC50), mRNA /cds=(37,366) /gb=NM_031210 /gi=24475712 /ug=Hs.324521 /len=442	NM_031210	Hs.324521	NP_112487
ncrb3702	NM_031229	chromosome 20 open reading frame 18 (C20orf18), transcript variant 2, mRNA /cds=(677,2179) /gb=NM_031229 /gi=14043035 /ug=Hs.247280 /len=2715	NM_006462; NM_031227; NM_031228; NM_031229	Hs.247280	NP_112506
ncrc1740	NM_031243	heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1), transcript variant B1, mRNA /cds=(170,1231) /gb=NM_031243 /gi=14043071 /ug=Hs.232400 /len=1780	NM_002137; NM_031243	Hs.232400	NP_112533
fcrb7098	NM_031298	hypothetical protein MGC2963 (MGC2963), mRNA /cds=(135,467) /gb=NM_031298 /gi=13775219 /ug=Hs.30011 /len=673	NM_031298	Hs.30011	NP_112588
fcrb1604	NM_031302	gycosyltransferase (LOC83468), mRNA /cds=(408,1457) /gb=NM_031302 /gi=21314737 /ug=Hs.159993 /len=1908	NM_031302	Hs.159993	NP_112592

ncrc5845	NM_031370	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa) (HNRPD), transcript variant 1, mRNA /cds=(286,1353) /gb=NM_031370 /gi=14110419 /ug=Hs.406404 /len=2197	NM_002138; NM_031369; NM_031370	Hs.406404	NP_112738
miob2192	NM_032174	hypothetical protein FLJ12770 (FLJ12770), mRNA /cds=(187,1113) /gb=NM_032174 /gi=21362029 /ug=Hs.321653 /len=2670	NM_032174	Hs.321653	NP_115550
ncrc2780	NM_032231	hypothetical protein FLJ22875 (FLJ22875), mRNA /cds=(152,634) /gb=NM_032231 /gi=15638951 /ug=Hs.406548 /len=1019	NM_032231	Hs.406548	NP_115607
seob8807	NM_032245	hypothetical protein DKFZp434I1916 (DKFZp434I1916), mRNA /cds=(144,563) /gb=NM_032245 /gi=14149959 /ug=Hs.334641 /len=800	NM_032245	Hs.334641	NP_115621
miod5190	NM_032280	hypothetical protein DKFZp761J139 (DKFZp761J139), mRNA /cds=(3155,3970) /gb=NM_032280 /gi=14150026 /ug=Hs.15536 /len=4635	NM_032280	Hs.15536	NP_115656

ncr8893	NM_032320	hypothetical protein MGC13007 (MGC13007), mRNA /cds=(1099,1653) /gb=NM_032320 /gi=14150091 /ug=Hs.332382 /len=2479	NM_032320	Hs.332382	NP_115696
mioa4782	NM_032328	hypothetical protein MGC12458 (MGC12458), mRNA /cds=(30,518) /gb=NM_032328 /gi=14150107 /ug=Hs.330664 /len=1026	NM_032328	Hs.330664	NP_115704
seoc4609	NM_032328	hypothetical protein MGC12458 (MGC12458), mRNA /cds=(30,518) /gb=NM_032328 /gi=14150107 /ug=Hs.330664 /len=1026	NM_032328	Hs.330664	NP_115704
ncrb0653	NM_032357	hypothetical protein MGC12981 (MGC12981), mRNA /cds=(225,767) /gb=NM_032357 /gi=21362049 /ug=Hs.104203 /len=1644	NM_032357	Hs.104203	NP_115733
fcrb4892	NM_018929	protocadherin gamma subfamily C, 5 (PCDHGC5), transcript variant 1, mRNA /cds=(1,2835) /gb=NM_018929 /gi=14277683 /ug=Hs.335001 /len=4641	NM_018929; NM_032407	Hs.335001	NP_115783
seob2337	NM_032549	inner mitochondrial membrane peptidase 2 like (IMMP2L), mRNA /cds=(444,971) /gb=NM_032549 /gi=14211844 /ug=Hs.89576 /len=1540	NM_032549	Hs.89576	NP_115938

ncrc4371	NM_032560	hypothetical protein FLJ20707 (FLJ20707), mRNA /cds=(83,2173) /gb=NM_032560 /gi=19923643 /ug=Hs.334657 /len=2794	NM_017936; NM_032560	Hs.334657	NP_115949
fcrb1381	NM_032560	hypothetical protein FLJ20707 (FLJ20707), mRNA /cds=(83,2173) /gb=NM_032560 /gi=19923643 /ug=Hs.334657 /len=2794	NM_017936; NM_032560	Hs.334657	NP_115949
fcrb5914	NM_032603	lysyl oxidase-like 3 (LOXL3), mRNA /cds=(73,2334) /gb=NM_032603 /gi=22095373 /ug=Hs.334702 /len=3121	NM_032603	Hs.334702	NP_115992
mioc8750	NM_032622	ligand of numb-protein X (LNX), mRNA /cds=(236,2134) /gb=NM_032622 /gi=14249127 /ug=Hs.66295 /len=3737	NM_032622	Hs.66295	NP_116011
hfcr2658	NM_006411	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha) (AGPAT1), transcript variant 1, mRNA /cds=(319,1170) /gb=NM_006411 /gi=26787964 /ug=Hs.240534 /len=2242	NM_006411; NM_032741	Hs.240534	NP_116130
fcrb9134	NM_032840	hypothetical protein FLJ14800 (FLJ14800), mRNA /cds=(22,1350) /gb=NM_032840 /gi=14249553 /ug=Hs.62119 /len=2568	NM_032840	Hs.62119	NP_116229

fcrb4231	NM_032849	hypothetical protein FLJ14834 (FLJ14834), mRNA /cds=(326,1237) /gb=NM_032849 /gi=21361885 /ug=Hs.62905 /len=2342	NM_032849	Hs.62905	NP_116238
ncrc4384	NM_032870	SR rich protein (DKFZp564B0769), mRNA /cds=(33,2450) /gb=NM_032870 /gi=18699723 /ug=Hs.18368 /len=2663	NM_032870	Hs.18368	NP_116259
mioc8479	NM_032870	SR rich protein (DKFZp564B0769), mRNA /cds=(33,2450) /gb=NM_032870 /gi=18699723 /ug=Hs.18368 /len=2663	NM_032870	Hs.18368	NP_116259
mioc2997	NM_032927	hypothetical protein MGC13159 (MGC13159), mRNA /cds=(592,1017) /gb=NM_032927 /gi=14249719 /ug=Hs.12845 /len=1759	NM_032927	Hs.12845	NP_116316
miob7627	NM_033111	CG016 (LOC88523), mRNA /cds=(323,2230) /gb=NM_033111 /gi=14916464 /ug=Hs.112434 /len=2431	NM_033111	Hs.112434	NP_149102
fcrb8060	BC040354	Similar to caldesmon 1, clone MGC:21352 IMAGE:4753285, mRNA, complete cds (=OK/SW-cl.14 mRNA, complete cds, AB062484.1)	NM_004342; NM_033138; NM_033139; NM_033140; NM_033157	Hs.325474	NP_149347

mioc3127	NM_033138	caldesmon 1 (CALD1), transcript variant 1, mRNA /cds=(230,2611) /gb=NM_033138 /gi=15149460 /ug=Hs.325474 /len=3610	NM_004342; NM_033138; NM_033139; NM_033140; NM_033157	Hs.325474	NP_149347
seob7404	NM_001656	ADP-ribosylation factor domain protein 1, 64kDa (ARFD1), transcript variant alpha, mRNA /cds=(23,1747) /gb=NM_001656 /gi=15208639 /ug=Hs.792 /len=3565	NM_001656; NM_033227; NM_033228	Hs.792	NP_150231
mioa9492	NM_033264	Mus musculus protein phosphatase 1, regulatory (inhibitor) subunit 1C (Ppp1r1c), mRNA	NM_033264	Mm.29963	NP_150289
seoa7296	NM_012142	cyclin D-type binding-protein 1 (CCNDBP1), transcript variant 1, mRNA /cds=(158,1240) /gb=NM_012142 /gi=16554565 /ug=Hs.36794 /len=1615	NM_012142; NM_037370	Hs.36794	NP_411241
miob6226	NM_052815	immediate early response 3 (IER3), transcript variant long, mRNA /cds=(30,611) /gb=NM_052815 /gi=16554596 /ug=Hs.76095 /len=1345	NM_003897; NM_052815	Hs.76095	NP_434702
hfcr2789	NM_052871	hypothetical protein MGC4677 (MGC4677), mRNA /cds=(1337,1495) /gb=NM_052871 /gi=16418372 /ug=Hs.432419 /len=1607	NM_052871	Hs.432419	NP_443103

fcr2821	NM_000075	cyclin-dependent kinase 4 (CDK4), transcript variant 1, mRNA /cds=(228,1139) /gb=NM_000075 /gi=16936531 /ug=Hs.95577 /len=1474	NM_000075; NM_052984	Hs.95577	NP_443710
seoa1104	NM_016071	mitochondrial ribosomal protein S33 (MRPS33), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA /cds=(139,459) /gb=NM_016071 /gi=16950595 /ug=Hs.83006 /len=727	NM_016071; NM_053035	Hs.83006	NP_444263
ncrc3526	NM_006625	FUS interacting protein (serine-arginine rich) 1 (FUSIP1), transcript variant 1, mRNA	NM_006625; NM_054016	Hs.3530	NP_473357
fcrb6890	NM_013354	CCR4-NOT transcription complex, subunit 7 (CNOT7), transcript variant 1, mRNA /cds=(340,1128) /gb=NM_013354 /gi=17978498 /ug=Hs.380963 /len=2653	NM_013354; NM_054026	Hs.380963	NP_473367
fcr2952	NM_058246	DnaJ (Hsp40) subfamily B, member 6 (DNAJB6), transcript variant 1, mRNA /cds=(156,1136) /gb=NM_058246 /gi=24234717 /ug=Hs.181195 /len=2495	NM_005494; NM_058246	Hs.181195	NP_490647

seob2974	NM_078467	cyclin-dependent kinase inhibitor 1A (p21, Cip1) (CDKN1A), transcript variant 2, mRNA /cds=(236,730) /gb=NM_078467 /gi=17978494 /ug=Hs.179665 /len=2281	NM_000389; NM_078467	Hs.179665	NP_510867
seob1801	NM_078469	BRCA2 and CDKN1A interacting protein (BCCIP), transcript variant C, mRNA /cds=(13,891) /gb=NM_078469 /gi=17402872 /ug=Hs.279862 /len=2338	NM_016567; NM_078468; NM_078469	Hs.279862	NP_510869
fcrb1834	NM_079425	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_021019; NM_079423; NM_079424; NM_079425	Hs.77385	NP_524149
fcrb2208	NM_079425	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_021019; NM_079423; NM_079424; NM_079425	Hs.77385	NP_524149
ncrc4135	NM_079425	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_021019; NM_079423; NM_079424; NM_079425	Hs.77385	NP_524149

ncrc0097	NM_079425	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA /cds=(41,514) /gb=NM_079425 /gi=17986263 /ug=Hs.77385 /len=717	NM_021019; NM_079423; NM_079424; NM_079425	Hs.77385	NP_524149
fcr3053	NM_080425	GNAS complex locus (GNAS), transcript variant 3, mRNA /cds=(1,2730) /gb=NM_080425 /gi=18426897 /ug=Hs.374523 /len=3091	NM_000516; NM_016592; NM_080425; NM_080426	Hs.374523	NP_536351
miob2855	NM_080425	GNAS complex locus (GNAS), transcript variant 3, mRNA /cds=(1,2730) /gb=NM_080425 /gi=18426897 /ug=Hs.374523 /len=3091	NM_000516; NM_016592; NM_080425; NM_080426	Hs.374523	NP_536351
fcrc1745	BQ066467	AGENCOURT_6861057 NIH_MGC_99 cDNA clone IMAGE:5931113 5', mRNA sequence /clone=IMAGE:5931113 /clone_end=5' /gb=BQ066467 /gi=19895513 /ug=Hs.446485 /len=1029		Hs.446485	NP_536351
hfcr5865	NM_080599	UPF2 regulator of nonsense transcripts (yeast) (UPF2), transcript variant 1, mRNA /cds=(130,3948) /gb=NM_080599 /gi=18375675 /ug=Hs.3862 /len=5223	NM_015542; NM_080599	Hs.3862	NP_542166

mioc5103	NM_080655	similar to RIKEN cDNA 5730528L13 gene (MGC17337), mRNA /cds=(68,895) /gb=NM_080655 /gi=18087818 /ug=Hs.78531 /len=1175	NM_080655	Hs.78531	NP_542386
miod4449	NM_080821	chromosome 20 open reading frame 108 (C20orf108), mRNA /cds=(41,619) /gb=NM_080821 /gi=18201877 /ug=Hs.352413 /len=3026	NM_080821	Hs.352413	NP_543011
mioa9189	NM_030781	collectin sub-family member 12 (COLEC12), transcript variant II, mRNA /cds=(172,2040) /gb=NM_030781 /gi=18641357 /ug=Hs.29423 /len=4685	NM_030781; NM_130386	Hs.29423	NP_569057
mioa6147	NM_133370	KIAA1966 protein (KIAA1966), mRNA /cds=(492,2468) /gb=NM_133370 /gi=21166354 /ug=Hs.158184 /len=3248	NM_133370	Hs.158184	NP_588611
ncrc1811	NM_005732	RAD50 (S. cerevisiae) (RAD50), transcript variant 1, mRNA /cds=(388,4326) /gb=NM_005732 /gi=19924128 /ug=Hs.41587 /len=5891	NM_005732; NM_133482	Hs.41587	NP_597816
seob4451	NM_133493	CD109 (CD109), mRNA /cds=(113,4450) /gb=NM_133493 /gi=19424129 /ug=Hs.55964 /len=5883	NM_133493	Hs.55964	NP_598000

ncrc2119	NM_001920	decorin (DCN), transcript variant A1, mRNA /cds=(200,1279) /gb=NM_001920 /gi=19743844 /ug=Hs.433989 /len=1751	NM_001920; NM_133503; NM_133504; NM_133505; NM_133506; NM_133507	Hs.433989	NP_598014
seoa2654	BC000626	clone MGC:3081 IMAGE:3347416, mRNA, complete cds	NM_015227	Hs.22982	NP_598368
mioa6731	NM_134264	SOCS box-containing WD protein SWiP-1 (WSB1), transcript variant 3, mRNA /cds=(317,1051) /gb=NM_134264 /gi=20143909 /ug=Hs.187991 /len=4243	NM_015626; NM_134264; NM_134265	Hs.187991	NP_599027
seob5379	NM_134408	Rattus norvegicus calcium-independent alpha-latrotoxin receptor 2 (Cirl2), mRNA	NM_134408	Rn.12089	NP_599235
ncrb8585	NM_138363	hypothetical protein BC009518 (LOC90799), mRNA /cds=(59,2524) /gb=NM_138363 /gi=19923898 /ug=Hs.135265 /len=2705	NM_138363	Hs.135265	NP_612372
fcrc2852	AK094179	cDNA FLJ36860 fis, clone ASTRO2015295. /gb=AK094179 /gi=21753186 /ug=Hs.352406 /len=2882		Hs.352406	NP_612398
fcr2220	NM_138619	golgi associated, gamma adaptin ear containing, ARF binding protein 3 (GGA3), transcript variant long, mRNA /cds=(10,2181) /gb=NM_138619 /gi=20336266 /ug=Hs.87726 /len=3860	NM_014001; NM_138619	Hs.87726	NP_619525

ncrb5060	NM_012104	beta-site APP-cleaving enzyme (BACE), transcript variant a, mRNA /cds=(447,1952) /gb=NM_012104 /gi=21040369 /ug=Hs.49349 /len=5832	NM_012104; NM_138971; NM_138972; NM_138973	Hs.49349	NP_620429
mioc9262	AJ345030	mRNA for presenilin-like protein 4 (PSL4 gene)	NM_139015	Hs.21143	NP_620584
ncr2717	NM_139078	mitogen-activated protein kinase-activated protein kinase 5 (MAPKAPK5), transcript variant 2, mRNA /cds=(260,1681) /gb=NM_139078 /gi=21237767 /ug=Hs.30327 /len=2066	NM_003668; NM_139078	Hs.30327	NP_620777
seoc2213	AK026207	cDNA: FLJ22554 fis, clone HSI01092		Hs.93842	NP_631903
fcrb4802	NM_139207	nucleosome assembly protein 1-like 1 (NAP1L1), transcript variant 1, mRNA /cds=(125,1300) /gb=NM_139207 /gi=21327707 /ug=Hs.302649 /len=3582	NM_004537; NM_139207	Hs.302649	NP_631946
mioc0107	NM_144596	tetratricopeptide repeat domain 8 (TTC8), mRNA /cds=(53,1648) /gb=NM_144596 /gi=21389382 /ug=Hs.55158 /len=2241	NM_144596	Hs.55158	NP_653197
ncr3976	NM_007200	A kinase (PRKA) anchor protein 13 (AKAP13), transcript variant 2, mRNA /cds=(214,8655) /gb=NM_007200 /gi=21493028 /ug=Hs.301946 /len=10156	NM_006738; NM_007200; NM_144767	Hs.301946	NP_658913

ncrc3276	NM_144772	apolipoprotein A-I binding protein (APOA1BP), mRNA /cds=(28,894) /gb=NM_144772 /gi=21426826 /ug=Hs.374850 /len=1120	NM_144772	Hs.374850	NP_658985
mioa4883	NM_144778	muscleblind-like protein MBLL39 (MBLL39), transcript variant 1, mRNA /cds=(782,1885) /gb=NM_144778 /gi=21464124 /ug=Hs.283609 /len=4665	NM_005757; NM_144778	Hs.283609	NP_659002
seob9435	NM_145040	protein kinase C, delta binding protein (PRKCDBP), mRNA /cds=(35,820) /gb=NM_145040 /gi=21450786 /ug=Hs.431979 /len=1053	NM_145040	Hs.431979	NP_659477
ncr3197	NM_145080	non-SMC (structural maintenance of chromosomes) element 1 protein (NSE1), mRNA /cds=(24,794) /gb=NM_145080 /gi=21489972 /ug=Hs.284295 /len=992	NM_145080	Hs.284295	NP_659547
seoa3106	NM_145080	non-SMC (structural maintenance of chromosomes) element 1 protein (NSE1), mRNA /cds=(24,794) /gb=NM_145080 /gi=21489972 /ug=Hs.284295 /len=992	NM_145080	Hs.284295	NP_659547
ncrc9280	NM_145283	similar to hypothetical protein BC014127 (LOC158046), mRNA	NM_145283	Hs.309216	NP_660326

seoa1427	NM_145690	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ), transcript variant 2, mRNA /cds=(127,864) /gb=NM_145690 /gi=21735624 /ug=Hs.75103 /len=2876	NM_003406; NM_145690	Hs.75103	NP_663723
miob7373	NM_145808	likely ortholog of rat V-1 protein (V-1), mRNA /cds=(229,585) /gb=NM_145808 /gi=21956644 /ug=Hs.21321 /len=3770	NM_145808	Hs.21321	NP_665807
ncr0663	NM_145869	annexin A11 (ANXA11), transcript variant c, mRNA /cds=(484,2001) /gb=NM_145869 /gi=22165432 /ug=Hs.75510 /len=2731	NM_001157; NM_145868; NM_145869	Hs.75510	NP_665876
seob9820	NM_002624	prefoldin 5 (PFDN5), transcript variant 1, mRNA /cds=(36,500) /gb=NM_002624 /gi=22202632 /ug=Hs.288856 /len=661	NM_002624; NM_145896; NM_145897	Hs.288856	NP_665904
miob4055	NM_007203	A kinase (PRKA) anchor protein 2 (AKAP2), transcript variant 1, mRNA /cds=(181,3492) /gb=NM_007203 /gi=22325354 /ug=Hs.42322 /len=7522	NM_007203; NM_147150	Hs.42322	NP_671492
mioc7471	NM_006277	intersectin 2 (ITSN2), transcript variant 1, mRNA /cds=(242,5332) /gb=NM_006277 /gi=22325384 /ug=Hs.166184 /len=6092	NM_006277; NM_019595; NM_147152	Hs.166184	NP_671494

miob5855	BC042899	Similar to hypothetical protein MGC30540, clone MGC:17342 IMAGE:4342258, mRNA, complete cds /cds=(216,1457) /gb=BC042899 /gi=27552863 /ug=Hs.153716 /len=3028	NM_147156	Hs.153716	NP_671512
seoa7443	NM_021249	sorting nexin 6 (SNX6), transcript variant 1, mRNA /cds=(498,1370) /gb=NM_021249 /gi=23111048 /ug=Hs.284291 /len=3041	NM_021249; NM_152233	Hs.284291	NP_689419
seob6572	NM_152255	proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7), transcript variant 2, mRNA /cds=(116,616) /gb=NM_152255 /gi=23110947 /ug=Hs.233952 /len=1069	NM_002792; NM_152255	Hs.233952	NP_689468
miod6560	NM_152261	hypothetical protein MGC17943 (MGC17943), mRNA /cds=(214,564) /gb=NM_152261 /gi=22748614 /ug=Hs.106390 /len=3167	NM_152261	Hs.106390	NP_689474
fcrc6043	NM_152344	hypothetical protein FLJ30656 (FLJ30656), mRNA /cds=(52,639) /gb=NM_152344 /gi=22748746 /ug=Hs.349887 /len=2212	NM_152344	Hs.349887	NP_689557
seob5632	NM_152391	hypothetical protein MGC33602 (MGC33602), mRNA /cds=(140,748) /gb=NM_152391 /gi=22748836 /ug=Hs.274415 /len=1790	NM_152391	Hs.274415	NP_689604

miob7550	NM_152392	hypothetical protein DKFZp564C236 (DKFZp564C236), mRNA /cds=(1590,2003) /gb=NM_152392 /gi=22748838 /ug=Hs.378856 /len=2161	NM_152392	Hs.378856	NP_689605
mioc7570	NM_152392	hypothetical protein DKFZp564C236 (DKFZp564C236), mRNA /cds=(1590,2003) /gb=NM_152392 /gi=22748838 /ug=Hs.378856 /len=2161	NM_152392	Hs.378856	NP_689605
miod2886	NM_152520	hypothetical protein FLJ25270 (FLJ25270), mRNA /cds=(244,1353) /gb=NM_152520 /gi=22749086 /ug=Hs.6295 /len=2493	NM_152520	Hs.6295	NP_689733
hfcr2389	NM_152544	hypothetical protein FLJ35725 (FLJ35725), mRNA /cds=(201,1298) /gb=NM_152544 /gi=22749134 /ug=Hs.380632 /len=1851	NM_152544	Hs.380632	NP_689757
seoc4762	NM_152553	hypothetical protein MGC26996 (MGC26996), mRNA /cds=(344,1171) /gb=NM_152553 /gi=22749144 /ug=Hs.307526 /len=1804	NM_152553	Hs.307526	NP_689766
ncrc4508	NM_152576	hypothetical protein MGC24103 (MGC24103), mRNA /cds=(445,549) /gb=NM_152576 /gi=22749194 /ug=Hs.287447 /len=1767	NM_152576	Hs.287447	NP_689789

ncrc5648	NM_152862	actin related protein 2/3 complex, subunit 2, 34kDa (ARPC2), transcript variant 1, mRNA /cds=(113,1015) /gb=NM_152862 /gi=23238210 /ug=Hs.83583 /len=1462	NM_005731; NM_152862	Hs.83583	NP_690601
ncrc0849	NM_152306	ubiquitin-like, containing PHD and RING finger domains 2 (URF2), transcript variant 1, mRNA /cds=(341,1852) /gb=NM_152306 /gi=23312361 /ug=Hs.348602 /len=3720	NM_152306; NM_152896	Hs.348602	NP_690856
seob0426	NM_152932	glycosyltransferase AD-017 (AD-017), transcript variant 1, mRNA /cds=(140,1255) /gb=NM_152932 /gi=23510345 /ug=Hs.283737 /len=1635	NM_018446; NM_152932	Hs.283737	NP_690909
seob4030	NM_153012	tumor necrosis factor (ligand) superfamily, member 12 (TNFSF12), transcript variant 2, mRNA /cds=(97,501) /gb=NM_153012 /gi=23510440 /ug=Hs.26401 /len=1642	NM_003809; NM_153012	Hs.26401	NP_694557
miod3983	AK057950	cDNA FLJ25221 fis, clone STM00723	NM_153013	Hs.81907	NP_694558
fcrc5713	NM_021090	myotubularin related protein 3 (MTMR3), transcript variant 3, mRNA /cds=(288,3884) /gb=NM_021090 /gi=23510385 /ug=Hs.63302 /len=5963	NM_021090; NM_153050; NM_153051	Hs.63302	NP_694691

miod1924	NM_153208	hypothetical protein MGC35048 (MGC35048), mRNA /cds=(700,1563) /gb=NM_153208 /gi=23397455 /ug=Hs.367493 /len=2603	NM_153208	Hs.367493	NP_694940
miod1814	NM_153267	hypothetical protein MGC21981 (MGC21981), mRNA /cds=(66,764) /gb=NM_153267 /gi=23397567 /ug=Hs.131987 /len=1727	NM_153267	Hs.131987	NP_694999
ncr9587	NM_003334	ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing) (UBE1), transcript variant 1, mRNA /cds=(130,3306) /gb=NM_003334 /gi=23510337 /ug=Hs.2055 /len=3504	NM_003334; NM_153280	Hs.2055	NP_695012
fcrb3843	BC028002	clone IMAGE:5212110, mRNA /gb=BC028002 /gi=24081066 /ug=Hs.386507 /len=2415	NM_032921; NM_153373	Hs.386507	NP_699204
seoa4598	NM_153425	TNFRSF1A-associated via death domain (TRADD), transcript variant 2, mRNA /cds=(731,1489) /gb=NM_153425 /gi=24234725 /ug=Hs.89862 /len=1959	NM_003789; NM_153425	Hs.89862	NP_700474
miob8816	NM_004516	interleukin enhancer binding factor 3, 90kDa (ILF3), transcript variant 2, mRNA	NM_004516; NM_012218; NM_153464	Hs.256583	NP_703194

miob8578	NM_153638	pantothenate kinase 2 (Hallervorden-Spatz syndrome) (PANK2), transcript variant 1, mRNA /cds=(56,1399) /gb=NM_153638 /gi=24430170 /ug=Hs.286212 /len=1959	NM_024960; NM_153637; NM_153638; NM_153639; NM_153640; NM_153641	Hs.286212	NP_705905
fcrb7833	NM_153649	tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=NM_153649 /gi=24119202 /ug=Hs.85844 /len=2089	NM_152263; NM_153649	Hs.85844	NP_705935
mioc2021	NM_153649	tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=NM_153649 /gi=24119202 /ug=Hs.85844 /len=2089	NM_152263; NM_153649	Hs.85844	NP_705935
fcrb3739	NM_018951	homeo box A10 (HOXA10), transcript variant 1, mRNA /cds=(50,1231) /gb=NM_018951 /gi=24497548 /ug=Hs.110637 /len=2618	NM_018951; NM_153715	Hs.110637	NP_714926
ncrc0807	AI498805	tm68a09.x1 NCI_CGAP_Brn25 cDNA clone IMAGE:2163256 3', mRNA sequence /clone=IMAGE:2163256 /clone_end=3' /gb=AI498805 /gi=4390787 /ug=Hs.436349 /len=460		Hs.436349	NP_722550
ncr1218	NM_170662	Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB), mRNA	NM_170662		NP_733762

miob3898	NM_006930	S-phase kinase-associated protein 1A (p19A) (SKP1A), transcript variant 1, mRNA /cds=(140,622) /gb=NM_006930 /gi=25777710 /ug=Hs.171626 /len=2172	NM_006930; NM_170679	Hs.171626	NP_733779
seoa1739	NM_006930	S-phase kinase-associated protein 1A (p19A) (SKP1A), transcript variant 1, mRNA /cds=(140,622) /gb=NM_006930 /gi=25777710 /ug=Hs.171626 /len=2172	NM_006930; NM_170679	Hs.171626	NP_733779
ncrc3358	NM_006930	S-phase kinase-associated protein 1A (p19A) (SKP1A), transcript variant 1, mRNA /cds=(140,622) /gb=NM_006930 /gi=25777710 /ug=Hs.171626 /len=2172	NM_006930; NM_170679	Hs.171626	NP_733779
fcrb2162	NM_170707	lamin A/C (LMNA), transcript variant 1, mRNA /cds=(213,2207) /gb=NM_170707 /gi=27436945 /ug=Hs.377973 /len=3181	NM_005572; NM_170707; NM_170708	Hs.377973	NP_733822
ncrb0303	NM_170746	selenoprotein H (SELH), mRNA /cds=(243,611) /gb=NM_170746 /gi=25014108 /ug=Hs.290874 /len=834	NM_170746	Hs.290874	NP_734467

miob3249	NM_013411	adenylate kinase 2 (AK2), nuclear gene encoding mitochondrial protein, transcript variant AK2B, mRNA /cds=(43,741) /gb=NM_013411 /gi=26665888 /ug=Hs.294008 /len=2146	NM_001625; NM_013411; NM_172199	Hs.294008	NP_751949
ncrc9736	NM_018672	ATP-binding cassette, sub-family A (ABC1), member 5 (ABCA5), transcript variant 1, mRNA /cds=(1219,6147) /gb=NM_018672 /gi=27262623 /ug=Hs.180513 /len=7044	NM_018672; NM_172232	Hs.180513	NP_758424
miod7367	NM_006186	nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, mRNA /cds=(336,2132) /gb=NM_006186 /gi=27894347 /ug=Hs.82120 /len=3447	NM_006186; NM_173171; NM_173172; NM_173173	Hs.82120	NP_775265
seoc4316	NM_006333	nuclear DNA-binding protein (C1D), transcript variant 1, mRNA /cds=(64,489) /gb=NM_006333 /gi=27894371 /ug=Hs.15164 /len=1200	NM_006333; NM_173177	Hs.15164	NP_775269
fcrb4375	NM_173354	SNF1-like kinase (SNF1LK), mRNA /cds=(98,2449) /gb=NM_173354 /gi=27597093 /ug=Hs.380991 /len=4726	NM_173354	Hs.380991	NP_775490

ncrb8220	NM_173471	hypothetical protein LOC115286 (LOC115286), mRNA /cds=(189,740) /gb=NM_173471 /gi=27735034 /ug=Hs.379386 /len=1873	NM_173471	Hs.379386	NP_775742
miob2067	NM_173474	hypothetical protein LOC123803 (LOC123803), mRNA /cds=(15,947) /gb=NM_173474 /gi=27735048 /ug=Hs.351573 /len=1146	NM_173474	Hs.351573	NP_775745
ncrb3373	NM_006785	mucosa associated lymphoid tissue lymphoma translocation gene 1 (MALT1), transcript variant 1, mRNA /cds=(259,2733) /gb=NM_006785 /gi=27886564 /ug=Hs.180566 /len=5029	NM_006785; NM_173844	Hs.180566	NP_776216
seoc4356	NM_173852	keratinocytes associated protein 2 (KCP2), mRNA /cds=(1,489) /gb=NM_173852 /gi=27777660 /ug=Hs.374854 /len=489	NM_173852	Hs.374854	NP_776251
mioa4628	NM_002816	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (PSMD12), mRNA /cds=(44,1414) /gb=NM_002816 /gi=4506220 /ug=Hs.4295 /len=3548	NM_002816; NM_174871	Hs.4295	NP_777360

miod0468	BC042754	Similar to low density lipoprotein receptor-related protein 2, clone IMAGE:4828259, mRNA, partial cds /cds=(1,1059) /gb=BC042754 /gi=27769271 /ug=Hs.205865 /len=3814	NM_174902	Hs.205865	NP_777562
miod5984	BC028585	hypothetical gene supported by AK000174; AK055070; AK055612, clone IMAGE:4836971, mRNA		Hs.374538	NP_777569
seob7613	NM_004349	core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1), transcript variant 1, mRNA /cds=(412,2145) /gb=NM_004349 /gi=28329413 /ug=Hs.31551 /len=3463	NM_004349; NM_175634; NM_175635; NM_175636	Hs.31551	NP_783554
seoa3885	AK090822	cDNA FLJ33503 fis, clone BRAMY2004521. /cds=(367,750) /gb=AK090822 /gi=21749052 /ug=Hs.356719 /len=2339	NM_175893	Hs.356719	NP_787089
seoa1559	AB011108	hypothetical protein (KIAA0536)	NM_003913; NM_176800	Hs.198891	NP_789770
seoc2470	BC033859	chromosome 20 open reading frame 178, clone MGC:45387 IMAGE:5173394, mRNA, complete cds	NM_176812	Hs.352579	NP_789782
seob7547	NM_014599	melanoma antigen, family D, 2 (MAGED2), mRNA /cds=(97,1917) /gb=NM_014599 /gi=21264316 /ug=Hs.4943 /len=2077	NM_014599; NM_177433	Hs.4943	NP_803182

fcrc1974	NM_014782	armadillo repeat protein ALEX2 (ALEX2), mRNA /cds=(458,2356) /gb=NM_014782 /gi=21361239 /ug=Hs.48924 /len=2788	NM_177949	Hs.48924	NP_808818
fcrb3476	NM_021131	protein phosphatase 2A, regulatory subunit B' (PR 53) (PPP2R4), mRNA /cds=(190,1161) /gb=NM_021131 /gi=10880986 /ug=Hs.400740 /len=2661	NM_021131; NM_178000; NM_178001; NM_178002; NM_178003	Hs.400740	NP_821070
seob5640	BC013374	clone MGC:16435 IMAGE:3946253, mRNA, complete cds /cds=(137,1471) /gb=BC013374 /gi=15426525 /ug=Hs.179661 /len=2519	NM_178014	Hs.179661	NP_821133
fcrb7780	NM_178148	solute carrier family 35, member B2 (SLC35B2), mRNA	NM_178148		NP_835361
fcrb8973	NM_030789	histocompatibility (minor) 13 (HM13), mRNA /cds=(86,1219) /gb=NM_030789 /gi=23308606 /ug=Hs.386538 /len=1584	NM_030789	Hs.386538	NP_848697
ncrc4320	NM_015339	activity-dependent neuroprotector (ADNP), mRNA /cds=(346,3654) /gb=NM_015339 /gi=12229216 /ug=Hs.3657 /len=4713	NM_015339	Hs.3657	NP_852107
hfcr2890	NM_144601	chemokine-like factor super family 3 (CKLFSF3), mRNA /cds=(527,1075) /gb=NM_144601 /gi=21389400 /ug=Hs.7773 /len=2318	NM_144601	Hs.7773	NP_853533

seob6131	NM_002916	replication factor C (activator 1) 4, 37kDa (RFC4), mRNA /cds=(284,1375) /gb=NM_002916 /gi=4506490 /ug=Hs.35120 /len=1446	NM_002916	Hs.35120	NP_853551
ncrc7040	NM_012094	peroxiredoxin 5 (PRDX5), mRNA /cds=(37,681) /gb=NM_012094 /gi=6912237 /ug=Hs.31731 /len=805	NM_012094	Hs.31731	NP_857635
mioc4994	AK026583	cDNA: FLJ22930 fis, clone KAT07255. /gb=AK026583 /gi=10439467 /ug=Hs.90790 /len=1600		Hs.90790	NP_858042
seob7409	NM_006534	nuclear receptor coactivator 3 (NCOA3), mRNA /cds=(184,4422) /gb=NM_006534 /gi=5729725 /ug=Hs.225977 /len=6754	NM_006534	Hs.225977	NP_858045
ncrc5688	NM_003605	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase) (OGT), mRNA /cds=(2040,4802) /gb=NM_003605 /gi=6006036 /ug=Hs.100293 /len=5733	NM_003605	Hs.100293	NP_858059
fcrc0631	AL834355	mRNA; cDNA DKFZp547F237 (from clone DKFZp547F237); complete cds (=AK024813.1)		Hs.6820	NP_859049

ncrc7016	NM_012381	origin recognition complex, subunit 3-like (yeast) (ORC3L), mRNA /cds=(27,2162) /gb=NM_012381 /gi=6912561 /ug=Hs.74420 /len=2510	NM_012381	Hs.74420	NP_862820
fcrb5313	NM_002654	pyruvate kinase, muscle (PKM2), mRNA /cds=(110,1705) /gb=NM_002654 /gi=4505838 /ug=Hs.198281 /len=2287	NM_002654	Hs.198281	NP_872271
mioa1163	BU727332	UI-E-CQ1-act-a-04-0-UI.s1 UI-E-CQ1 cDNA clone UI-E-CQ1-act-a-04-0-UI 3', mRNA sequence /clone=UI-E-CQ1-act-a-04-0-UI /clone_end=3' /gb=BU727332 /gi=23648099 /ug=Hs.116567 /len=1621		Hs.116567	NP_872297
seoa5090	NM_006754	synaptophysin-like protein (SYPL), mRNA /cds=(34,813) /gb=NM_006754 /gi=5803184 /ug=Hs.80919 /len=2130	NM_006754	Hs.80919	NP_874384
seob7229	NM_002493	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa (NDUFB6), mRNA /cds=(104,490) /gb=NM_002493 /gi=20149518 /ug=Hs.109646 /len=733	NM_002493	Hs.109646	NP_877416

seob4039	NM_021960	myeloid cell leukemia sequence 1 (BCL2-related) (MCL1), mRNA /cds=(64,1116) /gb=NM_021960 /gi=19923213 /ug=Hs.86386 /len=3953	NM_021960	Hs.86386	NP_877495
fcr5176	NM_001675	activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4), mRNA /cds=(882,1937) /gb=NM_001675 /gi=4502264 /ug=Hs.181243 /len=2015	NM_001675	Hs.181243	NP_877962
fcrb5840	NM_016240	scavenger receptor class A, member 3 (SCARA3), mRNA /cds=(142,1962) /gb=NM_016240 /gi=7705335 /ug=Hs.128856 /len=3636	NM_016240	Hs.128856	NP_878185
mioa1055	NM_016106	vesicle transport-related protein (RA410), mRNA /cds=(8,1930) /gb=NM_016106 /gi=7706370 /ug=Hs.27023 /len=2149	NM_016106; NM_016163	Hs.27023	NP_878255
mioa1708	NM_001969	eukaryotic translation initiation factor 5 (EIF5), mRNA /cds=(469,1764) /gb=NM_001969 /gi=21361336 /ug=Hs.433702 /len=3899	NM_001969	Hs.433702	NP_892116
fcr0018	NM_016208	vacuolar protein sorting 28 (yeast) (VPS28), mRNA /cds=(62,727) /gb=NM_016208 /gi=7705884 /ug=Hs.339697 /len=928	NM_016208	Hs.339697	NP_898880

seob6510	NM_000311	prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia) (PRNP), mRNA /cds=(50,811) /gb=NM_000311 /gi=4506112 /ug=Hs.74621 /len=2415	NM_000311	Hs.74621	NP_898902
miod0533	AF253417	microsomal epoxide hydrolase (EPHX1) gene, complete cds	NM_000120		NP_000111
seoa5679	X66503	adenylosuccinate synthetase mRNA	NM_001126		NP_001117
mioa1077	NM_018212	enabled (Drosophila) (ENAH), mRNA /cds=(77,646) /gb=NM_018212 /gi=8922657 /ug=Hs.14838 /len=2943	NM_018212	Hs.14838	NP_060682
fcrb8910	NM_006083	IK cytokine, down-regulator of HLA II (IK), mRNA /cds=(112,1785) /gb=NM_006083 /gi=11038650 /ug=Hs.8024 /len=1785	NM_006083	Hs.8024	NP_006074
mioa4677	AJ010770	hyperion gene, exons 1-50	NM_005751; NM_147166; NM_147171; NM_147185		NP_005742; NP_671695; NP_671700; NP_671714
fcr4024	AF058293	D-dopachrome tautomerase (=U49785; Y11151)	NM_001355		NP_001346
seob3386	AB017563	IGSF4 gene, exon 10 and complete cds	NM_014333		NP_055148
ncrc1032	NM_147185	A kinase (PRKA) anchor protein (yotiao) 9 (AKAP9), transcript variant 3, mRNA	NM_005751; NM_147166; NM_147171; NM_147185		NP_005742; NP_671695; NP_671700; NP_671714
ncr3139	AF038042	BRCA1-associated RING domain protein (BARD1) gene, exons 10, 11 and complete cds	NM_000465		NP_000456

seob6096	NM_002223	inositol 1,4,5-triphosphate receptor, type 2 (ITPR2), mRNA	NM_002223		NP_002214
mioc5061	NM_000489	alpha thalassemia/mental retardation syndrome X linked (RAD54 S. cerevisiae) (ATRX), transcript variant 1, mRNA	NM_000489; NM_138270; NM_138271		NP_000480; NP_612114; NP_612115
seob8489	NM_152724	hypothetical protein FLJ31034 (FLJ31034), mRNA /cds=(598,1023) /gb=NM_152724 /gi=22749438 /ug=Hs.351342 /len=2267	NM_152724	Hs.351342	NP_689937

FIGURE 6c: OA stage specific markers for Marked OA only				
Genbank	Description	RefSeq	UniGene	Rep_prot
NM_000019	acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase) (ACAT1), nuclear gene encoding mitochondrial protein, mRNA /cds=(77,1360) /gb=NM_000019 /gi=4557236 /ug=Hs.37 /len=1518	NM_000019	Hs.37	NP_000010
NM_000064	complement component 3 (C3), mRNA /cds=(61,5052) /gb=NM_000064 /gi=4557384 /ug=Hs.284394 /len=5067	NM_000064	Hs.284394	NP_000055
NM_000088	collagen, type I, alpha 1 (COL1A1), mRNA /cds=(120,4514) /gb=NM_000088 /gi=14719826 /ug=Hs.172928 /len=5921	NM_000088	Hs.172928	NP_000079
NM_000093	collagen, type V, alpha 1 (COL5A1), mRNA /cds=(383,5899) /gb=NM_000093 /gi=16554578 /ug=Hs.146428 /len=6496	NM_000093	Hs.146428	NP_000084
NM_000176	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), mRNA /cds=(133,2466) /gb=NM_000176 /gi=4504132 /ug=Hs.75772 /len=4788	NM_000176	Hs.75772	NP_000167

NM_000178	glutathione synthetase (GSS), mRNA /cds=(41,1465) /gb=NM_000178 /gi=4504168 /ug=Hs.82327 /len=1856	NM_000178	Hs.82327	NP_000169
NM_000216	Kallmann syndrome 1 sequence (KAL1), mRNA /cds=(151,2193) /gb=NM_000216 /gi=4557682 /ug=Hs.89591 /len=6314	NM_000216	Hs.89591	NP_000207
NM_000293	phosphorylase kinase, beta (PHKB), mRNA /cds=(25,3306) /gb=NM_000293 /gi=4505782 /ug=Hs.78060 /len=4284	NM_000293	Hs.78060	NP_000284
NM_000297	polycystic kidney disease 2 (autosomal dominant) (PKD2), mRNA /cds=(67,2973) /gb=NM_000297 /gi=4505834 /ug=Hs.82001 /len=5057	NM_000297	Hs.82001	NP_000288
NM_000351	steroid sulfatase (microsomal), arylsulfatase C, isozyme S (STS), mRNA /cds=(221,1972) /gb=NM_000351 /gi=13162281 /ug=Hs.79876 /len=6520	NM_000351	Hs.79876	NP_000342

NM_000582	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1) (SPP1), mRNA /cds=(88,990) /gb=NM_000582 /gi=4759165 /ug=Hs.313 /len=1524	NM_000582	Hs.313	NP_000573
NM_000903	NAD(P)H dehydrogenase, quinone 1 (NQO1), mRNA /cds=(51,875) /gb=NM_000903 /gi=4505414 /ug=Hs.406515 /len=2447	NM_000903	Hs.406515	NP_000894
NM_000968	ribosomal protein L4 (RPL4), mRNA /cds=(57,1340) /gb=NM_000968 /gi=16579884 /ug=Hs.286 /len=1449	NM_000968	Hs.286	NP_000959
NM_000968	ribosomal protein L4 (RPL4), mRNA /cds=(57,1340) /gb=NM_000968 /gi=16579884 /ug=Hs.286 /len=1449	NM_000968	Hs.286	NP_000959
NM_000998	ribosomal protein L37a (RPL37A), mRNA /cds=(36,314) /gb=NM_000998 /gi=16306561 /ug=Hs.296290 /len=392	NM_000998	Hs.296290	NP_000989
NM_001001	ribosomal protein L36a-like (RPL36AL), mRNA /cds=(95,415) /gb=NM_001001 /gi=16306559 /ug=Hs.419465 /len=537	NM_001001	Hs.419465	NP_000992

NM_001012	ribosomal protein S8 (RPS8), mRNA /cds=(24,650) /gb=NM_001012 /gi=4506742 /ug=Hs.399720 /len=705	NM_001012	Hs.399720	NP_001003
NM_001090	ATP-binding cassette, sub-family F (GCN20), member 1 (ABCF1), mRNA /cds=(95,2518) /gb=NM_001090 /gi=10947134 /ug=Hs.9573 /len=3141	NM_001090	Hs.9573	NP_001081
NM_001319	casein kinase 1, gamma 2 (CSNK1G2), mRNA /cds=(54,1301) /gb=NM_001319 /gi=21314777 /ug=Hs.181390 /len=2446	NM_001319	Hs.181390	NP_001310
NM_001378	dynein, cytoplasmic, intermediate polypeptide 2 (DNCI2), mRNA /cds=(166,2082) /gb=NM_001378 /gi=24307878 /ug=Hs.66881 /len=2602	NM_001378	Hs.66881	NP_001369
NM_001378	dynein, cytoplasmic, intermediate polypeptide 2 (DNCI2), mRNA /cds=(166,2082) /gb=NM_001378 /gi=24307878 /ug=Hs.66881 /len=2602	NM_001378	Hs.66881	NP_001369

NM_001404	eukaryotic translation elongation factor 1 gamma (EEF1G), mRNA /cds=(38,1351) /gb=NM_001404 /gi=25453475 /ug=Hs.256184 /len=1429	NM_001404	Hs.256184	NP_001395
NM_001446	fatty acid binding protein 7, brain (FABP7), mRNA /cds=(187,585) /gb=NM_001446 /gi=16950660 /ug=Hs.26770 /len=888	NM_001446	Hs.26770	NP_001437
NM_001457	filamin B, beta (actin binding protein 278) (FLNB), mRNA /cds=(132,7940) /gb=NM_001457 /gi=4503746 /ug=Hs.81008 /len=9432	NM_001457	Hs.81008	NP_001448
NM_001539	DnaJ (Hsp40) subfamily A, member 1 (DNAJA1), mRNA /cds=(83,1276) /gb=NM_001539 /gi=4504510 /ug=Hs.94 /len=1438	NM_001539	Hs.94	NP_001530
NM_001555	immunoglobulin superfamily, member 1 (IGSF1), mRNA /cds=(81,4091) /gb=NM_001555 /gi=4504624 /ug=Hs.22111 /len=4381	NM_001555	Hs.22111	NP_001546

NM_001634	S-adenosylmethionine decarboxylase 1 (AMD1), mRNA /cds=(321,1325) /gb=NM_001634 /gi=5209326 /ug=Hs.262476 /len=3414	NM_001634	Hs.262476	NP_001625
NM_001685	ATP synthase, H transporting, mitochondrial F0 complex, subunit F6 (ATP5J), nuclear gene encoding mitochondrial protein, mRNA /cds=(693,1019) /gb=NM_001685 /gi=19913429 /ug=Hs.73851 /len=1178	NM_001685	Hs.73851	NP_001676
NM_001698	AU RNA binding protein/enoyl-Coenzyme A hydratase (AUH), nuclear gene encoding mitochondrial protein, mRNA /cds=(5,1024) /gb=NM_001698 /gi=4502326 /ug=Hs.81886 /len=1548	NM_001698	Hs.81886	NP_001689
NM_001792	cadherin 2, type 1, N-cadherin (neuronal) (CDH2), mRNA /cds=(206,2926) /gb=NM_001792 /gi=14589888 /ug=Hs.161 /len=4122	NM_001792	Hs.161	NP_001783

NM_001855	collagen, type XV, alpha 1 (COL15A1), mRNA /cds=(166,4332) /gb=NM_001855 /gi=18641349 /ug=Hs.83164 /len=5222	NM_001855	Hs.83164	NP_001846
NM_001861	cytochrome c oxidase subunit IV isoform 1 (COX4I1), nuclear gene encoding mitochondrial protein, mRNA /cds=(165,674) /gb=NM_001861 /gi=17017985 /ug=Hs.433419 /len=802	NM_001861	Hs.433419	NP_001852
NM_001864	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) (COX7A1), nuclear gene encoding mitochondrial protein, mRNA /cds=(463,702) /gb=NM_001864 /gi=18105034 /ug=Hs.421621 /len=783	NM_001864	Hs.421621	NP_001855
NM_001873	carboxypeptidase E (CPE), mRNA /cds=(291,1721) /gb=NM_001873 /gi=4503008 /ug=Hs.75360 /len=2443	NM_001873	Hs.75360	NP_001864
NM_001923	damage-specific DNA binding protein 1, 127kDa (DDB1), mRNA /cds=(110,3532) /gb=NM_001923 /gi=13435358 /ug=Hs.108327 /len=4221	NM_001923	Hs.108327	NP_001914

BC033736	dermatopontin, clone MGC:45278 IMAGE:5176855, mRNA, complete cds		Hs.80552	NP_001928
NM_001951	E2F transcription factor 5, p130-binding (E2F5), mRNA /cds=(35,1075) /gb=NM_001951 /gi=12669916 /ug=Hs.2331 /len=1752	NM_001951	Hs.2331	NP_001942
NM_001964	early growth response 1 (EGR1), mRNA /cds=(271,1902) /gb=NM_001964 /gi=4503492 /ug=Hs.326035 /len=3132	NM_001964	Hs.326035	NP_001955
NM_002006	fibroblast growth factor 2 (basic) (FGF2), mRNA /cds=(302,934) /gb=NM_002006 /gi=15451897 /ug=Hs.284244 /len=6802	NM_002006	Hs.284244	NP_001997
NM_002018	flightless I (Drosophila) (FLII), mRNA /cds=(52,3861) /gb=NM_002018 /gi=22547155 /ug=Hs.83849 /len=4176	NM_002018	Hs.83849	NP_002009
NM_002027	farnesyltransferase, CAAX box, alpha (FNTA), mRNA /cds=(7,1146) /gb=NM_002027 /gi=4503770 /ug=Hs.356463 /len=1644	NM_002027	Hs.356463	NP_002018

NM_002032	ferritin, heavy polypeptide 1 (FTH1), mRNA /cds=(92,664) /gb=NM_002032 /gi=4503794 /ug=Hs.418650 /len=801	NM_002032	Hs.418650	NP_002023
NM_002035	follicular lymphoma variant translocation 1 (FVT1), mRNA /cds=(108,1106) /gb=NM_002035 /gi=4503816 /ug=Hs.74050 /len=2272	NM_002035	Hs.74050	NP_002026
NM_002065	glutamate-ammonia ligase (glutamine synthase) (GLUL), mRNA /cds=(461,1582) /gb=NM_002065 /gi=21361767 /ug=Hs.170171 /len=3137	NM_002065	Hs.170171	NP_002056
NM_002245	potassium channel, subfamily K, member 1 (KCNK1), mRNA /cds=(183,1193) /gb=NM_002245 /gi=15451900 /ug=Hs.79351 /len=1901	NM_002245	Hs.79351	NP_002236
NM_002439	mutS 3 (E. coli) (MSH3), mRNA /cds=(17,3403) /gb=NM_002439 /gi=4505248 /ug=Hs.42674 /len=4374	NM_002439	Hs.42674	NP_002430
NM_002475	myosin light chain 1 slow a (MLC1SA), mRNA /cds=(48,674) /gb=NM_002475 /gi=17986280 /ug=Hs.90318 /len=778	NM_002475	Hs.90318	NP_002466

NM_002480	protein phosphatase 1, regulatory (inhibitor) subunit 12A (PPP1R12A), mRNA /cds=(1,3093) /gb=NM_002480 /gi=4505316 /ug=Hs.16533 /len=4613	NM_002480	Hs.16533	NP_002471
NM_002512	non-metastatic cells 2, protein (NM23B) expressed in (NME2), nuclear gene encoding mitochondrial protein, mRNA /cds=(73,531) /gb=NM_002512 /gi=4505408 /ug=Hs.433416 /len=670	NM_002512	Hs.433416	NP_002503
NM_002579	paralemmin (PALM), mRNA /cds=(146,1309) /gb=NM_002579 /gi=4557041 /ug=Hs.78482 /len=2823	NM_002579	Hs.78482	NP_002570
NM_002600	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce Drosophila) (PDE4B), mRNA /cds=(766,2460) /gb=NM_002600 /gi=4505662 /ug=Hs.188 /len=4068	NM_002600	Hs.188	NP_002591
NM_002715	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA), mRNA /cds=(210,1139) /gb=NM_002715 /gi=4506016 /ug=Hs.91773 /len=2181	NM_002715	Hs.91773	NP_002706

NM_002721	protein phosphatase 6, catalytic subunit (PPP6C), mRNA /cds=(69,986) /gb=NM_002721 /gi=20127429 /ug=Hs.356739 /len=1563	NM_002721	Hs.356739	NP_002712
NM_002736	protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA /cds=(167,1423) /gb=NM_002736 /gi=4506064 /ug=Hs.77439 /len=3259	NM_002736	Hs.77439	NP_002727
NM_002765	phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA /cds=(61,1017) /gb=NM_002765 /gi=4506128 /ug=Hs.2910 /len=2457	NM_002765	Hs.2910	NP_002756
NM_002793	proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1), mRNA /cds=(48,773) /gb=NM_002793 /gi=22538462 /ug=Hs.407981 /len=872	NM_002793	Hs.407981	NP_002784
NM_002811	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 (PSMD7), mRNA /cds=(128,1102) /gb=NM_002811 /gi=25777614 /ug=Hs.155543 /len=1673	NM_002811	Hs.155543	NP_002802

NM_002857	peroxisomal farnesylated protein (PXF), mRNA /cds=(11,910) /gb=NM_002857 /gi=4506338 /ug=Hs.168670 /len=3662	NM_002857	Hs.168670	NP_002848
BC050558	RAB5B, member RAS oncogene family, clone IMAGE:6191566, mRNA, partial cds			NP_002859
NM_002937	ribonuclease, RNase A family, 4 (RNASE4), mRNA /cds=(173,616) /gb=NM_002937 /gi=20070170 /ug=Hs.283749 /len=1414	NM_002937	Hs.283749	NP_002928
NM_002945	replication protein A1, 70kDa (RPA1), mRNA /cds=(44,1894) /gb=NM_002945 /gi=20070171 /ug=Hs.84318 /len=2824	NM_002945	Hs.84318	NP_002936
NM_002998	syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) (SDC2), mRNA /cds=(460,1065) /gb=NM_002998 /gi=27804306 /ug=Hs.1501 /len=2172	NM_002998	Hs.1501	NP_002989

NM_003001	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa (SDHC), nuclear gene encoding mitochondrial protein, mRNA /cds=(27,536) /gb=NM_003001 /gi=9257243 /ug=Hs.433982 /len=1315	NM_003001	Hs.433982	NP_002992
AB011538	mRNA for MEGF5, partial cds	NM_003062	Hs.57929	NP_003053
BC034956	clone IMAGE:4821017, mRNA		Hs.77196	NP_003118
NM_003142	Sjogren syndrome antigen B (autoantigen La) (SSB), mRNA /cds=(73,1299) /gb=NM_003142 /gi=10835066 /ug=Hs.83715 /len=1619	NM_003142	Hs.83715	NP_003133
NM_003164	syntaxin 5A (STX5A), mRNA /cds=(27,932) /gb=NM_003164 /gi=4507292 /ug=Hs.302300 /len=1507	NM_003164	Hs.302300	NP_003155
NM_003193	tubulin-specific chaperone e (TBCE), mRNA /cds=(81,1664) /gb=NM_003193 /gi=6006029 /ug=Hs.343564 /len=1882	NM_003193	Hs.343564	NP_003184
NM_003265	toll-like receptor 3 (TLR3), mRNA /cds=(102,2816) /gb=NM_003265 /gi=19718735 /ug=Hs.29499 /len=3057	NM_003265	Hs.29499	NP_003256

NM_003295	tumor protein, translationally-controlled 1 (TPT1), mRNA /cds=(95,613) /gb=NM_003295 /gi=4507668 /ug=Hs.401448 /len=830	NM_003295	Hs.401448	NP_003286
NM_003310	tumor suppressing subtransferable candidate 1 (TSSC1), mRNA /cds=(152,1315) /gb=NM_003310 /gi=4507702 /ug=Hs.4992 /len=1705	NM_003310	Hs.4992	NP_003301
NM_003359	UDP-glucose dehydrogenase (UGDH), mRNA /cds=(79,1563) /gb=NM_003359 /gi=4507812 /ug=Hs.28309 /len=2950	NM_003359	Hs.28309	NP_003350
NM_003380	vimentin (VIM), mRNA /cds=(123,1523) /gb=NM_003380 /gi=4507894 /ug=Hs.297753 /len=1851	NM_003380	Hs.297753	NP_003371
X59739	ZFX mRNA for put. transcription activator, isoform 2	NM_003410	Hs.2074	NP_003401
NM_003418	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein) (ZNF9), mRNA /cds=(103,636) /gb=NM_003418 /gi=4827070 /ug=Hs.2110 /len=1500	NM_003418	Hs.2110	NP_003409
AF062089	leucine zipper protein Fip3p (=AF074382 IkB kinase gamma subunit)	NM_003639	Hs.43505	NP_003630

NM_003640	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein (IKBKAP), mRNA /cds=(304,4302) /gb=NM_003640 /gi=4504628 /ug=Hs.31323 /len=4803	NM_003640	Hs.31323	NP_003631
NM_003750	eukaryotic translation initiation factor 3, subunit 10 theta, 150/170kDa (EIF3S10), mRNA /cds=(114,4262) /gb=NM_003750 /gi=4503508 /ug=Hs.154796 /len=5256	NM_003750	Hs.154796	NP_003741
NM_003753	eukaryotic translation initiation factor 3, subunit 7 zeta, 66/67kDa (EIF3S7), mRNA /cds=(372,2018) /gb=NM_003753 /gi=23238220 /ug=Hs.55682 /len=2169	NM_003753	Hs.55682	NP_003744
NM_003836	delta-like 1 (Drosophila) (DLK1), mRNA /cds=(163,1314) /gb=NM_003836 /gi=21361079 /ug=Hs.169228 /len=1556	NM_003836	Hs.169228	NP_003827
NM_003918	glycogenin 2 (GYG2), mRNA /cds=(284,1789) /gb=NM_003918 /gi=5453673 /ug=Hs.380757 /len=3267	NM_003918	Hs.380757	NP_003909

NM_003981	protein regulator of cytokinesis 1 (PRC1), mRNA /cds=(79,1941) /gb=NM_003981 /gi=4506038 /ug=Hs.344037 /len=3044	NM_003981	Hs.344037	NP_003972
NM_004127	G protein pathway suppressor 1 (GPS1), mRNA /cds=(21,1523) /gb=NM_004127 /gi=13435380 /ug=Hs.268530 /len=1866	NM_004127	Hs.268530	NP_004118
NM_004145	myosin IXB (MYO9B), mRNA /cds=(1,6069) /gb=NM_004145 /gi=4758749 /ug=Hs.159629 /len=6069	NM_004145	Hs.159629	NP_004136
NM_004147	developmentally regulated GTP binding protein 1 (DRG1), mRNA /cds=(66,1169) /gb=NM_004147 /gi=4758795 /ug=Hs.115242 /len=1383	NM_004147	Hs.115242	NP_004138
AL831917	mRNA; cDNA DKFZp761F0118 (from clone DKFZp761F0118) /cds=(1,6490) /gb=AL831917 /gi=21732430 /ug=Hs.6685 /len=7334		Hs.6685	NP_004232
NM_004247	U5 snRNP-specific protein, 116 kD (U5-116KD), mRNA /cds=(61,2979) /gb=NM_004247 /gi=4759279 /ug=Hs.151787 /len=3784	NM_004247	Hs.151787	NP_004238

NM_004279	peptidase (mitochondrial processing) beta (PMPCB), mRNA /cds=(14,1483) /gb=NM_004279 /gi=4758733 /ug=Hs.184211 /len=1771	NM_004279	Hs.184211	NP_004270
NM_004330	BCL2/adenovirus E1B 19kDa interacting protein 2 (BNIP2), mRNA /cds=(212,1156) /gb=NM_004330 /gi=4757855 /ug=Hs.155596 /len=2382	NM_004330	Hs.155596	NP_004321
NM_004415	desmoplakin (DPI, DPII) (DSP), mRNA /cds=(280,8895) /gb=NM_004415 /gi=4758199 /ug=Hs.349499 /len=9588	NM_004415	Hs.349499	NP_004406
NM_004446	glutamyl-prolyl-tRNA synthetase (EPRS), mRNA /cds=(59,4381) /gb=NM_004446 /gi=4758293 /ug=Hs.55921 /len=4586	NM_004446	Hs.55921	NP_004437
NM_004450	enhancer of rudimentary (Drosophila) (ERH), mRNA /cds=(72,386) /gb=NM_004450 /gi=4758301 /ug=Hs.433413 /len=815	NM_004450	Hs.433413	NP_004441
NM_004505	ubiquitin specific protease 6 (Tre-2 oncogene) (USP6), mRNA /cds=(1697,4057) /gb=NM_004505 /gi=4758563 /ug=Hs.111065 /len=7878	NM_004505	Hs.111065	NP_004496

NM_004551	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase) (NDUFS3), mRNA /cds=(13,807) /gb=NM_004551 /gi=4758787 /ug=Hs.429506 /len=899	NM_004551	Hs.429506	NP_004542
NM_004554	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4 (NFATC4), mRNA /cds=(294,3002) /gb=NM_004554 /gi=27886562 /ug=Hs.77810 /len=3399	NM_004554	Hs.77810	NP_004545
NM_004630	splicing factor 1 (SF1), mRNA /cds=(383,2254) /gb=NM_004630 /gi=4759339 /ug=Hs.180677 /len=3131	NM_004630	Hs.180677	NP_004621
AK057605	cDNA FLJ33043 fis, clone THYMU2000440		Hs.193145	NP_004645
NM_004663	RAB11A, member RAS oncogene family (RAB11A), mRNA /cds=(104,754) /gb=NM_004663 /gi=20149549 /ug=Hs.75618 /len=2474	NM_004663	Hs.75618	NP_004654
NM_004719	splicing factor, arginine/serine-rich 2, interacting protein (SFRS2IP), mRNA /cds=(1211,4657) /gb=NM_004719 /gi=4759171 /ug=Hs.51957 /len=5307	NM_004719	Hs.51957	NP_004710

NM_004827	ATP-binding cassette, sub-family G (WHITE), member 2 (ABCG2), mRNA /cds=(205,2172) /gb=NM_004827 /gi=4757849 /ug=Hs.194720 /len=2719	NM_004827	Hs.194720	NP_004818
NM_005008	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae) (NHP2L1), mRNA /cds=(95,481) /gb=NM_005008 /gi=4826859 /ug=Hs.182255 /len=1475	NM_005008	Hs.182255	NP_004999
NM_005121	thyroid hormone receptor-associated protein, 240 kDa subunit (TRAP240), mRNA /cds=(78,6602) /gb=NM_005121 /gi=4827043 /ug=Hs.11861 /len=7389	NM_005121	Hs.11861	NP_005112
NM_005345	heat shock 70kDa protein 1A (HSPA1A), mRNA /cds=(198,2123) /gb=NM_005345 /gi=26787973 /ug=Hs.75452 /len=2383	NM_005345	Hs.75452	NP_005336
NM_005415	solute carrier family 20 (phosphate transporter), member 1 (SLC20A1), mRNA /cds=(371,2410) /gb=NM_005415 /gi=7382462 /ug=Hs.78452 /len=3220	NM_005415	Hs.78452	NP_005406

NM_005452	chromosome 6 open reading frame 11 (C6orf11), mRNA /cds=(54,1886) /gb=NM_005452 /gi=14550417 /ug=Hs.17930 /len=2074	NM_005452	Hs.17930	NP_005443
NM_005482	phosphatidylinositol glycan, class K (PIGK), mRNA /cds=(25,1212) /gb=NM_005482 /gi=23199982 /ug=Hs.62187 /len=1897	NM_005482	Hs.62187	NP_005473
NM_005496	SMC4 structural maintenance of chromosomes 4-like 1 (yeast) (SMC4L1), mRNA /cds=(233,4099) /gb=NM_005496 /gi=21361251 /ug=Hs.50758 /len=5261	NM_005496	Hs.50758	NP_005487
NM_005499	SUMO-1 activating enzyme subunit 2 (UBA2), mRNA /cds=(26,1948) /gb=NM_005499 /gi=4885648 /ug=Hs.4311 /len=2617	NM_005499	Hs.4311	NP_005490
AA705851	ah42f05.s1 Soares_testis_NHT cDNA clone 1292193 3' similar to P54687 BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, CYTOSOLIC ;, mRNA sequence /clone=1292193 /clone_end=3' /gb=AA705851 /gi=2715769 /ug=Hs.443872 /len=412		Hs.443872	NP_005495

NM_005514	major histocompatibility complex, class I, B (HLA-B), mRNA /cds=(11,1099) /gb=NM_005514 /gi=21327676 /ug=Hs.77961 /len=1310	NM_005514	Hs.77961	NP_005505
NM_005536	inositol(myo)-1(or 4)-monophosphatase 1 (IMPA1), mRNA /cds=(99,932) /gb=NM_005536 /gi=8393607 /ug=Hs.171776 /len=2349	NM_005536	Hs.171776	NP_005527
NM_005587	MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A) (MEF2A), mRNA /cds=(415,1938) /gb=NM_005587 /gi=5031906 /ug=Hs.182280 /len=2975	NM_005587	Hs.182280	NP_005578
NM_005594	nascent-polypeptide-associated complex alpha polypeptide (NACA), mRNA /cds=(26,673) /gb=NM_005594 /gi=5031930 /ug=Hs.32916 /len=797	NM_005594	Hs.32916	NP_005585
NM_005626	splicing factor, arginine/serine-rich 4 (SFRS4), mRNA /cds=(107,1591) /gb=NM_005626 /gi=21361281 /ug=Hs.76122 /len=2167	NM_005626	Hs.76122	NP_005617

NM_005628	solute carrier family 1 (neutral amino acid transporter), member 5 (SLC1A5), mRNA /cds=(591,2216) /gb=NM_005628 /gi=5032092 /ug=Hs.183556 /len=2856	NM_005628	Hs.183556	NP_005619
NM_005770	small EDRK-rich factor 2 (SERF2), mRNA /cds=(1023,1319) /gb=NM_005770 /gi=21361286 /ug=Hs.380718 /len=1408	NM_005770	Hs.380718	NP_005761
NM_005839	serine/arginine repetitive matrix 1 (SRRM1), mRNA /cds=(6,2468) /gb=NM_005839 /gi=5032118 /ug=Hs.18192 /len=3698	NM_005839	Hs.18192	NP_005830
NM_006191	proliferation-associated 2G4, 38kDa (PA2G4), mRNA /cds=(98,1282) /gb=NM_006191 /gi=5453841 /ug=Hs.374491 /len=1697	NM_006191	Hs.374491	NP_006182
NM_006294	ubiquinol-cytochrome c reductase binding protein (UQCRB), mRNA /cds=(54,389) /gb=NM_006294 /gi=20070231 /ug=Hs.131255 /len=965	NM_006294	Hs.131255	NP_006285

NM_006346	progesterone-induced blocking factor 1 (PIBF1), mRNA /cds=(1,2277) /gb=NM_006346 /gi=5453889 /ug=Hs.43913 /len=2277	NM_006346	Hs.43913	NP_006337
NM_006482	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 2, mRNA /cds=(161,1966) /gb=NM_006482 /gi=5922003 /ug=Hs.173135 /len=3615	NM_003583; NM_006482	Hs.173135	NP_006473
NM_006519	t-complex-associated-testis-expressed 1-like 1 (TCTEL1), mRNA /cds=(1,342) /gb=NM_006519 /gi=5730084 /ug=Hs.266940 /len=713	NM_006519	Hs.266940	NP_006510
NM_006620	HBS1-like (S. cerevisiae) (HBS1L), mRNA /cds=(194,2248) /gb=NM_006620 /gi=24431963 /ug=Hs.221040 /len=7163	NM_006620	Hs.221040	NP_006611
NM_006640	MLL septin-like fusion (MSF), mRNA /cds=(258,1964) /gb=NM_006640 /gi=19923366 /ug=Hs.181002 /len=3929	NM_006640	Hs.181002	NP_006631

NM_006699	mannosidase, alpha, class 1A, member 2 (MAN1A2), mRNA /cds=(521,2446) /gb=NM_006699 /gi=5729912 /ug=Hs.367638 /len=2792	NM_006699	Hs.367638	NP_006690
NM_006757	troponin T3, skeletal, fast (TNNT3), mRNA /cds=(13,789) /gb=NM_006757 /gi=5803202 /ug=Hs.73454 /len=1000	NM_006757	Hs.73454	NP_006748
NM_006773	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 18 (Myc regulated) (DDX18), mRNA /cds=(72,2084) /gb=NM_006773 /gi=13787205 /ug=Hs.100555 /len=2753	NM_006773	Hs.100555	NP_006764
NM_006820	chromosome 1 open reading frame 29 (C1orf29), mRNA /cds=(242,1483) /gb=NM_006820 /gi=5803026 /ug=Hs.75470 /len=2058	NM_006820	Hs.75470	NP_006811
NM_006965	zinc finger protein 24 (KOX 17) (ZNF24), mRNA /cds=(165,1271) /gb=NM_006965 /gi=5902161 /ug=Hs.183593 /len=2513	NM_006965	Hs.183593	NP_008896

NM_006988	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1 (ADAMTS1), mRNA /cds=(294,3146) /gb=NM_006988 /gi=11038653 /ug=Hs.8230 /len=4459	NM_006988	Hs.8230	NP_008919
NM_006997	transforming, acidic coiled-coil containing protein 2 (TACC2), mRNA /cds=(87,3167) /gb=NM_006997 /gi=11119413 /ug=Hs.272023 /len=3686	NM_006997	Hs.272023	NP_008928
NM_007106	ubiquitin-like 3 (UBL3), mRNA /cds=(110,463) /gb=NM_007106 /gi=6005927 /ug=Hs.173091 /len=3323	NM_007106	Hs.173091	NP_009037
NM_007115	tumor necrosis factor, alpha-induced protein 6 (TNFAIP6), mRNA /cds=(77,910) /gb=NM_007115 /gi=26051242 /ug=Hs.29352 /len=1440	NM_007115	Hs.29352	NP_009046
NM_007268	Ig superfamily protein (Z39IG), mRNA /cds=(46,1245) /gb=NM_007268 /gi=6005957 /ug=Hs.8904 /len=1787	NM_007268	Hs.8904	NP_009199

NM_007344	transcription termination factor, RNA polymerase I (TTF1), mRNA /cds=(45,2705) /gb=NM_007344 /gi=6678454 /ug=Hs.54780 /len=2847	NM_007344	Hs.54780	NP_031370
NM_007361	nidogen 2 (osteonidogen) (NID2), mRNA /cds=(1,4131) /gb=NM_007361 /gi=6679055 /ug=Hs.82733 /len=4829	NM_007361	Hs.82733	NP_031387
NM_007373	soc-2 suppressor of clear (C. elegans) (SHOC2), mRNA /cds=(278,2026) /gb=NM_007373 /gi=6677944 /ug=Hs.104315 /len=3872	NM_007373	Hs.104315	NP_031399
BC008272	Mus musculus neuron specific gene family member 1, mRNA (cDNA clone MGC:11446 IMAGE:3603440), complete cds	NM_010942	Mm.7414	NP_035072
NM_012201	golgi apparatus protein 1 (GLG1), mRNA /cds=(27,3560) /gb=NM_012201 /gi=6912389 /ug=Hs.78979 /len=3909	NM_012201	Hs.78979	NP_036333
NM_012215	meningioma expressed antigen 5 (hyaluronidase) (MGEA5), mRNA /cds=(396,3146) /gb=NM_012215 /gi=11024697 /ug=Hs.5734 /len=5147	NM_012215	Hs.5734	NP_036347

NM_012257	HMG-box containing protein 1 (HBP1), mRNA /cds=(187,1731) /gb=NM_012257 /gi=21361410 /ug=Hs.10882 /len=2857	NM_012257	Hs.10882	NP_036389
NM_012322	U6 snRNA-associated Sm-like protein (LSM5), mRNA /cds=(1,276) /gb=NM_012322 /gi=6912487 /ug=Hs.227280 /len=749	NM_012322	Hs.227280	NP_036454
NM_012332	likely ortholog of mouse acyl-Coenzyme A thioesterase 2, mitochondrial (ACATE2), mRNA /cds=(148,1368) /gb=NM_012332 /gi=6912517 /ug=Hs.18625 /len=1954	NM_012332	Hs.18625	NP_036464
NM_012333	c-myc binding protein (MYCBP), mRNA /cds=(39,350) /gb=NM_012333 /gi=8850230 /ug=Hs.78221 /len=2070	NM_012333	Hs.78221	NP_036465
NM_012339	transmembrane 4 superfamily member tetraspan NET-7 (NET-7), mRNA /cds=(122,1006) /gb=NM_012339 /gi=21264576 /ug=Hs.95583 /len=1727	NM_012339	Hs.95583	NP_036471
NM_013234	muscle specific gene (M9), mRNA /cds=(172,828) /gb=NM_013234 /gi=10801344 /ug=Hs.283781 /len=911	NM_013234	Hs.283781	NP_037366

NM_014033	DKFZP586A0522 protein (DKFZP586A0522), mRNA /cds=(21,755) /gb=NM_014033 /gi=13378140 /ug=Hs.288771 /len=1705	NM_014033	Hs.288771	NP_054752
NM_014041	signal peptidase 12kDa (SPC12), mRNA /cds=(169,444) /gb=NM_014041 /gi=7661745 /ug=Hs.11125 /len=798	NM_014041	Hs.11125	NP_054760
NM_014138	PRO0659 protein (PRO0659), mRNA /cds=(60,584) /gb=NM_014138 /gi=7662583 /ug=Hs.6451 /len=1416	NM_014138	Hs.6451	NP_054857
AK025603	cDNA: FLJ21950 fis, clone HEP04949	NM_014181	Hs.372208	NP_054900
NM_014285	of Yeast RRP4 (ribosomal RNA processing 4), 3'-5'-exoribonuclease (RRP4), mRNA	NM_014285	Hs.211973	NP_055100
NM_014347	zinc finger protein (ZF5128), mRNA /cds=(95,1756) /gb=NM_014347 /gi=7657692 /ug=Hs.296365 /len=3000	NM_014347	Hs.296365	NP_055162
NM_014399	transmembrane 4 superfamily member tetraspan NET-6 (NET-6), mRNA /cds=(207,821) /gb=NM_014399 /gi=21264573 /ug=Hs.284243 /len=1875	NM_014399	Hs.284243	NP_055214

NM_014411	brain and nasopharyngeal carcinoma susceptibility protein (NSG-X), mRNA /cds=(186,518) /gb=NM_014411 /gi=14149650 /ug=Hs.26937 /len=1897	NM_014411	Hs.26937	NP_055226
NM_014453	putative breast adenocarcinoma marker (32kD) (BC-2), mRNA /cds=(130,798) /gb=NM_014453 /gi=7656921 /ug=Hs.12107 /len=903	NM_014453	Hs.12107	NP_055268
NM_014489	FGF receptor activating protein 1 (FRAG1), mRNA /cds=(129,1076) /gb=NM_014489 /gi=7657101 /ug=Hs.133968 /len=2040	NM_014489	Hs.133968	NP_055304
NM_014500	HIV TAT specific factor 1 (HTATSF1), mRNA /cds=(183,2450) /gb=NM_014500 /gi=21361436 /ug=Hs.171595 /len=2785	NM_014500	Hs.171595	NP_055315
NM_014608	cytoplasmic FMR1 interacting protein 1 (CYFIP1), mRNA /cds=(53,3814) /gb=NM_014608 /gi=24307968 /ug=Hs.77257 /len=4394	NM_014608	Hs.77257	NP_055423

NM_014669	KIAA0095 gene product (KIAA0095), mRNA /cds=(67,2526) /gb=NM_014669 /gi=7661901 /ug=Hs.155314 /len=2681	NM_014669	Hs.155314	NP_055484
NM_014739	KIAA0164 gene product (KIAA0164), mRNA /cds=(254,3016) /gb=NM_014739 /gi=7661957 /ug=Hs.80338 /len=5538	NM_014739	Hs.80338	NP_055554
NM_014764	DAZ associated protein 2 (DAZAP2), mRNA /cds=(70,576) /gb=NM_014764 /gi=7661885 /ug=Hs.75416 /len=1897	NM_014764	Hs.75416	NP_055579
NM_014774	KIAA0494 gene product (KIAA0494), mRNA /cds=(978,2465) /gb=NM_014774 /gi=7662159 /ug=Hs.62515 /len=5766	NM_014774	Hs.62515	NP_055589
NM_014781	RB1-inducible coiled-coil 1 (RB1CC1), mRNA /cds=(516,5291) /gb=NM_014781 /gi=7661991 /ug=Hs.50421 /len=6614	NM_014781	Hs.50421	NP_055596
NM_014880	C-type lectin BIMLEC precursor (BIMLEC), mRNA /cds=(12,710) /gb=NM_014880 /gi=26892292 /ug=Hs.2441 /len=1033	NM_014880	Hs.2441	NP_055695

D87466	mRNA for KIAA0276 gene, partial cds. /cds=(1,932) /gb=D87466 /gi=1665816 /ug=Hs.240112 /len=4185		Hs.240112	NP_055930
D31888	KIAA0071 mRNA, partial cds	NM_015156	Hs.78398	NP_055971
NM_015161	ADP-ribosylation factor-like 6 interacting protein (ARL6IP), mRNA /cds=(70,681) /gb=NM_015161 /gi=24308006 /ug=Hs.75249 /len=2280	NM_015161	Hs.75249	NP_055976
AL096857	Novel mRNA from chromosome 1, which has similarities to BAT2 genes /cds=(58,8163) /gb=AL096857 /gi=5541862 /ug=Hs.69559 /len=10174	NM_015172	Hs.69559	NP_055987
NM_015469	DKFZp564D177 protein (DKFZp564D177), mRNA /cds=(106,849) /gb=NM_015469 /gi=22267435 /ug=Hs.24608 /len=1664	NM_015469	Hs.24608	NP_056284
BC001336	Similar to nectin 3; DKFZP566B0846 protein, clone IMAGE:3461033, mRNA, partial cds	NM_015480	Hs.21201	NP_056295
NM_015570	autism susceptibility candidate 2 (AUTS2), mRNA /cds=(322,4101) /gb=NM_015570 /gi=17864089 /ug=Hs.32168 /len=5972	NM_015570	Hs.32168	NP_056385

NM_015571	SUMO-1-specific protease (SUSP1), mRNA /cds=(1,3339) /gb=NM_015571 /gi=7662311 /ug=Hs.27197 /len=4210	NM_015571	Hs.27197	NP_056386
NM_015577	retinoic acid induced 14 (RAI14), mRNA /cds=(112,3054) /gb=NM_015577 /gi=13470085 /ug=Hs.15165 /len=4925	NM_015577	Hs.15165	NP_056392
NM_015640	PAI-1 mRNA-binding protein (PAI-RBP1), mRNA /cds=(86,1249) /gb=NM_015640 /gi=7661625 /ug=Hs.165998 /len=2201	NM_015640	Hs.165998	NP_056455
BC032345	DKFZP586D0824 protein, clone MGC:40527 IMAGE:5208411, mRNA, complete cds /cds=(65,1078) /gb=BC032345 /gi=21595443 /ug=Hs.128797 /len=1499	NM_015660	Hs.128797	NP_056475
NM_015683	hypothetical protein CLONE24945 (CLONE24945), mRNA /cds=(144,1367) /gb=NM_015683 /gi=18373304 /ug=Hs.30882 /len=2518	NM_015683	Hs.30882	NP_056498
NM_015866	PR domain containing 2, with ZNF domain (PRDM2), transcript variant 2, mRNA	NM_012231; NM_015866	Hs.26719	NP_056950

NM_015902	progestin induced protein (DD5), mRNA /cds=(34,8433) /gb=NM_015902 /gi=15147336 /ug=Hs.278428 /len=8838	NM_015902	Hs.278428	NP_056986
NM_015952	PTD013 protein (PTD013), mRNA /cds=(87,812) /gb=NM_015952 /gi=7706269 /ug=Hs.22679 /len=982	NM_015952	Hs.22679	NP_057036
BC010867	Similar to lymphocyte activation-associated protein, clone IMAGE:3892557, mRNA (=AK001698.1)		Hs.272239	NP_057074
NM_016009	SH3-domain GRB2-like endophilin B1 (SH3GLB1), mRNA /cds=(82,1179) /gb=NM_016009 /gi=21359904 /ug=Hs.136309 /len=1561	NM_016009	Hs.136309	NP_057093
NM_016037	CGI-94 protein (CGI-94), mRNA /cds=(70,831) /gb=NM_016037 /gi=7705808 /ug=Hs.111449 /len=1025	NM_016037	Hs.111449	NP_057121
NM_016052	CGI-115 protein (CGI-115), mRNA /cds=(35,814) /gb=NM_016052 /gi=7705619 /ug=Hs.56043 /len=1308	NM_016052	Hs.56043	NP_057136

NM_016065	mitochondrial ribosomal protein S16 (MRPS16), nuclear gene encoding mitochondrial protein, mRNA /cds=(170,583) /gb=NM_016065 /gi=16554612 /ug=Hs.180312 /len=704	NM_016065	Hs.180312	NP_057149
NM_016146	PTD009 protein (PTD009), mRNA	NM_016146	Hs.279901	NP_057230
NM_016250	NDRG family member 2 (NDRG2), mRNA /cds=(97,1170) /gb=NM_016250 /gi=10280619 /ug=Hs.243960 /len=2024	NM_016250	Hs.243960	NP_057334
NM_016312	WW domain binding protein 11 (WBP11), mRNA /cds=(162,2087) /gb=NM_016312 /gi=18375679 /ug=Hs.334811 /len=2690	NM_016312	Hs.334811	NP_057396
NM_016360	clone HQ0477 PRO0477p (LOC51204), mRNA /cds=(201,1094) /gb=NM_016360 /gi=27545314 /ug=Hs.174134 /len=1491	NM_016360	Hs.174134	NP_057444
NM_016494	hypothetical protein LOC51255 (LOC51255), mRNA /cds=(31,492) /gb=NM_016494 /gi=24475978 /ug=Hs.11156 /len=601	NM_016494	Hs.11156	NP_057578

NM_016525	ubiquitin associated protein 1 (UBAP1), mRNA /cds=(236,1744) /gb=NM_016525 /gi=22212941 /ug=Hs.75425 /len=2757	NM_016525	Hs.75425	NP_057609
NM_016578	hepatitis B virus x associated protein (HBXAP), mRNA /cds=(1062,4631) /gb=NM_016578 /gi=10835261 /ug=Hs.20509 /len=5323	NM_016578	Hs.20509	NP_057662
NM_016929	chloride intracellular channel 5 (CLIC5), mRNA /cds=(298,1053) /gb=NM_016929 /gi=8393146 /ug=Hs.283021 /len=2380	NM_016929	Hs.283021	NP_058625
NM_017571	hypothetical protein LOC55580 (LOC55580), mRNA /cds=(759,2987) /gb=NM_017571 /gi=8923837 /ug=Hs.254122 /len=3109	NM_017571	Hs.254122	NP_060041
NM_017599	transmembrane protein vezatin (VEZATIN), mRNA /cds=(177,1886) /gb=NM_017599 /gi=19923537 /ug=Hs.24135 /len=3949	NM_017599	Hs.24135	NP_060069
NM_017611	likely ortholog of mouse embryonic epithelial gene 1 (EEG1), mRNA /cds=(319,1794) /gb=NM_017611 /gi=18252046 /ug=Hs.274453 /len=2630	NM_014096; NM_017611	Hs.274453	NP_060081

AJ420591	mRNA full length insert cDNA clone EUROIMAGE 701679		Hs.10784	NP_060103
NM_017661	hypothetical protein FLJ20086 (FLJ20086), mRNA /cds=(48,1313) /gb=NM_017661 /gi=8923096 /ug=Hs.46821 /len=3572	NM_017661	Hs.46821	NP_060131
NM_017798	chromosome 20 open reading frame 21 (C20orf21), mRNA /cds=(10,603) /gb=NM_017798 /gi=8923363 /ug=Hs.11747 /len=2429	NM_017798	Hs.11747	NP_060268
NM_017807	O-sialoglycoprotein endopeptidase (OSGEP), mRNA /cds=(130,1137) /gb=NM_017807 /gi=8923379 /ug=Hs.108894 /len=1394	NM_017807	Hs.108894	NP_060277
NM_017822	hypothetical protein FLJ20436 (FLJ20436), mRNA /cds=(505,963) /gb=NM_017822 /gi=8923410 /ug=Hs.268189 /len=1901	NM_017822	Hs.268189	NP_060292
NM_017837	hypothetical protein FLJ20477 (FLJ20477), mRNA /cds=(332,1813) /gb=NM_017837 /gi=21361770 /ug=Hs.26994 /len=2380	NM_017837	Hs.26994	NP_060307

NM_017991	hypothetical protein FLJ10081 (FLJ10081), mRNA /cds=(437,2812) /gb=NM_017991 /gi=21361733 /ug=Hs.7871 /len=5249	NM_017991	Hs.7871	NP_060461
NM_018107	RNA-binding region (RNP1, RRM) containing 4 (RNPC4), mRNA /cds=(187,1461) /gb=NM_018107 /gi=21361701 /ug=Hs.4997 /len=2442	NM_018107	Hs.4997	NP_060577
NM_018155	hypothetical protein FLJ10618 (FLJ10618), mRNA /cds=(210,1142) /gb=NM_018155 /gi=8922550 /ug=Hs.42484 /len=2001	NM_018155	Hs.42484	NP_060625
NM_018204	cytoskeleton associated protein 2 (CKAP2), mRNA /cds=(97,2145) /gb=NM_018204 /gi=19923520 /ug=Hs.24641 /len=3626	NM_018204	Hs.24641	NP_060674
NM_018385	hypothetical protein FLJ11301 (FLJ11301), mRNA /cds=(21,1997) /gb=NM_018385 /gi=14149719 /ug=Hs.301724 /len=3290	NM_018385	Hs.301724	NP_060855

NM_018405	hypothetical protein, clone 2746033 (HSA272196), mRNA /cds=(39,593) /gb=NM_018405 /gi=24475639 /ug=Hs.8179 /len=861	NM_018405	Hs.8179	NP_060875
NM_018475	TPA regulated locus (TPARL), mRNA /cds=(195,1169) /gb=NM_018475 /gi=8923860 /ug=Hs.236510 /len=1913	NM_018475	Hs.236510	NP_060945
NM_018489	hypothetical protein ASH1 (ASH1), mRNA /cds=(310,9219) /gb=NM_018489 /gi=8922080 /ug=Hs.102652 /len=9926	NM_018489	Hs.102652	NP_060959
NM_018579	mitochondrial solute carrier protein (MSCP), mRNA	NM_016612; NM_018579	Hs.283716	NP_061049
NM_018589	chromosome 14 open reading frame 116 (C14orf116), mRNA /cds=(270,458) /gb=NM_018589 /gi=20127573 /ug=Hs.60548 /len=1654	NM_018589	Hs.60548	NP_061059
NM_018649	H2A histone family, member Y2 (H2AFY2), mRNA /cds=(214,1332) /gb=NM_018649 /gi=8923919 /ug=Hs.92023 /len=1932	NM_018649	Hs.92023	NP_061119

NM_018981	ER-resident protein ERdj5 (ERdj5), mRNA /cds=(416,2797) /gb=NM_018981 /gi=24308126 /ug=Hs.1098 /len=4193	NM_018981	Hs.1098	NP_061854
NM_019000	hypothetical protein FLJ20152 (FLJ20152), mRNA /cds=(217,1287) /gb=NM_019000 /gi=21361616 /ug=Hs.82273 /len=2989	NM_019000	Hs.82273	NP_061873
NM_019058	HIF-1 responsive RTP801 (RTP801), mRNA /cds=(198,896) /gb=NM_019058 /gi=9506686 /ug=Hs.111244 /len=1760	NM_019058	Hs.111244	NP_061931
BC009777	clone MGC:13446 IMAGE:4275731, mRNA, complete cds	NM_019071	Hs.143198	NP_061944
NM_020062	SLC2A4 regulator (SLC2A4RG), mRNA /cds=(1,1164) /gb=NM_020062 /gi=13236503 /ug=Hs.170088 /len=1727	NM_020062	Hs.170088	NP_064446
NM_020187	DC12 protein (DC12), mRNA	NM_020187	Hs.166096	NP_064572
NM_020188	DC13 protein (DC13), mRNA /cds=(176,415) /gb=NM_020188 /gi=9910183 /ug=Hs.6879 /len=716	NM_020188	Hs.6879	NP_064573

NM_020307	cyclin L ania-6a (LOC57018), mRNA /cds=(55,1635) /gb=NM_020307 /gi=9945319 /ug=Hs.4859 /len=2076	NM_020307	Hs.4859	NP_064703
NM_020432	hypothetical protein DKFZp564F013 (DKFZP564F013), mRNA /cds=(107,2194) /gb=NM_020432 /gi=24308192 /ug=Hs.128653 /len=4572	NM_020432	Hs.128653	NP_065165
NM_020470	Yip1p-interacting factor (YIF1P), mRNA /cds=(116,997) /gb=NM_020470 /gi=9994168 /ug=Hs.406422 /len=1078	NM_020470	Hs.406422	NP_065203
NM_020648	twisted gastrulation 1 (Drosophila) (TWSG1), mRNA /cds=(106,777) /gb=NM_020648 /gi=21314788 /ug=Hs.247302 /len=3693	NM_020648	Hs.247302	NP_065699
AK022459	cDNA FLJ12397 fis, clone MAMMA1002769, weakly similar to cell cycle progression restoration 8 protein (CPR8) mRNA	NM_004748	Hs.82506	NP_065790
NM_020873	KIAA1497 protein (KIAA1497), mRNA /cds=(10,1305) /gb=NM_020873 /gi=23308734 /ug=Hs.126085 /len=2728	NM_020873	Hs.126085	NP_065924

BC043352	Similar to RIKEN cDNA 2310026P19 gene, clone MGC:49935 IMAGE:6175382, mRNA, complete cds /cds=(288,3329) /gb=BC043352 /gi=27694113 /ug=Hs.35096 /len=5900		Hs.35096	NP_065950
NM_020978	amylase, alpha 2B; pancreatic (AMY2B), mRNA /cds=(365,1900) /gb=NM_020978 /gi=20070311 /ug=Hs.335493 /len=1963	NM_020978	Hs.335493	NP_066188
NM_015270	adenylate cyclase 6 (ADCY6), transcript variant 1, mRNA /cds=(695,4201) /gb=NM_015270 /gi=10947059 /ug=Hs.12373 /len=6594	NM_015270; NM_020983	Hs.12373	NP_066193
NM_021190	polypyrimidine tract binding protein 2 (PTBP2), mRNA /cds=(53,1648) /gb=NM_021190 /gi=10863996 /ug=Hs.34956 /len=3054	NM_021190	Hs.34956	NP_067013
NM_021633	kelch-like protein C3IP1 (C3IP1), mRNA /cds=(201,1907) /gb=NM_021633 /gi=21361889 /ug=Hs.3826 /len=3338	NM_021633	Hs.3826	NP_067646

NM_021738	supervillin (SVIL), transcript variant 2, mRNA /cds=(754,7398) /gb=NM_021738 /gi=11496981 /ug=Hs.154567 /len=8300	NM_003174; NM_021738	Hs.154567	NP_068506
NM_021820	MDS024 protein (MDS024), mRNA /cds=(65,838) /gb=NM_021820 /gi=11141892 /ug=Hs.425659 /len=2103	NM_021820	Hs.425659	NP_068592
NM_021826	hypothetical protein FLJ13149 (FLJ13149), mRNA /cds=(291,2585) /gb=NM_021826 /gi=11141902 /ug=Hs.112188 /len=2836	NM_021826	Hs.112188	NP_068598
NM_022063	hypothetical protein FLJ13188 (FLJ13188), mRNA /cds=(247,948) /gb=NM_022063 /gi=11545770 /ug=Hs.11859 /len=2746	NM_022063	Hs.11859	NP_071346
AK026797	cDNA: FLJ23144 fis, clone LNG09262	NM_022068	Hs.293907	NP_071351
NM_022366	transcription factor B2, mitochondrial (TFB2M), mRNA /cds=(125,1315) /gb=NM_022366 /gi=11641288 /ug=Hs.7395 /len=1803	NM_022366	Hs.7395	NP_071761
NM_022763	FAD104 (FAD104), mRNA /cds=(58,3672) /gb=NM_022763 /gi=27477058 /ug=Hs.299883 /len=6894	NM_022763	Hs.299883	NP_073600

NM_022772	EPS8-related protein 2 (EPS8R2), mRNA /cds=(273,2420) /gb=NM_022772 /gi=21264615 /ug=Hs.55016 /len=3181	NM_022772	Hs.55016	NP_073609
NM_022780	hypothetical protein FLJ13910 (FLJ13910), mRNA /cds=(99,1274) /gb=NM_022780 /gi=19923839 /ug=Hs.75277 /len=3239	NM_022780	Hs.75277	NP_073617
NM_022802	C-terminal binding protein 2 (CTBP2), transcript variant 2, mRNA /cds=(137,3094) /gb=NM_022802 /gi=12746589 /ug=Hs.171391 /len=3780	NM_001329; NM_022802	Hs.171391	NP_073713
NM_023018	NAD kinase (FLJ13052), mRNA /cds=(206,1978) /gb=NM_023018 /gi=20070325 /ug=Hs.220324 /len=3676	NM_023018	Hs.220324	NP_075394
AK025702	cDNA: FLJ22049 fis, clone HEP09444. /gb=AK025702 /gi=10438304 /ug=Hs.423737 /len=2435		Hs.423737	NP_075447
NM_023039	ankyrin repeat, family A (RFXANK-like), 2 (ANKRA2), mRNA /cds=(648,1589) /gb=NM_023039 /gi=21362082 /ug=Hs.239154 /len=2048	NM_023039	Hs.239154	NP_075526

NM_024051	hypothetical protein MGC3077 (MGC3077), mRNA /cds=(137,703) /gb=NM_024051 /gi=13129017 /ug=Hs.433404 /len=1195	NM_024051	Hs.433404	NP_076956
M80902	AHNAK nucleoprotein mRNA, 5' end		Hs.165215	NP_076965
NM_024065	likely ortholog of mouse phosducin-like 2 (PDCL2), mRNA /cds=(101,820) /gb=NM_024065 /gi=13129043 /ug=Hs.94576 /len=1044	NM_024065	Hs.94576	NP_076970
BE966653	601661342R1 NIH_MGC_72 cDNA clone IMAGE:3915994 3', mRNA sequence /clone=IMAGE:3915994 /clone_end=3' /gb=BE966653 /gi=11772295 /ug=Hs.330958 /len=703		Hs.330958	NP_076974
NM_024102	MEP50 protein (MEP50), mRNA /cds=(40,1068) /gb=NM_024102 /gi=20127622 /ug=Hs.11039 /len=2428	NM_024102	Hs.11039	NP_077007
NM_024120	chromosome 20 open reading frame 7 (C20orf7), mRNA /cds=(31,507) /gb=NM_024120 /gi=13129143 /ug=Hs.44296 /len=1715	NM_024120	Hs.44296	NP_077025

NM_024571	hypothetical protein FLJ22940 (FLJ22940), mRNA /cds=(984,1382) /gb=NM_024571 /gi=13443017 /ug=Hs.15277 /len=1704	NM_024571	Hs.15277	NP_078847
NM_024941	hypothetical protein FLJ13611 (FLJ13611), mRNA /cds=(207,1271) /gb=NM_024941 /gi=13376418 /ug=Hs.282958 /len=2726	NM_024941	Hs.282958	NP_079217
NM_025057	hypothetical protein FLJ23189 (FLJ23189), mRNA /cds=(60,746) /gb=NM_025057 /gi=13376590 /ug=Hs.287733 /len=2157	NM_025057	Hs.287733	NP_079333
NM_030571	Nedd4 family interacting protein 1 (NDFIP1), mRNA /cds=(105,770) /gb=NM_030571 /gi=13386479 /ug=Hs.9788 /len=1837	NM_030571	Hs.9788	NP_085048
BQ228526	AGENCOURT_7591767 NIH_MGC_92 cDNA clone IMAGE:6067123 5', mRNA sequence /clone=IMAGE:6067123 /clone_end=5' /gb=BQ228526 /gi=20409926 /ug=Hs.282204 /len=1263		Hs.282204	NP_110390

NM_030786	intermediate filament protein syncoilin (SYNCOILIN), mRNA /cds=(169,624) /gb=NM_030786 /gi=13540560 /ug=Hs.348415 /len=2114	NM_030786	Hs.348415	NP_110413
NM_030918	sorting nexin 27 (SNX27), mRNA	NM_030918	Hs.67619	NP_112180
NM_031219	hypothetical protein MGC12904 (MGC12904), mRNA /cds=(196,951) /gb=NM_031219 /gi=13654293 /ug=Hs.7739 /len=1143	NM_031219	Hs.7739	NP_112496
NM_031447	hypothetical protein MGC13033 (MGC13033), mRNA /cds=(201,305) /gb=NM_031447 /gi=13899280 /ug=Hs.423808 /len=1339	NM_031447	Hs.423808	NP_113635
NM_031866	frizzled 8 (Drosophila) (FZD8), mRNA /cds=(6,2090) /gb=NM_031866 /gi=13994189 /ug=Hs.302634 /len=3195	NM_031866	Hs.302634	NP_114072
NM_031934	RAB34, member RAS oncogene family (RAB34), mRNA /cds=(206,985) /gb=NM_031934 /gi=21361998 /ug=Hs.301853 /len=1340	NM_031934	Hs.301853	NP_114140

NM_005016	poly(rC) binding protein 2 (PCBP2), transcript variant 1, mRNA /cds=(89,1189) /gb=NM_005016 /gi=14141167 /ug=Hs.63525 /len=1362	NM_005016; NM_031989	Hs.63525	NP_114366
NM_032025	CDA02 protein (CDA02), mRNA /cds=(3,1832) /gb=NM_032025 /gi=14042940 /ug=Hs.332404 /len=2179	NM_032025	Hs.332404	NP_114414
NM_032141	hypothetical protein DKFZp434K1421 (DKFZP434K1421), mRNA /cds=(29,1705) /gb=NM_032141 /gi=14149806 /ug=Hs.374609 /len=2547	NM_032141	Hs.374609	NP_115517
NM_032377	hypothetical protein MGC4549 (MGC4549), mRNA /cds=(29,280) /gb=NM_032377 /gi=14150202 /ug=Hs.326422 /len=991	NM_032377	Hs.326422	NP_115753
NM_032378	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (EEF1D), transcript variant 1, mRNA /cds=(198,2141) /gb=NM_032378 /gi=25453473 /ug=Hs.334798 /len=2216	NM_001960; NM_032378	Hs.334798	NP_115754

NM_023005	bromodomain adjacent to zinc finger domain, 1B (BAZ1B), transcript variant 1, mRNA /cds=(353,4804) /gb=NM_023005 /gi=14670389 /ug=Hs.194688 /len=6079	NM_023005; NM_032408	Hs.194688	NP_115784
AB058707	mRNA for KIAA1804 protein, partial cds	NM_032435	Hs.50883	NP_115811
NM_032476	mitochondrial ribosomal protein S6 (MRPS6), nuclear gene encoding mitochondrial protein, mRNA /cds=(124,501) /gb=NM_032476 /gi=16554615 /ug=Hs.424751 /len=959	NM_032476	Hs.424751	NP_115865
NM_032557	HP43.8KD protein (HP43.8KD), mRNA /cds=(507,3635) /gb=NM_032557 /gi=27545312 /ug=Hs.332841 /len=4684	NM_032557	Hs.332841	NP_115946
NM_032739	hypothetical protein MGC5370 (MGC5370), mRNA /cds=(189,269) /gb=NM_032739 /gi=14249363 /ug=Hs.332938 /len=974	NM_032739	Hs.332938	NP_116128
NM_032810	hypothetical protein FLJ14600 (FLJ14600), mRNA /cds=(309,764) /gb=NM_032810 /gi=14249497 /ug=Hs.100861 /len=2334	NM_032810	Hs.100861	NP_116199

NM_032832	hypothetical protein FLJ14735 (FLJ14735), mRNA /cds=(7,1509) /gb=NM_032832 /gi=14249539 /ug=Hs.334762 /len=3260	NM_032832	Hs.334762	NP_116221
NM_032870	SR rich protein (DKFZp564B0769), mRNA /cds=(33,2450) /gb=NM_032870 /gi=18699723 /ug=Hs.18368 /len=2663	NM_032870	Hs.18368	NP_116259
NM_032997	ZW10 interactor (ZWINT), transcript variant 2, mRNA /cds=(25,858) /gb=NM_032997 /gi=14602426 /ug=Hs.42650 /len=1851	NM_007057; NM_032997	Hs.42650	NP_127490
BC009336	clone MGC:16714 IMAGE:4128220, mRNA, complete cds	NM_033116	Hs.7200	NP_149107
NM_033535	F-box and leucine-rich repeat protein 5 (FBXL5), transcript variant 2, mRNA /cds=(586,2283) /gb=NM_033535 /gi=21536439 /ug=Hs.5548 /len=3475	NM_012161; NM_033535	Hs.5548	NP_277077
NM_015414	ribosomal protein L36 (RPL36), transcript variant 2, mRNA /cds=(153,470) /gb=NM_015414 /gi=16117793 /ug=Hs.433411 /len=545	NM_015414; NM_033643	Hs.433411	NP_378669

NM_052957	acidic repeat containing (ACRC), mRNA /cds=(3,2078) /gb=NM_052957 /gi=16445032 /ug=Hs.135167 /len=2692	NM_052957	Hs.135167	NP_443189
NM_053045	hypothetical protein MGC14327 (MGC14327), mRNA /cds=(225,635) /gb=NM_053045 /gi=16596685 /ug=Hs.231029 /len=1576	NM_053045	Hs.231029	NP_444273
NM_057159	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 (EDG2), transcript variant 2, mRNA /cds=(394,1488) /gb=NM_057159 /gi=16950637 /ug=Hs.75794 /len=2732	NM_001401; NM_057159	Hs.75794	NP_476500
NM_003479	protein tyrosine phosphatase type IVA, member 2 (PTP4A2), transcript variant 1, mRNA /cds=(1011,1514) /gb=NM_003479 /gi=18104974 /ug=Hs.82911 /len=3925	NM_003479; NM_080391; NM_080392	Hs.82911	NP_536317
NM_080737	synaptotagmin-like 4 (granuphilin-a) (SYTL4), mRNA /cds=(333,2348) /gb=NM_080737 /gi=18152766 /ug=Hs.247525 /len=3914	NM_080737	Hs.247525	NP_542775

NM_080597	oxysterol binding protein-like 1A (OSBPL1A), transcript variant OSBPL1B, mRNA /cds=(175,3027) /gb=NM_080597 /gi=19718740 /ug=Hs.252716 /len=4165	NM_018030; NM_080597; NM_133268	Hs.252716	NP_579802
NM_133367	chromosome 6 open reading frame 33 (C6orf33), mRNA /cds=(165,1229) /gb=NM_133367 /gi=19115959 /ug=Hs.239388 /len=4650	NM_133367	Hs.239388	NP_588608
NM_134264	SOCS box-containing WD protein SWiP-1 (WSB1), transcript variant 3, mRNA /cds=(317,1051) /gb=NM_134264 /gi=20143909 /ug=Hs.187991 /len=4243	NM_015626; NM_134264; NM_134265	Hs.187991	NP_599027
NM_138792	hypothetical protein BC018147 (LOC123169), mRNA /cds=(29,2029) /gb=NM_138792 /gi=20270336 /ug=Hs.296420 /len=2174	NM_138792	Hs.296420	NP_620147
NM_004357	CD151 antigen (CD151), transcript variant 1, mRNA /cds=(130,891) /gb=NM_004357 /gi=21237747 /ug=Hs.75564 /len=1552	NM_004357; NM_139030	Hs.75564	NP_620599
AK026207	cDNA: FLJ22554 fis, clone HSI01092		Hs.93842	NP_631903

AK095110	cDNA FLJ37791 fis, clone BRHIP3000131. /gb=AK095110 /gi=21754304 /ug=Hs.350534 /len=3820	NM_144628	Hs.350534	NP_653229
NM_144721	hypothetical protein MGC30052 (MGC30052), mRNA /cds=(35,703) /gb=NM_144721 /gi=21389506 /ug=Hs.143692 /len=2260	NM_144721	Hs.143692	NP_653322
NM_003188	mitogen-activated protein kinase kinase kinase 7 (MAP3K7), transcript variant A, mRNA /cds=(306,2045) /gb=NM_003188 /gi=21735560 /ug=Hs.7510 /len=2912	NM_003188; NM_145331; NM_145332; NM_145333	Hs.7510	NP_663306
AJ295983	mRNA for hypothetical protein (ORF1), clone Telethon(Italy_B41)_Strait15106_FL304		Hs.292653	NP_689526
NM_152388	hypothetical protein FLJ33282 (FLJ33282), mRNA /cds=(225,1523) /gb=NM_152388 /gi=22748830 /ug=Hs.346509 /len=2078	NM_152388	Hs.346509	NP_689601
NM_152408	hypothetical protein FLJ35779 (FLJ35779), mRNA /cds=(42,1694) /gb=NM_152408 /gi=22748864 /ug=Hs.432726 /len=1698	NM_152408	Hs.432726	NP_689621

NM_152520	hypothetical protein FLJ25270 (FLJ25270), mRNA /cds=(244,1353) /gb=NM_152520 /gi=22749086 /ug=Hs.6295 /len=2493	NM_152520	Hs.6295	NP_689733
NM_012425	Ras suppressor protein 1 (RSU1), mRNA /cds=(70,903) /gb=NM_012425 /gi=10800408 /ug=Hs.75551 /len=1436	NM_012425	Hs.75551	NP_689937
NM_153649	tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=NM_153649 /gi=24119202 /ug=Hs.85844 /len=2089	NM_152263; NM_153649	Hs.85844	NP_705935
NM_138962	musashi 2 (Drosophila) (MSI2), transcript variant 1, mRNA	NM_138962; NM_170721	Hs.103512	NP_733839
NM_172070	similar to F10G7.10.p (KIAA2024), mRNA /cds=(343,1374) /gb=NM_172070 /gi=25453393 /ug=Hs.46826 /len=3703	NM_172070	Hs.46826	NP_742067
NM_172239	exonuclease GOR (GOR), mRNA /cds=(628,1584) /gb=NM_172239 /gi=26665874 /ug=Hs.373854 /len=6609	NM_172239	Hs.373854	NP_758439

NM_003971	sperm associated antigen 9 (SPAG9), transcript variant 1, mRNA /cds=(79,4002) /gb=NM_003971 /gi=27436919 /ug=Hs.129872 /len=4663	NM_003971; NM_172345	Hs.129872	NP_758853
NM_176824	Bardet-Biedl syndrome 7 (BBS7), transcript variant 1, mRNA	NM_018190; NM_176824		NP_789794
BC013374	clone MGC:16435 IMAGE:3946253, mRNA, complete cds /cds=(137,1471) /gb=BC013374 /gi=15426525 /ug=Hs.179661 /len=2519	NM_178014	Hs.179661	NP_821133
AK023762	cDNA FLJ13700 fis, clone PLACE2000216, highly similar to SPECTRIN BETA CHAIN, BRAIN	NM_003128; NM_178313	Hs.107164	NP_842565
NM_004953	eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA /cds=(369,4559) /gb=NM_004953 /gi=4826709 /ug=Hs.433750 /len=5018	NM_004953	Hs.433750	NP_886553
NM_018682	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax Drosophila) (MLL5), mRNA /cds=(202,5778) /gb=NM_018682 /gi=23503326 /ug=Hs.333300 /len=6543	NM_018682	Hs.333300	NP_891847

AL833458	mRNA; cDNA DKFZp686J19116 (from clone DKFZp686J19116) /gb=AL833458 /gi=21734100 /ug=Hs.428760 /len=3297		Hs.428760	NP_037387
U55184	G protein Golf alpha gene, exon 12 and complete cds	NM_002071		NP_002062
U18270	thymopoietin (TMPO) gene, exons 4 and 5, and complete cds for thymopoietin alpha	NM_003276		NP_003267
NM_131105	Danio rerio alpha-tropomyosin (tpma), mRNA	NM_131105	Dr.20815	NP_571180
NM_138713	nuclear factor of activated T-cells 5, tonicity-responsive (NFAT5), transcript variant 2, mRNA	NM_006599; NM_138713; NM_138714; NM_173214; NM_173215		NP_006590; NP_619727; NP_619728; NP_775321; NP_775322
J00123	preproenkephalin precursor (PEN) gene, exon 3 and complete cds	NM_006211		NP_006202
AB030001	gene for SGRF, complete cds	NM_016584		NP_057668
NM_033071	spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant longest, mRNA	NM_015293; NM_033071; NM_133650		NP_056108; NP_149062; NP_598411
NM_025199	hypothetical protein FLJ20886 (FLJ20886), mRNA	NM_025199	Hs.241558	NP_079475
AL832582	mRNA; cDNA DKFZp451G0416 (from clone DKFZp451G0416)	NM_015878; NM_148174		NP_056962; NP_680479
AY207372	cyclin I (CCNI) gene, complete cds			AAO13492

AF539738	Danio rerio troponin mRNA, complete cds			AAN31755

FIGURE 6d: OA stage specific markers for severe OA only

Clone name	Genbank	Description	RefSeq	UniGene	Rep_prot
ncrb8285	NM_000088	collagen, type I, alpha 1 (COL1A1), mRNA /cds=(120,4514) /gb=NM_000088 /gi=14719826 /ug=Hs.172928 /len=5921	NM_000088	Hs.172928	NP_000079
ncrc2319	NM_000146	ferritin, light polypeptide (FTL), mRNA /cds=(189,716) /gb=NM_000146 /gi=20149497 /ug=Hs.430150 /len=878	NM_000146	Hs.430150	NP_000137
mioc4119	NM_000161	GTP cyclohydrolase 1 (dopa-responsive dystonia) (GCH1), mRNA /cds=(149,901) /gb=NM_000161 /gi=4503948 /ug=Hs.86724 /len=2921	NM_000161	Hs.86724	NP_000152
fcrc1965	NM_000175	glucose phosphate isomerase (GPI), mRNA /cds=(104,1780) /gb=NM_000175 /gi=18201904 /ug=Hs.406458 /len=2075	NM_000175	Hs.406458	NP_000166
mioa9147	NM_000237	lipoprotein lipase (LPL), mRNA /cds=(175,1602) /gb=NM_000237 /gi=4557726 /ug=Hs.180878 /len=3549	NM_000237	Hs.180878	NP_000228

seob2750	NM_000291	phosphoglycerate kinase 1 (PGK1), mRNA /cds=(70,1323) /gb=NM_000291 /gi=22095338 /ug=Hs.78771 /len=2338	NM_000291	Hs.78771	NP_000282
mioa0218	NM_000361	thrombomodulin (THBD), mRNA /cds=(542,2269) /gb=NM_000361 /gi=4507482 /ug=Hs.2030 /len=4050	NM_000361	Hs.2030	NP_000352
ncrb7675	NM_000380	xeroderma pigmentosum, complementation group A (XPA), mRNA /cds=(27,848) /gb=NM_000380 /gi=4507936 /ug=Hs.192803 /len=1377	NM_000380	Hs.192803	NP_000371
fcr7059	NM_000386	bleomycin hydrolase (BLMH), mRNA /cds=(79,1446) /gb=NM_000386 /gi=4557366 /ug=Hs.78943 /len=1932	NM_000386	Hs.78943	NP_000377
seoc0394	NM_000406	gonadotropin-releasing hormone receptor (GNRHR), mRNA /cds=(1749,2735) /gb=NM_000406 /gi=4504058 /ug=Hs.73064 /len=2735	NM_000406	Hs.73064	NP_000397
fcrb2704	NM_000517	hemoglobin, alpha 2 (HBA2), mRNA /cds=(38,466) /gb=NM_000517 /gi=14043068 /ug=Hs.347939 /len=575	NM_000517	Hs.347939	NP_000508

fcr2546	NM_000598	insulin-like growth factor binding protein 3 (IGFBP3), mRNA /cds=(88,963) /gb=NM_000598 /gi=19923110 /ug=Hs.77326 /len=2506	NM_000598	Hs.77326	NP_000589
fcrb3205	NM_000633	B-cell CLL/lymphoma 2 (BCL2), nuclear gene encoding mitochondrial protein, transcript variant alpha, mRNA /cds=(32,751) /gb=NM_000633 /gi=4557354 /ug=Hs.79241 /len=6030	NM_000633; NM_000657	Hs.79241	NP_000648
fcrb9371	NM_000701	ATPase, Na /K transporting, alpha 1 polypeptide (ATP1A1), mRNA /cds=(262,3333) /gb=NM_000701 /gi=21361180 /ug=Hs.76549 /len=3680	NM_000701	Hs.76549	NP_000692
fcrc3704	NM_000786	cytochrome P450, family 51 (CYP51), mRNA /cds=(332,1861) /gb=NM_000786 /gi=13929427 /ug=Hs.226213 /len=3381	NM_000786	Hs.226213	NP_000777
ncr5719	NM_000898	monoamine oxidase B (MAOB), nuclear gene encoding mitochondrial protein, mRNA /cds=(78,1640) /gb=NM_000898 /gi=4505092 /ug=Hs.82163 /len=2491	NM_000898	Hs.82163	NP_000889

ncrc3544	NM_000970	ribosomal protein L6 (RPL6), mRNA /cds=(32,898) /gb=NM_000970 /gi=16753226 /ug=Hs.409045 /len=950	NM_000970	Hs.409045	NP_000961
seob7309	NM_000970	ribosomal protein L6 (RPL6), mRNA /cds=(32,898) /gb=NM_000970 /gi=16753226 /ug=Hs.409045 /len=950	NM_000970	Hs.409045	NP_000961
mioa0607	NM_000971	ribosomal protein L7 (RPL7), mRNA /cds=(22,768) /gb=NM_000971 /gi=15431300 /ug=Hs.153 /len=838	NM_000971	Hs.153	NP_000962
ncrc5230	NM_000976	ribosomal protein L12 (RPL12), mRNA /cds=(89,586) /gb=NM_000976 /gi=15431291 /ug=Hs.405042 /len=632	NM_000976	Hs.405042	NP_000967
seoa7605	NM_000981	ribosomal protein L19 (RPL19), mRNA /cds=(29,619) /gb=NM_000981 /gi=17158042 /ug=Hs.426977 /len=698	NM_000981	Hs.426977	NP_000972
miod2225	NM_000985	ribosomal protein L17 (RPL17), mRNA /cds=(287,841) /gb=NM_000985 /gi=14591906 /ug=Hs.82202 /len=898	NM_000985	Hs.82202	NP_000976
fcrb6000	NM_000998	ribosomal protein L37a (RPL37A), mRNA /cds=(36,314) /gb=NM_000998 /gi=16306561 /ug=Hs.296290 /len=392	NM_000998	Hs.296290	NP_000989

mioa0909	NM_001000	ribosomal protein L39 (RPL39), mRNA /cds=(68,223) /gb=NM_001000 /gi=16306563 /ug=Hs.300141 /len=401	NM_001000	Hs.300141	NP_000991
fcrb5503	NM_001007	ribosomal protein S4, X-linked (RPS4X), mRNA /cds=(36,827) /gb=NM_001007 /gi=17981705 /ug=Hs.389933 /len=916	NM_001007	Hs.389933	NP_000998
mioa8984	NM_001012	ribosomal protein S8 (RPS8), mRNA /cds=(24,650) /gb=NM_001012 /gi=4506742 /ug=Hs.399720 /len=705	NM_001012	Hs.399720	NP_001003
mioa3987	NM_001021	ribosomal protein S17 (RPS17), mRNA /cds=(26,433) /gb=NM_001021 /gi=14591913 /ug=Hs.5174 /len=515	NM_001021	Hs.5174	NP_001012
fcrb5756	NM_001102	actinin, alpha 1 (ACTN1), mRNA /cds=(184,2862) /gb=NM_001102 /gi=12025669 /ug=Hs.119000 /len=3398	NM_001102	Hs.119000	NP_001093
fcrb1809	NM_001207	basic transcription factor 3 (BTF3), mRNA /cds=(240,728) /gb=NM_001207 /gi=20070129 /ug=Hs.101025 /len=952	NM_001207	Hs.101025	NP_001198

seoa3555	NM_001207	basic transcription factor 3 (BTF3), mRNA /cds=(240,728) /gb=NM_001207 /gi=20070129 /ug=Hs.101025 /len=952	NM_001207	Hs.101025	NP_001198
seob5942	NM_001239	cyclin H (CCNH), mRNA /cds=(233,1204) /gb=NM_001239 /gi=17738313 /ug=Hs.514 /len=1398	NM_001239	Hs.514	NP_001230
fcr7060	NM_001428	enolase 1, (alpha) (ENO1), mRNA /cds=(152,1456) /gb=NM_001428 /gi=16507965 /ug=Hs.254105 /len=1812	NM_001428	Hs.254105	NP_001419
hfcr2664	NM_001428	enolase 1, (alpha) (ENO1), mRNA /cds=(152,1456) /gb=NM_001428 /gi=16507965 /ug=Hs.254105 /len=1812	NM_001428	Hs.254105	NP_001419
ncrc1531	AF001862	FYN binding protein mRNA, complete cds	NM_001465	Hs.58435	NP_001456
seob6156	NM_001494	GDP dissociation inhibitor 2 (GDI2), mRNA /cds=(153,1490) /gb=NM_001494 /gi=6598322 /ug=Hs.56845 /len=2274	NM_001494	Hs.56845	NP_001485
miob2257	BC039726	Similar to general transcription factor IIH, polypeptide 3, 34kDa, clone IMAGE:5582960, mRNA		Hs.30724	NP_001507

fcrb6574	NM_001568	eukaryotic translation initiation factor 3, subunit 6 48kDa (EIF3S6), mRNA /cds=(23,1360) /gb=NM_001568 /gi=4503520 /ug=Hs.106673 /len=1510	NM_001568	Hs.106673	NP_001559
fcrb2745	NM_001613	actin, alpha 2, smooth muscle, aorta (ACTA2), mRNA /cds=(48,1181) /gb=NM_001613 /gi=4501882 /ug=Hs.195851 /len=1330	NM_001613	Hs.195851	NP_001604
mioa8034	NM_001690	ATPase, H transporting, lysosomal 70kDa, V1 subunit A, isoform 1 (ATP6V1A1), mRNA /cds=(67,1920) /gb=NM_001690 /gi=19913423 /ug=Hs.281866 /len=4567	NM_001690	Hs.281866	NP_001681
ncr1428	NM_001693	ATPase, H transporting, lysosomal 56/58kDa, V1 subunit B, isoform 2 (ATP6V1B2), mRNA /cds=(208,1743) /gb=NM_001693 /gi=19913427 /ug=Hs.1697 /len=3054	NM_001693	Hs.1697	NP_001684

seob1860	NM_001754	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene) (RUNX1), mRNA /cds=(445,1887) /gb=NM_001754 /gi=19923197 /ug=Hs.129914 /len=6212	NM_001754	Hs.129914	NP_001745
ncr3642	NM_001759	cyclin D2 (CCND2), mRNA /cds=(270,1139) /gb=NM_001759 /gi=16950656 /ug=Hs.75586 /len=6480	NM_001759	Hs.75586	NP_001750
fcrb3966	NM_001766	CD1D antigen, d polypeptide (CD1D), mRNA /cds=(165,1172) /gb=NM_001766 /gi=4502648 /ug=Hs.1799 /len=1903	NM_001766	Hs.1799	NP_001757
seoa0913	NM_001769	CD9 antigen (p24) (CD9), mRNA /cds=(112,798) /gb=NM_001769 /gi=21237762 /ug=Hs.1244 /len=1246	NM_001769	Hs.1244	NP_001760
seob0752	NM_001827	CDC28 protein kinase regulatory subunit 2 (CKS2), mRNA /cds=(96,335) /gb=NM_001827 /gi=4502858 /ug=Hs.83758 /len=627	NM_001827	Hs.83758	NP_001818
seoa0526	BC025372	calponin 3, acidic, clone MGC:1775 IMAGE:3505668, mRNA, complete cds	NM_001839	Hs.194662	NP_001830

fcrb2993	NM_001861	cytochrome c oxidase subunit IV isoform 1 (COX4I1), nuclear gene encoding mitochondrial protein, mRNA /cds=(165,674) /gb=NM_001861 /gi=17017985 /ug=Hs.433419 /len=802	NM_001861	Hs.433419	NP_001852
fcr4308	NM_001878	cellular retinoic acid binding protein 2 (CRABP2), mRNA /cds=(138,554) /gb=NM_001878 /gi=6382069 /ug=Hs.183650 /len=969	NM_001878	Hs.183650	NP_001869
fcr7656	NM_001896	casein kinase 2, alpha prime polypeptide (CSNK2A2), mRNA /cds=(164,1216) /gb=NM_001896 /gi=4503096 /ug=Hs.82201 /len=1677	NM_001896	Hs.82201	NP_001887
ncrc2495	NM_001967	eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), mRNA /cds=(16,1239) /gb=NM_001967 /gi=9945313 /ug=Hs.173912 /len=1864	NM_001967	Hs.173912	NP_001958
fcrc6452	NM_002047	glycyl-tRNA synthetase (GARS), mRNA /cds=(519,2576) /gb=NM_002047 /gi=6996009 /ug=Hs.293885 /len=2742	NM_002047	Hs.293885	NP_002038

ncr5066	NM_002117	major histocompatibility complex, class I, C (HLA-C), mRNA /cds=(16,1116) /gb=NM_002117 /gi=19557676 /ug=Hs.277477 /len=1549	NM_002117	Hs.277477	NP_002108
seoc5963	AL110194	mRNA; cDNA DKFZp566M063 (from clone DKFZp566M063)		Hs.6727	NP_002119
seob5976	NM_002210	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) (ITGAV), mRNA /cds=(42,3188) /gb=NM_002210 /gi=4504762 /ug=Hs.295726 /len=5717	NM_002210	Hs.295726	NP_002201
ncrc9228	NM_002295	laminin receptor 1 (ribosomal protein SA, 67kDa) (LAMR1), mRNA /cds=(86,973) /gb=NM_002295 /gi=9845501 /ug=Hs.181357 /len=1039	NM_002295	Hs.181357	NP_002286
seob0810	NM_002305	lectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1), mRNA /cds=(69,476) /gb=NM_002305 /gi=6006015 /ug=Hs.382367 /len=526	NM_002305	Hs.382367	NP_002296
ncr8780	NM_002395	malic enzyme 1, NADP( )-dependent, cytosolic (ME1), mRNA /cds=(108,1826) /gb=NM_002395 /gi=13435400 /ug=Hs.14732 /len=2212	NM_002395	Hs.14732	NP_002386

hfcr2696	NM_002417	antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA /cds=(197,9967) /gb=NM_002417 /gi=19923216 /ug=Hs.80976 /len=12515	NM_002417	Hs.80976	NP_002408
fcr2218	NM_002477	myosin, light polypeptide 5, regulatory (MYL5), mRNA /cds=(106,627) /gb=NM_002477 /gi=4505304 /ug=Hs.170482 /len=661	NM_002477	Hs.170482	NP_002468
seoa4400	BC045606	Similar to nidogen (enactin), clone MGC:33141 IMAGE:5271590, mRNA, complete cds		Hs.356624	NP_002499
seoa2726	NM_002526	5'-nucleotidase, ecto (CD73) (NT5E), mRNA	NM_002526	Hs.153952	NP_002517
hfcr1724	NM_002615	serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1 (SERPINF1), mRNA /cds=(39,1082) /gb=NM_002615 /gi=4505708 /ug=Hs.173594 /len=1199	NM_002615	Hs.173594	NP_002606
ncrb8191	NM_002616	period 1 (Drosophila) (PER1), mRNA /cds=(188,4060) /gb=NM_002616 /gi=4505712 /ug=Hs.68398 /len=4656	NM_002616	Hs.68398	NP_002607

hfcr1689	NM_002676	phosphomannomutase 1 (PMM1), mRNA /cds=(5,793) /gb=NM_002676 /gi=4505904 /ug=Hs.75835 /len=1210	NM_002676	Hs.75835	NP_002667
ncrb4402	NM_002696	polymerase (RNA) II (DNA directed) polypeptide G (POLR2G), mRNA /cds=(107,625) /gb=NM_002696 /gi=4505946 /ug=Hs.14839 /len=828	NM_002696	Hs.14839	NP_002687
miob0175	NM_002734	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1) (PRKAR1A), mRNA /cds=(88,1233) /gb=NM_002734 /gi=4506062 /ug=Hs.183037 /len=3036	NM_002734	Hs.183037	NP_002725
fcrb9420	NM_002778	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), mRNA /cds=(39,1613) /gb=NM_002778 /gi=11386146 /ug=Hs.406455 /len=2767	NM_002778	Hs.406455	NP_002769
seob0928	NM_002790	proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5), mRNA /cds=(86,811) /gb=NM_002790 /gi=23110941 /ug=Hs.76913 /len=1023	NM_002790	Hs.76913	NP_002781

fcrb8937	J03580	parathyroid-like protein (associated with humoral hypercalcemia of malignancy) mRNA, complete cds	NM_002820	Hs.89626	NP_002811
ncrc1247	NM_002835	protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA /cds=(30,2372) /gb=NM_002835 /gi=18375651 /ug=Hs.62 /len=3161	NM_002835	Hs.62	NP_002826
seob6395	NM_002841	protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA /cds=(718,5055) /gb=NM_002841 /gi=18860897 /ug=Hs.89627 /len=5787	NM_002841	Hs.89627	NP_002832
ncrb3989	BC050558	RAB5B, member RAS oncogene family, clone IMAGE:6191566, mRNA, partial cds			NP_002859
fcr4984	NM_002951	ribophorin II (RPN2), mRNA /cds=(289,2184) /gb=NM_002951 /gi=4506676 /ug=Hs.406532 /len=2509	NM_002951	Hs.406532	NP_002942
fcr2427	NM_002997	syndecan 1 (SDC1), mRNA /cds=(253,1185) /gb=NM_002997 /gi=21359855 /ug=Hs.82109 /len=2484	NM_002997	Hs.82109	NP_002988
seob6153	NM_003113	nuclear antigen Sp100 (SP100), mRNA /cds=(32,2671) /gb=NM_003113 /gi=19923235 /ug=Hs.77617 /len=3579	NM_003113	Hs.77617	NP_003104

seob0376	NM_003392	wingless-type MMTV integration site family, member 5A (WNT5A), mRNA /cds=(758,1855) /gb=NM_003392 /gi=17402917 /ug=Hs.152213 /len=4428	NM_003392	Hs.152213	NP_003383
fcr3001	NM_003405	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide (YWHAH), mRNA /cds=(198,938) /gb=NM_003405 /gi=21464102 /ug=Hs.349530 /len=1775	NM_003405	Hs.349530	NP_003396
mioa0400	AF025771	C2H2 zinc finger protein splicing variant b2 (ZNF189) mRNA, complete cds	NM_003452	Hs.50123	NP_003443
mioa3528	NM_003455	zinc finger protein 202 (ZNF202), mRNA /cds=(11,1957) /gb=NM_003455 /gi=10835040 /ug=Hs.9443 /len=4053	NM_003455	Hs.9443	NP_003446
hfcr6164	NM_003505	frizzled 1 (Drosophila) (FZD1), mRNA /cds=(414,2357) /gb=NM_003505 /gi=4503824 /ug=Hs.94234 /len=4350	NM_003505	Hs.94234	NP_003496
miob3252	NM_003613	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase (CILP), mRNA /cds=(130,3684) /gb=NM_003613 /gi=4502844 /ug=Hs.151407 /len=4175	NM_003613	Hs.151407	NP_003604

miob5675	NM_003630	peroxisomal biogenesis factor 3 (PEX3), mRNA /cds=(64,1185) /gb=NM_003630 /gi=4505726 /ug=Hs.7277 /len=1979	NM_003630	Hs.7277	NP_003621
ncr0179	NM_003729	RTC domain containing 1 (RTCD1), mRNA /cds=(171,1271) /gb=NM_003729 /gi=4506588 /ug=Hs.27076 /len=1539	NM_003729	Hs.27076	NP_003720
fcrb7588	NM_003746	dynein, cytoplasmic, light polypeptide 1 (DNCL1), mRNA /cds=(94,363) /gb=NM_003746 /gi=4505812 /ug=Hs.5120 /len=643	NM_003746	Hs.5120	NP_003737
ncr3948	NM_003851	cellular repressor of E1A-stimulated genes (CREG), mRNA /cds=(34,696) /gb=NM_003851 /gi=4503036 /ug=Hs.5710 /len=1989	NM_003851	Hs.5710	NP_003842
seob1078	NM_003881	WNT1 inducible signaling pathway protein 2 (WISP2), mRNA /cds=(148,900) /gb=NM_003881 /gi=18491001 /ug=Hs.194679 /len=1433	NM_003881	Hs.194679	NP_003872

ncrc6678	NM_003906	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) associated protein (MCM3AP), mRNA /cds=(38,5980) /gb=NM_003906 /gi=19923190 /ug=Hs.168481 /len=6114	NM_003906	Hs.168481	NP_003897
seob3869	NM_003919	sarcoglycan, epsilon (SGCE), mRNA /cds=(69,1382) /gb=NM_003919 /gi=10835046 /ug=Hs.110708 /len=1658	NM_003919	Hs.110708	NP_003910
hfcr3444	NM_003992	CDC-like kinase 3 (CLK3), transcript variant phclk3, mRNA /cds=(57,1529) /gb=NM_003992 /gi=4502884 /ug=Hs.73987 /len=1762	NM_001292; NM_003992	Hs.73987	NP_003983
fcrb6181	NM_004152	ornithine decarboxylase antizyme 1 (OAZ1), mRNA /gb=NM_004152 /gi=9845504 /ug=Hs.281960 /len=986	NM_004152	Hs.281960	NP_004143
fcr1182	NM_004181	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) (UCHL1), mRNA /cds=(75,746) /gb=NM_004181 /gi=21361090 /ug=Hs.76118 /len=1119	NM_004181	Hs.76118	NP_004172

fcr6915	NM_004192	acetylserotonin O-methyltransferase-like (ASMTL), mRNA /cds=(1,1890) /gb=NM_004192 /gi=4757793 /ug=Hs.70327 /len=1890	NM_004192	Hs.70327	NP_004183
hfcr1639	NM_004265	fatty acid desaturase 2 (FADS2), mRNA /cds=(151,1485) /gb=NM_004265 /gi=14141180 /ug=Hs.184641 /len=3149	NM_004265	Hs.184641	NP_004256
fcrb5455	NM_004269	cofactor required for Sp1 transcriptional activation, subunit 8, 34kDa (CRSP8), mRNA /cds=(1,822) /gb=NM_004269 /gi=4758065 /ug=Hs.374262 /len=822	NM_004269	Hs.374262	NP_004260
ncrb5254	NM_004339	pituitary tumor-transforming 1 interacting protein (PTTG1IP), mRNA /cds=(211,753) /gb=NM_004339 /gi=11038670 /ug=Hs.111126 /len=2737	NM_004339	Hs.111126	NP_004330
ncr3825	NM_004344	centrin, EF-hand protein, 2 (CETN2), mRNA /cds=(48,566) /gb=NM_004344 /gi=4757901 /ug=Hs.82794 /len=1087	NM_004344	Hs.82794	NP_004335

ncrc5464	NM_004552	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase) (NDUFS5), mRNA /cds=(72,392) /gb=NM_004552 /gi=4758789 /ug=Hs.409829 /len=540	NM_004552	Hs.409829	NP_004543
seob7928	NM_004642	CDK2-associated protein 1 (CDK2AP1), mRNA /cds=(523,870) /gb=NM_004642 /gi=17978492 /ug=Hs.433201 /len=1627	NM_004642	Hs.433201	NP_004633
miob0496	NM_004719	splicing factor, arginine/serine-rich 2, interacting protein (SFRS2IP), mRNA /cds=(1211,4657) /gb=NM_004719 /gi=4759171 /ug=Hs.51957 /len=5307	NM_004719	Hs.51957	NP_004710
seoa4102	NM_004780	transcription elongation factor A (SII)-like 1 (TCEAL1), mRNA /cds=(165,638) /gb=NM_004780 /gi=4759215 /ug=Hs.95243 /len=1174	NM_004780	Hs.95243	NP_004771
seoa6930	NM_004798	kinesin family member 3B (KIF3B), mRNA	NM_004798	Hs.301206	NP_004789
ncrc0174	NM_004837	geranylgeranyl diphosphate synthase 1 (GGPS1), mRNA /cds=(233,1135) /gb=NM_004837 /gi=21359876 /ug=Hs.55498 /len=1489	NM_004837	Hs.55498	NP_004828

seob2161	NM_004905	anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2) (AOP2), mRNA /cds=(44,718) /gb=NM_004905 /gi=4758637 /ug=Hs.120 /len=1653	NM_004905	Hs.120	NP_004896
seoa0066	NM_005006	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase) (NDUFS1), mRNA /cds=(85,2268) /gb=NM_005006 /gi=28269700 /ug=Hs.8248 /len=2382	NM_005006	Hs.8248	NP_004997
ncr7915	NM_005083	U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 1 (U2AF1RS1), mRNA /cds=(112,1551) /gb=NM_005083 /gi=13186299 /ug=Hs.103962 /len=1566	NM_005083	Hs.103962	NP_005074
ncr3380	NM_005178	B-cell CLL/lymphoma 3 (BCL3), mRNA /cds=(42,1382) /gb=NM_005178 /gi=20336471 /ug=Hs.31210 /len=1813	NM_005178	Hs.31210	NP_005169

fcrb3288	NM_005216	dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST), mRNA /cds=(60,1430) /gb=NM_005216 /gi=20070196 /ug=Hs.34789 /len=2045	NM_005216	Hs.34789	NP_005207
seoa4548	NM_005336	high density lipoprotein binding protein (vigilin) (HDLBP), mRNA	NM_005336	Hs.177516	NP_005327
seoc3552	BC041849	Similar to Rho-associated, coiled-coil containing protein kinase 1, clone IMAGE:5269982, mRNA		Hs.17820	NP_005397
seoa5473	NM_005408	chemokine (C-C motif) ligand 13 (CCL13), mRNA /cds=(76,372) /gb=NM_005408 /gi=22538799 /ug=Hs.11383 /len=861	NM_005408	Hs.11383	NP_005399
seoc4060	AF006516	eps8 binding protein e3B1 mRNA, complete cds	NM_005470	Hs.24752	NP_005461
miob7231	AA705851	ah42f05.s1 Soares_testis_NHT cDNA clone 1292193 3' similar to P54687 BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, CYTOSOLIC ;, mRNA sequence /clone=1292193 /clone_end=3' /gb=AA705851 /gi=2715769 /ug=Hs.443872 /len=412		Hs.443872	NP_005495

fcrb0623	NM_005517	high-mobility group nucleosomal binding domain 2 (HMGN2), mRNA /cds=(108,380) /gb=NM_005517 /gi=5031748 /ug=Hs.181163 /len=1198	NM_005517	Hs.181163	NP_005508
seoc0514	NM_005531	interferon, gamma-inducible protein 16 (IFI16), mRNA /cds=(265,2454) /gb=NM_005531 /gi=5031778 /ug=Hs.155530 /len=2709	NM_005531	Hs.155530	NP_005522
seoa6393	NM_005537	inhibitor of growth family, member 1 (ING1), mRNA /cds=(433,1701) /gb=NM_005537 /gi=19923770 /ug=Hs.46700 /len=2886	NM_005537	Hs.46700	NP_005528
fcr0535	NM_005539	inositol polyphosphate-5-phosphatase, 40kDa (INPP5A), mRNA /cds=(102,1193) /gb=NM_005539 /gi=5031796 /ug=Hs.124029 /len=2640	NM_005539	Hs.124029	NP_005530
seoa2639	NM_005545	immunoglobulin superfamily containing leucine-rich repeat (ISLR), mRNA /cds=(99,1385) /gb=NM_005545 /gi=5031808 /ug=Hs.102171 /len=2110	NM_005545	Hs.102171	NP_005536

mioc1440	NM_005578	LIM domain containing preferred translocation partner in lipoma (LPP), mRNA /cds=(247,2085) /gb=NM_005578 /gi=5031886 /ug=Hs.180398 /len=5656	NM_005578	Hs.180398	NP_005569
seoa0737	NM_005591	MRE11 meiotic recombination 11 A (S. cerevisiae) (MRE11A), transcript variant 1, mRNA /cds=(160,2286) /gb=NM_005591 /gi=24234691 /ug=Hs.20555 /len=4852	NM_005590; NM_005591	Hs.20555	NP_005582
seoa8669	NM_005638	synaptobrevin-like 1 (SYBL1), mRNA /cds=(115,777) /gb=NM_005638 /gi=27545446 /ug=Hs.24167 /len=2588	NM_005638	Hs.24167	NP_005629
seob1744	NM_005652	telomeric repeat binding factor 2 (TERF2), mRNA /cds=(126,1628) /gb=NM_005652 /gi=21536372 /ug=Hs.100030 /len=2909	NM_005652	Hs.100030	NP_005643
seoa7910	AK055659	cDNA FLJ31097 fis, clone IMR321000210	NM_005723	Hs.8037	NP_005714
miod5622	NM_005725	tetraspan 2 (TSPAN-2), mRNA /cds=(33,698) /gb=NM_005725 /gi=21264579 /ug=Hs.234863 /len=3179	NM_005725	Hs.234863	NP_005716

mioc5226	NM_005786	serologically defined colon cancer antigen 33 (SDCCAG33), mRNA /cds=(295,2358) /gb=NM_005786 /gi=15451922 /ug=Hs.284217 /len=2858	NM_005786	Hs.284217	NP_005777
mioc8793	NM_005795	calcitonin receptor-like (CALCRL), mRNA /cds=(555,1940) /gb=NM_005795 /gi=5031620 /ug=Hs.152175 /len=3018	NM_005795	Hs.152175	NP_005786
mioa6807	NM_005800	highly charged protein (D13S106E), mRNA /cds=(178,3456) /gb=NM_005800 /gi=5031648 /ug=Hs.151236 /len=3650	NM_005800	Hs.151236	NP_005791
miob5010	NM_005849	immunoglobulin superfamily, member 6 (IGSF6), mRNA /cds=(45,770) /gb=NM_005849 /gi=5031672 /ug=Hs.135194 /len=1019	NM_005849	Hs.135194	NP_005840
mioa9510	NM_005857	zinc metalloproteinase (STE24 yeast) (ZMPSTE24), mRNA /cds=(166,1593) /gb=NM_005857 /gi=18379365 /ug=Hs.25846 /len=3103	NM_005857	Hs.25846	NP_005848

mioa3080	NM_005903	MAD, mothers against decapentaplegic 5 (Drosophila) (MADH5), mRNA /cds=(193,1590) /gb=NM_005903 /gi=20070216 /ug=Hs.37501 /len=2049	NM_005903	Hs.37501	NP_005894
ncrc2289	NM_005907	mannosidase, alpha, class 1A, member 1 (MAN1A1), mRNA /cds=(443,2404) /gb=NM_005907 /gi=24497518 /ug=Hs.25253 /len=4139	NM_005907	Hs.25253	NP_005898
seob1161	NM_006003	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRFS1), nuclear gene encoding mitochondrial protein, mRNA /cds=(91,915) /gb=NM_006003 /gi=5174742 /ug=Hs.3712 /len=1203	NM_006003	Hs.3712	NP_005994
fcrb9454	NM_006067	neighbor of COX4 (NOC4), mRNA /cds=(209,841) /gb=NM_006067 /gi=19923775 /ug=Hs.173162 /len=1950	NM_006067	Hs.173162	NP_006058
hfcr4114	NM_006086	tubulin, beta, 4 (TUBB4), mRNA /cds=(1,1353) /gb=NM_006086 /gi=5174736 /ug=Hs.159154 /len=1648	NM_006086	Hs.159154	NP_006077

fcrb5181	NM_006184	nucleobindin 1 (NUCB1), mRNA /cds=(27,1412) /gb=NM_006184 /gi=20070227 /ug=Hs.172609 /len=2311	NM_006184	Hs.172609	NP_006175
seob3148	NM_006216	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPINE2), mRNA /cds=(210,1406) /gb=NM_006216 /gi=24307906 /ug=Hs.21858 /len=2129	NM_006216	Hs.21858	NP_006207
fcr2611	NM_006230	polymerase (DNA directed), delta 2, regulatory subunit 50kDa (POLD2), mRNA /cds=(79,1488) /gb=NM_006230 /gi=5453923 /ug=Hs.74598 /len=1584	NM_006230	Hs.74598	NP_006221
hfcr6600	NM_006233	polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa (POLR2I), mRNA /cds=(36,413) /gb=NM_006233 /gi=14589954 /ug=Hs.47062 /len=458	NM_006233	Hs.47062	NP_006224
seoa1582	NM_006306	SMC1 structural maintenance of chromosomes 1-like 1 (yeast) (SMC1L1), mRNA	NM_006306	Hs.211602	NP_006297

fcrb8162	NM_006322	tubulin, gamma complex associated protein 3 (TUBGCP3), mRNA /cds=(85,2808) /gb=NM_006322 /gi=5453659 /ug=Hs.9884 /len=3795	NM_006322	Hs.9884	NP_006313
fcr3367	NM_006325	RAN, member RAS oncogene family (RAN), mRNA /cds=(115,765) /gb=NM_006325 /gi=6042206 /ug=Hs.10842 /len=1656	NM_006325	Hs.10842	NP_006316
ncr5509	NM_006329	fibulin 5 (FBLN5), mRNA /cds=(463,1809) /gb=NM_006329 /gi=19743802 /ug=Hs.11494 /len=2646	NM_006329	Hs.11494	NP_006320
hfcr4446	NM_006353	high mobility group nucleosomal binding domain 4 (HMGN4), mRNA /cds=(239,511) /gb=NM_006353 /gi=23238232 /ug=Hs.236774 /len=1980	NM_006353	Hs.236774	NP_006344
hfcr2524	NM_006372	NS1-associated protein 1 (NSAP1), mRNA /cds=(526,2397) /gb=NM_006372 /gi=23397426 /ug=Hs.373499 /len=2932	NM_006372	Hs.373499	NP_006363
mioa0072	NM_006409	actin related protein 2/3 complex, subunit 1A, 41kDa (ARPC1A), mRNA /cds=(148,1260) /gb=NM_006409 /gi=22907051 /ug=Hs.90370 /len=1619	NM_006409	Hs.90370	NP_006400

seob5792	NM_006431	chaperonin containing TCP1, subunit 2 (beta) (CCT2), mRNA /cds=(58,1665) /gb=NM_006431 /gi=5453602 /ug=Hs.432970 /len=1935	NM_006431	Hs.432970	NP_006422
seoc1058	NM_006474	lung type-I cell membrane-associated glycoprotein (T1A-2), mRNA /cds=(234,722) /gb=NM_006474 /gi=18767663 /ug=Hs.135150 /len=1081	NM_006474	Hs.135150	NP_006465
ncrb7586	NM_006530	glioma-amplified sequence-41 (GAS41), mRNA /cds=(222,905) /gb=NM_006530 /gi=5729837 /ug=Hs.4029 /len=1404	NM_006530	Hs.4029	NP_006521
hfcr3007	NM_006561	CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA /cds=(35,1564) /gb=NM_006561 /gi=5729815 /ug=Hs.211610 /len=5516	NM_006561	Hs.211610	NP_006552
ncr9502	NM_006682	fibrinogen-like 2 (FGL2), mRNA /cds=(34,1353) /gb=NM_006682 /gi=5730074 /ug=Hs.351808 /len=1496	NM_006682	Hs.351808	NP_006673
fcrc1738	NM_006701	similar to S. pombe dim1 (DIM1), mRNA /cds=(141,569) /gb=NM_006701 /gi=20070233 /ug=Hs.433683 /len=1415	NM_006701	Hs.433683	NP_006692

fcrc5160	NM_002313	actin binding LIM protein 1 (ABLIM1), transcript variant ABLIM-l, mRNA /cds=(100,2436) /gb=NM_002313 /gi=21284382 /ug=Hs.158203 /len=7581	NM_002313; NM_006719; NM_006720	Hs.158203	NP_006711
ncrb3541	NM_006766	runt-related transcription factor binding protein 2 (RUNXBP2), mRNA /cds=(394,6408) /gb=NM_006766 /gi=5803097 /ug=Hs.82210 /len=7869	NM_006766	Hs.82210	NP_006757
ncrc3690	BG166990	602344930F1 NIH_MGC_89 cDNA clone IMAGE:4454934 5', mRNA sequence /clone=IMAGE:4454934 /clone_end=5' /gb=BG166990 /gi=12673693 /ug=Hs.440568 /len=1137		Hs.440568	NP_006764
mioc5751	NM_006795	EH-domain containing 1 (EHD1), mRNA /cds=(247,1851) /gb=NM_006795 /gi=5803008 /ug=Hs.155119 /len=3508	NM_006795	Hs.155119	NP_006786
hfcr1918	NM_006868	RAB31, member RAS oncogene family (RAB31), mRNA /cds=(61,645) /gb=NM_006868 /gi=5803130 /ug=Hs.223025 /len=921	NM_006868	Hs.223025	NP_006859

fcrc6409	AF022654	homeodomain protein (OG12) mRNA, complete cds	NM_003030; NM_006884	Hs.55967	NP_006875
fcr0955	NM_006886	ATP synthase, H transporting, mitochondrial F1 complex, epsilon subunit (ATP5E), nuclear gene encoding mitochondrial protein, mRNA /cds=(95,250) /gb=NM_006886 /gi=21327678 /ug=Hs.177530 /len=417	NM_006886	Hs.177530	NP_008817
miob5752	NM_006925	splicing factor, arginine/serine-rich 5 (SFRS5), mRNA /cds=(219,542) /gb=NM_006925 /gi=5902077 /ug=Hs.166975 /len=1865	NM_006925	Hs.166975	NP_008856
ncrb0462	NM_006996	solute carrier family 19 (thiamine transporter), member 2 (SLC19A2), mRNA /cds=(238,1731) /gb=NM_006996 /gi=27734718 /ug=Hs.30246 /len=3668	NM_006996	Hs.30246	NP_008927
mioc3107	NM_006997	transforming, acidic coiled-coil containing protein 2 (TACC2), mRNA /cds=(87,3167) /gb=NM_006997 /gi=11119413 /ug=Hs.272023 /len=3686	NM_006997	Hs.272023	NP_008928

fcrb1406	NM_007007	cleavage and polyadenylation specific factor 6, 68kDa (CPSF6), mRNA /cds=(35,1690) /gb=NM_007007 /gi=5901927 /ug=Hs.64542 /len=3426	NM_007007	Hs.64542	NP_008938
fcrb6874	NM_007100	ATP synthase, H transporting, mitochondrial F0 complex, subunit e (ATP5I), mRNA /cds=(64,273) /gb=NM_007100 /gi=6005716 /ug=Hs.85539 /len=336	NM_007100	Hs.85539	NP_009031
fcrb2334	NM_007104	ribosomal protein L10a (RPL10A), mRNA /cds=(16,669) /gb=NM_007104 /gi=15431287 /ug=Hs.425293 /len=700	NM_007104	Hs.425293	NP_009035
miob7223	NM_007149	zinc finger protein 184 (Kruppel-like) (ZNF184), mRNA /cds=(268,2523) /gb=NM_007149 /gi=24307934 /ug=Hs.158174 /len=3095	NM_007149	Hs.158174	NP_009080
seoc1561	NM_007218	patched related protein translocated in renal cancer (TRC8), mRNA /cds=(215,2209) /gb=NM_007218 /gi=21314653 /ug=Hs.28285 /len=2481	NM_007218	Hs.28285	NP_009149

fcrb0993	NM_007242	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 19 (DBP5 yeast) (DDX19), mRNA /cds=(105,1544) /gb=NM_007242 /gi=13787207 /ug=Hs.289097 /len=1806	NM_007242	Hs.289097	NP_009173
fcrb4860	NM_007255	xylosylprotein beta 1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I) (B4GALT7), mRNA /cds=(41,1024) /gb=NM_007255 /gi=6005951 /ug=Hs.54702 /len=1669	NM_007255	Hs.54702	NP_009186
hfcr6394	NM_007263	coatomer protein complex, subunit epsilon (COPE), mRNA /cds=(43,969) /gb=NM_007263 /gi=6005734 /ug=Hs.10326 /len=1130	NM_007263	Hs.10326	NP_009194
fcrb7051	NM_007358	putative DNA binding protein (M96), mRNA /cds=(244,2025) /gb=NM_007358 /gi=6678763 /ug=Hs.31016 /len=2648	NM_007358	Hs.31016	NP_031384
fcrb7852	NM_012073	chaperonin containing TCP1, subunit 5 (epsilon) (CCT5), mRNA /cds=(92,1717) /gb=NM_012073 /gi=24307938 /ug=Hs.1600 /len=1961	NM_012073	Hs.1600	NP_036205

miod5114	NM_012086	general transcription factor IIIC, polypeptide 3, 102kDa (GTF3C3), mRNA /cds=(94,2754) /gb=NM_012086 /gi=6912397 /ug=Hs.90847 /len=2961	NM_012086	Hs.90847	NP_036218
hfcr2201	NM_012201	golgi apparatus protein 1 (GLG1), mRNA /cds=(27,3560) /gb=NM_012201 /gi=6912389 /ug=Hs.78979 /len=3909	NM_012201	Hs.78979	NP_036333
fcr6866	NM_012321	U6 snRNA-associated Sm-like protein (LSM4), mRNA /cds=(49,468) /gb=NM_012321 /gi=6912485 /ug=Hs.76719 /len=1033	NM_012321	Hs.76719	NP_036453
fcrb9448	AK022921	cDNA FLJ12859 fis, clone NT2RP2003522, highly similar to zinc finger DNA binding protein 99 (ZNF281) mRNA		Hs.59757	NP_036614
seoc3229	NM_013250	zinc finger protein 215 (ZNF215), mRNA /cds=(589,2142) /gb=NM_013250 /gi=7019582 /ug=Hs.161427 /len=3480	NM_013250	Hs.161427	NP_037382

seoc6295	NM_013252	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 5 (CLECSF5), mRNA /cds=(198,764) /gb=NM_013252 /gi=10281668 /ug=Hs.126355 /len=3510	NM_013252	Hs.126355	NP_037384
hfcr6376	NM_013277	Rac GTPase activating protein 1 (RACGAP1), mRNA /cds=(225,2123) /gb=NM_013277 /gi=21361396 /ug=Hs.23900 /len=3237	NM_013277	Hs.23900	NP_037409
ncr0531	NM_013332	hypoxia-inducible protein 2 (HIG2), mRNA /cds=(206,397) /gb=NM_013332 /gi=7019408 /ug=Hs.61762 /len=1372	NM_013332	Hs.61762	NP_037464
mioc5113	NM_013943	chloride intracellular channel 4 (CLIC4), mRNA /cds=(198,959) /gb=NM_013943 /gi=7330334 /ug=Hs.25035 /len=4318	NM_013943	Hs.25035	NP_039234
miob7970	NM_014033	DKFZP586A0522 protein (DKFZP586A0522), mRNA /cds=(21,755) /gb=NM_014033 /gi=13378140 /ug=Hs.288771 /len=1705	NM_014033	Hs.288771	NP_054752

ncrc5335	NM_014046	mitochondrial ribosomal protein S18B (MRPS18B), nuclear gene encoding mitochondrial protein, mRNA /cds=(38,814) /gb=NM_014046 /gi=16554601 /ug=Hs.274417 /len=1439	NM_014046	Hs.274417	NP_054765
fcrb1890	NM_014077	DKFZP586O0120 protein (DKFZP586O0120), mRNA /cds=(21,359) /gb=NM_014077 /gi=7661695 /ug=Hs.4766 /len=1465	NM_014077	Hs.4766	NP_054796
seob5629	AK096676	cDNA FLJ39357 fis, clone PEBLM2003914. /gb=AK096676 /gi=21756220 /ug=Hs.22635 /len=2315		Hs.22635	NP_054874
seoa6395	NM_014160	HSPC070 protein (HSPC070), mRNA /cds=(332,1582) /gb=NM_014160 /gi=8850222 /ug=Hs.279474 /len=3050	NM_014160	Hs.279474	NP_054879
miob3411	NM_014210	ecotropic viral integration site 2A (EVI2A), mRNA /cds=(220,918) /gb=NM_014210 /gi=7657074 /ug=Hs.70499 /len=1563	NM_014210	Hs.70499	NP_055025
mioa1944	NM_014280	DnaJ (Hsp40) subfamily C, member 8 (DNAJC8), mRNA /cds=(8,802) /gb=NM_014280 /gi=7657610 /ug=Hs.433540 /len=1525	NM_014280	Hs.433540	NP_055095

seob4197	NM_014287	pM5 protein (PM5), mRNA /cds=(1,3669) /gb=NM_014287 /gi=10947030 /ug=Hs.439182 /len=4182	NM_014287	Hs.439182	NP_055102
fcrb7760	NM_014292	chromobox 6 (CBX6), mRNA /cds=(30,1268) /gb=NM_014292 /gi=10140848 /ug=Hs.107374 /len=6014	NM_014292	Hs.107374	NP_055107
ncrc2227	NM_014319	integral inner nuclear membrane protein (MAN1), mRNA /cds=(7,2742) /gb=NM_014319 /gi=7706606 /ug=Hs.7256 /len=4703	NM_014319	Hs.7256	NP_055134
miod2255	NM_014333	immunoglobulin superfamily, member 4 (IGSF4), mRNA /cds=(4,1332) /gb=NM_014333 /gi=22095346 /ug=Hs.70337 /len=3512	NM_014333	Hs.70337	NP_055148
seoa0388	NM_014341	mitochondrial carrier 1 (MTCH1), nuclear gene encoding mitochondrial protein, mRNA /cds=(1,1119) /gb=NM_014341 /gi=7657344 /ug=Hs.279939 /len=1890	NM_014341	Hs.279939	NP_055156
seob9574	NM_014394	growth hormone inducible transmembrane protein (GHITM), mRNA /cds=(130,1089) /gb=NM_014394 /gi=7657479 /ug=Hs.433957 /len=2374	NM_014394	Hs.433957	NP_055209

mioa4770	NM_014409	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa (TAF5L), mRNA /cds=(98,1867) /gb=NM_014409 /gi=21269865 /ug=Hs.26782 /len=3065	NM_014409	Hs.26782	NP_055224
miob0487	NM_014575	schwannomin interacting protein 1 (SCHIP1), mRNA /cds=(70,1533) /gb=NM_014575 /gi=7657539 /ug=Hs.61490 /len=2112	NM_014575	Hs.61490	NP_055390
fcr6801	NM_014628	gene predicted from cDNA with a complete coding sequence (CMT2), mRNA /cds=(4,828) /gb=NM_014628 /gi=7661917 /ug=Hs.124 /len=1233	NM_014628	Hs.124	NP_055443
seoa7542	NM_014656	KIAA0040 gene product (KIAA0040), mRNA /cds=(921,1382) /gb=NM_014656 /gi=7657258 /ug=Hs.158282 /len=4564	NM_014656	Hs.158282	NP_055471
seob3105	NM_014730	KIAA0152 gene product (KIAA0152), mRNA /cds=(129,1007) /gb=NM_014730 /gi=7661947 /ug=Hs.181418 /len=6322	NM_014730	Hs.181418	NP_055545
fcr4376	D14657	hypothetical protein (KIAA0101)	NM_014736	Hs.81892	NP_055551

miod4140	NM_014781	RB1-inducible coiled-coil 1 (RB1CC1), mRNA /cds=(516,5291) /gb=NM_014781 /gi=7661991 /ug=Hs.50421 /len=6614	NM_014781	Hs.50421	NP_055596
fcr5029	NM_014828	chromosome 14 open reading frame 92 (C14orf92), mRNA /cds=(33,1898) /gb=NM_014828 /gi=7662273 /ug=Hs.194035 /len=4174	NM_014828	Hs.194035	NP_055643
miob0986	NM_014828	chromosome 14 open reading frame 92 (C14orf92), mRNA /cds=(33,1898) /gb=NM_014828 /gi=7662273 /ug=Hs.194035 /len=4174	NM_014828	Hs.194035	NP_055643
ncrb3942	NM_014892	KIAA1116 protein (KIAA1116), mRNA /cds=(186,4001) /gb=NM_014892 /gi=7662491 /ug=Hs.227602 /len=4664	NM_014892	Hs.227602	NP_055707
miob3314	NM_014950	zinc finger and BTB domain containing 1 (ZBTB1), mRNA /cds=(263,2197) /gb=NM_014950 /gi=7662437 /ug=Hs.372699 /len=3990	NM_014950	Hs.372699	NP_055765
miod1316	NM_014953	mitotic control protein dis3 (DIS3), mRNA /cds=(37,2913) /gb=NM_014953 /gi=19923415 /ug=Hs.323346 /len=7320	NM_014953	Hs.323346	NP_055768

mioa9062	NM_014999	RAB21, member RAS oncogene family (RAB21), mRNA /cds=(256,933) /gb=NM_014999 /gi=7661921 /ug=Hs.184627 /len=2630	NM_014999	Hs.184627	NP_055814
mioc1697	BC014378	clone IMAGE:4044107, mRNA		Hs.64691	NP_055991
mioc2082	NM_015247	cylindromatosis (turban tumor syndrome) (CYLD), mRNA /cds=(392,3262) /gb=NM_015247 /gi=14165257 /ug=Hs.18827 /len=5371	NM_015247	Hs.18827	NP_056062
mioa6404	NM_015252	KIAA0903 protein (KIAA0903), mRNA /cds=(349,4044) /gb=NM_015252 /gi=24308022 /ug=Hs.16218 /len=5048	NM_015252	Hs.16218	NP_056067
seoa4422	NM_015338	additional sex combs like 1 (Drosophila) (ASXL1), mRNA /cds=(259,4884) /gb=NM_015338 /gi=27734730 /ug=Hs.3686 /len=6864	NM_015338	Hs.3686	NP_056153
fcrc5789	NM_015416	cervical cancer 1 protooncogene (DKFZP586A011), mRNA /cds=(9,1091) /gb=NM_015416 /gi=21166356 /ug=Hs.75884 /len=2118	NM_015416	Hs.75884	NP_056231

mioa4196	NM_015435	ring finger protein 19 (RNF19), mRNA /cds=(318,2834) /gb=NM_015435 /gi=19923421 /ug=Hs.48320 /len=4357	NM_015435	Hs.48320	NP_056250
mioa8607	NM_015440	DKFZP586G1517 protein (DKFZP586G1517), mRNA /cds=(127,2328) /gb=NM_015440 /gi=24308062 /ug=Hs.44155 /len=2749	NM_015440	Hs.44155	NP_056255
mioc7209	AL833852	mRNA; cDNA DKFZp761G0111 (from clone DKFZp761G0111)	NM_015472	Hs.24341	NP_056287
seoa7373	NM_015558	synovial sarcoma translocation gene on chromosome 18-like 1 (SS18L1), mRNA /cds=(61,1251) /gb=NM_015558 /gi=27754185 /ug=Hs.154429 /len=3723	NM_015558	Hs.154429	NP_056373
ncrc2507	AB014542	mRNA for KIAA0642 protein, partial cds. /cds=(200,4189) /gb=AB014542 /gi=20521116 /ug=Hs.323317 /len=5937		Hs.323317	NP_056390
fcrb6587	NM_015702	hypothetical protein CL25022 (CL25022), mRNA /cds=(158,1048) /gb=NM_015702 /gi=7661547 /ug=Hs.5324 /len=1416	NM_015702	Hs.5324	NP_056517

seoa5665	NM_015899	putative glycolipid transfer protein (LOC51054), mRNA /cds=(538,1713) /gb=NM_015899 /gi=7705683 /ug=Hs.334649 /len=1839	NM_015899	Hs.334649	NP_056983
seob2155	AL833555	mRNA; cDNA DKFZp686A1444 (from clone DKFZp686A1444)		Hs.278428	NP_056986
fcrb2353	NM_015965	cell death-regulatory protein GRIM19 (GRIM19), mRNA /cds=(212,895) /gb=NM_015965 /gi=21361821 /ug=Hs.279574 /len=1023	NM_015965	Hs.279574	NP_057049
mioc2891	NM_016059	peptidylprolyl isomerase (cyclophilin)-like 1 (PPIL1), mRNA /cds=(222,722) /gb=NM_016059 /gi=22035675 /ug=Hs.27693 /len=1723	NM_016059	Hs.27693	NP_057143
fcr6011	AK055223	cDNA FLJ30661 fis, clone DFNES2000526		Hs.432729	NP_057178
mioa5729	NM_016103	GTP-binding protein Sara (LOC51128), mRNA /cds=(151,747) /gb=NM_016103 /gi=7705826 /ug=Hs.279582 /len=1280	NM_016103	Hs.279582	NP_057187
ncrc6888	NM_016107	zinc finger RNA binding protein (ZFR), mRNA /cds=(44,1300) /gb=NM_016107 /gi=7706372 /ug=Hs.173518 /len=2734	NM_016107	Hs.173518	NP_057191

seob7369	NM_016129	COP9 constitutive photomorphogenic subunit 4 (Arabidopsis) (COPS4), mRNA /cds=(7,1224) /gb=NM_016129 /gi=7705844 /ug=Hs.6671 /len=1613	NM_016129	Hs.6671	NP_057213
seoa4464	NM_000965	retinoic acid receptor, beta (RARB), transcript variant 1, mRNA /cds=(469,1815) /gb=NM_000965 /gi=14916493 /ug=Hs.171495 /len=3119	NM_000965; NM_016152	Hs.171495	NP_057236
fcrb5166	NM_016221	dynactin 4 (p62) (DCTN4), mRNA /cds=(22,1404) /gb=NM_016221 /gi=19923450 /ug=Hs.328865 /len=3837	NM_016221	Hs.328865	NP_057305
miob4793	NM_016258	high-glucose-regulated protein 8 (HGRG8), mRNA /cds=(151,1863) /gb=NM_016258 /gi=7705410 /ug=Hs.20993 /len=2730	NM_016258	Hs.20993	NP_057342
seoa3578	NM_016302	protein x 0001 (LOC51185), mRNA /cds=(34,1044) /gb=NM_016302 /gi=10047097 /ug=Hs.18925 /len=1668	NM_016302	Hs.18925	NP_057386
miob6721	NM_016315	CED-6 protein (CED-6), mRNA /cds=(429,1343) /gb=NM_016315 /gi=7705317 /ug=Hs.107056 /len=3277	NM_016315	Hs.107056	NP_057399

mioa5902	NM_016331	zinc finger protein ANC_2H01 (LOC51193), mRNA /cds=(446,1903) /gb=NM_016331 /gi=7705934 /ug=Hs.22879 /len=3013	NM_016331	Hs.22879	NP_057415
fcrb4280	NM_016404	hypothetical protein HSPC152 (HSPC152), mRNA /cds=(36,413) /gb=NM_016404 /gi=7705476 /ug=Hs.79259 /len=612	NM_016404	Hs.79259	NP_057488
seoa7583	NM_016570	CDA14 (LOC51290), mRNA /cds=(89,1225) /gb=NM_016570 /gi=7706104 /ug=Hs.26813 /len=1378	NM_016570	Hs.26813	NP_057654
ncrc6015	NM_016617	hypothetical protein BM-002 (BM-002), mRNA /cds=(40,297) /gb=NM_016617 /gi=7705299 /ug=Hs.367646 /len=2529	NM_016617	Hs.367646	NP_057701
seob7614	NM_016648	HDCMA18P protein (HDCMA18P), mRNA /cds=(532,1176) /gb=NM_016648 /gi=7705400 /ug=Hs.278635 /len=1438	NM_016648	Hs.278635	NP_057732
seob5556	NM_016947	chromosome 6 open reading frame 48 (C6orf48), mRNA /cds=(42,422) /gb=NM_016947 /gi=8393383 /ug=Hs.109798 /len=711	NM_016947	Hs.109798	NP_058643

miod5060	NM_017426	nucleoporin 54kDa (NUP54), mRNA /cds=(129,1652) /gb=NM_017426 /gi=26051236 /ug=Hs.9082 /len=2358	NM_017426	Hs.9082	NP_059122
fcrb3615	NM_017510	gp25L2 protein (HSGP25L2G), mRNA /cds=(76,720) /gb=NM_017510 /gi=24475637 /ug=Hs.279929 /len=1420	NM_017510	Hs.279929	NP_059980
fcr5836	NM_017510	gp25L2 protein (HSGP25L2G), mRNA /cds=(76,720) /gb=NM_017510 /gi=24475637 /ug=Hs.279929 /len=1420	NM_017510	Hs.279929	NP_059980
fcrb5536	NM_017607	protein phosphatase 1, regulatory (inhibitor) subunit 12C (PPP1R12C), mRNA /cds=(19,2367) /gb=NM_017607 /gi=14149715 /ug=Hs.235975 /len=2944	NM_017607	Hs.235975	NP_060077
mioc0222	NM_017654	hypothetical protein FLJ20073 (FLJ20073), mRNA /cds=(17,1909) /gb=NM_017654 /gi=8923080 /ug=Hs.65641 /len=3401	NM_017654	Hs.65641	NP_060124
miod3739	NM_017851	hypothetical protein FLJ20509 (FLJ20509), mRNA /cds=(418,1041) /gb=NM_017851 /gi=8923470 /ug=Hs.30634 /len=2369	NM_017851	Hs.30634	NP_060321

ncr2842	NM_017876	hypothetical protein FLJ20552 (FLJ20552), mRNA /cds=(130,1065) /gb=NM_017876 /gi=21361772 /ug=Hs.69554 /len=1681	NM_017876	Hs.69554	NP_060346
ncr1941	NM_017987	RUN and FYVE domain containing 2 (RUFY2), mRNA /cds=(12,1832) /gb=NM_017987 /gi=24850106 /ug=Hs.154091 /len=2080	NM_017987	Hs.154091	NP_060457
fcrc0039	NM_018011	hypothetical protein FLJ10154 (FLJ10154), mRNA /cds=(246,1067) /gb=NM_018011 /gi=8922258 /ug=Hs.179972 /len=1734	NM_018011	Hs.179972	NP_060481
ncr8156	NM_018013	hypothetical protein FLJ10159 (FLJ10159), mRNA /cds=(1,807) /gb=NM_018013 /gi=8922262 /ug=Hs.22505 /len=2070	NM_018013	Hs.22505	NP_060483
seoc5911	NM_018019	hypothetical protein FLJ10193 (FLJ10193), mRNA /cds=(57,497) /gb=NM_018019 /gi=22907057 /ug=Hs.235195 /len=2222	NM_018019	Hs.235195	NP_060489
fcrc5850	NM_018067	hypothetical protein FLJ10350 (FLJ10350), mRNA /cds=(676,2340) /gb=NM_018067 /gi=21361780 /ug=Hs.177596 /len=2811	NM_018067	Hs.177596	NP_060537

mioa3939	NM_018158	solute carrier family 4 (anion exchanger), member 1, adaptor protein (SLC4A1AP), mRNA /cds=(283,2673) /gb=NM_018158 /gi=8922556 /ug=Hs.306000 /len=2954	NM_018158	Hs.306000	NP_060628
miod6646	NM_018178	hypothetical protein FLJ10687 (FLJ10687), mRNA /cds=(46,903) /gb=NM_018178 /gi=21361715 /ug=Hs.29379 /len=2992	NM_018178	Hs.29379	NP_060648
fcrb6202	NM_018182	hypothetical protein FLJ10700 (FLJ10700), mRNA /cds=(184,1872) /gb=NM_018182 /gi=8922595 /ug=Hs.295909 /len=3434	NM_018182	Hs.295909	NP_060652
seoc1163	AF225871	polybromo-1 (PB1) mRNA, complete cds, alternatively spliced	NM_018165; NM_018313	Hs.44143	NP_060783
seob6139	NM_018352	hypothetical protein FLJ11184 (FLJ11184), mRNA /cds=(113,724) /gb=NM_018352 /gi=8922922 /ug=Hs.267446 /len=1748	NM_018352	Hs.267446	NP_060822
seob6084	NM_018421	TBC1 domain family, member 2 (TBC1D2), mRNA /cds=(1622,3028) /gb=NM_018421 /gi=8922166 /ug=Hs.135917 /len=3431	NM_018421	Hs.135917	NP_060891

mioc6970	NM_018465	uncharacterized hematopoietic stem/progenitor cells protein MDS030 (MDS030), mRNA /cds=(206,649) /gb=NM_018465 /gi=8923931 /ug=Hs.181385 /len=927	NM_018465	Hs.181385	NP_060935
ncrc0151	NM_018507	hypothetical protein PRO1843 (PRO1843), mRNA /cds=(965,1255) /gb=NM_018507 /gi=8924082 /ug=Hs.283330 /len=1268	NM_018507	Hs.283330	NP_060977
ncrb0757	BC029427	clone MGC:32681 IMAGE:4809776, mRNA, complete cds		Hs.410294	NP_061008
mioc6360	NM_018675	zinc finger protein 302 (ZNF302), mRNA /cds=(337,1773) /gb=NM_018675 /gi=11034834 /ug=Hs.125287 /len=2978	NM_018443; NM_018675	Hs.125287	NP_061145
ncr0004	NM_018847	KIAA1354 protein (KIAA1354), mRNA /cds=(514,2367) /gb=NM_018847 /gi=24308180 /ug=Hs.106283 /len=4373	NM_018847	Hs.106283	NP_061335
seoa5586	AL133623	mRNA; cDNA DKFZp434P0721 (from clone DKFZp434P0721); partial cds /cds=(1,3481) /gb=AL133623 /gi=6599261 /ug=Hs.82501 /len=8281		Hs.82501	NP_061874
fcrb6613	NM_019095	chromosome 20 open reading frame 155 (C20orf155), mRNA	NM_019095	Hs.3569	NP_061968

seoc2614	NM_019095	hypothetical protein (LOC54675), mRNA /cds=(1,906) /gb=NM_019095 /gi=10092646 /ug=Hs.3569 /len=906	NM_019095	Hs.3569	NP_061968
mioc5039	NM_020038	ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA /cds=(71,1603) /gb=NM_020038 /gi=9955973 /ug=Hs.90786 /len=5380	NM_003786; NM_020037; NM_020038	Hs.90786	NP_064422
fcrb2317	NM_020150	SAR1 protein (SAR1), mRNA /cds=(125,721) /gb=NM_020150 /gi=21361614 /ug=Hs.110796 /len=3003	NM_020150	Hs.110796	NP_064535
mioa5059	NM_020166	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) (MCCC1), mRNA /cds=(133,2310) /gb=NM_020166 /gi=13518227 /ug=Hs.47649 /len=2528	NM_020166	Hs.47649	NP_064551
seoc3854	NM_020368	disrupter of silencing 10 (SAS10), mRNA /cds=(162,1601) /gb=NM_020368 /gi=9966798 /ug=Hs.322901 /len=2035	NM_020368	Hs.322901	NP_065101

miob2601	NM_020443	neuron navigator 1 (NAV1), mRNA /cds=(348,5972) /gb=NM_020443 /gi=27262621 /ug=Hs.6298 /len=11365	NM_020443	Hs.6298	NP_065176
miod0935	AL080079	mRNA; cDNA DKFZp564D0462 (from clone DKFZp564D0462)	NM_020455	Hs.44197	NP_065188
fcr4056	AF004876	54TMp (54tm) (=S83365 RAB5-interaction protein)	NM_020470	Hs.406422	NP_065203
ncrc9528	NM_020529	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), mRNA /cds=(95,1048) /gb=NM_020529 /gi=10092618 /ug=Hs.81328 /len=1550	NM_020529	Hs.81328	NP_065390
mioa7955	NM_020905	retinol dehydrogenase 14 (all-trans and 9-cis) (RDH14), mRNA /cds=(64,1074) /gb=NM_020905 /gi=10190745 /ug=Hs.288880 /len=1538	NM_020905	Hs.288880	NP_065956
fcrb8134	NM_021070	latent transforming growth factor beta binding protein 3 (LTBP3), mRNA /cds=(1,3771) /gb=NM_021070 /gi=18497287 /ug=Hs.289019 /len=4064	NM_021070	Hs.289019	NP_066548
seoa0302	NM_021088	zinc finger protein 2 (A1-5) (ZNF2), mRNA /cds=(855,1733) /gb=NM_021088 /gi=20304090 /ug=Hs.192285 /len=2630	NM_021088	Hs.192285	NP_066574

seoa0040	NM_021109	thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(78,212) /gb=NM_021109 /gi=11056060 /ug=Hs.75968 /len=556	NM_021109	Hs.75968	NP_066932
miob0931	NM_021111	reversion-inducing-cysteine-rich protein with kazal motifs (RECK), mRNA /cds=(93,3008) /gb=NM_021111 /gi=11863155 /ug=Hs.29640 /len=4414	NM_021111	Hs.29640	NP_066934
seoc7910	NM_021183	hypothetical protein similar to small G proteins, especially RAP-2A (LOC57826), mRNA /cds=(17,568) /gb=NM_021183 /gi=10880976 /ug=Hs.225979 /len=3165	NM_021183	Hs.225979	NP_067006
fcrb5961	NM_021227	DC2 protein (DC2), mRNA /cds=(60,509) /gb=NM_021227 /gi=24308270 /ug=Hs.103180 /len=1090	NM_021227	Hs.103180	NP_067050
fcrb6279	NM_004069	adaptor-related protein complex 2, sigma 1 subunit (AP2S1), transcript variant AP17, mRNA /cds=(71,499) /gb=NM_004069 /gi=11038644 /ug=Hs.119591 /len=781	NM_004069; NM_021575	Hs.119591	NP_067586

seob3404	NM_021632	zinc-finger protein ZBRK1 (ZBRK1), mRNA /cds=(184,1782) /gb=NM_021632 /gi=11056003 /ug=Hs.130965 /len=2260	NM_021632	Hs.130965	NP_067645
fcrb5051	NM_021825	hypothetical protein MDS025 (MDS025), mRNA /cds=(363,1127) /gb=NM_021825 /gi=21361605 /ug=Hs.154938 /len=1585	NM_021825	Hs.154938	NP_068597
seoc1216	AL049447	mRNA; cDNA DKFZp586A0722 (from clone DKFZp586A0722)		Hs.433334	NP_068603
fcrb1547	NM_022003	FXYD domain containing ion transport regulator 6 (FXYD6), mRNA /cds=(67,354) /gb=NM_022003 /gi=11612654 /ug=Hs.3807 /len=1677	NM_022003	Hs.3807	NP_071286
seoa9665	NM_022145	leucine zipper protein FKSG14 (FKSG14), mRNA /cds=(265,1074) /gb=NM_022145 /gi=16905072 /ug=Hs.192843 /len=1794	NM_022145	Hs.192843	NP_071428
miod7052	NM_022483	hypothetical protein FLJ21657 (FLJ21657), mRNA /cds=(342,989) /gb=NM_022483 /gi=19923589 /ug=Hs.26498 /len=2995	NM_022483	Hs.26498	NP_071928

mioa2851	NM_022731	similar to rat nuclear ubiquitous casein kinase 2 (NUCKS), mRNA /cds=(67,558) /gb=NM_022731 /gi=12232386 /ug=Hs.118064 /len=1811	NM_022731	Hs.118064	NP_073568
mioc0121	NM_022731	similar to rat nuclear ubiquitous casein kinase 2 (NUCKS), mRNA /cds=(67,558) /gb=NM_022731 /gi=12232386 /ug=Hs.118064 /len=1811	NM_022731	Hs.118064	NP_073568
ncrc9642	NM_022756	hypothetical protein FLJ11730 (FLJ11730), mRNA /cds=(33,608) /gb=NM_022756 /gi=20149668 /ug=Hs.17118 /len=1558	NM_022756	Hs.17118	NP_073593
mioa8074	NM_022763	FAD104 (FAD104), mRNA	NM_022763	Hs.299883	NP_073600
seob3747	NM_022763	FAD104 (FAD104), mRNA /cds=(58,3672) /gb=NM_022763 /gi=27477058 /ug=Hs.299883 /len=6894	NM_022763	Hs.299883	NP_073600
miod6988	NM_022845	core-binding factor, beta subunit (CBFB), transcript variant 1, mRNA	NM_001755; NM_022845	Hs.179881	NP_074036
seoc0422	AL161991	mRNA; cDNA DKFZp761C169 (from clone DKFZp761C169); partial cds /cds=(997,2475) /gb=AL161991 /gi=7328122 /ug=Hs.71252 /len=3324	NM_022913	Hs.71252	NP_075064

seob4011	AL161991	mRNA; cDNA DKFZp761C169 (from clone DKFZp761C169); partial cds /cds=(997,2475) /gb=AL161991 /gi=7328122 /ug=Hs.71252 /len=3324	NM_022913	Hs.71252	NP_075064
ncrc3116	NM_023926	hypothetical protein FLJ12895 (FLJ12895), mRNA /cds=(410,1942) /gb=NM_023926 /gi=21314715 /ug=Hs.235390 /len=2804	NM_023926	Hs.235390	NP_076415
fcrc1849	NM_024297	hypothetical protein MGC2941 (MGC2941), mRNA /cds=(172,969) /gb=NM_024297 /gi=13236519 /ug=Hs.288217 /len=2005	NM_024297	Hs.288217	NP_077273
miob2944	NM_024520	hypothetical protein FLJ22555 (FLJ22555), mRNA /cds=(323,1198) /gb=NM_024520 /gi=13375659 /ug=Hs.3592 /len=1530	NM_024520	Hs.3592	NP_078796
ncrc7038	NM_024551	hypothetical protein FLJ21432 (FLJ21432), mRNA /cds=(110,886) /gb=NM_024551 /gi=13375714 /ug=Hs.334854 /len=3500	NM_024551	Hs.334854	NP_078827
seob8986	NM_024568	chromodomain helicase DNA binding protein 1-like (CHD1L), mRNA /cds=(332,1897) /gb=NM_024568 /gi=24308292 /ug=Hs.14570 /len=2936	NM_024568	Hs.14570	NP_078844

seoa6389	BC013945	Similar to hypothetical protein FLJ21212, clone MGC:24384 IMAGE:4064736, mRNA, complete cds	NM_024642	Hs.47099	NP_078918
ncr2899	NM_024657	hypothetical protein FLJ11565 (FLJ11565), mRNA /cds=(19,2301) /gb=NM_024657 /gi=21362027 /ug=Hs.61763 /len=3037	NM_024657	Hs.61763	NP_078933
miod4023	NM_024659	hypothetical protein FLJ11753 (FLJ11753), mRNA /cds=(14,832) /gb=NM_024659 /gi=13375910 /ug=Hs.62348 /len=1868	NM_024659	Hs.62348	NP_078935
mioc4929	NM_024699	hypothetical protein FLJ14007 (FLJ14007), mRNA /cds=(15,821) /gb=NM_024699 /gi=13375984 /ug=Hs.99519 /len=1793	NM_024699	Hs.99519	NP_078975
mioa7617	NM_024755	hypothetical protein FLJ13213 (FLJ13213), mRNA /cds=(234,1670) /gb=NM_024755 /gi=13376087 /ug=Hs.331328 /len=2617	NM_024755	Hs.331328	NP_079031
ncr7532	NM_024945	hypothetical protein FLJ12888 (FLJ12888), mRNA /cds=(333,2210) /gb=NM_024945 /gi=13376426 /ug=Hs.284137 /len=3413	NM_024945	Hs.284137	NP_079221
seoc3801	AL832993	mRNA; cDNA DKFZp666L233 (from clone DKFZp666L233)	NM_030571	Hs.9788	NP_085048

mioa4183	NM_002380	matrilin 2 (MATN2), transcript variant 1, mRNA /cds=(126,2996) /gb=NM_002380 /gi=13518036 /ug=Hs.19368 /len=3496	NM_002380; NM_030583	Hs.19368	NP_085072
mioa2970	NM_030751	transcription factor 8 (represses interleukin 2 expression) (TCF8), mRNA /cds=(25,3399) /gb=NM_030751 /gi=28077090 /ug=Hs.232068 /len=3952	NM_030751	Hs.232068	NP_110378
miob9233	BC050366	thioredoxin domain containing, clone IMAGE:5764221, mRNA			NP_110382
seoa3274	NM_031214	hypothetical protein AF311304 (AF311304), mRNA /cds=(21,185) /gb=NM_031214 /gi=13654285 /ug=Hs.300624 /len=1138	NM_031214	Hs.300624	NP_112491
seob7637	NM_031216	sec13-like protein (SEC13L), mRNA /cds=(107,1189) /gb=NM_031216 /gi=14591917 /ug=Hs.301048 /len=3492	NM_031216	Hs.301048	NP_112493
fcrb2933	NM_031286	SH3 domain binding glutamic acid-rich protein like 3 (SH3BGRL3), mRNA /cds=(72,353) /gb=NM_031286 /gi=13775197 /ug=Hs.109051 /len=764	NM_031286	Hs.109051	NP_112576
seoa4324	NM_031287	SF3b10 (SF3b10), mRNA	NM_031287	Hs.110695	NP_112577

mioc1808	NM_031452	hypothetical protein MGC2560 (MGC2560), mRNA /cds=(195,551) /gb=NM_031452 /gi=13899288 /ug=Hs.80624 /len=1229	NM_031452	Hs.80624	NP_113640
fcrb7247	NM_031453	hypothetical protein MGC11034 (MGC11034), mRNA /cds=(246,641) /gb=NM_031453 /gi=13899290 /ug=Hs.103378 /len=3301	NM_031453	Hs.103378	NP_113641
ncrc2705	NM_031461	CocoaCrisp (LOC83690), mRNA /cds=(376,1878) /gb=NM_031461 /gi=21314740 /ug=Hs.182364 /len=2962	NM_031461	Hs.182364	NP_113649
miod6896	NM_031469	SH3 domain binding glutamic acid-rich protein like 2 (SH3BGRL2), mRNA /cds=(180,503) /gb=NM_031469 /gi=13899316 /ug=Hs.9167 /len=4676	NM_031469	Hs.9167	NP_113657
mioc3370	NM_031483	itchy E3 ubiquitin protein ligase (mouse) (ITCH), mRNA /cds=(171,2759) /gb=NM_031483 /gi=27477108 /ug=Hs.98074 /len=6357	NM_031483	Hs.98074	NP_113671

mioa2173	NM_005016	poly(rC) binding protein 2 (PCBP2), transcript variant 1, mRNA /cds=(89,1189) /gb=NM_005016 /gi=14141167 /ug=Hs.63525 /len=1362	NM_005016; NM_031989	Hs.63525	NP_114366
seoc0861	NM_032041	neurocalcin delta (NCALD), mRNA /cds=(121,702) /gb=NM_032041 /gi=14042973 /ug=Hs.90063 /len=3300	NM_032041	Hs.90063	NP_114430
mioa9007	NM_032121	hypothetical protein DKFZp564K142 similar to implantation-associated protein (DKFZp564K142), mRNA /cds=(30,1037) /gb=NM_032121 /gi=14149774 /ug=Hs.323562 /len=2241	NM_032121	Hs.323562	NP_115497
mioc8079	NM_032148	hypothetical protein DKFZp434K0427 (DKFZP434K0427), mRNA /cds=(342,1814) /gb=NM_032148 /gi=14149818 /ug=Hs.238996 /len=2375	NM_032148	Hs.238996	NP_115524
fcrc0134	NM_032211	lysyl oxidase-like 4 (LOXL4), mRNA /cds=(152,2422) /gb=NM_032211 /gi=19923658 /ug=Hs.306814 /len=3665	NM_032211	Hs.306814	NP_115587

seob2953	NM_032273	hypothetical protein DKFZp586C1924 (DKFZp586C1924), mRNA /cds=(106,693) /gb=NM_032273 /gi=14150016 /ug=Hs.108338 /len=782	NM_032273	Hs.108338	NP_115649
ncrc9055	NM_032313	hypothetical protein MGC3232 (MGC3232), mRNA /cds=(85,2181) /gb=NM_032313 /gi=14150077 /ug=Hs.8715 /len=2316	NM_032313	Hs.8715	NP_115689
fcrb8110	NM_032347	zinc finger protein 397 (ZNF397), mRNA /cds=(136,963) /gb=NM_032347 /gi=14150142 /ug=Hs.269914 /len=1439	NM_032347	Hs.269914	NP_115723
mioa9258	NM_032661	hypothetical protein MGC5139 (MGC5139), mRNA /cds=(14,115) /gb=NM_032661 /gi=14249217 /ug=Hs.127610 /len=457	NM_032661	Hs.127610	NP_116050
ncr2304	NM_032682	forkhead box P1 (FOXP1), mRNA /cds=(432,2465) /gb=NM_032682 /gi=19923670 /ug=Hs.274344 /len=4954	NM_032682	Hs.274344	NP_116071
seoc3443	NM_032822	hypothetical protein FLJ14668 (FLJ14668), mRNA /cds=(59,475) /gb=NM_032822 /gi=14249519 /ug=Hs.334644 /len=1786	NM_032822	Hs.334644	NP_116211

miod2082	NM_032859	hypothetical protein FLJ14906 (FLJ14906), mRNA /cds=(131,736) /gb=NM_032859 /gi=14249591 /ug=Hs.183528 /len=2492	NM_032859	Hs.183528	NP_116248
ncrc3773	NM_032870	SR rich protein (DKFZp564B0769), mRNA /cds=(33,2450) /gb=NM_032870 /gi=18699723 /ug=Hs.18368 /len=2663	NM_032870	Hs.18368	NP_116259
fcrb7573	NM_032907	hypothetical protein MGC14421 (MGC14421), mRNA /cds=(474,1616) /gb=NM_032907 /gi=14249681 /ug=Hs.334713 /len=1772	NM_032907	Hs.334713	NP_116296
fcr3287	NM_002607	platelet-derived growth factor alpha polypeptide (PDGFA), transcript variant 1, mRNA /cds=(839,1474) /gb=NM_002607 /gi=15208657 /ug=Hs.37040 /len=2797	NM_002607; NM_033023	Hs.37040	NP_148983
ncr7768	NM_033055	likely ortholog of mouse hippocampus abundant gene transcript 1 (HIAT1), mRNA /cds=(6,1124) /gb=NM_033055 /gi=24308343 /ug=Hs.21015 /len=2230	NM_033055	Hs.21015	NP_149044

fcr1150	NM_033209	Thy-1 co-transcribed (LOC94105), mRNA /cds=(1289,1717) /gb=NM_033209 /gi=24475732 /ug=Hs.345643 /len=1818	NM_033209	Hs.345643	NP_149986
fcr6395	NM_003672	CDC14 cell division cycle 14 A (S. cerevisiae) (CDC14A), transcript variant 1, mRNA /cds=(466,2250) /gb=NM_003672 /gi=15451928 /ug=Hs.65993 /len=4262	NM_003672; NM_033312; NM_033313	Hs.65993	NP_201570
miod2665	NM_033318	hypothetical gene supported by AL449243 (LOC91689), mRNA /cds=(80,403) /gb=NM_033318 /gi=21314768 /ug=Hs.306083 /len=1586	NM_033318	Hs.306083	NP_201575
mioc2720	NM_033495	KIAA1309 protein (KIAA1309), mRNA /cds=(211,2025) /gb=NM_033495 /gi=15741229 /ug=Hs.348262 /len=3119	NM_033495	Hs.348262	NP_277030
fcrb1296	NM_015414	ribosomal protein L36 (RPL36), transcript variant 2, mRNA /cds=(153,470) /gb=NM_015414 /gi=16117793 /ug=Hs.433411 /len=545	NM_015414; NM_033643	Hs.433411	NP_378669

mioa4542	NM_033655	cell recognition molecule CASPR3 (CASPR3), transcript variant 1, mRNA /cds=(408,3872) /gb=NM_033655 /gi=16306508 /ug=Hs.212839 /len=5017	NM_024879; NM_033655	Hs.212839	NP_387504
ncrc9916	BQ109159	imageqc_6_2001/snk86bdrr81.y1 NIH_MGC_12 cDNA clone IMAGE:5110111 5', mRNA sequence /clone=IMAGE:5110111 /clone_end=5' /gb=BQ109159 /gi=20158813 /ug=Hs.433575 /len=604		Hs.433575	NP_387506
fcrb6870	NM_007103	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa (NDUFV1), mRNA /cds=(70,1464) /gb=NM_007103 /gi=20149567 /ug=Hs.7744 /len=1566	NM_007103	Hs.7744	NP_438172
ncrc9758	NM_052966	chromosome 1 open reading frame 24 (C1orf24), mRNA /cds=(195,2981) /gb=NM_052966 /gi=16757969 /ug=Hs.48778 /len=6919	NM_022083; NM_052966	Hs.48778	NP_443198
ncr1912	NM_053025	myosin, light polypeptide kinase (MYLK), transcript variant 1, mRNA /cds=(120,5864) /gb=NM_053025 /gi=16950610 /ug=Hs.211582 /len=5925	NM_005965; NM_053025; NM_053026; NM_053027; NM_053028; NM_053029; NM_053030; NM_053031; NM_053032	Hs.211582	NP_444260

ncr5909	BC036034	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2, clone MGC:33157 IMAGE:5272431, mRNA, complete cds	NM_001401; NM_057159	Hs.75794	NP_476500
seoa2795	NM_080821	chromosome 20 open reading frame 108 (C20orf108), mRNA /cds=(41,619) /gb=NM_080821 /gi=18201877 /ug=Hs.352413 /len=3026	NM_080821	Hs.352413	NP_543011
miod7066	NM_030781	collectin sub-family member 12 (COLEC12), transcript variant II, mRNA /cds=(172,2040) /gb=NM_030781 /gi=18641357 /ug=Hs.29423 /len=4685	NM_030781; NM_130386	Hs.29423	NP_569057
mioc8640	NM_133259	leucine-rich PPR-motif containing (LRPPRC), mRNA /cds=(46,3867) /gb=NM_133259 /gi=18959201 /ug=Hs.182490 /len=4782	NM_133259	Hs.182490	NP_573566
seoa1661	NM_133493	CD109 (CD109), mRNA /cds=(113,4450) /gb=NM_133493 /gi=19424129 /ug=Hs.55964 /len=5883	NM_133493	Hs.55964	NP_598000
mioc2340	NM_133502	zinc finger protein 274 (ZNF274), transcript variant ZNF274c, mRNA /cds=(460,2421) /gb=NM_133502 /gi=19743800 /ug=Hs.83761 /len=2839	NM_016324; NM_016325; NM_133502	Hs.83761	NP_598009

seob3112	NM_001920	decorin (DCN), transcript variant A1, mRNA /cds=(200,1279) /gb=NM_001920 /gi=19743844 /ug=Hs.433989 /len=1751	NM_001920; NM_133503; NM_133504; NM_133505; NM_133506; NM_133507	Hs.433989	NP_598014
seob6379	NM_015293	synaptic nuclei expressed gene 1 (SYNE-1), transcript variant beta, mRNA /cds=(121,10086) /gb=NM_015293 /gi=19526752 /ug=Hs.192102 /len=10742	NM_015293; NM_033071; NM_133650	Hs.192102	NP_598411
fcr4784	NM_134269	smoothelin (SMTN), transcript variant 2, mRNA /cds=(219,2966) /gb=NM_134269 /gi=19913395 /ug=Hs.149098 /len=3294	NM_006932; NM_134269; NM_134270	Hs.149098	NP_599032
seob0047	U09820	helicase II (RAD54L) mRNA, complete cds. /cds=(54,4979) /gb=U09820 /gi=606832 /ug=Hs.96264 /len=6115	NM_000489; NM_138270; NM_138271	Hs.96264	NP_612115
seoc1948	NM_138436	hypothetical protein BC013035 (LOC114926), mRNA /cds=(128,430) /gb=NM_138436 /gi=19923964 /ug=Hs.10018 /len=836	NM_138436	Hs.10018	NP_612445
ncr5529	BC014000	clone MGC:20208 IMAGE:3936339, mRNA, complete cds /cds=(330,1832) /gb=BC014000 /gi=15559281 /ug=Hs.58461 /len=2733		Hs.58461	NP_612456

fcrb5507	NM_138455	collagen triple helix repeat containing 1 (CTHRC1), mRNA /cds=(109,840) /gb=NM_138455 /gi=19923988 /ug=Hs.283713 /len=1245	NM_138455	Hs.283713	NP_612464
fcrb5705	NM_138555	kinesin family member 23 (KIF23), transcript variant 1, mRNA /cds=(118,3000) /gb=NM_138555 /gi=20143966 /ug=Hs.270845 /len=3636	NM_004856; NM_138555	Hs.270845	NP_612565
fcrb5164	NM_138785	hypothetical protein BC014320 (LOC116254), mRNA /cds=(28,1020) /gb=NM_138785 /gi=20302037 /ug=Hs.240767 /len=1143	NM_138785	Hs.240767	NP_620140
mioa4326	NM_000919	peptidylglycine alpha-amidating monooxygenase (PAM), transcript variant 1, mRNA /cds=(374,3298) /gb=NM_000919 /gi=21070983 /ug=Hs.83920 /len=3960	NM_000919; NM_138766; NM_138821; NM_138822	Hs.83920	NP_620177
seoa5894	NM_058183	SON DNA binding protein (SON), transcript variant e, mRNA /cds=(50,6376) /gb=NM_058183 /gi=21040317 /ug=Hs.92909 /len=8482	NM_003103; NM_032195; NM_058183; NM_138925; NM_138926; NM_138927	Hs.92909	NP_620305

fcrc4896	NM_139168	splicing factor, arginine/serine-rich 12 (SFRS12), mRNA /cds=(342,1868) /gb=NM_139168 /gi=21040254 /ug=Hs.381165 /len=3811	NM_139168	Hs.381165	NP_631907
seoa1480	NM_139207	nucleosome assembly protein 1-like 1 (NAP1L1), transcript variant 1, mRNA /cds=(125,1300) /gb=NM_139207 /gi=21327707 /ug=Hs.302649 /len=3582	NM_004537; NM_139207	Hs.302649	NP_631946
miod0642	AW071632	wt94d09.x1 NCI_CGAP_GC6 cDNA clone IMAGE:2515121 3', mRNA sequence /clone=IMAGE:2515121 /clone_end=3' /gb=AW071632 /gi=6026630 /ug=Hs.414880 /len=122		Hs.414880	NP_653087
fcrb5439	NM_007040	E1B-55kDa-associated protein 5 (E1B-AP5), transcript variant 1, mRNA /cds=(174,2744) /gb=NM_007040 /gi=21536325 /ug=Hs.155218 /len=3872	NM_007040; NM_144732; NM_144733; NM_144734	Hs.155218	NP_653335
seoc1504	NM_144976	hypothetical protein MGC26914 (MGC26914), mRNA /cds=(148,1809) /gb=NM_144976 /gi=21699059 /ug=Hs.202974 /len=2900	NM_144976	Hs.202974	NP_659413

seoc0149	NM_004619	TNF receptor-associated factor 5 (TRAF5), transcript variant 1, mRNA /cds=(194,1867) /gb=NM_004619 /gi=22027625 /ug=Hs.29736 /len=4132	NM_004619; NM_145759	Hs.29736	NP_665702
seob0850	NM_017613	downstream neighbor of SON (DONSON), transcript variant 1, mRNA /cds=(68,1768) /gb=NM_017613 /gi=22035582 /ug=Hs.17834 /len=2189	NM_017613; NM_145794; NM_145795	Hs.17834	NP_665738
fcrb5296	NM_015129	septin 6 (SEPT6), transcript variant II, mRNA /cds=(257,1561) /gb=NM_015129 /gi=22035575 /ug=Hs.90998 /len=2686	NM_015129; NM_145799; NM_145800; NM_145802	Hs.90998	NP_665801
miob8373	NM_007217	programmed cell death 10 (PDCD10), transcript variant 1, mRNA /cds=(399,1037) /gb=NM_007217 /gi=22538790 /ug=Hs.28866 /len=1454	NM_007217; NM_145859; NM_145860	Hs.28866	NP_665859
ncrc9784	NM_002624	prefoldin 5 (PFDN5), transcript variant 1, mRNA /cds=(36,500) /gb=NM_002624 /gi=22202632 /ug=Hs.288856 /len=661	NM_002624; NM_145896; NM_145897	Hs.288856	NP_665904

miob4886	NM_148954	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2) (PSMB9), transcript variant 2, mRNA /cds=(52,681) /gb=NM_148954 /gi=23110931 /ug=Hs.381081 /len=748	NM_002800; NM_148954	Hs.381081	NP_683756
fcrb3519	NM_148980	Williams Beuren syndrome chromosome region 20C (WBSCR20C), transcript variant 3, mRNA /cds=(794,1399) /gb=NM_148980 /gi=23200003 /ug=Hs.334837 /len=1857	NM_032158; NM_148936; NM_148980; NM_149379	Hs.334837	NP_684281
seoa0511	NM_015976	sorting nexin 7 (SNX7), transcript variant 1, mRNA /cds=(268,1431) /gb=NM_015976 /gi=23111053 /ug=Hs.127241 /len=1798	NM_015976; NM_152238	Hs.127241	NP_689424
miod1450	NM_152334	hypothetical protein FLJ25005 (FLJ25005), mRNA /cds=(166,1467) /gb=NM_152334 /gi=22748728 /ug=Hs.181426 /len=2109	NM_152334	Hs.181426	NP_689547
seob7747	NM_152367	hypothetical protein FLJ38716 (FLJ38716), mRNA /cds=(266,1354) /gb=NM_152367 /gi=22748790 /ug=Hs.376194 /len=3229	NM_152367	Hs.376194	NP_689580

fcrb1687	NM_152573	hypothetical protein FLJ31614 (FLJ31614), mRNA /cds=(312,881) /gb=NM_152573 /gi=22749180 /ug=Hs.351442 /len=1766	NM_152573	Hs.351442	NP_689786
ncrc9549	NM_152683	hypothetical protein FLJ33167 (FLJ33167), mRNA /cds=(217,1899) /gb=NM_152683 /gi=22749372 /ug=Hs.351470 /len=2078	NM_152683	Hs.351470	NP_689896
fcr1883	NM_152713	integral membrane protein 1 (ITM1), mRNA /cds=(130,2247) /gb=NM_152713 /gi=22749414 /ug=Hs.287850 /len=2553	NM_152713	Hs.287850	NP_689926
seoa3109	NM_006597	heat shock 70kDa protein 8 (HSPA8), transcript variant 1, mRNA /cds=(79,2019) /gb=NM_006597 /gi=24234684 /ug=Hs.180414 /len=2276	NM_006597; NM_153201	Hs.180414	NP_694881
mioa8831	NM_153225	hypothetical protein FLJ40021 (FLJ40021), mRNA /cds=(364,792) /gb=NM_153225 /gi=23397486 /ug=Hs.41185 /len=1972	NM_153225	Hs.41185	NP_694957
mioc4009	NM_153348	F-box only protein 29 (FBXO29), mRNA /cds=(88,1884) /gb=NM_153348 /gi=24158491 /ug=Hs.350985 /len=4874	NM_153348	Hs.350985	NP_699179

mioc0350	NM_153373	hypothetical protein MGC15875 (MGC15875), mRNA /cds=(235,1587) /gb=NM_153373 /gi=24119276 /ug=Hs.315054 /len=2010	NM_032921; NM_153373	Hs.315054	NP_699204
fcrb8196	NM_153649	tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=NM_153649 /gi=24119202 /ug=Hs.85844 /len=2089	NM_152263; NM_153649	Hs.85844	NP_705935
seoc1167	NM_153812	hypothetical protein MGC43399 (MGC43399), mRNA /cds=(383,1285) /gb=NM_153812 /gi=24432092 /ug=Hs.7299 /len=3684	NM_153812	Hs.7299	NP_722519
ncr7570	NM_153831	PTK2 protein tyrosine kinase 2 (PTK2), transcript variant 1, mRNA /cds=(231,3389) /gb=NM_153831 /gi=27886591 /ug=Hs.740 /len=4453	NM_005607; NM_153831	Hs.740	NP_722560
seob5007	NM_170705	isoprenylcysteine carboxyl methyltransferase (ICMT), transcript variant 2, mRNA /cds=(457,1023) /gb=NM_170705 /gi=24797155 /ug=Hs.183212 /len=3654	NM_012405; NM_170705	Hs.183212	NP_733806
fcrb5146	NM_170707	lamin A/C (LMNA), transcript variant 1, mRNA /cds=(213,2207) /gb=NM_170707 /gi=27436945 /ug=Hs.377973 /len=3181	NM_005572; NM_170707; NM_170708	Hs.377973	NP_733822

miob9506	NM_172240	TUWD12 (TUWD12), mRNA /cds=(106,1542) /gb=NM_172240 /gi=26665868 /ug=Hs.25130 /len=2984	NM_172240	Hs.25130	NP_758440
ncrc4907	NM_004555	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 (NFATC3), transcript variant 2, mRNA /cds=(211,3417) /gb=NM_004555 /gi=27886542 /ug=Hs.172674 /len=4005	NM_004555; NM_173163; NM_173164; NM_173165	Hs.172674	NP_775188
ncrb8134	NM_173473	hypothetical protein LOC119504 (LOC119504), mRNA /cds=(119,451) /gb=NM_173473 /gi=27735038 /ug=Hs.426296 /len=1177	NM_173473	Hs.426296	NP_775744
mioc7700	NM_173473	hypothetical protein LOC119504 (LOC119504), mRNA /cds=(119,451) /gb=NM_173473 /gi=27735038 /ug=Hs.426296 /len=1177	NM_173473	Hs.426296	NP_775744
ncr2861	AK074985	cDNA FLJ90504 fis, clone NT2RP3004090, weakly similar to GOLIATH PROTEIN. /cds=(103,1305) /gb=AK074985 /gi=22760786 /ug=Hs.171802 /len=2452	NM_173647	Hs.171802	NP_775918

seob9694	NM_173852	keratinocytes associated protein 2 (KCP2), mRNA /cds=(1,489) /gb=NM_173852 /gi=27777660 /ug=Hs.374854 /len=489	NM_173852	Hs.374854	NP_776251
hfcr1694	NM_004135	isocitrate dehydrogenase 3 (NAD) gamma (IDH3G), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA	NM_004135; NM_174869	Hs.75253	NP_777358
mioc1117	NM_174890	hypothetical protein LOC93550 (LOC93550), mRNA /cds=(217,2400) /gb=NM_174890 /gi=28376663 /ug=Hs.377945 /len=3256	NM_174890	Hs.377945	NP_777550
mioc0621	NM_174909	hypothetical protein LOC153339 (LOC153339), mRNA /cds=(21,239) /gb=NM_174909 /gi=28372532 /ug=Hs.374538 /len=726	NM_174909	Hs.374538	NP_777569
fcrb3285	NM_014599	melanoma antigen, family D, 2 (MAGED2), mRNA /cds=(97,1917) /gb=NM_014599 /gi=21264316 /ug=Hs.4943 /len=2077	NM_014599; NM_177433	Hs.4943	NP_803182

miod6500	BQ181216	UI-H-EU0-azl-k-15-0-UI.s1 NCI_CGAP_Car1 cDNA clone IMAGE: 5850374 3', mRNA sequence /clone=IMAGE:_5850374 /clone_end=3' /gb=BQ181216 /gi=20356708 /ug=Hs.442170 /len=1044		Hs.442170	NP_835228
miod0500	NM_032023	AD037 protein (AD037), mRNA /cds=(107,1072) /gb=NM_032023 /gi=23510359 /ug=Hs.296162 /len=2481	NM_032023	Hs.296162	NP_835281
miod4216	BC041375	clone IMAGE:5274527, mRNA /gb=BC041375 /gi=27370608 /ug=Hs.11700 /len=3905	NM_178314	Hs.11700	NP_847884
fcrb6483	NM_020830	WD40 and FYVE domain containing 1 (WDFY1), mRNA /cds=(30,1262) /gb=NM_020830 /gi=18482372 /ug=Hs.44743 /len=4585	NM_020830	Hs.44743	NP_848127
miob9458	AI377292	te65d01.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2091553 3', mRNA sequence /clone=IMAGE:2091553 /clone_end=3' /gb=AI377292 /gi=4187145 /ug=Hs.410753 /len=238		Hs.410753	NP_848642

mioc2216	NM_006814	proteasome (prosome, macropain) inhibitor subunit 1 (PI31) (PSMF1), mRNA /cds=(127,942) /gb=NM_006814 /gi=5803122 /ug=Hs.405813 /len=3188	NM_006814	Hs.405813	NP_848694
ncrc3073	NM_006348	component of oligomeric golgi complex 5 (COG5), mRNA /cds=(52,2571) /gb=NM_006348 /gi=5453669 /ug=Hs.239631 /len=3105	NM_006348	Hs.239631	NP_859422
fcrb7072	AK075459	cDNA PSEC0152 fis, clone PLACE1007885. /cds=(20,1144) /gb=AK075459 /gi=22761560 /ug=Hs.350475 /len=2130		Hs.350475	NP_877437
ncr1692	NM_133171	engulfment and cell motility 2 (ced-12 C. elegans) (ELMO2), transcript variant 1, mRNA /cds=(141,2303) /gb=NM_133171 /gi=19718768 /ug=Hs.96560 /len=3630	NM_022086; NM_133171	Hs.96560	NP_877496
hfcr1433	NM_016240	scavenger receptor class A, member 3 (SCARA3), mRNA /cds=(142,1962) /gb=NM_016240 /gi=7705335 /ug=Hs.128856 /len=3636	NM_016240	Hs.128856	NP_878185

seoa3752	NM_000935	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 (PLOD2), mRNA /cds=(1,2214) /gb=NM_000935 /gi=4505888 /ug=Hs.41270 /len=3503	NM_000935	Hs.41270	NP_891988
seob5748	NM_031268	PRO0461 protein (PRO0461), mRNA /gb=NM_031268 /gi=20588827 /ug=Hs.25063 /len=1100	NM_031268	Hs.25063	NP_112558
seob7984	AF094481	trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds	NM_003663		NP_003654
seoc4654	X07718	fibronectin gene ED-A region	NM_002026; NM_054034		NP_002017; NP_473375
ncrb2544	NM_018996	hypothetical protein FLJ20015 (FLJ20015), mRNA /cds=(32,523) /gb=NM_018996 /gi=9506648 /ug=Hs.375614 /len=1457	NM_018996	Hs.375614	NP_061869
ncrc1316	XM_294901	hypothetical gene supported by U79248; AK056929; BC041875 (LOC339290), mRNA			XP_294901
ncr1954	AB042297	PTS gene for 6-pyruvoyltetrahydropterin synthase, complete cds	NM_031938		NP_114144

Figure 7a: Mild OA stage-specific markers (Affymetrix data)					
Gene name	Common name	Genbank	Description	RefSeq	UniGene
203400_s_at		NM_001063	gb:NM_001063.1 /DEF=Homo sapiens transferrin (TF), mRNA. /FEA=mRNA /GEN=TF /PROD=transferrin precursor /DB_XREF=gi:4557870 /UG=Hs.284176 transferrin /FL=gb:M12530.1 gb:NM_001063.1		
214674_at	USP19	AW451502	ubiquitin specific protease 19		Hs.301373
210794_s_at		AF119863	Consensus includes gb:AF119863.1 /DEF=Homo sapiens PRO2160 mRNA, complete cds. /FEA=mRNA /PROD=PRO2160 /DB_XREF=gi:7770162 /UG=Hs.112844 maternally expressed 3 /FL=gb:AF119863.1		

202994_s_at		Z95331	Consensus includes gb:Z95331 /DEF=Human DNA sequence from clone CTA-941F9 on chromosome 22q13 Contains the 3 end of the FBLN1 gene for Fibulin 1 isoforms B, C and D, the first exon of the gene for a novel protein (the ortholog of mouse brain protein E46), ESTs, STSs, GSSs and two... /FEA=mRNA_1 /DB_XREF=gi:6572282 /UG=Hs.79732 fibulin 1 /FL=gb:U01244.1 gb:NM_006486.1		
218630_at		NM_017777	gb:NM_017777.1 /DEF=Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA. /FEA=mRNA /GEN=FLJ20345 /PROD=hypothetical protein FLJ20345 /DB_XREF=gi:8923323 /UG=Hs.20558 hypothetical protein FLJ20345 /FL=gb:NM_017777.1		

222186_at		AL109684	Consensus includes gb:AL109684.1 /DEF=Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 27080. /FEA=mRNA /DB_XREF=gi:5689805 /UG=Hs.306329 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 27080		
201791_s_at		NM_001360	gb:NM_001360.1 /DEF=Homo sapiens 7-dehydrocholesterol reductase (DHCR7), mRNA. /FEA=mRNA /GEN=DHCR7 /PROD=7-dehydrocholesterol reductase /DB_XREF=gi:4503320 /UG=Hs.11806 7-dehydrocholesterol reductase /FL=gb:BC000054.1 gb:AF034544.1 gb:AF067127.1 gb:AF096305.1 gb:NM_001360.1		

213147_at		NM_018951	Consensus includes gb:AI375919 /FEA=EST /DB_XREF=gi:4175909 /DB_XREF=est:tc14d04.x1 /CLONE=IMAGE:2063815 /UG=Hs.110637 homeo box A10 /FL=gb:NM_018951.1		
204153_s_at		NM_002405	gb:NM_002405.1 /DEF=Homo sapiens manic fringe (Drosophila) homolog (MFNG), mRNA. /FEA=mRNA /GEN=MFNG /PROD=manic fringe (Drosophila) homolog /DB_XREF=gi:4505158 /UG=Hs.31939 manic fringe (Drosophila) homolog /FL=gb:U94352.1 gb:NM_002405.1		

205702_at		NM_006608	gb:NM_006608.1 /DEF=Homo sapiens putative homeodomain transcription factor (PHTF1), mRNA. /FEA=mRNA /GEN=PHTF1 /PROD=putative homeodomain transcription factor /DB_XREF=gi:5729975 /UG=Hs.123637 putative homeodomain transcription factor /FL=gb:NM_006608.1		
210355_at		J03580	gb:J03580.1 /DEF=Human, parathyroid-like protein (associated with humoral hypercalcemia of malignancy) mRNA, complete cds. /FEA=mRNA /GEN=PTHLH /DB_XREF=gi:190705 /UG=Hs.89626 parathyroid hormone-like hormone /FL=gb:J03580.1		

211252_x_at		U36759	gb:U36759.1 /DEF=Human pre-T cell receptor alpha-type chain precursor, mRNA, complete cds. /FEA=mRNA /PROD=pre-T cell receptor alpha-type chain precursor /DB_XREF=gi:1127580 /UG=Hs.169002 Human pre TCR alpha mRNA, partial cds /FL=gb:U36759.1		
217566_s_at		BF222018	ESTs, Moderately similar to S71105 protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) 4, prostate specific - human [H.sapiens]		Hs.289803
33814_at	PAK4	AF005046	p21(CDKN1A)-activated kinase 4	NM_005884	Hs.20447
216521_s_at	c6.1A-TCRC	S72931	This sequence comes from Fig. 1; author's translation differs from conceptual translation; Homo sapiens T-cell receptor alpha chain-c6.1A fusion protein (c6.1A-TCRC) gene, partial cds.		

219961_s_at		NM_018474	gb:NM_018474.1 /DEF=Homo sapiens uncharacterized hypothalamus protein HT013 (HT013), mRNA. /FEA=mRNA /GEN=HT013 /PROD=uncharacterized hypothalamus protein HT013 /DB_XREF=gi:8923814 /UG=Hs.173515 uncharacterized hypothalamus protein HT013 /FL=gb:AF220187.1 gb:NM_018474.1		
208463_at		NM_000809	gb:NM_000809.1 /DEF=Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 4 (GABRA4), mRNA. /FEA=CDS /GEN=GABRA4 /PROD=gamma-aminobutyric acid A receptor, alpha 4precursor /DB_XREF=gi:4557604 /UG=Hs.248112 gamma-aminobutyric acid (GABA) A receptor, alpha 4 /FL=gb:NM_000809.1 gb:U30461.1		

218743_at		NM_024591	gb:NM_024591.1 /DEF=Homo sapiens hypothetical protein FLJ11749 (FLJ11749), mRNA. /FEA=mRNA /GEN=FLJ11749 /PROD=hypothetical protein FLJ11749 /DB_XREF=gi:13375782 /UG=Hs.22897 hypothetical protein FLJ11749 /FL=gb:NM_024591.1		
219184_x_at		NM_013337	gb:NM_013337.1 /DEF=Homo sapiens translocase of inner mitochondrial membrane 22 (yeast) homolog (TIM22), mRNA. /FEA=mRNA /GEN=TIM22 /PROD=translocase of inner mitochondrial membrane 22(yeast) homolog /DB_XREF=gi:7019552 /UG=Hs.87595 translocase of inner mitochondrial membrane 22 (yeast) homolog /FL=gb:BC002324.1 gb:AF155330.1 gb:NM_013337.1		

219645_at		NM_001231	gb:NM_001231.1 /DEF=Homo sapiens calsequestrin 1 (fast-twitch, skeletal muscle) (CASQ1), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=CASQ1 /PROD=skeletal muscle calsequestrin 1 /DB_XREF=gi:4557406 /UG=Hs.60708 calsequestrin 1 (fast-twitch, skeletal muscle) /FL=gb:NM_001231.1 gb:S73775.1		
204479_at		NM_012383	gb:NM_012383.1 /DEF=Homo sapiens osteoclast stimulating factor 1 (OSTF1), mRNA. /FEA=mRNA /GEN=OSTF1 /PROD=osteoclast stimulating factor 1 /DB_XREF=gi:6912563 /UG=Hs.95821 osteoclast stimulating factor 1 /FL=gb:U63717.1 gb:NM_012383.1		

201878_at		NM_005744	Consensus includes gb:N25546 /FEA=EST /DB_XREF=gi:1139894 /DB_XREF=est:yx76e05.s1 /CLONE=IMAGE:267680 /UG=Hs.181461 ariadne (Drosophila) homolog, ubiquitin-conjugating enzyme E2-binding protein, 1 /FL=gb:AF072832.1 gb:NM_005744.2		
212729_at		AB033058	Consensus includes gb:AI916274 /FEA=EST /DB_XREF=gi:5636129 /DB_XREF=est:wg99e04.x1 /CLONE=IMAGE:2379390 /UG=Hs.11101 KIAA1232 protein		
212726_at		AB014562	Consensus includes gb:AB014562.1 /DEF=Homo sapiens mRNA for KIAA0662 protein, partial cds. /FEA=mRNA /GEN=KIAA0662 /PROD=KIAA0662 protein /DB_XREF=gi:3327137 /UG=Hs.93868 KIAA0662 gene product		

203338_at		NM_006246	gb:NM_006246.1 /DEF=Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E), mRNA. /FEA=mRNA /GEN=PPP2R5E /PROD=protein phosphatase 2, regulatory subunit B(B56), epsilon isoform /DB_XREF=gi:5453955 /UG=Hs.173328 protein phosphatase 2, regulatory subunit B (B56), epsilon isoform /FL=gb:L76703.1 gb:NM_006246.1		
215985_at		X92110	Consensus includes gb:X92110.1 /DEF=H.sapiens mRNA for hcgVIII protein. /FEA=mRNA /DB_XREF=gi:1216163 /UG=Hs.153618 HCGVIII-1 protein		

201511_at		NM_001087	gb:NM_001087.1 /DEF=Homo sapiens angio-associated, migratory cell protein (AAMP), mRNA. /FEA=mRNA /GEN=AAMP /PROD=angio-associated, migratory cell protein /DB_XREF=gi:4557228 /UG=Hs.83347 angio-associated, migratory cell protein /FL=gb:NM_001087.1 gb:M95627.1		
205231_s_at		NM_005670	gb:NM_005670.1 /DEF=Homo sapiens epilepsy, progressive myoclonus type 2, Lafora disease (laforin) (EPM2A), mRNA. /FEA=mRNA /GEN=EPM2A /PROD=epilepsy, progressive myoclonus type 2, Laforadisease (laforin) /DB_XREF=gi:11321612 /UG=Hs.22464 epilepsy, progressive myoclonus type 2, Lafora disease (laforin) /FL=gb:AF284580.1 gb:NM_005670.1 gb:AF084535.2		
212337_at		AI687738	ESTs		Hs.409222

219920_s_at		NM_021971	gb:NM_021971.1 /DEF=Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB), transcript variant 2, mRNA. /FEA=mRNA /GEN=GMPPB /PROD=GDP-mannose pyrophosphorylase B, isoform 2 /DB_XREF=gi:11761620 /UG=Hs.28077 GDP-mannose pyrophosphorylase B /FL=gb:NM_021971.1 gb:BC001141.1 gb:AF135421.1		
211139_s_at		AF045452	gb:AF045452.1 /DEF=Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds. /FEA=mRNA /PROD=transcriptional regulatory protein p54 /DB_XREF=gi:3282824 /UG=Hs.107474 NGFI-A binding protein 1 (ERG1 binding protein 1) /FL=gb:AF045452.1		

209984_at		AB037901	gb:AB037901.1 /DEF=Homo sapiens GASC-1 mRNA, complete cds. /FEA=mRNA /GEN=GASC-1 /DB_XREF=gi:10567163 /UG=Hs.149918 gene amplified in squamous cell carcinoma 1; KIAA0780 protein /FL=gb:AB037901.1		
218761_at		NM_017610	gb:NM_017610.1 /DEF=Homo sapiens hypothetical protein DKFZp761D081 (DKFZp761D081), mRNA. /FEA=mRNA /GEN=DKFZp761D081 /PROD=hypothetical protein DKFZp761D081 /DB_XREF=gi:8922164 /UG=Hs.12504 hypothetical protein DKFZp761D081 /FL=gb:NM_017610.1		
201983_s_at	EGFR	AW157070	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)		Hs.77432
215499_at	MAP2K3	AA780381	mitogen-activated protein kinase kinase 3		Hs.180533

219626_at		NM_024597	gb:NM_024597.1 /DEF=Homo sapiens hypothetical protein FLJ12649 (FLJ12649), mRNA. /FEA=mRNA /GEN=FLJ12649 /PROD=hypothetical protein FLJ12649 /DB_XREF=gi:13375794 /UG=Hs.24078 hypothetical protein FLJ12649 /FL=gb:NM_024597.1		
222209_s_at		AK000684	Consensus includes gb:AK000684.1 /DEF=Homo sapiens cDNA FLJ20677 fis, clone KAIA4183. /FEA=mRNA /DB_XREF=gi:7020930 /UG=Hs.183887 hypothetical protein FLJ22104		

203300_x_at		NM_003916	gb:NM_003916.1 /DEF=Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA. /FEA=mRNA /GEN=AP1S2 /PROD=adaptor-related protein complex 1, sigma 2subunit /DB_XREF=gi:4506956 /UG=Hs.40368 adaptor-related protein complex 1, sigma 2 subunit /FL=gb:AF251295.1 gb:BC001117.1 gb:AB015320.1 gb:NM_003916.1		
203269_at		NM_003580	gb:NM_003580.1 /DEF=Homo sapiens neutral sphingomyelinase (N-SMase) activation associated factor (NSMAF), mRNA. /FEA=mRNA /GEN=NSMAF /PROD=neutral sphingomyelinase (N-SMase) activationassociated factor /DB_XREF=gi:4505464 /UG=Hs.78687 neutral sphingomyelinase (N-SMase) activation associated factor /FL=gb:NM_003580.1		
214151_s_at	PIGB	AU144243	phosphatidylinositol glycan, class B		Hs.247118

212989_at	TUBGCP2	AI377497	tubulin, gamma complex associated protein 2		Hs.13386
201661_s_at		NM_004457	gb:NM_004457.2 /DEF=Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 3 (FACL3), mRNA. /FEA=mRNA /GEN=FACL3 /PROD=long-chain fatty-acid-Coenzyme A ligase 3 /DB_XREF=gi:12669907 /UG=Hs.268012 fatty-acid-Coenzyme A ligase, long-chain 3 /FL=gb:NM_004457.2 gb:D89053.1 gb:AF116690.1		
201664_at		AL136877	gb:AL136877.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434F205 (from clone DKFZp434F205); complete cds. /FEA=mRNA /GEN=DKFZp434F205 /PROD=hypothetical protein /DB_XREF=gi:6807670 /UG=Hs.50758 SMC4 (structural maintenance of chromosomes 4, yeast)-like 1 /FL=gb:AB019987.1 gb:NM_005496.1 gb:AL136877.1		

201681_s_at		AB011155	Consensus includes gb:AB011155.1 /DEF=Homo sapiens mRNA for KIAA0583 protein, partial cds. /FEA=mRNA /GEN=KIAA0583 /PROD=KIAA0583 protein /DB_XREF=gi:3043689 /UG=Hs.170290 discs, large (Drosophila) homolog 5 /FL=gb:U61843.1 gb:NM_004747.1		
210653_s_at		M55575	gb:M55575.1 /DEF=Human branched chain alpha-keto acid dehydrogenase (BCKDHB) E1-beta subunit mRNA, complete cds. /FEA=mRNA /GEN=BCKDHB /PROD=branched chain alpha-keto acid dehydrogenaseE1-beta subunit /DB_XREF=gi:179361 /UG=Hs.1265 branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease) /FL=gb:M55575.1		

210691_s_at		AF275803	gb:AF275803.1 /DEF=Homo sapiens PNAS-107 mRNA, complete cds. /FEA=mRNA /PROD=PNAS-107 /DB_XREF=gi:10834769 /UG=Hs.27258 calcyclin binding protein /FL=gb:AF275803.1		
210839_s_at		D45421	gb:D45421.1 /DEF=Human mRNA for phosphodiesterase I alpha, complete cds. /FEA=mRNA /PROD=phosphodiesterase I alpha /DB_XREF=gi:662289 /UG=Hs.174185 ectonucleotide pyrophosphatasephosphodiesterase 2 (autotaxin) /FL=gb:NM_006209.1 gb:D45421.1		
218143_s_at		NM_005697	gb:NM_005697.2 /DEF=Homo sapiens secretory carrier membrane protein 2 (SCAMP2), mRNA. /FEA=mRNA /GEN=SCAMP2 /PROD=secretory carrier membrane protein 2 /DB_XREF=gi:5730030 /UG=Hs.238030 secretory carrier membrane protein 2 /FL=gb:BC001376.1 gb:BC004385.1 gb:AF005038.2 gb:NM_005697.2		

219973_at		NM_024590	gb:NM_024590.1 /DEF=Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA. /FEA=mRNA /GEN=FLJ23548 /PROD=hypothetical protein FLJ23548 /DB_XREF=gi:13375780 /UG=Hs.22895 hypothetical protein FLJ23548 /FL=gb:NM_024590.1		
203460_s_at		NM_007318	gb:NM_007318.1 /DEF=Homo sapiens presenilin 1 (Alzheimer disease 3) (PSEN1), transcript variant I-463, mRNA. /FEA=mRNA /GEN=PSEN1 /PROD=presenilin 1 isoform I-463 /DB_XREF=gi:7549812 /UG=Hs.3260 presenilin 1 (Alzheimer disease 3) /FL=gb:U40379.1 gb:L76517.1 gb:NM_007318.1		

201524_x_at		NM_003348	gb:NM_003348.1 /DEF=Homo sapiens ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13) (UBE2N), mRNA. /FEA=mRNA /GEN=UBE2N /PROD=ubiquitin-conjugating enzyme E2N (homologous toyeast UBC13) /DB_XREF=gi:4507792 /UG=Hs.75355 ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13) /FL=gb:D83004.1 gb:BC000396.1 gb:BC003365.1 gb:NM_003348.1		
216005_at		BF434846	ESTs, Weakly similar to hypothetical protein FLJ20234 [Homo sapiens] [H.sapiens]		Hs.392339

201519_at		NM_014820	gb:NM_014820.1 /DEF=Homo sapiens translocase of outer mitochondrial membrane 70 (yeast) homolog A (TOMM70A), mRNA. /FEA=mRNA /GEN=TOMM70A /PROD=translocase of outer mitochondrial membrane 70(yeast) homolog A /DB_XREF=gi:7662672 /UG=Hs.21198 translocase of outer mitochondrial membrane 70 (yeast) homolog A /FL=gb:BC003633.1 gb:AB018262.1 gb:NM_014820.1		
201824_at		AB022663	gb:AB022663.1 /DEF=Homo sapiens HFB30 mRNA, complete cds. /FEA=mRNA /GEN=HFB30 /DB_XREF=gi:5019617 /UG=Hs.215857 ring finger protein 14 /FL=gb:AF060544.1 gb:NM_004290.1 gb:AB022663.1		
219540_at	ZNF267	AU150728	zinc finger protein 267		Hs.145498

201807_at		NM_004896	gb:NM_004896.1 /DEF=Homo sapiens vacuolar protein sorting 26 (yeast homolog) (VPS26), mRNA. /FEA=mRNA /GEN=VPS26 /PROD=vacuolar protein sorting 26 (yeast homolog) /DB_XREF=gi:4758509 /UG=Hs.67052 vacuolar protein sorting 26 (yeast homolog) /FL=gb:AF054179.1 gb:NM_004896.1 gb:AF175266.1		
206858_s_at		NM_004503	gb:NM_004503.1 /DEF=Homo sapiens homeo box C6 (HOXC6), mRNA. /FEA=mRNA /GEN=HOXC6 /PROD=homeo box C6 /DB_XREF=gi:4758553 /UG=Hs.820 homeo box C6 /FL=gb:NM_004503.1		

210993_s_at		U54826	gb:U54826.1 /DEF=Human mad-related protein MADR1 mRNA, complete cds. /FEA=mRNA /PROD=mad-related protein MADR1 /DB_XREF=gi:1332713 /UG=Hs.79067 MAD (mothers against decapentaplegic, Drosophila) homolog 1 /FL=gb:U54826.1 gb:U59912.1		
209099_x_at		U73936	gb:U73936.1 /DEF=Homo sapiens Jagged 1 (HJ1) mRNA, complete cds. /FEA=mRNA /GEN=HJ1 /PROD=Jagged 1 /DB_XREF=gi:1695273 /UG=Hs.91143 jagged 1 (Alagille syndrome) /FL=gb:U61276.1 gb:U73936.1 gb:AF003837.1 gb:AF028593.1 gb:NM_000214.1		
210944_s_at		BC003169	gb:BC003169.1 /DEF=Homo sapiens, Similar to calpain 3, (p94), clone MGC:4403, mRNA, complete cds. /FEA=mRNA /PROD=Similar to calpain 3, (p94) /DB_XREF=gi:13111992 /UG=Hs.40300 calpain 3, (p94) /FL=gb:BC003169.1		

216941_s_at		AK026521	Consensus includes gb:AK026521.1 /DEF=Homo sapiens cDNA: FLJ22868 fis, clone KAT02340, highly similar to HUMTFSL1C Homo sapiens transcription factor SL1 mRNA. /FEA=mRNA /DB_XREF=gi:10439398 /UG=Hs.121044 TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kD		
36030_at	DKFZP586I2223	AL080214	intermediate filament-like MGC:2625	NM_015438; NM_080730; NM_080731	Hs.408973
201736_s_at	TEB4	BF000409	similar to S. cerevisiae SSM4		Hs.380875
201752_s_at	ADD3	AI763123	adducin 3 (gamma)		Hs.98834
205554_s_at		NM_004944	gb:NM_004944.1 /DEF=Homo sapiens deoxyribonuclease I-like 3 (DNASE1L3), mRNA. /FEA=mRNA /GEN=DNASE1L3 /PROD=deoxyribonuclease I-like 3 /DB_XREF=gi:4826697 /UG=Hs.88646 deoxyribonuclease I-like 3 /FL=gb:U56814.1 gb:AF047354.1 gb:NM_004944.1		
213350_at	RPS11	BF680255	ribosomal protein S11		Hs.182740

202876_s_at		NM_002586	gb:NM_002586.1 /DEF=Homo sapiens pre-B-cell leukemia transcription factor 2 (PBX2), mRNA. /FEA=mRNA /GEN=PBX2 /PROD=pre-B-cell leukemia transcription factor 2 /DB_XREF=gi:4505624 /UG=Hs.93728 pre-B-cell leukemia transcription factor 2 /FL=gb:NM_002586.1		
214805_at		U79273	Consensus includes gb:U79273.1 /DEF=Human clone 23933 mRNA sequence. /FEA=mRNA /DB_XREF=gi:1710239 /UG=Hs.239483 Human clone 23933 mRNA sequence		
212535_at	MEF2A	AA142929	MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A)		Hs.277806
221865_at	DKFZp547P234	BF969986	hypothetical protein DKFZp547P234		Hs.170226

218957_s_at		NM_025155	gb:NM_025155.1 /DEF=Homo sapiens hypothetical protein FLJ11848 (FLJ11848), mRNA. /FEA=mRNA /GEN=FLJ11848 /PROD=hypothetical protein FLJ11848 /DB_XREF=gi:13376750 /UG=Hs.289031 hypothetical protein FLJ11848 /FL=gb:NM_025155.1		
218124_at		NM_017750	gb:NM_017750.1 /DEF=Homo sapiens hypothetical protein FLJ20296 (FLJ20296), mRNA. /FEA=mRNA /GEN=FLJ20296 /PROD=hypothetical protein FLJ20296 /DB_XREF=gi:8923274 /UG=Hs.6603 hypothetical protein FLJ20296 /FL=gb:NM_017750.1		

205511_at		NM_017976	gb:NM_017976.1 /DEF=Homo sapiens hypothetical protein FLJ10038 (FLJ10038), mRNA. /FEA=mRNA /GEN=FLJ10038 /PROD=hypothetical protein FLJ10038 /DB_XREF=gi:8922197 /UG=Hs.181202 hypothetical protein FLJ10038 /FL=gb:NM_017976.1		
221617_at		AF077053	Consensus includes gb:AF077053.1 /DEF=Homo sapiens neuronal cell death-related protein mRNA, complete cds. /FEA=mRNA /PROD=neuronal cell death-related protein /DB_XREF=gi:4689153 /UG=Hs.171723 neuronal cell death-related protein /FL=gb:AF077053.1 gb:NM_015975.1 gb:AF220509.1		
221922_at	MCLC	AW195581	Mid-1-related chloride channel 1		Hs.93121

209317_at		AF008442	gb:AF008442.1 /DEF=Homo sapiens RNA polymerase I subunit hRPA39 mRNA, complete cds. /FEA=mRNA /PROD=RNA polymerase I subunit hRPA39 /DB_XREF=gi:2266928 /UG=Hs.5409 RNA polymerase I subunit /FL=gb:AF008442.1		
205711_x_at		NM_005174	gb:NM_005174.1 /DEF=Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1 (ATP5C1), mRNA. /FEA=mRNA /GEN=ATP5C1 /PROD=ATP synthase, H+ transporting, mitochondrial F1complex, gamma polypeptide 1 /DB_XREF=gi:4885078 /UG=Hs.155433 ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1 /FL=gb:D16563.1 gb:NM_005174.1		

218937_at		NM_017810	gb:NM_017810.1 /DEF=Homo sapiens hypothetical protein FLJ20417 (FLJ20417), mRNA. /FEA=mRNA /GEN=FLJ20417 /PROD=hypothetical protein FLJ20417 /DB_XREF=gi:8923385 /UG=Hs.10710 hypothetical protein FLJ20417 /FL=gb:NM_017810.1		
221731_x_at		J02814	Consensus includes gb:BF218922 /FEA=EST /DB_XREF=gi:11112418 /DB_XREF=est:601885091F1 /CLONE=IMAGE:4103447 /UG=Hs.81800 chondroitin sulfate proteoglycan 2 (versican)		
214695_at	NICE-4	AW051361	NICE-4 protein		Hs.8127
221745_at		AK026008	Consensus includes gb:BE538424 /FEA=EST /DB_XREF=gi:9767069 /DB_XREF=est:601068256F1 /CLONE=IMAGE:3454693 /UG=Hs.288283 Homo sapiens cDNA: FLJ22355 fis, clone HRC06344		

202656_s_at	TRIP-Br2	BG107456	transcriptional regulator interacting with the PHS-bromodomain 2		Hs.77293
209508_x_at		AF005774	gb:AF005774.1 /DEF=Homo sapiens caspase-like apoptosis regulatory protein (clarp) mRNA, alternatively spliced, complete cds. /FEA=mRNA /GEN=clarp /PROD=caspase-like apoptosis regulatory protein /DB_XREF=gi:2286144 /UG=Hs.195175 CASP8 and FADD-like apoptosis regulator /FL=gb:BC001602.1 gb:U97074.1 gb:AF010127.1 gb:AF005774.1 gb:AF009618.1 gb:U85059.1 gb:AF041458.1 gb:AF041460.1		

202529_at		NM_002766	gb:NM_002766.1 /DEF=Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 1 (PRPSAP1), mRNA. /FEA=mRNA /GEN=PRPSAP1 /PROD=phosphoribosyl pyrophosphatesynthetase-associated protein 1 /DB_XREF=gi:4506130 /UG=Hs.77498 phosphoribosyl pyrophosphate synthetase-associated protein 1 /FL=gb:D61391.1 gb:NM_002766.1		
213344_s_at	H2AFX	H51429	H2A histone family, member X		Hs.147097

209523_at		AK001618	Consensus includes gb:AK001618.1 /DEF=Homo sapiens cDNA FLJ10756 fis, clone NT2RP3004572, highly similar to Homo sapiens cofactor of initiator function mRNA. /FEA=mRNA /DB_XREF=gi:7022983 /UG=Hs.122752 TATA box binding protein (TBP)-associated factor, RNA polymerase II, B, 150kD /FL=gb:AF026445.1 gb:AF040701.1 gb:AF057694.1 gb:NM_003184.1		
202621_at		NM_001571	gb:NM_001571.1 /DEF=Homo sapiens interferon regulatory factor 3 (IRF3), mRNA. /FEA=mRNA /GEN=IRF3 /PROD=interferon regulatory factor 3 /DB_XREF=gi:4504724 /UG=Hs.75254 interferon regulatory factor 3 /FL=gb:NM_001571.1		

203169_at		NM_014785	gb:NM_014785.1 /DEF=Homo sapiens KIAA0258 gene product (KIAA0258), mRNA. /FEA=mRNA /GEN=KIAA0258 /PROD=KIAA0258 gene product /DB_XREF=gi:7662029 /UG=Hs.47313 KIAA0258 gene product /FL=gb:BC001725.1 gb:D87447.1 gb:NM_014785.1		
214193_s_at	DJ434O14.5	AI770084	novel putative protein similar to YIL091C yeast hypothetical 84 kD protein from SGA1-KTR7		Hs.194754
202211_at		BC005122	gb:BC005122.1 /DEF=Homo sapiens, ADP-ribosylation factor GTPase activating protein 1, clone MGC:10272, mRNA, complete cds. /FEA=mRNA /PROD=ADP-ribosylation factor GTPase activatingprotein 1 /DB_XREF=gi:13477296 /UG=Hs.13014 ADP-ribosylation factor GTPase activating protein 1 /FL=gb:BC005122.1 gb:AF111847.1 gb:NM_014570.1		

202215_s_at		NM_014223	gb:NM_014223.2 /DEF=Homo sapiens nuclear transcription factor Y, gamma (NFYC), mRNA. /FEA=mRNA /GEN=NFYC /PROD=nuclear transcription factor Y, gamma /DB_XREF=gi:11496977 /UG=Hs.168157 nuclear transcription factor Y, gamma /FL=gb:NM_014223.2 gb:D85425.1 gb:BC005003.1 gb:D89986.1		
202165_at		NM_006241	Consensus includes gb:BF966540 /FEA=EST /DB_XREF=gi:12333755 /DB_XREF=est:602287009T1 /CLONE=IMAGE:4375586 /UG=Hs.267819 protein phosphatase 1, regulatory (inhibitor) subunit 2 /FL=gb:NM_006241.1		

203136_at		NM_006423	gb:NM_006423.1 /DEF=Homo sapiens Rab acceptor 1 (prenylated) (RABAC1), mRNA. /FEA=mRNA /GEN=RABAC1 /PROD=Rab acceptor 1 (prenylated) /DB_XREF=gi:5453959 /UG=Hs.11417 Rab acceptor 1 (prenylated) /FL=gb:NM_006423.1 gb:AF112202.1		
208003_s_at		NM_006599	gb:NM_006599.1 /DEF=Homo sapiens nuclear factor of activated T-cells 5, tonicity-resonsive (NFAT5), mRNA. /FEA=mRNA /GEN=NFAT5 /PROD=nuclear factor of activated T-cells 5,tonicity-resonsive /DB_XREF=gi:5729944 /UG=Hs.86998 nuclear factor of activated T-cells 5, tonicity-responsive /FL=gb:AB020634.1 gb:AF163836.1 gb:NM_006599.1		

202113_s_at		AF043453	gb:AF043453.1 /DEF=Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds. /FEA=mRNA /GEN=SNX2 /PROD=sorting nexin 2 /DB_XREF=gi:2827433 /UG=Hs.11183 sorting nexin 2 /FL=gb:BC003382.1 gb:AF043453.1 gb:AF065482.1 gb:NM_003100.1		
202069_s_at	BG1	AI826060	lipidosin		Hs.277543
213217_at	ADCY2	AU149572	adenylate cyclase 2 (brain)		Hs.2352
209620_s_at		AB005289	gb:AB005289.1 /DEF=Homo sapiens mRNA for ABC transporter 7 protein, complete cds. /FEA=mRNA /GEN=hABC7 /PROD=ABC transporter 7 protein /DB_XREF=gi:3228278 /UG=Hs.125856 ATP-binding cassette, sub-family B (MDRTAP), member 7 /FL=gb:AB005289.1 gb:AF038950.1 gb:AF133659.1 gb:NM_004299.2		

202979_s_at		NM_021212	gb:NM_021212.1 /DEF=Homo sapiens HCF-binding transcription factor Zhangfei (ZF), mRNA. /FEA=mRNA /GEN=ZF /PROD=HCF-binding transcription factor Zhangfei /DB_XREF=gi:10864024 /UG=Hs.29417 HCF-binding transcription factor Zhangfei /FL=gb:NM_021212.1 gb:AF039942.1		
208073_x_at		NM_003316	gb:NM_003316.1 /DEF=Homo sapiens tetratricopeptide repeat domain 3 (TTC3), mRNA. /FEA=mRNA /GEN=TTC3 /PROD=tetratricopeptide repeat domain 3 /DB_XREF=gi:10835036 /UG=Hs.118174 tetratricopeptide repeat domain 3 /FL=gb:NM_003316.1 gb:D84295.1		

208216_at		NM_001934	gb:NM_001934.1 /DEF=Homo sapiens distal-less homeobox 4 (DLX4), mRNA. /FEA=mRNA /GEN=DLX4 /PROD=distal-less homeobox 4 /DB_XREF=gi:4503342 /UG=Hs.172648 distal-less homeobox 4 /FL=gb:U73328.1 gb:NM_001934.1		
214934_at	ATP9B	AW411030	ATPase, Class II, type 9B		Hs.91471
214749_s_at		AK000818	Consensus includes gb:AK000818.1 /DEF=Homo sapiens cDNA FLJ20811 fis, clone ADSE01435. /FEA=mRNA /DB_XREF=gi:7021128 /UG=Hs.83530 hypothetical protein		
208424_s_at		NM_020313	gb:NM_020313.1 /DEF=Homo sapiens hypothetical protein (LOC57019), mRNA. /FEA=mRNA /GEN=LOC57019 /PROD=hypothetical protein /DB_XREF=gi:10092672 /UG=Hs.4900 hypothetical protein /FL=gb:NM_020313.1		

209610_s_at	SLC1A4	BF340083	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4		Hs.323878
203046_s_at		NM_003920	gb:NM_003920.1 /DEF=Homo sapiens timeless (Drosophila) homolog (TIMELESS), mRNA. /FEA=mRNA /GEN=TIMELESS /PROD=timeless (Drosophila) homolog /DB_XREF=gi:4507506 /UG=Hs.118631 timeless (Drosophila) homolog /FL=gb:AF098162.1 gb:AB015597.1 gb:NM_003920.1		
219854_at		NM_021030	gb:NM_021030.1 /DEF=Homo sapiens zinc finger protein 14 (KOX 6) (ZNF14), mRNA. /FEA=mRNA /GEN=ZNF14 /PROD=zinc finger protein 14 (KOX 6) /DB_XREF=gi:11139306 /UG=Hs.197219 zinc finger protein 14 (KOX 6) /FL=gb:NM_021030.1 gb:AB021644.1		
212699_at	SCAMP5	BE222801	secretory carrier membrane protein 5		Hs.7934

222028_at	ZNF45	AI967981	zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)		Hs.41728
214319_at		W58342	Homo sapiens cDNA FLJ34103 fis, clone FCBBF3007859, moderately similar to Human putative protein B2 mRNA		Hs.406809
213436_at	CNR1; CB1; CB-R; CB1A; CANN6; CB1K5	U73304	G protein-coupled receptor; Human CB1 cannabinoid receptor (CNR1) gene, complete cds.	NM_001840; NM_016083; NM_033181	
208881_x_at		BC005247	gb:BC005247.1 /DEF=Homo sapiens, isopentenyl-diphosphate delta isomerase, clone MGC:12281, mRNA, complete cds. /FEA=mRNA /PROD=isopentenyl-diphosphate delta isomerase /DB_XREF=gi:13528899 /UG=Hs.76038 isopentenyl-diphosphate delta isomerase /FL=gb:BC005247.1		

200886_s_at		NM_002629	gb:NM_002629.1 /DEF=Homo sapiens phosphoglycerate mutase 1 (brain) (PGAM1), mRNA. /FEA=mRNA /GEN=PGAM1 /PROD=phosphoglycerate mutase 1 (brain) /DB_XREF=gi:4505752 /UG=Hs.181013 phosphoglycerate mutase 1 (brain) /FL=gb:BC000455.1 gb:NM_002629.1 gb:J04173.1		
212018_s_at		AK025446	Consensus includes gb:AK000822.1 /DEF=Homo sapiens cDNA FLJ20815 fis, clone ADSE01038, highly similar to AJ007398 Homo sapiens mRNA for PBK1 protein. /FEA=mRNA /DB_XREF=gi:7021134 /UG=Hs.85963 DKFZP564M182 protein		

200800_s_at		NM_005345	gb:NM_005345.3 /DEF=Homo sapiens heat shock 70kD protein 1A (HSPA1A), mRNA. /FEA=mRNA /GEN=HSPA1A /PROD=heat shock 70kD protein 1A /DB_XREF=gi:5579469 /UG=Hs.8997 heat shock 70kD protein 1A /FL=gb:BC002453.1 gb:NM_005345.3		
204186_s_at	PPID	AI014573	peptidylprolyl isomerase D (cyclophilin D)		Hs.143482
204180_s_at		NM_014007	Consensus includes gb:AI745225 /FEA=EST /DB_XREF=gi:5113513 /DB_XREF=est:wg10d12.x1 /CLONE=IMAGE:2364695 /UG=Hs.127649 KIAA0414 protein /FL=gb:NM_014007.1		
212060_at		AB002330	Consensus includes gb:AU152088 /FEA=EST /DB_XREF=gi:11013609 /DB_XREF=est:AU152088 /CLONE=NT2RP3000162 /UG=Hs.7976 KIAA0332 protein		

64418_at		AI472320	ESTs, Weakly similar to I38022 hypothetical protein - human [H.sapiens]		Hs.48504
200857_s_at		NM_006311	gb:NM_006311.1 /DEF=Homo sapiens nuclear receptor co-repressor 1 (NCOR1), mRNA. /FEA=mRNA /GEN=NCOR1 /PROD=nuclear receptor co-repressor 1 /DB_XREF=gi:5454137 /UG=Hs.144904 nuclear receptor co-repressor 1 /FL=gb:AF044209.1 gb:NM_006311.1		
217925_s_at		NM_022758	gb:NM_022758.1 /DEF=Homo sapiens hypothetical protein FLJ22195 (FLJ22195), mRNA. /FEA=mRNA /GEN=FLJ22195 /PROD=hypothetical protein FLJ22195 /DB_XREF=gi:12232426 /UG=Hs.25999 hypothetical protein FLJ22195 /FL=gb:NM_022758.1		
208883_at	DD5	U69567	progestin induced protein		Hs.278428

217783_s_at		NM_016061	gb:NM_016061.1 /DEF=Homo sapiens CGI-127 protein (LOC51646), mRNA. /FEA=mRNA /GEN=LOC51646 /PROD=CGI-127 protein /DB_XREF=gi:7706340 /UG=Hs.184542 CGI-127 protein /FL=gb:BC000836.1 gb:AF151885.1 gb:NM_016061.1		
201023_at		NM_005642	gb:NM_005642.1 /DEF=Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, F, 55kD (TAF2F), mRNA. /FEA=mRNA /GEN=TAF2F /PROD=TATA box binding protein (TBP)-associatedfactor, RNA polymerase II, F, 55kD /DB_XREF=gi:5032148 /UG=Hs.155188 TATA box binding protein (TBP)-associated factor, RNA polymerase II, F, 55kD /FL=gb:NM_005642.1 gb:U18062.1		

205053_at		NM_000946	gb:NM_000946.1 /DEF=Homo sapiens primase, polypeptide 1 (49kD) (PRIM1), mRNA. /FEA=mRNA /GEN=PRIM1 /PROD=primase, polypeptide 1 (49kD) /DB_XREF=gi:4506050 /UG=Hs.82741 primase, polypeptide 1 (49kD) /FL=gb:BC005266.1 gb:NM_000946.1		
204038_s_at		NM_001401	gb:NM_001401.1 /DEF=Homo sapiens endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 (EDG2), mRNA. /FEA=mRNA /GEN=EDG2 /PROD=endothelial differentiation, lysophosphatidicacid G-protein-coupled receptor, 2 /DB_XREF=gi:4503456 /UG=Hs.75794 endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 /FL=gb:U78192.1 gb:U80811.1 gb:NM_001401.1		

207434_s_at		NM_021603	gb:NM_021603.1 /DEF=Homo sapiens FXYD domain-containing ion transport regulator 2 (FXYD2), transcript variant b, mRNA. /FEA=mRNA /GEN=FXYD2 /PROD=FXYD domain-containing ion transport regulator2, isoform 2 /DB_XREF=gi:11125763 /UG=Hs.19520 FXYD domain-containing ion transport regulator 2 /FL=gb:NM_021603.1 gb:BC005302.1		
200973_s_at		NM_005724	gb:NM_005724.1 /DEF=Homo sapiens tetraspan 3 (TSPAN-3), mRNA. /FEA=mRNA /GEN=TSPAN-3 /PROD=tetraspan 3 /DB_XREF=gi:5032200 /UG=Hs.100090 tetraspan 3 /FL=gb:BC000704.1 gb:BC004280.1 gb:AF054840.1 gb:NM_005724.1 gb:AF133423.1		

212008_at		D87684	Consensus includes gb:N29889 /FEA=EST /DB_XREF=gi:1148409 /DB_XREF=est:yy11e11.s1 /CLONE=IMAGE:270956 /UG=Hs.77495 UBX domain-containing 1		
51146_at	FLJ20477	AA203365	hypothetical protein FLJ20477		Hs.26994
219266_at		NM_021632	gb:NM_021632.1 /DEF=Homo sapiens zinc-finger protein ZBRK1 (ZBRK1), mRNA. /FEA=mRNA /GEN=ZBRK1 /PROD=zinc-finger protein ZBRK1 /DB_XREF=gi:11056003 /UG=Hs.130965 zinc-finger protein ZBRK1 /FL=gb:AF295096.1 gb:AF309561.1 gb:NM_021632.1		
204556_s_at	DZIP1	AL568422	zinc-finger protein DZIP1		Hs.60177
200630_x_at	SET	AV702810	SET translocation (myeloid leukemia-associated)		Hs.145279

217860_at		NM_004544	gb:NM_004544.1 /DEF=Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10 (42kD) (NDUFA10), mRNA. /FEA=mRNA /GEN=NDUFA10 /PROD=NADH dehydrogenase (ubiquinone) 1 alphasubcomplex, 10 (42kD) /DB_XREF=gi:4758767 /UG=Hs.198271 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10 (42kD) /FL=gb:BC003417.1 gb:AF087661.1 gb:NM_004544.1		
213650_at	GOLGIN-67	AW006438	golgin-67		Hs.182982

220287_at		NM_020249	gb:NM_020249.1 /DEF=Homo sapiens disintegrin metalloproteinase with thrombospondin repeats (ADAMTS9), mRNA. /FEA=mRNA /GEN=ADAMTS9 /PROD=a disintegrin and metalloproteinase withthrombospondin motifs-9 preproprotein /DB_XREF=gi:9910121 /UG=Hs.126855 disintegrin metalloproteinase with thrombospondin repeats /FL=gb:AF261918.1 gb:NM_020249.1		
208775_at		D89729	gb:D89729.1 /DEF=Homo sapiens mRNA for CRM1 protein, complete cds. /FEA=mRNA /PROD=CRM1 protein /DB_XREF=gi:2626839 /UG=Hs.79090 exportin 1 (CRM1, yeast, homolog) /FL=gb:D89729.1 gb:NM_003400.2		
213684_s_at	LIM	BF671400	LIM protein (similar to rat protein kinase C-binding enigma)		Hs.154103

212086_x_at		M13452	Consensus includes gb:AK026584.1 /DEF=Homo sapiens cDNA: FLJ22931 fis, clone KAT07501, highly similar to HSLAMAR Human mRNA for nuclear envelope protein lamin A precursor. /FEA=mRNA /DB_XREF=gi:10439468 /UG=Hs.77886 lamin AC		
204489_s_at		NM_000610	gb:NM_000610.1 /DEF=Homo sapiens CD44 antigen (homing function and Indian blood group system) (CD44), mRNA. /FEA=mRNA /GEN=CD44 /PROD=CD44 antigen (homing function and Indian bloodgroup system) /DB_XREF=gi:10835162 /UG=Hs.169610 CD44 antigen (homing function and Indian blood group system) /FL=gb:NM_000610.1 gb:U40373.1 gb:M59040.1 gb:M24915.1		

208734_x_at		M28213	gb:M28213.1 /DEF=Homo sapiens GTP-binding protein (RAB2) mRNA, complete cds. /FEA=mRNA /GEN=RAB2 /PROD=GTP-binding protein /DB_XREF=gi:550061 /UG=Hs.78305 RAB2, member RAS oncogene family /FL=gb:NM_002865.1 gb:M28213.1		
213572_s_at	SERPINB1	AI554300	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1		Hs.183583
200071_at	SPF30	BF224259	splicing factor 30, survival of motor neuron-related		Hs.79968
200060_s_at		BC001659	gb:BC001659.1 /DEF=Homo sapiens, RNA-binding protein S1, serine-rich domain, clone MGC:1125, mRNA, complete cds. /FEA=mRNA /PROD=RNA-binding protein S1, serine-rich domain /DB_XREF=gi:12804496 /UG=Hs.75104 RNA-binding protein S1, serine-rich domain /FL=gb:BC001659.1 gb:BC001838.1		

220261_s_at		NM_018106	gb:NM_018106.1 /DEF=Homo sapiens hypothetical protein FLJ10479 (FLJ10479), mRNA. /FEA=mRNA /GEN=FLJ10479 /PROD=hypothetical protein FLJ10479 /DB_XREF=gi:8922447 /UG=Hs.5268 hypothetical protein FLJ10479 /FL=gb:AL136674.1 gb:BC001239.1 gb:NM_018106.1		
200066_at		AF182645	gb:AF182645.1 /DEF=Homo sapiens chondrosarcoma-associated protein 2 (CSA2) mRNA, complete cds. /FEA=mRNA /GEN=CSA2 /PROD=chondrosarcoma-associated protein 2 /DB_XREF=gi:5901877 /UG=Hs.8024 IK cytokine, down-regulator of HLA II /FL=gb:NM_006083.2 gb:AF182645.1		

200754_x_at		NM_003016	gb:NM_003016.1 /DEF=Homo sapiens splicing factor, arginineserine-rich 2 (SFRS2), mRNA. /FEA=mRNA /GEN=SFRS2 /PROD=splicing factor, arginineserine-rich 2 /DB_XREF=gi:4506898 /UG=Hs.73965 splicing factor, arginineserine-rich 2 /FL=gb:BC000339.1 gb:BC001303.1 gb:M90104.1 gb:NM_003016.1		
218598_at		NM_021930	gb:NM_021930.1 /DEF=Homo sapiens hypothetical protein FLJ11785 (FLJ11785), mRNA. /FEA=mRNA /GEN=FLJ11785 /PROD=hypothetical protein FLJ11785 /DB_XREF=gi:11345465 /UG=Hs.44625 Rad50-interacting protein 1 /FL=gb:NM_021930.1 gb:AF317622.1		

200744_s_at		NM_002074	Consensus includes gb:AI741124 /FEA=EST /DB_XREF=gi:5109412 /DB_XREF=est:wg19c04.x1 /CLONE=IMAGE:2365542 /UG=Hs.215595 guanine nucleotide binding protein (G protein), beta polypeptide 1 /FL=gb:NM_002074.1 gb:BC004186.1		
65472_at		AI161338	qb80a04.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1706382 3' similar to TR:O21123 O21123 CYTOCHROME OXIDASE I ;, mRNA sequence.		
200770_s_at		J03202	gb:J03202.1 /DEF=Human laminin B2 chain mRNA, complete cds. /FEA=mRNA /GEN=LAMB2 /DB_XREF=gi:186916 /UG=Hs.214982 laminin, gamma 1 (formerly LAMB2) /FL=gb:J03202.1 gb:NM_002293.2		
54632_at	FLJ21877	AI286226	hypothetical protein FLJ21877		Hs.16063
217798_at	CNOT2	AI123426	CCR4-NOT transcription complex, subunit 2		Hs.239720

204353_s_at		BC002923	gb:BC002923.1 /DEF=Homo sapiens, clone MGC:10280, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:10280) /DB_XREF=gi:12804138 /UG=Hs.31968 DKFZP586D211 protein /FL=gb:BC002923.1 gb:NM_015450.1		
200704_at		AB034747	gb:AB034747.1 /DEF=Homo sapiens SIMPLE mRNA for small integral membrane protein of lysosomelate endosome, complete cds. /FEA=mRNA /GEN=SIMPLE /PROD=small integral membrane protein of lysosomelateendosome /DB_XREF=gi:12862475 /UG=Hs.76507 LPS-induced TNF-alpha factor /FL=gb:AB034747.1 gb:U77396.1 gb:AF010312.1 gb:NM_004862.1		

200693_at		NM_006826	gb:NM_006826.1 /DEF=Homo sapiens tyrosine 3-monooxygenasetryptophan 5-monooxygenase activation protein, theta polypeptide (YWHAQ), mRNA. /FEA=mRNA /GEN=YWHAQ /PROD=tyrosine 3-monooxygenasetryptophan5-monooxygenase activation protein, theta polypeptide /DB_XREF=gi:5803226 /UG=Hs.74405 tyrosine 3-monooxygenasetryptophan 5-monooxygenase activation protein, theta polypeptide /FL=gb:NM_006826.1		
217795_s_at	MGC3222	W74580	hypothetical protein MGC3222		Hs.323193

208810_at		AF080569	gb:AF080569.1 /DEF=Homo sapiens DnaJ-like 2 protein (HSJ2) mRNA, complete cds. /FEA=mRNA /GEN=HSJ2 /PROD=DnaJ-like 2 protein /DB_XREF=gi:4322314 /UG=Hs.181195 DnaJ (Hsp40) homolog, subfamily B, member 6 /FL=gb:AL136707.1 gb:BC000177.2 gb:AB014888.1 gb:AF080569.1 gb:NM_005494.1 gb:AF075601.1 gb:AF060703.1 gb:AB015799.1		
200712_s_at	MAPRE1	AI633566	microtubule-associated protein, RP/EB family, member 1		Hs.234279
200713_s_at		NM_012325	gb:NM_012325.1 /DEF=Homo sapiens microtubule-associated protein, RPEB family, member 1 (MAPRE1), mRNA. /FEA=mRNA /GEN=MAPRE1 /PROD=microtubule-associated protein, RPEB family,member 1 /DB_XREF=gi:6912493 /UG=Hs.234279 microtubule-associated protein, RPEB family, member 1 /FL=gb:NM_012325.1 gb:U24166.1		

211569_s_at		AF001903	gb:AF001903.1 /DEF=Human 3-hydroxyacyl-CoA dehydrogenase, isoform 2 mRNA, complete cds. /FEA=mRNA /PROD=3-hydroxyacyl-CoA dehydrogenase, isoform 2 /DB_XREF=gi:2078328 /UG=Hs.8110 L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain /FL=gb:AF001903.1		
207239_s_at		NM_006201	gb:NM_006201.1 /DEF=Homo sapiens PCTAIRE protein kinase 1 (PCTK1), mRNA. /FEA=mRNA /GEN=PCTK1 /PROD=PCTAIRE protein kinase 1 /DB_XREF=gi:5453859 /UG=Hs.171834 PCTAIRE protein kinase 1 /FL=gb:NM_006201.1		

208955_at		AB049113	gb:AB049113.1 /DEF=Homo sapiens DUT mRNA for dUTP pyrophosphatase, complete cds. /FEA=mRNA /GEN=DUT /PROD=dUTP pyrophosphatase /DB_XREF=gi:10257384 /UG=Hs.82113 dUTP pyrophosphatase /FL=gb:AB049113.1 gb:U31930.1 gb:U62891.1 gb:M89913.1 gb:NM_001948.1		
219599_at		NM_018507	gb:NM_018507.1 /DEF=Homo sapiens hypothetical protein PRO1843 (PRO1843), mRNA. /FEA=mRNA /GEN=PRO1843 /PROD=hypothetical protein PRO1843 /DB_XREF=gi:8924082 /UG=Hs.283330 hypothetical protein PRO1843 /FL=gb:AF119854.1 gb:NM_018507.1		

218532_s_at		NM_019000	gb:NM_019000.1 /DEF=Homo sapiens hypothetical protein (FLJ20152), mRNA. /FEA=mRNA /GEN=FLJ20152 /PROD=hypothetical protein /DB_XREF=gi:9506660 /UG=Hs.82273 hypothetical protein /FL=gb:NM_019000.1		
201210_at		NM_001356	gb:NM_001356.2 /DEF=Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide 3 (DDX3), transcript variant 2, mRNA. /FEA=mRNA /GEN=DDX3 /PROD=DEADH (Asp-Glu-Ala-AspHis) box polypeptide 3 /DB_XREF=gi:13514812 /UG=Hs.147916 DEADH (Asp-Glu-Ala-AspHis) box polypeptide 3 /FL=gb:NM_001356.2 gb:U50553.1 gb:AF000982.1 gb:AF061337.1		

218347_at		NM_018264	gb:NM_018264.1 /DEF=Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA. /FEA=mRNA /GEN=FLJ10900 /PROD=hypothetical protein FLJ10900 /DB_XREF=gi:8922751 /UG=Hs.16277 hypothetical protein FLJ10900 /FL=gb:NM_018264.1		
205100_at		NM_005110	gb:NM_005110.1 /DEF=Homo sapiens glutamine-fructose-6-phosphate transaminase 2 (GFPT2), mRNA. /FEA=mRNA /GEN=GFPT2 /PROD=glutamine-fructose-6-phosphate transaminase 2 /DB_XREF=gi:4826741 /UG=Hs.30332 glutamine-fructose-6-phosphate transaminase 2 /FL=gb:BC000012.1 gb:AB016789.1 gb:NM_005110.1		

218696_at		NM_004836	gb:NM_004836.1 /DEF=Homo sapiens eukaryotic translation initiation factor 2-alpha kinase 3 (EIF2AK3), mRNA. /FEA=mRNA /GEN=EIF2AK3 /PROD=eukaryotic translation initiation factor 2-alphakinase 3 /DB_XREF=gi:4758891 /UG=Hs.102506 eukaryotic translation initiation factor 2-alpha kinase 3 /FL=gb:AF110146.1 gb:NM_004836.1 gb:AF193339.1		
205091_x_at		NM_002907	gb:NM_002907.1 /DEF=Homo sapiens RecQ protein-like (DNA helicase Q1-like) (RECQL), mRNA. /FEA=mRNA /GEN=RECQL /PROD=RecQ protein-like (DNA helicase Q1-like) /DB_XREF=gi:4506468 /UG=Hs.235069 RecQ protein-like (DNA helicase Q1-like) /FL=gb:NM_002907.1 gb:L36140.1		

201403_s_at		NM_004528	gb:NM_004528.1 /DEF=Homo sapiens microsomal glutathione S-transferase 3 (MGST3), mRNA. /FEA=mRNA /GEN=MGST3 /PROD=microsomal glutathione S-transferase 3 /DB_XREF=gi:4758713 /UG=Hs.111811 microsomal glutathione S-transferase 3 /FL=gb:BC000505.1 gb:BC003034.1 gb:AF026977.1 gb:NM_004528.1		
211296_x_at		AB009010	gb:AB009010.1 /DEF=Homo sapiens mRNA for polyubiquitin UbC, complete cds. /FEA=mRNA /GEN=UbC1 /PROD=polyubiquitin UbC /DB_XREF=gi:2647407 /UG=Hs.183704 ubiquitin C /FL=gb:BC000449.1 gb:AB009010.1		
201381_x_at		AF057356	gb:AF057356.1 /DEF=Homo sapiens calcyclin binding protein mRNA, complete cds. /FEA=mRNA /PROD=calcyclin binding protein /DB_XREF=gi:3063652 /UG=Hs.27258 calcyclin binding protein /FL=gb:AF314752.1 gb:AF057356.1 gb:NM_014412.1		

43544_at	TRAP95	AA314406	thyroid hormone receptor-associated protein, 95-kD subunit		Hs.31659
211509_s_at		AB015639	gb:AB015639.1 /DEF=Homo sapiens ASY mRNA, complete cds. /FEA=mRNA /GEN=ASY /DB_XREF=gi:5821139 /UG=Hs.65450 reticulon 4 /FL=gb:AB015639.1		
201190_s_at	PITPN	H15647	phosphotidylinositol transfer protein		Hs.409367
201218_at		NM_001329	Consensus includes gb:N23018 /FEA=EST /DB_XREF=gi:1137168 /DB_XREF=est:yx65d12.s1 /CLONE=IMAGE:266615 /UG=Hs.171391 C-terminal binding protein 2 /FL=gb:AF016507.1 gb:NM_001329.1		

201272_at		NM_001628	gb:NM_001628.1 /DEF=Homo sapiens aldo-keto reductase family 1, member B1 (aldose reductase) (AKR1B1), mRNA. /FEA=mRNA /GEN=AKR1B1 /PROD=aldo-keto reductase family 1, member B1 (aldosereductase) /DB_XREF=gi:4502048 /UG=Hs.75313 aldo-keto reductase family 1, member B1 (aldose reductase) /FL=gb:BC000260.1 gb:BC005387.1 gb:J04795.1 gb:J05017.1 gb:J05474.1 gb:M34720.1 gb:NM_001628.1		
201245_s_at	FLJ20113	AL523776	hypothetical protein FLJ20113		Hs.108504

203961_at		AL157398	Consensus includes gb:AL157398 /DEF=Human DNA sequence from clone RP11-56H7 on chromosome 10. Contains ESTs, STSs and GSSs. Contains the gene for the nebulette protein (NEBL, actin-binding Z-disc protein) /FEA=mRNA_1 /DB_XREF=gi:10045326 /UG=Hs.5025 nebulette /FL=gb:NM_006393.1		
218552_at		NM_018281	gb:NM_018281.1 /DEF=Homo sapiens hypothetical protein FLJ10948 (FLJ10948), mRNA. /FEA=mRNA /GEN=FLJ10948 /PROD=hypothetical protein FLJ10948 /DB_XREF=gi:8922786 /UG=Hs.9670 hypothetical protein FLJ10948 /FL=gb:NM_018281.1		

218656_s_at		NM_005780	gb:NM_005780.1 /DEF=Homo sapiens lipoma HMGIC fusion partner (LHFP), mRNA. /FEA=mRNA /GEN=LHFP /PROD=lipoma HMGIC fusion partner /DB_XREF=gi:5031864 /UG=Hs.93765 lipoma HMGIC fusion partner /FL=gb:AF098807.1 gb:NM_005780.1		
213413_at		BG434174	ESTs, Weakly similar to PRO0478 protein [Homo sapiens] [H.sapiens]		Hs.409046
213916_at	ZNF20	AU154474	zinc finger protein 20 (KOX 13)		Hs.110956
218430_s_at		NM_022841	gb:NM_022841.1 /DEF=Homo sapiens hypothetical protein FLJ12994 (FLJ12994), mRNA. /FEA=mRNA /GEN=FLJ12994 /PROD=hypothetical protein FLJ12994 /DB_XREF=gi:12383091 /UG=Hs.126908 hypothetical protein FLJ12994 /FL=gb:NM_022841.1		

204879_at		NM_006474	gb:NM_006474.1 /DEF=Homo sapiens lung type-I cell membrane-associated glycoprotein (T1A-2), transcript variant 2, mRNA. /FEA=mRNA /GEN=T1A-2 /PROD=lung type-I cell membrane-associatedglycoprotein, isoform 2 precursor /DB_XREF=gi:5454097 /UG=Hs.135150 lung type-I cell membrane-associated glycoprotein /FL=gb:AF030428.1 gb:NM_006474.1		
213813_x_at		AI345238	ESTs, Highly similar to FRIL_HUMAN Ferritin light chain (Ferritin L subunit) [H.sapiens]		Hs.356834
205425_at		NM_005338	gb:NM_005338.3 /DEF=Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA. /FEA=mRNA /GEN=HIP1 /PROD=huntingtin interacting protein 1 /DB_XREF=gi:12545385 /UG=Hs.97206 huntingtin interacting protein 1 /FL=gb:NM_005338.3 gb:U79734.1		

214806_at		U90030	Consensus includes gb:U90030.1 /DEF=Homo sapiens bicaudal-D (BICD) mRNA, alternatively spliced, partial cds. /FEA=mRNA /GEN=BICD /PROD=bicaudal-D /DB_XREF=gi:2745977 /UG=Hs.164975 Bicaudal D (Drosophila) homolog 1		
201691_s_at		NM_005079	gb:NM_005079.1 /DEF=Homo sapiens tumor protein D52 (TPD52), mRNA. /FEA=mRNA /GEN=TPD52 /PROD=tumor protein D52 /DB_XREF=gi:4827037 /UG=Hs.2384 tumor protein D52 /FL=gb:NM_005079.1 gb:U18914.1		
213753_x_at		BF541557	ESTs, Highly similar to IF5A_HUMAN Initiation factor 5A (eIF-5A) (eIF-4D) (Rev-binding factor) [H.sapiens]		Hs.381005

220596_at		NM_015590	gb:NM_015590.1 /DEF=Homo sapiens DKFZP434F1735 protein (DKFZP434F1735), mRNA. /FEA=mRNA /GEN=DKFZP434F1735 /PROD=DKFZP434F1735 protein /DB_XREF=gi:7661571 /UG=Hs.306189 DKFZP434F1735 protein /FL=gb:NM_015590.1		
206608_s_at		NM_020366	gb:NM_020366.1 /DEF=Homo sapiens retinitis pigmentosa GTPase regulator interacting protein 1 (RPGRIP1), mRNA. /FEA=mRNA /GEN=RPGRIP1 /PROD=retinitis pigmentosa GTPase regulatorinteracting protein 1 /DB_XREF=gi:9966834 /UG=Hs.131917 retinitis pigmentosa GTPase regulator interacting protein 1 /FL=gb:AF260257.1 gb:AF227257.1 gb:NM_020366.1		

220542_s_at		NM_016583	gb:NM_016583.1 /DEF=Homo sapiens LUNX protein; PLUNC (palate lung and nasal epithelium clone); tracheal epithelium enriched protein (LOC51297), mRNA. /FEA=mRNA /GEN=LOC51297 /PROD=LUNX protein; PLUNC (palate lung and nasalepithelium clone); tracheal epithelium enriched protein /DB_XREF=gi:7706118 /UG=Hs.211092 LUNX protein; PLUNC (palate lung and nasal epithelium clone); tracheal epithelium enriched protein /FL=gb:AB024937.1 gb:NM_016583.1 gb:AF172993.1		
201655_s_at		M85289	gb:M85289.1 /DEF=Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds. /FEA=mRNA /GEN=HSPG2 /PROD=heparan sulfate proteoglycan /DB_XREF=gi:184426 /UG=Hs.211573 heparan sulfate proteoglycan 2 (perlecan) /FL=gb:M85289.1 gb:NM_005529.2		

221728_x_at		AK025198	Consensus includes gb:AA628440 /FEA=EST /DB_XREF=gi:2540827 /DB_XREF=est:af26f02.s1 /CLONE=IMAGE:1032795 /UG=Hs.83623 nuclear receptor subfamily 1, group I, member 3		
220241_at		NM_017905	gb:NM_017905.1 /DEF=Homo sapiens hypothetical protein FLJ20623 (FLJ20623), mRNA. /FEA=mRNA /GEN=FLJ20623 /PROD=hypothetical protein FLJ20623 /DB_XREF=gi:8923574 /UG=Hs.27337 hypothetical protein FLJ20623 /FL=gb:NM_017905.1		

219993_at		NM_022454	gb:NM_022454.1 /DEF=Homo sapiens hypothetical protein FLJ22252 similar to SRY-box containing gene 17 (FLJ22252), mRNA. /FEA=mRNA /GEN=FLJ22252 /PROD=hypothetical protein FLJ22252 similar to SRY-boxcontaining gene 17 /DB_XREF=gi:11967990 /UG=Hs.97984 hypothetical protein FLJ22252 similar to SRY-box containing gene 17 /FL=gb:NM_022454.1		
206003_at		NM_014645	gb:NM_014645.1 /DEF=Homo sapiens KIAA0635 gene product (KIAA0635), mRNA. /FEA=mRNA /GEN=KIAA0635 /PROD=KIAA0635 gene product /DB_XREF=gi:7662215 /UG=Hs.185091 KIAA0635 gene product /FL=gb:AB014535.1 gb:NM_014645.1		

209408_at		U63743	gb:U63743.1 /DEF=Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds. /FEA=mRNA /PROD=mitotic centromere-associated kinesin /DB_XREF=gi:1695881 /UG=Hs.69360 kinesin-like 6 (mitotic centromere-associated kinesin) /FL=gb:NM_006845.2 gb:U63743.1		
177_at	PLD1	U38545	phospholipase D1, phophatidylcholine-specific	NM_002662	Hs.82587
221335_x_at		NM_019108	gb:NM_019108.1 /DEF=Homo sapiens hypothetical protein F17127_1 (F17127_1), mRNA. /FEA=CDS /GEN=F17127_1 /PROD=hypothetical protein F17127_1 /DB_XREF=gi:10092658 /UG=Hs.10116 hypothetical protein F17127_1 /FL=gb:NM_019108.1		

205995_x_at		NM_014642	gb:NM_014642.1 /DEF=Homo sapiens KIAA0036 gene product (KIAA0036), mRNA. /FEA=mRNA /GEN=KIAA0036 /PROD=KIAA0036 gene product /DB_XREF=gi:7661875 /UG=Hs.169387 KIAA0036 gene product /FL=gb:D25278.1 gb:NM_014642.1		
205215_at		NM_007212	gb:NM_007212.1 /DEF=Homo sapiens ring finger protein 2 (RNF2), mRNA. /FEA=mRNA /GEN=RNF2 /PROD=ring finger protein 2 /DB_XREF=gi:6005746 /UG=Hs.124186 ring finger protein 2 /FL=gb:AF141327.1 gb:NM_007212.1		

201206_s_at		NM_004587	gb:NM_004587.1 /DEF=Homo sapiens ribosome binding protein 1 (dog 180kD homolog) (RRBP1), mRNA. /FEA=mRNA /GEN=RRBP1 /PROD=ribosome binding protein 1 /DB_XREF=gi:4759055 /UG=Hs.98614 ribosome binding protein 1 (dog 180kD homolog) /FL=gb:AF006751.1 gb:NM_004587.1		
218756_s_at		NM_024308	gb:NM_024308.1 /DEF=Homo sapiens hypothetical protein MGC4172 (MGC4172), mRNA. /FEA=mRNA /GEN=MGC4172 /PROD=hypothetical protein MGC4172 /DB_XREF=gi:13236541 /UG=Hs.8949 hypothetical protein MGC4172 /FL=gb:BC002731.1 gb:NM_024308.1		

204572_s_at		NM_006223	gb:NM_006223.1 /DEF=Homo sapiens protein (peptidyl-prolyl cistrans isomerase) NIMA-interacting, 4 (parvulin) (PIN4), mRNA. /FEA=mRNA /GEN=PIN4 /PROD=protein (peptidyl-prolyl cistrans isomerase)NIMA-interacting, 4 (parvulin) /DB_XREF=gi:5453901 /UG=Hs.11774 protein (peptidyl-prolyl cistrans isomerase) NIMA-interacting, 4 (parvulin) /FL=gb:BC005234.1 gb:AF143096.1 gb:AB009690.1 gb:NM_006223.1		
210117_at		AF311312	gb:AF311312.1 /DEF=Homo sapiens infertility-related sperm protein mRNA, complete cds. /FEA=mRNA /PROD=infertility-related sperm protein /DB_XREF=gi:10863767 /UG=Hs.153057 sperm associated antigen 1 /FL=gb:AF311312.1 gb:NM_003114.1		

204819_at		NM_004463	gb:NM_004463.1 /DEF=Homo sapiens faciogenital dysplasia (Aarskog-Scott syndrome) (FGD1), mRNA. /FEA=mRNA /GEN=FGD1 /PROD=faciogenital dysplasia protein /DB_XREF=gi:4758357 /UG=Hs.1572 faciogenital dysplasia (Aarskog-Scott syndrome) /FL=gb:NM_004463.1 gb:U11690.1		
202763_at		NM_004346	gb:NM_004346.1 /DEF=Homo sapiens caspase 3, apoptosis-related cysteine protease (CASP3), mRNA. /FEA=mRNA /GEN=CASP3 /PROD=caspase 3, apoptosis-related cysteine protease /DB_XREF=gi:4757911 /UG=Hs.74552 caspase 3, apoptosis-related cysteine protease /FL=gb:NM_004346.1 gb:U13737.1 gb:U13738.1 gb:U26943.1		
222341_x_at		AW973235	ESTs		Hs.293697

215293_s_at		AL049261	Consensus includes gb:AL049261.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564E053 (from clone DKFZp564E053). /FEA=mRNA /DB_XREF=gi:4500009 /UG=Hs.133968 FGF receptor activating protein 1		
203226_s_at	SAS	AL514076	sarcoma amplified sequence		Hs.50984
207780_at		NM_001340	gb:NM_001340.1 /DEF=Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA. /FEA=mRNA /GEN=CYLC2 /PROD=cylicin 2 /DB_XREF=gi:4557508 /UG=Hs.3232 cylicin, basic protein of sperm head cytoskeleton 2 /FL=gb:NM_001340.1		

208914_at		NM_015044	Consensus includes gb:BE646414 /FEA=EST /DB_XREF=gi:9970725 /DB_XREF=est:7e86d08.x1 /CLONE=IMAGE:3292047 /UG=Hs.155546 KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2 /FL=gb:AF190863.1 gb:AF233522.1 gb:AF165531.1 gb:NM_015044.1		
214920_at		R33964	ESTs, Weakly similar to T45117 hU1-70K protein (286 AA) [imported] human (fragment) [H.sapiens]		Hs.23799
214765_s_at		AK024677	Consensus includes gb:AK024677.1 /DEF=Homo sapiens cDNA: FLJ21024 fis, clone CAE06651, highly similar to HUMPLT Human LTR mRNA. /FEA=mRNA /DB_XREF=gi:10437016 /UG=Hs.264330 N-acylsphingosine amidohydrolase (acid ceramidase)-like		

201294_s_at		NM_015626	Consensus includes gb:N24643 /FEA=EST /DB_XREF=gi:1138793 /DB_XREF=est:yx89f11.s1 /CLONE=IMAGE:268941 /UG=Hs.187991 DKFZP564A122 protein /FL=gb:AF106684.1 gb:NM_015626.1		
205074_at		NM_003060	gb:NM_003060.1 /DEF=Homo sapiens solute carrier family 22 (organic cation transporter), member 5 (SLC22A5), mRNA. /FEA=mRNA /GEN=SLC22A5 /PROD=solute carrier family 22 (organic cationtransporter), member 5 /DB_XREF=gi:4507004 /UG=Hs.15813 solute carrier family 22 (organic cation transporter), member 5 /FL=gb:AB015050.1 gb:AF057164.1 gb:NM_003060.1		

203119_at		NM_024098	gb:NM_024098.1 /DEF=Homo sapiens hypothetical protein MGC2574 (MGC2574), mRNA. /FEA=mRNA /GEN=MGC2574 /PROD=hypothetical protein MGC2574 /DB_XREF=gi:13129103 /UG=Hs.4253 hypothetical protein MGC2574 /FL=gb:BC001378.1 gb:NM_024098.1		
217212_s_at		Z84723	Human DNA sequence from phage LAW2 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains Interleukin 9 receptor pseudogene.		
201085_s_at	SON	AA664291	SON DNA binding protein		Hs.92909
214060_at	SSBP1	BE220360	single-stranded DNA binding protein		Hs.923

217207_s_at		AK025267	Consensus includes gb:AK025267.1 /DEF=Homo sapiens cDNA: FLJ21614 fis, clone COL07391, highly similar to AB020625 Homo sapiens mRNA for butyrophilin like receptor. /FEA=mRNA /DB_XREF=gi:10437746 /UG=Hs.225949 butyrophilin-like 3		
208963_x_at	FADS1	BE540552	fatty acid desaturase 1		Hs.132898
201082_s_at		NM_004082	gb:NM_004082.2 /DEF=Homo sapiens dynactin 1 (p150, Glued (Drosophila) homolog) (DCTN1), transcript variant 1, mRNA. /FEA=mRNA /GEN=DCTN1 /PROD=dynactin 1, isoform 1 /DB_XREF=gi:13259509 /UG=Hs.74617 dynactin 1 (p150, Glued (Drosophila) homolog) /FL=gb:NM_023019.1 gb:NM_004082.2		

217253_at		L37198	Consensus includes gb:L37198.1 /DEF=Homo sapiens (clone B3B3E13) Huntingtons disease candidate region mRNA fragment. /FEA=mRNA /DB_XREF=gi:600519 /UG=Hs.233617 Homo sapiens (clone B3B3E13) Huntingtons disease candidate region mRNA fragment		
218766_s_at		NM_015836	gb:NM_015836.1 /DEF=Homo sapiens tryptophanyl tRNA synthetase 2 (mitochondrial) (WARS2), nuclear gene encoding mitochondrial protein, mRNA. /FEA=mRNA /GEN=WARS2 /PROD=tryptophanyl tRNA synthetase 2 (mitochondrial) /DB_XREF=gi:7710153 /UG=Hs.227274 tryptophanyl tRNA synthetase 2 (mitochondrial) /FL=gb:NM_015836.1		

209073_s_at		AF015040	gb:AF015040.1 /DEF=Homo sapiens NUMB protein (NUMB) mRNA, complete cds. /FEA=mRNA /GEN=NUMB /PROD=NUMB protein /DB_XREF=gi:4102704 /UG=Hs.78890 numb (Drosophila) homolog /FL=gb:AF015040.1 gb:AF108092.1 gb:AF171939.1		
37170_at	BIKE	AB015331	BMP-2 inducible kinase	NM_017593	Hs.198642
52837_at	KIAA1644	AL047020	KIAA1644 protein		Hs.6829
209431_s_at		AF254083	gb:AF254083.1 /DEF=Homo sapiens zinc finger sarcoma gene long A isoform (ZSG) mRNA, complete cds. /FEA=mRNA /GEN=ZSG /PROD=zinc finger sarcoma gene long A isoform /DB_XREF=gi:9954374 /UG=Hs.27801 zinc finger protein 278 /FL=gb:NM_014323.1 gb:AF254083.1		

209994_s_at		AF016535	gb:AF016535.1 /DEF=Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds. /FEA=mRNA /GEN=mdr1 /PROD=P-glycoprotein /DB_XREF=gi:2353263 /UG=Hs.21330 ATP-binding cassette, sub-family B (MDRTAP), member 1 /FL=gb:M14758.1 gb:AF016535.1 gb:NM_000927.2		
216210_x_at	HRIHFB2122	AA046650	Tara-like protein		Hs.40342
207338_s_at		NM_003454	gb:NM_003454.1 /DEF=Homo sapiens zinc finger protein 200 (ZNF200), mRNA. /FEA=mRNA /GEN=ZNF200 /PROD=zinc finger protein 200 /DB_XREF=gi:4508012 /UG=Hs.88219 zinc finger protein 200 /FL=gb:AF060866.1 gb:NM_003454.1		

218883_s_at		NM_024629	gb:NM_024629.1 /DEF=Homo sapiens hypothetical protein FLJ23468 (FLJ23468), mRNA. /FEA=mRNA /GEN=FLJ23468 /PROD=hypothetical protein FLJ23468 /DB_XREF=gi:13375855 /UG=Hs.38178 hypothetical protein FLJ23468 /FL=gb:NM_024629.1		
219354_at		NM_018316	gb:NM_018316.1 /DEF=Homo sapiens hypothetical protein FLJ11078 (FLJ11078), mRNA. /FEA=mRNA /GEN=FLJ11078 /PROD=hypothetical protein FLJ11078 /DB_XREF=gi:8922853 /UG=Hs.250632 hypothetical protein FLJ11078 /FL=gb:NM_018316.1		

215785_s_at		AL161999	Consensus includes gb:AL161999.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761H087 (from clone DKFZp761H087); partial cds. /FEA=mRNA /GEN=DKFZp761H087 /PROD=hypothetical protein /DB_XREF=gi:7328000 /UG=Hs.258503 p53 inducible protein		
209584_x_at		AF165520	gb:AF165520.1 /DEF=Homo sapiens phorbolin I protein (PBI) mRNA, complete cds. /FEA=mRNA /GEN=PBI /PROD=phorbolin I protein /DB_XREF=gi:9294746 /UG=Hs.8583 similar to APOBEC1 /FL=gb:AF165520.1		
214082_at		AW003516	ESTs, Moderately similar to cytokine receptor-like factor 2; cytokine receptor CRL2 precusor [Homo sapiens] [H.sapiens]		Hs.13503

211756_at		BC005961	gb:BC005961.1 /DEF=Homo sapiens, parathyroid hormone-like hormone, clone MGC:14611, mRNA, complete cds. /FEA=mRNA /PROD=parathyroid hormone-like hormone /DB_XREF=gi:13543620 /FL=gb:BC005961.1		
204762_s_at	GNAO1	BE670563	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O		Hs.296184
202688_at		NM_003810	gb:NM_003810.1 /DEF=Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10), mRNA. /FEA=mRNA /GEN=TNFSF10 /PROD=tumor necrosis factor (ligand) superfamily,member 10 /DB_XREF=gi:4507592 /UG=Hs.83429 tumor necrosis factor (ligand) superfamily, member 10 /FL=gb:U37518.1 gb:U57059.1 gb:NM_003810.1		
209163_at	CYB561	AL514271	cytochrome b-561		Hs.355264

213332_at		AL031290	Consensus includes gb:AL031290 /DEF=Human DNA sequence from clone 774I24 on chromosome 1q24.1-24.3 Contains protein similar to pregnancy-associated plasma protein A precursor neuronal migration protein astrotactin, ESTs, STS and GSS /FEA=mRNA_1 /DB_XREF=gi:3550114 /UG=Hs.9654 similar to pregnancy-associated plasma protein A precursor		
219818_s_at		NM_018025	gb:NM_018025.1 /DEF=Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA. /FEA=mRNA /GEN=FLJ10206 /PROD=hypothetical protein FLJ10206 /DB_XREF=gi:8922282 /UG=Hs.55014 hypothetical protein FLJ10206 /FL=gb:NM_018025.1		

220019_s_at		NM_005774	gb:NM_005774.1 /DEF=Homo sapiens zinc finger protein 255 (ZNF255), mRNA. /FEA=mRNA /GEN=ZNF255 /PROD=zinc finger protein 255 /DB_XREF=gi:5031614 /UG=Hs.181696 zinc finger protein 255 /FL=gb:AF067164.1 gb:NM_005774.1		
216288_at		AU159276	AU159276 THYRO1 Homo sapiens cDNA clone THYRO1001262 3', mRNA sequence.		
219736_at		NM_018700	gb:NM_018700.1 /DEF=Homo sapiens zinc-binding protein Rbcc728 (Rbcc728), mRNA. /FEA=mRNA /GEN=Rbcc728 /PROD=zinc-binding protein Rbcc728 /DB_XREF=gi:8924237 /UG=Hs.121429 zinc-binding protein Rbcc728 /FL=gb:NM_018700.1		
203213_at	CDC2	AL524035	cell division cycle 2, G1 to S and G2 to M		Hs.334562

202791_s_at		AK022669	Consensus includes gb:AK022669.1 /DEF=Homo sapiens cDNA FLJ12607 fis, clone NT2RM4001489, highly similar to Homo sapiens mRNA for KIAA0685 protein. /FEA=mRNA /DB_XREF=gi:10434196 /UG=Hs.296406 KIAA0685 gene product /FL=gb:AB014585.1 gb:NM_014678.1		
215916_at		AL157418	Consensus includes gb:AL157418.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761K18121 (from clone DKFZp761K18121). /FEA=mRNA /DB_XREF=gi:7018439 /UG=Hs.112028 MisshapenNIK-related kinase		

221155_x_at		NM_018603	gb:NM_018603.1 /DEF=Homo sapiens hypothetical protein PRO1496 (PRO1496), mRNA. /FEA=mRNA /GEN=PRO1496 /PROD=hypothetical protein PRO1496 /DB_XREF=gi:8924053 /UG=Hs.283617 hypothetical protein PRO1496 /FL=gb:AF116665.1 gb:NM_018603.1		
52255_s_at	COL5A3	AI984221	collagen, type V, alpha 3		Hs.235368
216175_at		AK025276	Consensus includes gb:AK025276.1 /DEF=Homo sapiens cDNA: FLJ21623 fis, clone COL07915. /FEA=mRNA /DB_XREF=gi:10437759 /UG=Hs.306791 Homo sapiens cDNA: FLJ21623 fis, clone COL07915		

213105_s_at		AL031709	Consensus includes gb:AI799802 /FEA=EST /DB_XREF=gi:5365274 /DB_XREF=est:wc43d09.x1 /CLONE=IMAGE:2321393 /UG=Hs.134846 Human DNA sequence from clone 316G12 on chromosome 16. Contains the gene for C2 domain protein KIAA0734, the gene for a novel protein similar to predicted yeast, worm and archae-bacterial proteins, a novel gene and the 3 part of the gene for a novel prot		
200720_s_at	ACTR1A	AL532341	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast)		Hs.153961

208299_at		NM_021096	gb:NM_021096.1 /DEF=Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA. /FEA=mRNA /GEN=CACNA1I /PROD=calcium channel, voltage-dependent, alpha 1Isubunit /DB_XREF=gi:10863882 /UG=Hs.125116 calcium channel, voltage-dependent, alpha 1I subunit /FL=gb:NM_021096.1 gb:AF129133.1		
205503_at		NM_005401	gb:NM_005401.1 /DEF=Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), mRNA. /FEA=mRNA /GEN=PTPN14 /PROD=protein tyrosine phosphatase, non-receptor type14 /DB_XREF=gi:4885566 /UG=Hs.159238 protein tyrosine phosphatase, non-receptor type 14 /FL=gb:NM_005401.1		
396_f_at	EPOR	X97671	erythropoietin receptor	NM_000121	Hs.127826

221815_at		BE671816	Homo sapiens, Similar to hypothetical protein PRO2831, clone MGC:23813 IMAGE:4273837, mRNA, complete cds		Hs.351935
220777_at		NM_022113	gb:NM_022113.1 /DEF=Homo sapiens kinesin family member 13A (KIF13A), mRNA. /FEA=mRNA /GEN=KIF13A /PROD=kinesin family member 13A /DB_XREF=gi:11545828 /UG=Hs.146286 kinesin family member 13A /FL=gb:NM_022113.1		
212997_s_at	TLK2	AU119586	tousled-like kinase 2		Hs.57553

205288_at		NM_003672	gb:NM_003672.1 /DEF=Homo sapiens CDC14 (cell division cycle 14, S. cerevisiae) homolog A (CDC14A), mRNA. /FEA=mRNA /GEN=CDC14A /PROD=CDC14 (cell division cycle 14, S. cerevisiae)homolog A /DB_XREF=gi:4502696 /UG=Hs.65993 CDC14 (cell division cycle 14, S. cerevisiae) homolog A /FL=gb:AF000367.1 gb:NM_003672.1 gb:AF122013.1		
209457_at		U16996	gb:U16996.1 /DEF=Human protein tyrosine phosphatase mRNA, complete cds. /FEA=mRNA /PROD=protein tyrosine phosphatase /DB_XREF=gi:642012 /UG=Hs.2128 dual specificity phosphatase 5 /FL=gb:NM_004419.2 gb:U16996.1 gb:U15932.2		

207571_x_at		NM_004848	gb:NM_004848.1 /DEF=Homo sapiens basement membrane-induced gene (ICB-1), mRNA. /FEA=mRNA /GEN=ICB-1 /PROD=basement membrane-induced gene /DB_XREF=gi:4758579 /UG=Hs.10649 basement membrane-induced gene /FL=gb:AF044896.1 gb:NM_004848.1		
222034_at	GNB2L1	AA443762	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1		Hs.5662
215651_at		AK026682	Consensus includes gb:AK026682.1 /DEF=Homo sapiens cDNA: FLJ23029 fis, clone LNG01883. /FEA=mRNA /DB_XREF=gi:10439589 /UG=Hs.306864 Homo sapiens cDNA: FLJ23029 fis, clone LNG01883		

219470_x_at		NM_019084	gb:NM_019084.1 /DEF=Homo sapiens hypothetical protein FLJ10895 (FLJ10895), mRNA. /FEA=mRNA /GEN=FLJ10895 /PROD=hypothetical protein FLJ10895 /DB_XREF=gi:9506628 /UG=Hs.281348 hypothetical protein FLJ10895 /FL=gb:NM_019084.1		
208911_s_at		M34055	gb:M34055.1 /DEF=Human pyruvate dehydrogenase E1-beta subunit mRNA, complete cds. /FEA=mRNA /GEN=PDHB /DB_XREF=gi:190791 /UG=Hs.979 pyruvate dehydrogenase (lipoamide) beta /FL=gb:BC000439.1 gb:BC001924.1 gb:J03576.1 gb:M34479.1 gb:M54788.1 gb:M34055.1 gb:NM_000925.1		

203970_s_at		NM_003630	gb:NM_003630.1 /DEF=Homo sapiens peroxisomal biogenesis factor 3 (PEX3), mRNA. /FEA=mRNA /GEN=PEX3 /PROD=peroxisomal biogenesis factor 3 /DB_XREF=gi:4505726 /UG=Hs.7277 peroxisomal biogenesis factor 3 /FL=gb:NM_003630.1 gb:AB035307.1		
204000_at		NM_016194	gb:NM_016194.1 /DEF=Homo sapiens hypothetical protein (DKFZp586O1922), mRNA. /FEA=mRNA /GEN=DKFZp586O1922 /PROD=hypothetical protein /DB_XREF=gi:7705366 /UG=Hs.155090 hypothetical protein /FL=gb:AL117471.1 gb:NM_016194.1		
203906_at	KIAA0763	AI652645	KIAA0763 gene product		Hs.409124
213398_s_at	HCDI	AI347090	HCDI protein		Hs.7911

201117_s_at		NM_001873	gb:NM_001873.1 /DEF=Homo sapiens carboxypeptidase E (CPE), mRNA. /FEA=mRNA /GEN=CPE /PROD=carboxypeptidase E precursor /DB_XREF=gi:4503008 /UG=Hs.75360 carboxypeptidase E /FL=gb:NM_001873.1		
207394_at		NM_003438	gb:NM_003438.1 /DEF=Homo sapiens zinc finger protein 137 (clone pHZ-30) (ZNF137), mRNA. /FEA=mRNA /GEN=ZNF137 /PROD=zinc finger protein 137 (clone pHZ-30) /DB_XREF=gi:4507988 /UG=Hs.151689 zinc finger protein 137 (clone pHZ-30) /FL=gb:NM_003438.1 gb:U09414.1		

208922_s_at		BC004904	gb:BC004904.1 /DEF=Homo sapiens, nuclear RNA export factor 1, clone MGC:4612, mRNA, complete cds. /FEA=mRNA /PROD=nuclear RNA export factor 1 /DB_XREF=gi:13436184 /UG=Hs.323502 nuclear RNA export factor 1 /FL=gb:BC004904.1 gb:U80073.1 gb:AF126246.1 gb:AF112880.1 gb:NM_006362.1		
211939_x_at		X74070	Consensus includes gb:X74070.1 /DEF=H.sapiens mRNA for transcription factor BTF 3. /FEA=mRNA /PROD=transcription factor BTF3 /DB_XREF=gi:395086 /UG=Hs.101025 basic transcription factor 3		

200912_s_at		NM_001967	gb:NM_001967.2 /DEF=Homo sapiens eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), mRNA. /FEA=mRNA /GEN=EIF4A2 /PROD=eukaryotic translation initiation factor 4A,isoform 2 /DB_XREF=gi:9945313 /UG=Hs.173912 eukaryotic translation initiation factor 4A, isoform 2 /FL=gb:D30655.1 gb:NM_001967.2		
208880_s_at		AB019219	gb:AB019219.1 /DEF=Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1Zer1 and Prp6. /FEA=mRNA /DB_XREF=gi:4164165 /UG=Hs.31334 putative mitochondrial outer membrane protein import receptor /FL=gb:BC001666.1 gb:AF026031.1 gb:AB019219.1 gb:NM_012469.1 gb:AF221842.1		

212037_at		Y09703	Consensus includes gb:BF508848 /FEA=EST /DB_XREF=gi:11592146 /DB_XREF=est:UI-H-BI4-aor-e-06-0-UI.s1 /CLONE=IMAGE:3085907 /UG=Hs.44499 pinin, desmosome associated protein		
205042_at		NM_005476	gb:NM_005476.2 /DEF=Homo sapiens UDP-N-acetylglucosamine-2-epimeraseN-acetylmannosamine kinase (GNE), mRNA. /FEA=mRNA /GEN=GNE /PROD=UDP-N-acetylglucosamine-2-epimeraseN-acetylmannosamine kinase /DB_XREF=gi:6382074 /UG=Hs.5920 UDP-N-acetylglucosamine-2-epimeraseN-acetylmannosamine kinase /FL=gb:AF051852.1 gb:AF155663.1 gb:NM_005476.2		

211959_at		L27560	Consensus includes gb:AW007532 /FEA=EST /DB_XREF=gi:5856310 /DB_XREF=est:ws52h07.x1 /CLONE=IMAGE:2500861 /UG=Hs.103391 Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA		
213982_s_at	KIAA0471	BG107203	KIAA0471 gene product		Hs.242271
203729_at		NM_001425	gb:NM_001425.1 /DEF=Homo sapiens epithelial membrane protein 3 (EMP3), mRNA. /FEA=mRNA /GEN=EMP3 /PROD=epithelial membrane protein 3 /DB_XREF=gi:4503562 /UG=Hs.9999 epithelial membrane protein 3 /FL=gb:U52101.1 gb:U87947.1 gb:NM_001425.1		
209007_s_at		AF267856	gb:AF267856.1 /DEF=Homo sapiens HT033 mRNA, complete cds. /FEA=mRNA /PROD=HT033 /DB_XREF=gi:12006038 /UG=Hs.8084 hypothetical protein dJ465N24.2.1 /FL=gb:AF247168.1 gb:AF267856.1		

207069_s_at		NM_005585	gb:NM_005585.1 /DEF=Homo sapiens MAD (mothers against decapentaplegic, Drosophila) homolog 6 (MADH6), mRNA. /FEA=mRNA /GEN=MADH6 /PROD=MAD (mothers against decapentaplegic,Drosophila) homolog 6 /DB_XREF=gi:5031898 /UG=Hs.153863 MAD (mothers against decapentaplegic, Drosophila) homolog 6 /FL=gb:U59914.1 gb:NM_005585.1		
39549_at	NPAS2	AI743090	neuronal PAS domain protein 2		Hs.321164
212328_at		AK027231	Consensus includes gb:AB029025.1 /DEF=Homo sapiens mRNA for KIAA1102 protein, partial cds. /FEA=mRNA /GEN=KIAA1102 /PROD=KIAA1102 protein /DB_XREF=gi:5689540 /UG=Hs.202949 KIAA1102 protein		

217225_x_at		AL512687	Consensus includes gb:AL512687.1 /DEF=Homo sapiens mRNA; cDNA DKFZp547A1913 (from clone DKFZp547A1913). /FEA=mRNA /GEN=DKFZp547A1913 /PROD=hypothetical protein /DB_XREF=gi:12224839 /UG=Hs.227823 pM5 protein		
201293_x_at		NM_021130	gb:NM_021130.1 /DEF=Homo sapiens peptidylprolyl isomerase A (cyclophilin A) (PPIA), mRNA. /FEA=mRNA /GEN=PPIA /PROD=peptidylprolyl isomerase A (cyclophilin A) /DB_XREF=gi:10863926 /UG=Hs.182937 peptidylprolyl isomerase A (cyclophilin A) /FL=gb:NM_021130.1 gb:BC000689.1 gb:BC005320.1		

221046_s_at		NM_014170	gb:NM_014170.1 /DEF=Homo sapiens HSPC135 protein (HSPC135), mRNA. /FEA=mRNA /GEN=HSPC135 /PROD=HSPC135 protein /DB_XREF=gi:7661795 /UG=Hs.127496 HSPC135 protein /FL=gb:AF161484.1 gb:NM_014170.1		
221104_s_at		NM_018376	gb:NM_018376.1 /DEF=Homo sapiens hypothetical protein FLJ11275 (FLJ11275), mRNA. /FEA=mRNA /GEN=FLJ11275 /PROD=hypothetical protein FLJ11275 /DB_XREF=gi:8922969 /UG=Hs.272248 hypothetical protein FLJ11275 /FL=gb:NM_018376.1		

209022_at		AK026678	Consensus includes gb:AK026678.1 /DEF=Homo sapiens cDNA: FLJ23025 fis, clone LNG01702, highly similar to HUMAUTOND Human autonomously replicating sequence (ARS) mRNA. /FEA=mRNA /DB_XREF=gi:10439584 /UG=Hs.8217 stromal antigen 2 /FL=gb:BC001765.1		
213918_s_at	IDN3	BF221673	IDN3 protein		Hs.225767
201173_x_at		NM_006600	gb:NM_006600.1 /DEF=Homo sapiens nuclear distribution gene C (A.nidulans) homolog (NUDC), mRNA. /FEA=mRNA /GEN=NUDC /PROD=nuclear distribution gene C (A.nidulans)homolog /DB_XREF=gi:5729952 /UG=Hs.263812 nuclear distribution gene C (A.nidulans) homolog /FL=gb:BC002399.1 gb:BC003132.1 gb:AB019408.1 gb:AF130736.1 gb:AF125465.1 gb:AF100760.1 gb:NM_006600.1		

203869_at		NM_022832	Consensus includes gb:AK024318.1 /DEF=Homo sapiens cDNA FLJ14256 fis, clone PLACE1000007, weakly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15). /FEA=mRNA /DB_XREF=gi:10436669 /UG=Hs.109268 hypothetical protein FLJ12552 /FL=gb:NM_022832.1		
201011_at		NM_002950	gb:NM_002950.1 /DEF=Homo sapiens ribophorin I (RPN1), mRNA. /FEA=mRNA /GEN=RPN1 /PROD=ribophorin I /DB_XREF=gi:4506674 /UG=Hs.2280 ribophorin I /FL=gb:NM_002950.1		
213951_s_at		BE964655	EST		Hs.385022
212289_at	KIAA0874	AW572909	KIAA0874 protein		Hs.27973
213931_at	ID2	AI819238	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein		Hs.180919

213666_at		AK026589	Consensus includes gb:AK026589.1 /DEF=Homo sapiens cDNA: FLJ22936 fis, clone KAT07936. /FEA=mRNA /DB_XREF=gi:10439473 /UG=Hs.90998 KIAA0128 protein; septin 2		
212887_at	SEC23A	AI753659	Sec23 homolog A (S. cerevisiae)		Hs.272927
200614_at		NM_004859	gb:NM_004859.1 /DEF=Homo sapiens clathrin, heavy polypeptide (Hc) (CLTC), mRNA. /FEA=mRNA /GEN=CLTC /PROD=clathrin heavy chain /DB_XREF=gi:4758011 /UG=Hs.178710 clathrin, heavy polypeptide (Hc) /FL=gb:D21260.1 gb:NM_004859.1		
207765_s_at		NM_025182	gb:NM_025182.1 /DEF=Homo sapiens hypothetical protein FLJ11560 (FLJ11560), mRNA. /FEA=mRNA /GEN=FLJ11560 /PROD=hypothetical protein FLJ11560 /DB_XREF=gi:13378154 /UG=Hs.301696 hypothetical protein FLJ11560 /FL=gb:NM_025182.1		

212944_at		AK024896	Consensus includes gb:AK024896.1 /DEF=Homo sapiens cDNA: FLJ21243 fis, clone COL01164. /FEA=mRNA /DB_XREF=gi:10437310 /UG=Hs.268016 Homo sapiens cDNA: FLJ21243 fis, clone COL01164		
213469_at		AV705244	ESTs, Weakly similar to hypothetical protein FLJ20234 [Homo sapiens] [H.sapiens]		Hs.409229
218589_at		NM_005767	gb:NM_005767.1 /DEF=Homo sapiens purinergic receptor (family A group 5) (P2Y5), mRNA. /FEA=mRNA /GEN=P2Y5 /PROD=purinergic receptor (family A group 5) /DB_XREF=gi:5031968 /UG=Hs.189999 purinergic receptor (family A group 5) /FL=gb:AF000546.1 gb:NM_005767.1		

204524_at		NM_002613	gb:NM_002613.1 /DEF=Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PDPK1), mRNA. /FEA=mRNA /GEN=PDPK1 /PROD=3-phosphoinositide dependent protein kinase-1 /DB_XREF=gi:4505694 /UG=Hs.154729 3-phosphoinositide dependent protein kinase-1 /FL=gb:AF017995.1 gb:NM_002613.1		
200627_at		BC003005	gb:BC003005.1 /DEF=Homo sapiens, unactive progesterone receptor, 23 kD, clone MGC:4004, mRNA, complete cds. /FEA=mRNA /PROD=unactive progesterone receptor, 23 kD /DB_XREF=gi:12804292 /UG=Hs.278270 unactive progesterone receptor, 23 kD /FL=gb:BC003005.1 gb:L24804.1 gb:NM_006601.1		

200640_at		NM_003406	gb:NM_003406.1 /DEF=Homo sapiens tyrosine 3-monooxygenasetryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ), mRNA. /FEA=mRNA /GEN=YWHAZ /PROD=tyrosine 3-monooxygenasetryptophan5-monooxygenase activation protein, zeta polypeptide /DB_XREF=gi:4507952 /UG=Hs.75103 tyrosine 3-monooxygenasetryptophan 5-monooxygenase activation protein, zeta polypeptide /FL=gb:BC003623.1 gb:M86400.1 gb:NM_003406.1 gb:U28964.1		
204714_s_at		NM_000130	gb:NM_000130.2 /DEF=Homo sapiens coagulation factor V (proaccelerin, labile factor) (F5), mRNA. /FEA=mRNA /GEN=F5 /PROD=coagulation factor V precursor /DB_XREF=gi:10518500 /UG=Hs.30054 coagulation factor V (proaccelerin, labile factor) /FL=gb:NM_000130.2 gb:M16967.1 gb:M14335.1		

217906_at		NM_014315	gb:NM_014315.1 /DEF=Homo sapiens host cell factor homolog (LCP), mRNA. /FEA=mRNA /GEN=LCP /PROD=host cell factor homolog /DB_XREF=gi:7657300 /UG=Hs.20597 host cell factor homolog /FL=gb:BC002335.1 gb:AF113131.1 gb:NM_014315.1 gb:AF244137.1		
218249_at		NM_022494	gb:NM_022494.1 /DEF=Homo sapiens hypothetical protein FLJ21952 (FLJ21952), mRNA. /FEA=mRNA /GEN=FLJ21952 /PROD=hypothetical protein FLJ21952 /DB_XREF=gi:11968052 /UG=Hs.22353 hypothetical protein FLJ21952 /FL=gb:NM_022494.1		

212158_at		J04621	Consensus includes gb:AL577322 /FEA=EST /DB_XREF=gi:12940338 /DB_XREF=est:AL577322 /CLONE=CS0DI085YI06 (3 prime) /UG=Hs.1501 syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)		
200594_x_at		NM_004501	gb:NM_004501.1 /DEF=Homo sapiens heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) (HNRPU), mRNA. /FEA=mRNA /GEN=HNRPU /PROD=heterogeneous nuclear ribonucleoprotein U(scaffold attachment factor A) /DB_XREF=gi:4758545 /UG=Hs.103804 heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) /FL=gb:BC003367.1 gb:BC003621.1 gb:NM_004501.1		

204640_s_at		NM_003563	gb:NM_003563.1 /DEF=Homo sapiens speckle-type POZ protein (SPOP), mRNA. /FEA=mRNA /GEN=SPOP /PROD=speckle-type POZ protein /DB_XREF=gi:4507182 /UG=Hs.129951 speckle-type POZ protein /FL=gb:BC003385.1 gb:NM_003563.1		
218258_at		NM_015972	gb:NM_015972.1 /DEF=Homo sapiens RNA polymerase I 16 kDa subunit (LOC51082), mRNA. /FEA=mRNA /GEN=LOC51082 /PROD=RNA polymerase I 16 kDa subunit /DB_XREF=gi:7705739 /UG=Hs.106127 RNA polymerase I 16 kDa subunit /FL=gb:BC000889.1 gb:AF077044.1 gb:NM_015972.1		
212875_s_at		AP001745	Consensus includes gb:AP001745 /DEF=Homo sapiens genomic DNA, chromosome 21q, section 89105 /FEA=mRNA_3 /DB_XREF=gi:7768737 /UG=Hs.16007 chromosome 21 open reading frame 25		

218610_s_at		NM_018340	gb:NM_018340.1 /DEF=Homo sapiens hypothetical protein FLJ11151 (FLJ11151), mRNA. /FEA=mRNA /GEN=FLJ11151 /PROD=hypothetical protein FLJ11151 /DB_XREF=gi:8922900 /UG=Hs.14992 hypothetical protein FLJ11151 /FL=gb:NM_018340.1		
220525_s_at		NM_012103	gb:NM_012103.1 /DEF=Homo sapiens ancient ubiquitous protein 1 (AUP1), mRNA. /FEA=mRNA /GEN=AUP1 /PROD=ancient ubiquitous protein 1 /DB_XREF=gi:6912259 /UG=Hs.173736 ancient ubiquitous protein 1 /FL=gb:AF100754.1 gb:NM_012103.1		
65438_at	KIAA1609	AA195124	KIAA1609 protein		Hs.14449

204137_at		NM_003272	gb:NM_003272.1 /DEF=Homo sapiens transmembrane 7 superfamily member 1 (upregulated in kidney) (TM7SF1), mRNA. /FEA=mRNA /GEN=TM7SF1 /PROD=transmembrane 7 superfamily member 1(upregulated in kidney) /DB_XREF=gi:4507544 /UG=Hs.15791 transmembrane 7 superfamily member 1 (upregulated in kidney) /FL=gb:AF027826.1 gb:NM_003272.1		
212221_x_at		AL117536	Consensus includes gb:AV703259 /FEA=EST /DB_XREF=gi:10720588 /DB_XREF=est:AV703259 /CLONE=ADBCRE12 /UG=Hs.303154 popeye protein 3		

204354_at		NM_015450	gb:NM_015450.1 /DEF=Homo sapiens DKFZP586D211 protein (DKFZP586D211), mRNA. /FEA=mRNA /GEN=DKFZP586D211 /PROD=DKFZP586D211 protein /DB_XREF=gi:13123773 /UG=Hs.31968 DKFZP586D211 protein /FL=gb:BC002923.1 gb:NM_015450.1		
208795_s_at		D55716	gb:D55716.1 /DEF=Human mRNA for P1cdc47, complete cds. /FEA=mRNA /GEN=P1cdc47 /PROD=P1cdc47 /DB_XREF=gi:1255616 /UG=Hs.77152 minichromosome maintenance deficient (S. cerevisiae) 7 /FL=gb:D55716.1		

217835_x_at		NM_018840	gb:NM_018840.1 /DEF=Homo sapiens putative Rab5-interacting protein (LOC55969), mRNA. /FEA=mRNA /GEN=LOC55969 /PROD=putative Rab5-interacting protein /DB_XREF=gi:10047115 /UG=Hs.184062 putative Rab5-interacting protein /FL=gb:NM_018840.1 gb:AF274936.1 gb:AF112213.1		
218593_at		NM_018077	gb:NM_018077.1 /DEF=Homo sapiens hypothetical protein FLJ10377 (FLJ10377), mRNA. /FEA=mRNA /GEN=FLJ10377 /PROD=hypothetical protein FLJ10377 /DB_XREF=gi:8922387 /UG=Hs.274263 hypothetical protein FLJ10377 /FL=gb:NM_018077.1		

217808_s_at		NM_024117	gb:NM_024117.1 /DEF=Homo sapiens hypothetical protein MGC2745 (MGC2745), mRNA. /FEA=mRNA /GEN=MGC2745 /PROD=hypothetical protein MGC2745 /DB_XREF=gi:13129137 /UG=Hs.324178 hypothetical protein MGC2745 /FL=gb:BC002326.1 gb:BC003044.1 gb:NM_024117.1		
213062_at		AA643304	Homo sapiens, Similar to N-terminal Asn amidase, clone MGC:29626 IMAGE:4872717, mRNA, complete cds		Hs.351573
218875_s_at		NM_012177	gb:NM_012177.1 /DEF=Homo sapiens F-box only protein 5 (FBXO5), mRNA. /FEA=mRNA /GEN=FBXO5 /PROD=F-box only protein 5 /DB_XREF=gi:6912365 /UG=Hs.272027 F-box only protein 5 /FL=gb:AF129535.1 gb:NM_012177.1		
212684_at	ZNF3	AI752257	zinc finger protein 3 (A8-51)		Hs.155470

202365_at		BC004815	gb:BC004815.1 /DEF=Homo sapiens, clone MGC:5139, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:5139) /DB_XREF=gi:13435956 /UG=Hs.127610 acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain /FL=gb:BC004815.1 gb:M26393.1 gb:NM_000017.1		
214328_s_at	HSPCA	R01140	heat shock 90kDa protein 1, alpha		Hs.289088
221667_s_at		AF133207	gb:AF133207.1 /DEF=Homo sapiens protein kinase (H11) mRNA, complete cds. /FEA=mRNA /GEN=H11 /PROD=protein kinase /DB_XREF=gi:5901654 /UG=Hs.111676 protein kinase H11; small stress protein-like protein HSP22 /FL=gb:AF133207.1		

202348_s_at		BC000674	gb:BC000674.1 /DEF=Homo sapiens, dystonia 1, torsion (autosomal dominant; torsin A), clone MGC:1558, mRNA, complete cds. /FEA=mRNA /PROD=dystonia 1, torsion (autosomal dominant; torsinA) /DB_XREF=gi:12653776 /UG=Hs.19261 dystonia 1, torsion (autosomal dominant; torsin A) /FL=gb:BC000674.1 gb:AF007871.1 gb:NM_000113.1		
221984_s_at	MGC3035	AL040896	hypothetical protein MGC3035		Hs.22412
202975_s_at	RHOBTB3	N21138	Rho-related BTB domain containing 3		Hs.10432
218448_at		NM_017896	gb:NM_017896.1 /DEF=Homo sapiens hypothetical protein FLJ20602 (FLJ20602), mRNA. /FEA=mRNA /GEN=FLJ20602 /PROD=hypothetical protein FLJ20602 /DB_XREF=gi:8923556 /UG=Hs.103808 hypothetical protein FLJ20602 /FL=gb:NM_017896.1		

202168_at		NM_003187	gb:NM_003187.1 /DEF=Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, G, 32kD (TAF2G), mRNA. /FEA=mRNA /GEN=TAF2G /PROD=TATA box binding protein (TBP)-associatedfactor, RNA polymerase II, G, 32kD /DB_XREF=gi:4507350 /UG=Hs.60679 TATA box binding protein (TBP)-associated factor, RNA polymerase II, G, 32kD /FL=gb:BC003400.1 gb:NM_003187.1 gb:U21858.1 gb:U25112.1 gb:U30504.1		
209227_at	N33	AU158251	Putative prostate cancer tumor suppressor		Hs.71119

209212_s_at		AB030824	gb:AB030824.1 /DEF=Homo sapiens mRNA for transcription factor BTEB2, complete cds. /FEA=mRNA /GEN=bteb2 /PROD=transcription factor BTEB2 /DB_XREF=gi:8272417 /UG=Hs.84728 Kruppel-like factor 5 (intestinal) /FL=gb:D14520.1 gb:NM_001730.1 gb:AF132818.1 gb:AB030824.1 gb:AF287272.1		
218133_s_at		NM_021824	gb:NM_021824.1 /DEF=Homo sapiens NIF3 (Ngg1 interacting factor 3, S.pombe homolog)-like 1 (NIF3L1), mRNA. /FEA=mRNA /GEN=NIF3L1 /PROD=NIF3 (Ngg1 interacting factor 3, S.pombehomolog)-like 1 /DB_XREF=gi:11141898 /UG=Hs.21943 NIF3 (Ngg1 interacting factor 3, S.pombe homolog)-like 1 /FL=gb:AF182416.1 gb:NM_021824.1 gb:AF060513.1 gb:AB038949.1		
212689_s_at		AA524505	Human putative zinc finger protein mRNA		Hs.383008

202238_s_at		NM_006169	gb:NM_006169.1 /DEF=Homo sapiens nicotinamide N-methyltransferase (NNMT), mRNA. /FEA=mRNA /GEN=NNMT /PROD=nicotinamide N-methyltransferase /DB_XREF=gi:5453789 /UG=Hs.76669 nicotinamide N-methyltransferase /FL=gb:BC000234.1 gb:U08021.1 gb:NM_006169.1		
202596_at		BC000436	gb:BC000436.1 /DEF=Homo sapiens, endosulfine alpha, clone MGC:8394, mRNA, complete cds. /FEA=mRNA /PROD=endosulfine alpha /DB_XREF=gi:12653334 /UG=Hs.111680 endosulfine alpha /FL=gb:BC000436.1 gb:BC004461.1 gb:NM_004436.1 gb:AF157509.1		
221806_s_at	FLJ10707	BF590997	hypothetical protein FLJ10707		Hs.7187

202775_s_at		NM_004592	gb:NM_004592.1 /DEF=Homo sapiens splicing factor, arginineserine-rich 8 (suppressor-of-white-apricot, Drosophila homolog) (SFRS8), mRNA. /FEA=mRNA /GEN=SFRS8 /PROD=splicing factor, arginineserine-rich 8(suppressor-of-white-apricot, Drosophila homolog) /DB_XREF=gi:4759101 /UG=Hs.84229 splicing factor, arginineserine-rich 8 (suppressor-of-white-apricot, Drosophila homolog) /FL=gb:NM_004592.1 gb:U08377.1		

202501_at		NM_014268	gb:NM_014268.1 /DEF=Homo sapiens microtubule-associated protein, RPEB family, member 2 (MAPRE2), mRNA. /FEA=mRNA /GEN=MAPRE2 /PROD=microtubule associated protein, RPEB family,member 2 /DB_XREF=gi:10346134 /UG=Hs.78335 microtubule-associated protein, RPEB family, member 2 /FL=gb:NM_014268.1		
209386_at	TM4SF1	AI346835	transmembrane 4 superfamily member 1		Hs.351316
208315_x_at		NM_003300	gb:NM_003300.1 /DEF=Homo sapiens TNF receptor-associated factor 3 (TRAF3), mRNA. /FEA=mRNA /GEN=TRAF3 /PROD=TNF receptor-associated factor 3 /DB_XREF=gi:4507678 /UG=Hs.297660 TNF receptor-associated factor 3 /FL=gb:NM_003300.1 gb:U21092.1		

209413_at		BC002431	gb:BC002431.1 /DEF=Homo sapiens, Similar to UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2, clone MGC:2008, mRNA, complete cds. /FEA=mRNA /PROD=Similar to UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2 /DB_XREF=gi:12803236 /UG=Hs.206713 UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2 /FL=gb:BC002431.1 gb:AF038660.1 gb:NM_003780.1 gb:AB024434.1		
214700_x_at		AK000323	Consensus includes gb:AK000323.1 /DEF=Homo sapiens cDNA FLJ20316 fis, clone HEP07903, highly similar to U79263 Human clone 23760 mRNA. /FEA=mRNA /DB_XREF=gi:7020332 /UG=Hs.225841 DKFZP434D193 protein		
213318_s_at	APOM	BG028844	apolipoprotein M		Hs.274348

202693_s_at		NM_004760	Consensus includes gb:AW194730 /FEA=EST /DB_XREF=gi:6473630 /DB_XREF=est:xn43d11.x1 /CLONE=IMAGE:2696469 /UG=Hs.9075 serinethreonine kinase 17a (apoptosis-inducing) /FL=gb:AB011420.1 gb:NM_004760.1		
214919_s_at	FLJ20288	R39094	FLJ20288 protein		Hs.84045
221920_s_at	MSCP	BE677761	likely ortholog of mouse mitochondrial solute carrier protein		Hs.300496
218285_s_at		NM_020139	gb:NM_020139.1 /DEF=Homo sapiens oxidoreductase UCPA (LOC56898), mRNA. /FEA=mRNA /GEN=LOC56898 /PROD=oxidoreductase UCPA /DB_XREF=gi:10047131 /UG=Hs.124696 oxidoreductase UCPA /FL=gb:NM_020139.1 gb:AF164790.1		

202886_s_at		M65254	gb:M65254.1 /DEF=Protein phosphatase 2A 65 kDa regulatory subunit-beta mRNA, complete cds. /FEA=mRNA /GEN=SNRPEP1 /PROD=protein phosphatase-2A regulatory subunit-beta /DB_XREF=gi:189429 /UG=Hs.108705 protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform /FL=gb:NM_002716.1 gb:AF163473.1 gb:M65254.1 gb:AF087438.1		
218431_at		NM_022067	gb:NM_022067.1 /DEF=Homo sapiens hypothetical protein FLJ12707 (FLJ12707), mRNA. /FEA=mRNA /GEN=FLJ12707 /PROD=hypothetical protein FLJ12707 /DB_XREF=gi:11545778 /UG=Hs.16157 hypothetical protein FLJ12707 /FL=gb:NM_022067.1		

221669_s_at		BC001964	gb:BC001964.1 /DEF=Homo sapiens, acyl-Coenzyme A dehydrogenase family, member 8, clone MGC:4966, mRNA, complete cds. /FEA=mRNA /PROD=acyl-Coenzyme A dehydrogenase family, member 8 /DB_XREF=gi:12805020 /UG=Hs.14791 acyl Coenzyme A dehydrogenase family, member 8 /FL=gb:BC001964.1		
205523_at		U43328	gb:U43328.1 /DEF=Human link protein mRNA, complete cds. /FEA=mRNA /PROD=link protein /DB_XREF=gi:1151008 /UG=Hs.2799 cartilage linking protein 1 /FL=gb:U43328.1 gb:NM_001884.1		

202439_s_at		NM_000202	gb:NM_000202.2 /DEF=Homo sapiens iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 1, mRNA. /FEA=mRNA /GEN=IDS /PROD=iduronate-2-sulfatase isoform a precursor /DB_XREF=gi:5360215 /UG=Hs.172458 iduronate 2-sulfatase (Hunter syndrome) /FL=gb:M58342.1 gb:NM_000202.2		
221693_s_at		AB049952	gb:AB049952.1 /DEF=Homo sapiens MRPS18a mRNA for mitochondrial ribosomal protein S18a, complete cds. /FEA=mRNA /GEN=MRPS18a /PROD=mitochondrial ribosomal protein S18a /DB_XREF=gi:13620904 /FL=gb:AB049952.1		

202436_s_at		NM_000104	Consensus includes gb:AU144855 /FEA=EST /DB_XREF=gi:11006376 /DB_XREF=est:AU144855 /CLONE=HEMBA1003161 /UG=Hs.154654 cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) /FL=gb:NM_000104.2 gb:U03688.1		
202437_s_at		NM_000104	gb:NM_000104.2 /DEF=Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1), mRNA. /FEA=mRNA /GEN=CYP1B1 /PROD=cytochrome P450, subfamily I (dioxin-inducible),polypeptide 1 /DB_XREF=gi:13325059 /UG=Hs.154654 cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) /FL=gb:NM_000104.2 gb:U03688.1		

218482_at		NM_020189	gb:NM_020189.1 /DEF=Homo sapiens DC6 protein (DC6), mRNA. /FEA=mRNA /GEN=DC6 /PROD=DC6 protein /DB_XREF=gi:9910185 /UG=Hs.283740 DC6 protein /FL=gb:AF201940.1 gb:AF173296.1 gb:NM_020189.1		
201713_s_at		D42063	gb:D42063.1 /DEF=Human mRNA for RanBP2 (Ran-binding protein 2), complete cds. /FEA=mRNA /PROD=RanBP2 (Ran-binding protein 2) /DB_XREF=gi:924266 /UG=Hs.199179 RAN binding protein 2 /FL=gb:NM_006267.2 gb:D42063.1		
203511_s_at		AF041432	gb:AF041432.1 /DEF=Homo sapiens bet3 (BET3) mRNA, complete cds. /FEA=mRNA /GEN=BET3 /PROD=bet3 /DB_XREF=gi:2791803 /UG=Hs.288013 similar to yeast BET3 (S. cerevisiae) /FL=gb:AF041432.1 gb:NM_014408.1		

212793_at	DAAM2	BF513244	dishevelled associated activator of morphogenesis 2		Hs.387175
206744_s_at		NM_014242	gb:NM_014242.1 /DEF=Homo sapiens zinc finger protein 237 (ZNF237), mRNA. /FEA=mRNA /GEN=ZNF237 /PROD=zinc finger protein 237 /DB_XREF=gi:7657706 /UG=Hs.124386 zinc finger protein 237 /FL=gb:NM_014242.1		
212756_s_at	KIAA0349	AI761518	KIAA0349 protein		Hs.15303
209149_s_at	TM9SF1	BE899402	transmembrane 9 superfamily member 1		Hs.91586
201779_s_at		AF070558	gb:AF070558.1 /DEF=Homo sapiens clone 24450 RING zinc finger protein RZF mRNA, complete cds. /FEA=mRNA /PROD=RING zinc finger protein RZF /DB_XREF=gi:3387924 /UG=Hs.6900 ring finger protein 13 /FL=gb:AF037204.1 gb:AF070558.1 gb:NM_007282.1		

201753_s_at		NM_019903	gb:NM_019903.1 /DEF=Homo sapiens adducin 3 (gamma) (ADD3), transcript variant 2, mRNA. /FEA=mRNA /GEN=ADD3 /PROD=adducin 3, isoform b /DB_XREF=gi:9951926 /UG=Hs.324470 adducin 3 (gamma) /FL=gb:D67031.1 gb:NM_019903.1		
212796_s_at	KIAA1055	BF195608	KIAA1055 protein		Hs.126084
201443_s_at		AF248966	gb:AF248966.1 /DEF=Homo sapiens HT028 mRNA, complete cds. /FEA=mRNA /PROD=HT028 /DB_XREF=gi:12005668 /UG=Hs.183434 ATPase, H+ transporting, lysosomal (vacuolar proton pump) membrane sector associated protein M8-9 /FL=gb:AF248966.1 gb:NM_005765.1		

203620_s_at		NM_014824	gb:NM_014824.1 /DEF=Homo sapiens KIAA0769 gene product (KIAA0769), mRNA. /FEA=mRNA /GEN=KIAA0769 /PROD=KIAA0769 gene product /DB_XREF=gi:7662295 /UG=Hs.19056 KIAA0769 gene product /FL=gb:AB018312.1 gb:NM_014824.1		
203599_s_at		NM_007187	gb:NM_007187.2 /DEF=Homo sapiens WW domain binding protein 4 (formin binding protein 21) (WBP4), mRNA. /FEA=mRNA /GEN=WBP4 /PROD=WW domain-containing binding protein 4 /DB_XREF=gi:9943844 /UG=Hs.28307 WW domain binding protein 4 (formin binding protein 21) /FL=gb:AF071185.1 gb:NM_007187.2		

208625_s_at		AF104913	gb:AF104913.1 /DEF=Homo sapiens eukaryotic protein synthesis initiation factor mRNA, complete cds. /FEA=mRNA /PROD=eukaryotic protein synthesis initiation factor /DB_XREF=gi:3941723 /UG=Hs.211568 eukaryotic translation initiation factor 4 gamma, 1 /FL=gb:AF104913.1		
206766_at		AF112345	gb:AF112345.1 /DEF=Homo sapiens integrin alpha 10 subunit (ITGA10) mRNA, complete cds. /FEA=mRNA /GEN=ITGA10 /PROD=integrin alpha 10 subunit /DB_XREF=gi:6650627 /UG=Hs.158237 integrin, alpha 10 /FL=gb:AF074015.1 gb:NM_003637.2 gb:AF112345.1		

210962_s_at		AB019691	gb:AB019691.1 /DEF=Homo sapiens mRNA for Centrosome- and Golgi-localized PKN-associated protein (CG-NAP), complete cds. /FEA=mRNA /GEN=cg-nap /PROD=Centrosome- and Golgi-localized PKN-associatedprotein (CG-NAP) /DB_XREF=gi:5051742 /UG=Hs.58103 A kinase (PRKA) anchor protein (yotiao) 9 /FL=gb:AB019691.1		
34726_at	CACNB3	U07139	calcium channel, voltage-dependent, beta 3 subunit		Hs.250712
213101_s_at	ACTR3	Z78330	ARP3 actin-related protein 3 homolog (yeast)		Hs.5321
213015_at		BF448315	ESTs		Hs.171553

217995_at		NM_021199	gb:NM_021199.1 /DEF=Homo sapiens CGI-44 protein; sulfide dehydrogenase like (yeast) (CGI-44), mRNA. /FEA=mRNA /GEN=CGI-44 /PROD=CGI-44 protein; sulfide dehydrogenase like(yeast) /DB_XREF=gi:10864010 /UG=Hs.8185 CGI-44 protein; sulfide dehydrogenase like (yeast) /FL=gb:NM_021199.1 gb:AF151802.1 gb:AF118085.1		
210119_at		U73191	gb:U73191.1 /DEF=Human inward rectifier potassium channel (Kir1.3), complete cds. /FEA=mRNA /GEN=Kir1.3 /PROD=inward rectifier potassium channel /DB_XREF=gi:1765984 /UG=Hs.17287 potassium inwardly-rectifying channel, subfamily J, member 15 /FL=gb:U73191.1 gb:NM_002243.1		

219644_at		NM_016122	gb:NM_016122.1 /DEF=Homo sapiens NY-REN-58 antigen (LOC51134), mRNA. /FEA=mRNA /GEN=LOC51134 /PROD=NY-REN-58 antigen /DB_XREF=gi:7705838 /UG=Hs.56148 NY-REN-58 antigen /FL=gb:AF155115.1 gb:NM_016122.1		
219032_x_at		NM_014322	gb:NM_014322.1 /DEF=Homo sapiens opsin 3 (encephalopsin) (OPN3), mRNA. /FEA=mRNA /GEN=OPN3 /PROD=opsin 3 (encephalopsin) /DB_XREF=gi:7657070 /UG=Hs.279926 opsin 3 (encephalopsin) /FL=gb:AF140242.1 gb:NM_014322.1		

219064_at		NM_030569	gb:NM_030569.1 /DEF=Homo sapiens hypothetical protein MGC10848 (MGC10848), mRNA. /FEA=mRNA /GEN=MGC10848 /PROD=hypothetical protein MGC10848 /DB_XREF=gi:13386477 /UG=Hs.207443 hypothetical protein MGC10848 /FL=gb:BC004282.1 gb:NM_030569.1		
219015_s_at		NM_018466	gb:NM_018466.1 /DEF=Homo sapiens uncharacterized hematopoietic stemprogenitor cells protein MDS031 (MDS031), mRNA. /FEA=mRNA /GEN=MDS031 /PROD=uncharacterized hematopoietic stemprogenitorcells protein MDS031 /DB_XREF=gi:8923933 /UG=Hs.110853 uncharacterized hematopoietic stemprogenitor cells protein MDS031 /FL=gb:BC005336.1 gb:AF220051.1 gb:NM_018466.1		
203181_x_at	SRPK2	AW149364	SFRS protein kinase 2		Hs.78353

202157_s_at		U69546	gb:U69546.1 /DEF=Homo sapiens RNA-binding protein BRUNOL3 (BRUNOL3) mRNA, complete cds. /FEA=mRNA /GEN=BRUNOL3 /PROD=RNA-binding protein BRUNOL3 /DB_XREF=gi:1568642 /UG=Hs.211610 CUG triplet repeat, RNA-binding protein 2 /FL=gb:U69546.1 gb:AF036956.1 gb:AF090694.1 gb:NM_006561.1		
213253_at	SMC2L1	AU154486	SMC2 structural maintenance of chromosomes 2-like 1 (yeast)		Hs.381940
202022_at		NM_005165	gb:NM_005165.1 /DEF=Homo sapiens aldolase C, fructose-bisphosphate (ALDOC), mRNA. /FEA=mRNA /GEN=ALDOC /PROD=aldolase C, fructose-bisphosphate /DB_XREF=gi:4885062 /UG=Hs.155247 aldolase C, fructose-bisphosphate /FL=gb:BC003613.1 gb:AF054987.1 gb:NM_005165.1		

206015_s_at		NM_014947	gb:NM_014947.1 /DEF=Homo sapiens KIAA1041 protein (KIAA1041), mRNA. /FEA=mRNA /GEN=KIAA1041 /PROD=KIAA1041 protein /DB_XREF=gi:7662455 /UG=Hs.26023 KIAA1041 protein /FL=gb:AB028964.1 gb:NM_014947.1		
203211_s_at		AK027038	Consensus includes gb:AK027038.1 /DEF=Homo sapiens cDNA: FLJ23385 fis, clone HEP16802. /FEA=mRNA /DB_XREF=gi:10440053 /UG=Hs.181326 KIAA1073 protein /FL=gb:AB028996.1 gb:NM_016156.1		
221509_at		AB014731	gb:AB014731.1 /DEF=Homo sapiens mRNA for SMAP-3, complete cds. /FEA=mRNA /GEN=smap-3 /PROD=SMAP-3 /DB_XREF=gi:12248760 /UG=Hs.22393 density-regulated protein /FL=gb:AB014731.1		

203375_s_at		NM_003291	gb:NM_003291.1 /DEF=Homo sapiens tripeptidyl peptidase II (TPP2), mRNA. /FEA=mRNA /GEN=TPP2 /PROD=tripeptidyl peptidase II /DB_XREF=gi:4507656 /UG=Hs.1117 tripeptidyl peptidase II /FL=gb:M73047.1 gb:NM_003291.1		
201859_at		NM_002727	gb:NM_002727.1 /DEF=Homo sapiens proteoglycan 1, secretory granule (PRG1), mRNA. /FEA=mRNA /GEN=PRG1 /PROD=proteoglycan 1, secretory granule /DB_XREF=gi:4506044 /UG=Hs.1908 proteoglycan 1, secretory granule /FL=gb:J03223.1 gb:NM_002727.1		
212737_at	GM2A	AL513583	GM2 ganglioside activator protein		Hs.289082

206414_s_at		NM_003887	gb:NM_003887.1 /DEF=Homo sapiens development and differentiation enhancing factor 2 (DDEF2), mRNA. /FEA=mRNA /GEN=DDEF2 /PROD=ADP-ribosylation factorarf-directed GTPaseactivating protein /DB_XREF=gi:4502248 /UG=Hs.12802 development and differentiation enhancing factor 2 /FL=gb:AB007860.1 gb:NM_003887.1		
212388_at		AB028980	Consensus includes gb:AB028980.1 /DEF=Homo sapiens mRNA for KIAA1057 protein, partial cds. /FEA=mRNA /GEN=KIAA1057 /PROD=KIAA1057 protein /DB_XREF=gi:5689450 /UG=Hs.7243 ubiquitin specific protease 24		

219080_s_at		NM_019857	gb:NM_019857.1 /DEF=Homo sapiens CTP synthase II (CTPS2), mRNA. /FEA=mRNA /GEN=CTPS2 /PROD=CTP synthase II /DB_XREF=gi:9789918 /UG=Hs.58553 CTP synthase II /FL=gb:AF226667.1 gb:NM_019857.1		
218515_at		NM_016631	gb:NM_016631.1 /DEF=Homo sapiens hypothetical protein (LOC51325), mRNA. /FEA=mRNA /GEN=LOC51325 /PROD=hypothetical protein /DB_XREF=gi:7706175 /UG=Hs.26461 hypothetical protein /FL=gb:AF208862.1 gb:NM_016631.1		

218324_s_at		NM_023071	gb:NM_023071.1 /DEF=Homo sapiens hypothetical protein FLJ13117 (FLJ13117), mRNA. /FEA=mRNA /GEN=FLJ13117 /PROD=hypothetical protein FLJ13117 /DB_XREF=gi:12751480 /UG=Hs.152982 hypothetical protein FLJ13117 /FL=gb:NM_023071.1		
201901_s_at		NM_003403	Consensus includes gb:Z14077.1 /DEF=H.sapiens mRNA for YY1NF-E1 protein. /FEA=mRNA /PROD=YY1 NF-E1 /DB_XREF=gi:38010 /UG=Hs.97496 YY1 transcription factor /FL=gb:M77698.1 gb:M76541.1 gb:NM_003403.2		

206342_x_at		NM_006123	gb:NM_006123.1 /DEF=Homo sapiens iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 2, mRNA. /FEA=mRNA /GEN=IDS /PROD=iduronate-2-sulfatase isoform b precursor /DB_XREF=gi:5360207 /UG=Hs.172458 iduronate 2-sulfatase (Hunter syndrome) /FL=gb:L40586.1 gb:NM_006123.1		
214150_x_at	ATP6V0E	BE043477	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e		Hs.24322
209911_x_at		BC002842	gb:BC002842.1 /DEF=Homo sapiens, H2B histone family, member B, clone MGC:3802, mRNA, complete cds. /FEA=mRNA /PROD=H2B histone family, member B /DB_XREF=gi:12803984 /UG=Hs.180779 H2B histone family, member B /FL=gb:NM_021063.1 gb:BC002842.1		

205401_at		NM_003659	gb:NM_003659.1 /DEF=Homo sapiens alkylglycerone phosphate synthase (AGPS), mRNA. /FEA=mRNA /GEN=AGPS /PROD=alkylglycerone phosphate synthase precursor /DB_XREF=gi:4501992 /UG=Hs.22580 alkylglycerone phosphate synthase /FL=gb:NM_003659.1		
206571_s_at		NM_004834	gb:NM_004834.1 /DEF=Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4), mRNA. /FEA=mRNA /GEN=MAP4K4 /PROD=mitogen-activated protein kinase kinase kinasekinase 4 /DB_XREF=gi:4758523 /UG=Hs.3628 mitogen-activated protein kinase kinase kinase kinase 4 /FL=gb:AF096300.1 gb:NM_004834.1		

214959_s_at		AF229253	Consensus includes gb:AF229253.1 /DEF=Homo sapiens clone FIF N1 fibroblast growth factor 2-interacting factor (API5) mRNA, partial cds.; alternatively spliced. /FEA=mRNA /GEN=API5 /PROD=fibroblast growth factor 2-interacting factor /DB_XREF=gi:12656082 /UG=Hs.227913 API5-like 1		
218002_s_at		NM_004887	gb:NM_004887.1 /DEF=Homo sapiens small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK) (SCYB14), mRNA. /FEA=mRNA /GEN=SCYB14 /PROD=small inducible cytokine subfamily B(Cys-X-Cys), member 14 (BRAK) /DB_XREF=gi:4757869 /UG=Hs.24395 small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK) /FL=gb:BC003513.1 gb:AF073957.1 gb:NM_004887.1 gb:AF144103.1 gb:AF106911.1		

220575_at		NM_024974	gb:NM_024974.1 /DEF=Homo sapiens hypothetical protein FLJ11800 (FLJ11800), mRNA. /FEA=mRNA /GEN=FLJ11800 /PROD=hypothetical protein FLJ11800 /DB_XREF=gi:13376473 /UG=Hs.287456 hypothetical protein FLJ11800 /FL=gb:NM_024974.1		
211084_x_at		Z25429	gb:Z25429.1 /DEF=H.sapiens protein-serinethreonine kinase gene, complete CDS. /FEA=mRNA /PROD=protein-serinethreonine kinase /DB_XREF=gi:405736 /FL=gb:Z25429.1		
209339_at		U76248	gb:U76248.1 /DEF=Human hSIAH2 mRNA, complete cds. /FEA=mRNA /PROD=hSIAH2 /DB_XREF=gi:2673967 /UG=Hs.20191 seven in absentia (Drosophila) homolog 2 /FL=gb:U76248.1 gb:NM_005067.1		

210973_s_at		M63889	gb:M63889.1 /DEF=Human heparin-binding growth factor receptor (HBGF-R-alpha-a3) mRNA, complete cds. /FEA=mRNA /GEN=HBGF-R /PROD=heparin-binding growth factor receptor /DB_XREF=gi:183882 /UG=Hs.748 fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome) /FL=gb:M63889.1		
214697_s_at	ROD1	AW190873	ROD1 regulator of differentiation 1 (S. pombe)		Hs.145078
209229_s_at		BC002799	gb:BC002799.1 /DEF=Homo sapiens, KIAA1115 protein, clone MGC:3534, mRNA, complete cds. /FEA=mRNA /PROD=KIAA1115 protein /DB_XREF=gi:12803904 /UG=Hs.72172 KIAA1115 protein /FL=gb:BC002799.1		
217496_s_at	IDE	AA918442	insulin-degrading enzyme		Hs.1508

212046_x_at		X60188	Consensus includes gb:X60188.1 /DEF=Human ERK1 mRNA for protein serinethreonine kinase. /FEA=mRNA /GEN=ERK1 /PROD=protein serinethreonine kinase /DB_XREF=gi:31220 /UG=Hs.861 mitogen-activated protein kinase 3		
209587_at		U70370	gb:U70370.1 /DEF=Human hindlimb expressed homeobox protein backfoot (Bft) mRNA, complete cds. /FEA=mRNA /GEN=Bft /PROD=hindlimb expressed homeobox protein backfoot /DB_XREF=gi:1870670 /UG=Hs.84136 paired-like homeodomain transcription factor 1 /FL=gb:BC003685.1 gb:U70370.1		

205431_s_at		NM_021073	gb:NM_021073.1 /DEF=Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA. /FEA=mRNA /GEN=BMP5 /PROD=bone morphogenetic protein 5 /DB_XREF=gi:10835090 /UG=Hs.1104 bone morphogenetic protein 5 /FL=gb:NM_021073.1 gb:M60314.1		
202075_s_at		NM_006227	gb:NM_006227.1 /DEF=Homo sapiens phospholipid transfer protein (PLTP), mRNA. /FEA=mRNA /GEN=PLTP /PROD=phospholipid transfer protein /DB_XREF=gi:5453913 /UG=Hs.283007 phospholipid transfer protein /FL=gb:L26232.1 gb:NM_006227.1		
215203_at		AW438464	ESTs, Weakly similar to hypothetical protein FLJ20378 [Homo sapiens] [H.sapiens]		Hs.288760

206685_at		NM_018985	gb:NM_018985.1 /DEF=Homo sapiens hypothetical protein (HCGIV.9), mRNA. /FEA=mRNA /GEN=HCGIV.9 /PROD=hypothetical protein /DB_XREF=gi:9506770 /UG=Hs.60856 hypothetical protein /FL=gb:NM_018985.1		
210493_s_at		BC001279	gb:BC001279.1 /DEF=Homo sapiens, Similar to KIAA0626 gene product, clone MGC:5129, mRNA, complete cds. /FEA=mRNA /PROD=Similar to KIAA0626 gene product /DB_XREF=gi:12654870 /UG=Hs.285318 Homo sapiens, Similar to KIAA0626 gene product, clone MGC:5129, mRNA, complete cds /FL=gb:BC001279.1		
215392_at		AU148154	AU148154 MAMMA1 Homo sapiens cDNA clone MAMMA1002744 3', mRNA sequence.		

210378_s_at		BC004118	gb:BC004118.1 /DEF=Homo sapiens, clone MGC:11170, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:11170) /DB_XREF=gi:13278674 /UG=Hs.18528 Sjogrens syndrome nuclear autoantigen 1 /FL=gb:BC004118.1		
217608_at		AW408767	ESTs, Moderately similar to hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]		Hs.383211
205211_s_at		NM_004292	gb:NM_004292.1 /DEF=Homo sapiens ras inhibitor (RIN1), mRNA. /FEA=mRNA /GEN=RIN1 /PROD=ras inhibitor /DB_XREF=gi:4759039 /UG=Hs.1030 ras inhibitor /FL=gb:L36463.1 gb:NM_004292.1		
214258_x_at	HTATIP	AA886971	HIV-1 Tat interactive protein, 60kDa		Hs.6364

204488_at		NM_014908	gb:NM_014908.1 /DEF=Homo sapiens KIAA1094 protein (KIAA1094), mRNA. /FEA=mRNA /GEN=KIAA1094 /PROD=KIAA1094 protein /DB_XREF=gi:7662481 /UG=Hs.161166 KIAA1094 protein /FL=gb:AB029017.1 gb:NM_014908.1		
218578_at		NM_024529	gb:NM_024529.1 /DEF=Homo sapiens hypothetical protein FLJ23316 (FLJ23316), mRNA. /FEA=mRNA /GEN=FLJ23316 /PROD=hypothetical protein FLJ23316 /DB_XREF=gi:13375677 /UG=Hs.5722 hypothetical protein FLJ23316 /FL=gb:AF312865.1 gb:NM_024529.1		

208916_at		AF105230	gb:AF105230.1 /DEF=Homo sapiens neutral amino acid transporter (SLC1A5) mRNA, complete cds. /FEA=mRNA /GEN=SLC1A5 /PROD=neutral amino acid transporter /DB_XREF=gi:4191561 /UG=Hs.183556 solute carrier family 1 (neutral amino acid transporter), member 5 /FL=gb:BC000062.1 gb:U53347.1 gb:AF102826.1 gb:AF105230.1 gb:AF105423.1 gb:NM_005628.1		
202687_s_at		U57059	gb:U57059.1 /DEF=Homo sapiens Apo-2 ligand mRNA, complete cds. /FEA=mRNA /PROD=Apo-2 ligand /DB_XREF=gi:1336207 /UG=Hs.83429 tumor necrosis factor (ligand) superfamily, member 10 /FL=gb:U37518.1 gb:U57059.1 gb:NM_003810.1		

201297_s_at		NM_018221	Consensus includes gb:AK023321.1 /DEF=Homo sapiens cDNA FLJ13259 fis, clone OVARC1000876, moderately similar to MOB1 PROTEIN. /FEA=mRNA /DB_XREF=gi:10435206 /UG=Hs.196437 hypothetical protein FLJ10788 /FL=gb:AB016839.1 gb:BC003398.1 gb:NM_018221.1		
207565_s_at		NM_001531	gb:NM_001531.1 /DEF=Homo sapiens major histocompatibility complex, class I-like sequence (HLALS), mRNA. /FEA=mRNA /GEN=HLALS /PROD=major histocompatibility complex, class I-likesequence /DB_XREF=gi:4504416 /UG=Hs.101840 major histocompatibility complex, class I-like sequence /FL=gb:NM_001531.1 gb:U22963.1		

220761_s_at		NM_016281	gb:NM_016281.1 /DEF=Homo sapiens STE20-like kinase (JIK), mRNA. /FEA=mRNA /GEN=JIK /PROD=STE20-like kinase /DB_XREF=gi:7705559 /UG=Hs.12040 STE20-like kinase /FL=gb:AF179867.1 gb:NM_016281.1		
221978_at	HLA-F	BE138825	major histocompatibility complex, class I, F		Hs.377850
221490_at		AL136733	gb:AL136733.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434N1010 (from clone DKFZp434N1010); complete cds. /FEA=mRNA /GEN=DKFZp434N1010 /PROD=hypothetical protein /DB_XREF=gi:12052984 /UG=Hs.75425 ubiquitin associated protein /FL=gb:AL136733.1 gb:AF222043.2 gb:NM_016525.2		
213182_x_at	CDKN1C	R78668	cyclin-dependent kinase inhibitor 1C (p57, Kip2)		Hs.106070
217704_x_at		AI820796	ESTs, Weakly similar to hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]		Hs.310806

209398_at		BC002649	gb:BC002649.1 /DEF=Homo sapiens, H1 histone family, member 2, clone MGC:3992, mRNA, complete cds. /FEA=mRNA /PROD=H1 histone family, member 2 /DB_XREF=gi:12803628 /UG=Hs.7644 H1 histone family, member 2 /FL=gb:BC002649.1 gb:NM_005319.1		
202254_at		AB007900	Consensus includes gb:AB007900.1 /DEF=Homo sapiens KIAA0440 mRNA, partial cds. /FEA=mRNA /GEN=KIAA0440 /DB_XREF=gi:2662160 /UG=Hs.172180 KIAA0440 protein /FL=gb:AF090990.1 gb:NM_015556.1		
203836_s_at		D84476	gb:D84476.1 /DEF=Homo sapiens mRNA for ASK1, complete cds. /FEA=mRNA /PROD=ASK1 /DB_XREF=gi:1805499 /UG=Hs.151988 mitogen-activated protein kinase kinase kinase 5 /FL=gb:U67156.1 gb:D84476.1 gb:NM_005923.2		

210837_s_at		AF012074	gb:AF012074.1 /DEF=Homo sapiens cAMP-specific phosphodiesterase PDE4D2 (PDE4D) mRNA, complete cds. /FEA=mRNA /GEN=PDE4D /PROD=cAMP-specific phosphodiesterase PDE4D2 /DB_XREF=gi:2735858 /UG=Hs.172081 phosphodiesterase 4D, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E3) /FL=gb:U50158.1 gb:AF012074.1		
213815_x_at	LOC58509	AI913329	NY-REN-24 antigen		Hs.128425
203498_at		NM_005822	gb:NM_005822.1 /DEF=Homo sapiens Down syndrome critical region gene 1-like 1 (DSCR1L1), mRNA. /FEA=mRNA /GEN=DSCR1L1 /PROD=Down syndrome critical region gene 1-like 1protein /DB_XREF=gi:5032234 /UG=Hs.156007 Down syndrome critical region gene 1-like 1 /FL=gb:D83407.1 gb:NM_005822.1		

220751_s_at		NM_016348	gb:NM_016348.1 /DEF=Homo sapiens chromosome 5 open reading frame 4 (C5ORF4), mRNA. /FEA=mRNA /GEN=C5ORF4 /PROD=putative tumor suppressor /DB_XREF=gi:7705942 /UG=Hs.10235 chromosome 5 open reading frame 4 /FL=gb:AF159165.1 gb:NM_016348.1		
219255_x_at		NM_018725	gb:NM_018725.1 /DEF=Homo sapiens IL-17B receptor (IL17BR), mRNA. /FEA=mRNA /GEN=IL17BR /PROD=IL-17B receptor /DB_XREF=gi:8923816 /UG=Hs.5470 IL-17B receptor /FL=gb:BC000980.1 gb:AF212365.1 gb:NM_018725.1 gb:AF208110.1		

221073_s_at		NM_006092	gb:NM_006092.1 /DEF=Homo sapiens caspase recruitment domain 4 (NOD1), mRNA. /FEA=mRNA /GEN=NOD1 /PROD=caspase recruitment domain 4 /DB_XREF=gi:5174616 /UG=Hs.19405 caspase recruitment domain 4 /FL=gb:AF113925.1 gb:NM_006092.1		
204116_at		NM_000206	gb:NM_000206.1 /DEF=Homo sapiens interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG), mRNA. /FEA=mRNA /GEN=IL2RG /PROD=interleukin 2 receptor, gamma chain, precursor /DB_XREF=gi:4557881 /UG=Hs.84 interleukin 2 receptor, gamma (severe combined immunodeficiency) /FL=gb:NM_000206.1		

218953_s_at		NM_024028	gb:NM_024028.1 /DEF=Homo sapiens hypothetical protein MGC3265 (MGC3265), mRNA. /FEA=mRNA /GEN=MGC3265 /PROD=hypothetical protein MGC3265 /DB_XREF=gi:13128973 /UG=Hs.257111 hypothetical protein MGC3265 /FL=gb:BC000014.1 gb:NM_024028.1		
213312_at		NM_020425	Consensus includes gb:NM_020425.1 /DEF=Homo sapiens hypothetical protein DKFZp586E1923 (DKFZP586E1923), mRNA. /FEA=CDS /GEN=DKFZP586E1923 /PROD=hypothetical protein DKFZp586E1923 /DB_XREF=gi:10092684 /UG=Hs.70769 hypothetical protein DKFZp586E1923 /FL=gb:NM_020425.1		

206928_at		NM_003431	gb:NM_003431.1 /DEF=Homo sapiens zinc finger protein 124 (HZF-16) (ZNF124), mRNA. /FEA=mRNA /GEN=ZNF124 /PROD=zinc finger protein 124 (HZF-16) /DB_XREF=gi:4507976 /UG=Hs.180248 zinc finger protein 124 (HZF-16) /FL=gb:NM_003431.1		
220898_at		NM_024972	gb:NM_024972.1 /DEF=Homo sapiens hypothetical protein FLJ11736 (FLJ11736), mRNA. /FEA=mRNA /GEN=FLJ11736 /PROD=hypothetical protein FLJ11736 /DB_XREF=gi:13376469 /UG=Hs.287448 hypothetical protein FLJ11736 /FL=gb:NM_024972.1		

202367_at		NM_001913	gb:NM_001913.1 /DEF=Homo sapiens cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1), mRNA. /FEA=mRNA /GEN=CUTL1 /PROD=cut (Drosophila)-like 1 (CCAAT displacementprotein) /DB_XREF=gi:4503168 /UG=Hs.147049 cut (Drosophila)-like 1 (CCAAT displacement protein) /FL=gb:NM_001913.1 gb:L12579.1		
217120_s_at		AK023368	Consensus includes gb:AK023368.1 /DEF=Homo sapiens cDNA FLJ13306 fis, clone OVARC1001417, highly similar to Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170 mRNA. /FEA=mRNA /DB_XREF=gi:10435273 /UG=Hs.21586 cofactor required for Sp1 transcriptional activation, subunit 2 (150kD)		

206044_s_at		NM_004333	gb:NM_004333.1 /DEF=Homo sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF), mRNA. /FEA=mRNA /GEN=BRAF /PROD=v-raf murine sarcoma viral oncogene homolog B1 /DB_XREF=gi:4757867 /UG=Hs.622 v-raf murine sarcoma viral oncogene homolog B1 /FL=gb:M95712.1 gb:NM_004333.1		
220453_at		NM_017765	gb:NM_017765.1 /DEF=Homo sapiens hypothetical protein FLJ20320 (FLJ20320), mRNA. /FEA=mRNA /GEN=FLJ20320 /PROD=hypothetical protein FLJ20320 /DB_XREF=gi:8923300 /UG=Hs.263081 hypothetical protein FLJ20320 /FL=gb:NM_017765.1		

201714_at		NM_001070	gb:NM_001070.1 /DEF=Homo sapiens tubulin, gamma 1 (TUBG1), mRNA. /FEA=mRNA /GEN=TUBG1 /PROD=tubulin, gamma 1 /DB_XREF=gi:4507730 /UG=Hs.21635 tubulin, gamma 1 /FL=gb:BC000619.1 gb:M61764.1 gb:NM_001070.1		
218816_at		NM_018214	gb:NM_018214.1 /DEF=Homo sapiens hypothetical protein FLJ10775 (FLJ10775), mRNA. /FEA=mRNA /GEN=FLJ10775 /PROD=hypothetical protein FLJ10775 /DB_XREF=gi:8922660 /UG=Hs.35091 hypothetical protein FLJ10775 /FL=gb:BC003193.1 gb:NM_018214.1		
213839_at		AW028110	ESTs		Hs.301478

203205_at		NM_014663	gb:NM_014663.1 /DEF=Homo sapiens KIAA0677 gene product (KIAA0677), mRNA. /FEA=mRNA /GEN=KIAA0677 /PROD=KIAA0677 gene product /DB_XREF=gi:7662245 /UG=Hs.155983 KIAA0677 gene product /FL=gb:BC002558.1 gb:AB014577.1 gb:NM_014663.1		
210330_at		U58331	gb:U58331.1 /DEF=Human placental delta sarcoglycan mRNA, complete cds. /FEA=mRNA /PROD=delta sarcoglycan /DB_XREF=gi:1695856 /UG=Hs.151899 sarcoglycan, delta (35kD dystrophin-associated glycoprotein) /FL=gb:U58331.1		

215506_s_at		AK021882	Consensus includes gb:AK021882.1 /DEF=Homo sapiens cDNA FLJ11820 fis, clone HEMBA1006445, highly similar to Homo sapiens putative tumor supressor NOEY2 mRNA. /FEA=mRNA /DB_XREF=gi:10433168 /UG=Hs.194695 ras homolog gene family, member I		
202409_at		X07868	Consensus includes gb:X07868 /DEF=Human DNA for insulin-like growth factor II (IGF-2); exon 7 and additional ORF /FEA=mRNA_1 /DB_XREF=gi:32998 /UG=Hs.251664 insulin-like growth factor 2 (somatomedin A) /FL=gb:BC000531.1 gb:J03242.1 gb:M17426.1 gb:NM_000612.2		

216347_s_at		AK023188	Consensus includes gb:AK023188.1 /DEF=Homo sapiens cDNA FLJ13126 fis, clone NT2RP3002909, weakly similar to P53-BINDING PROTEIN 2. /FEA=mRNA /DB_XREF=gi:10435002 /UG=Hs.6162 KIAA0771 protein		
205527_s_at		NM_015487	gb:NM_015487.1 /DEF=Homo sapiens DKFZP434D174 protein (DKFZP434D174), mRNA. /FEA=mRNA /GEN=DKFZP434D174 /PROD=DKFZP434D174 protein /DB_XREF=gi:11094402 /UG=Hs.302421 DKFZP434D174 protein /FL=gb:NM_015487.1		
221430_s_at		NM_030963	gb:NM_030963.1 /DEF=Homo sapiens hypothetical protein DKFZp434O1427 (DKFZP434O1427), mRNA. /FEA=CDS /GEN=DKFZP434O1427 /PROD=hypothetical protein DKFZp434O1427 /DB_XREF=gi:13624336 /FL=gb:NM_030963.1		

204724_s_at		NM_001853	gb:NM_001853.1 /DEF=Homo sapiens collagen, type IX, alpha 3 (COL9A3), mRNA. /FEA=mRNA /GEN=COL9A3 /PROD=collagen, type IX, alpha 3 /DB_XREF=gi:4502966 /UG=Hs.53563 collagen, type IX, alpha 3 /FL=gb:L41162.1 gb:NM_001853.1		
204602_at		NM_012242	gb:NM_012242.1 /DEF=Homo sapiens dickkopf (Xenopus laevis) homolog 1 (DKK1), mRNA. /FEA=mRNA /GEN=DKK1 /PROD=dickkopf (Xenopus laevis) homolog 1 /DB_XREF=gi:7110718 /UG=Hs.40499 dickkopf (Xenopus laevis) homolog 1 /FL=gb:AF127563.1 gb:AF177394.1 gb:NM_012242.1		

204010_s_at		NM_004985	gb:NM_004985.1 /DEF=Homo sapiens v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog (KRAS2), mRNA. /FEA=mRNA /GEN=KRAS2 /PROD=v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogenehomolog /DB_XREF=gi:4826811 /UG=Hs.184050 v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog /FL=gb:M54968.1 gb:NM_004985.1		
206279_at		NM_002760	gb:NM_002760.1 /DEF=Homo sapiens protein kinase, Y-linked (PRKY), mRNA. /FEA=mRNA /GEN=PRKY /PROD=protein kinase, Y-linked /DB_XREF=gi:10835064 /UG=Hs.56336 protein kinase, Y-linked /FL=gb:NM_002760.1		

219983_at		NM_020386	gb:NM_020386.1 /DEF=Homo sapiens H-REV107 protein-related protein (LOC57110), mRNA. /FEA=mRNA /GEN=LOC57110 /PROD=H-REV107 protein-related protein /DB_XREF=gi:9966858 /UG=Hs.36761 H-REV107 protein-related protein /FL=gb:AB030816.1 gb:NM_020386.1		
219954_s_at		NM_020973	gb:NM_020973.1 /DEF=Homo sapiens cytosolic beta-glucosidase (GLUC), mRNA. /FEA=mRNA /GEN=GLUC /PROD=cytosolic beta-glucosidase /DB_XREF=gi:13273312 /UG=Hs.146182 cytosolic beta-glucosidase /FL=gb:AB017913.1 gb:AF317840.1 gb:NM_020973.1		

219460_s_at		NM_017849	gb:NM_017849.1 /DEF=Homo sapiens hypothetical protein FLJ20507 (FLJ20507), mRNA. /FEA=mRNA /GEN=FLJ20507 /PROD=hypothetical protein FLJ20507 /DB_XREF=gi:8923465 /UG=Hs.202955 hypothetical protein FLJ20507 /FL=gb:NM_017849.1		
205394_at		NM_001274	gb:NM_001274.1 /DEF=Homo sapiens CHK1 (checkpoint, S.pombe) homolog (CHEK1), mRNA. /FEA=mRNA /GEN=CHEK1 /PROD=CHK1 (checkpoint, S.pombe) homolog /DB_XREF=gi:4502802 /UG=Hs.20295 CHK1 (checkpoint, S.pombe) homolog /FL=gb:AF016582.1 gb:NM_001274.1		
214140_at	SLC25A16	AI827990	solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16		Hs.180408

209008_x_at		U76549	gb:U76549.1 /DEF=Human cytokeratin 8 mRNA, complete cds. /FEA=mRNA /PROD=cytokeratin 8 /DB_XREF=gi:1673574 /UG=Hs.242463 keratin 8 /FL=gb:BC000654.1 gb:U76549.1 gb:M34225.1 gb:M26324.1 gb:NM_002273.1		
212948_at		AB020716	Consensus includes gb:AB020716.1 /DEF=Homo sapiens mRNA for KIAA0909 protein, partial cds. /FEA=mRNA /GEN=KIAA0909 /PROD=KIAA0909 protein /DB_XREF=gi:4240306 /UG=Hs.107362 KIAA0909 protein		

210910_s_at		BC000487	gb:BC000487.1 /DEF=Homo sapiens, Similar to POM (POM121 rat homolog) and ZP3 fusion protein, clone MGC:8359, mRNA, complete cds. /FEA=mRNA /PROD=Similar to POM (POM121 rat homolog) and ZP3fusion protein /DB_XREF=gi:12653432 /UG=Hs.296380 POM (POM121 rat homolog) and ZP3 fusion protein /FL=gb:BC000487.1		
210715_s_at		AF027205	gb:AF027205.1 /DEF=Homo sapiens Kunitz-type protease inhibitor (kop) mRNA, complete cds. /FEA=mRNA /GEN=kop /PROD=Kunitz-type protease inhibitor /DB_XREF=gi:2598967 /UG=Hs.31439 serine protease inhibitor, Kunitz type, 2 /FL=gb:AF027205.1		

209006_s_at		AF247168	gb:AF247168.1 /DEF=Homo sapiens NPD014 (NPD014) mRNA, complete cds. /FEA=mRNA /GEN=NPD014 /PROD=NPD014 /DB_XREF=gi:12005626 /UG=Hs.8084 hypothetical protein dJ465N24.2.1 /FL=gb:AF247168.1 gb:AF267856.1		
219292_at		NM_018105	gb:NM_018105.1 /DEF=Homo sapiens hypothetical protein FLJ10477 (FLJ10477), mRNA. /FEA=mRNA /GEN=FLJ10477 /PROD=hypothetical protein FLJ10477 /DB_XREF=gi:8922445 /UG=Hs.7432 hypothetical protein FLJ10477 /FL=gb:NM_018105.1		
212232_at		AB023231	Consensus includes gb:AB023231.1 /DEF=Homo sapiens mRNA for KIAA1014 protein, partial cds. /FEA=mRNA /GEN=KIAA1014 /PROD=KIAA1014 protein /DB_XREF=gi:4589677 /UG=Hs.6834 KIAA1014 protein		

208718_at		Z97056	Consensus includes gb:Z97056 /DEF=Human DNA sequence from clone RP3-434P1 on chromosome 22 Contains the KCNJ4 gene for inwardly rectifying potassium channel J4 (hippocampal inward rectifier, HIR, HRK1, HIRK2, KIR2.3), the KDELR3 gene for KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulu... /FEA=mRNA_5 /DB_XREF=gi:2832593 /UG=Hs.6179 DEADH (Asp-Glu-Ala-AspHis) box polypeptide 17 (72kD) /FL=gb:BC000595.1 gb:NM_006386.2 gb:U59321.1		
212145_at		D87453	Consensus includes gb:D87453.1 /DEF=Human mRNA for KIAA0264 gene, partial cds. /FEA=mRNA /GEN=KIAA0264 /DB_XREF=gi:1665794 /UG=Hs.122669 KIAA0264 protein		
208752_x_at	NAP1L1	AI888672	nucleosome assembly protein 1-like 1		Hs.302649
212077_at		AL583520	Homo sapiens OK/SW-cl.14 mRNA, complete cds		Hs.374993
212919_at	KIAA1096	AV715578	KIAA1096 protein		Hs.69559

211406_at		AF119875	gb:AF119875.1 /DEF=Homo sapiens PRO2309 mRNA, complete cds. /FEA=mRNA /PROD=PRO2309 /DB_XREF=gi:7770186 /UG=Hs.283037 HSPC039 protein /FL=gb:AF119875.1		
208787_at		BC003375	gb:BC003375.1 /DEF=Homo sapiens, mitochondrial ribosomal protein L3, clone MGC:5219, mRNA, complete cds. /FEA=mRNA /PROD=mitochondrial ribosomal protein L3 /DB_XREF=gi:13097224 /UG=Hs.79086 mitochondrial ribosomal protein L3 /FL=gb:BC003375.1 gb:NM_007208.1		
218362_s_at		NM_014953	gb:NM_014953.1 /DEF=Homo sapiens KIAA1008 protein (KIAA1008), mRNA. /FEA=mRNA /GEN=KIAA1008 /PROD=KIAA1008 protein /DB_XREF=gi:7662443 /UG=Hs.323346 KIAA1008 protein /FL=gb:AB023225.1 gb:NM_014953.1		

219377_at		NM_022751	gb:NM_022751.1 /DEF=Homo sapiens hypothetical protein FLJ21610 (FLJ21610), mRNA. /FEA=mRNA /GEN=FLJ21610 /PROD=hypothetical protein FLJ21610 /DB_XREF=gi:12232414 /UG=Hs.12727 hypothetical protein FLJ21610 /FL=gb:NM_022751.1		
208093_s_at		NM_030808	gb:NM_030808.1 /DEF=Homo sapiens LIS1-interacting protein NUDEL; endooligopeptidase A (NUDEL), mRNA. /FEA=mRNA /GEN=NUDEL /PROD=LIS1-interacting protein NUDEL;endooligopeptidase A /DB_XREF=gi:13540599 /FL=gb:NM_030808.1		
212491_s_at	DNAJC8	AA843895	DnaJ (Hsp40) homolog, subfamily C, member 8		Hs.74711

213005_s_at		D79994	Consensus includes gb:D79994.1 /DEF=Human mRNA for KIAA0172 gene, partial cds. /FEA=mRNA /GEN=KIAA0172 /DB_XREF=gi:1136403 /UG=Hs.77546 KIAA0172 protein		
209632_at		L07590	Consensus includes gb:AI760130 /FEA=EST /DB_XREF=gi:5175797 /DB_XREF=est:wg58b07.x1 /CLONE=IMAGE:2369269 /UG=Hs.28219 protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 72), alpha isoform and (PR 130), beta isoform /FL=gb:L07590.1		
218356_at		NM_013393	gb:NM_013393.1 /DEF=Homo sapiens cell division protein FtsJ (FJH1), mRNA. /FEA=mRNA /GEN=FJH1 /PROD=cell division protein FtsJ /DB_XREF=gi:7019376 /UG=Hs.279877 cell division protein FtsJ /FL=gb:AF093415.1 gb:NM_013393.1		

212560_at	COX6B	AV728268	cytochrome c oxidase subunit VIb		Hs.174031
212628_at		AK023692	Consensus includes gb:BG292065 /FEA=EST /DB_XREF=gi:13050507 /DB_XREF=est:602386350F1 /CLONE=IMAGE:4515036 /UG=Hs.69171 protein kinase C-like 2		
209404_s_at		AF151867	gb:AF151867.1 /DEF=Homo sapiens CGI-109 protein mRNA, complete cds. /FEA=mRNA /PROD=CGI-109 protein /DB_XREF=gi:4929686 /UG=Hs.278391 CGI-109 protein /FL=gb:AF151867.1		

209444_at		BC001851	gb:BC001851.1 /DEF=Homo sapiens, Similar to RAP1, GTP-GDP dissociation stimulator 1, clone MGC:4525, mRNA, complete cds. /FEA=mRNA /PROD=Similar to RAP1, GTP-GDP dissociation stimulator1 /DB_XREF=gi:12804812 /UG=Hs.7940 RAP1, GTP-GDP dissociation stimulator 1 /FL=gb:NM_021159.1 gb:BC001851.1 gb:BC001816.1 gb:AF215923.1 gb:AF237413.1		
209534_x_at	AKAP13	BF222823	A kinase (PRKA) anchor protein 13		Hs.301946
212499_s_at		AK025580	Consensus includes gb:AK025580.1 /DEF=Homo sapiens cDNA: FLJ21927 fis, clone HEP04178, highly similar to HSU90909 Human clone 23722 mRNA sequence. /FEA=mRNA /DB_XREF=gi:10438139 /UG=Hs.81360 Homo sapiens cDNA: FLJ21927 fis, clone HEP04178, highly similar to HSU90909 Human clone 23722 mRNA sequence		

209392_at		L35594	gb:L35594.1 /DEF=Human autotaxin mRNA, complete cds. /FEA=mRNA /PROD=autotaxin /DB_XREF=gi:537905 /UG=Hs.174185 ectonucleotide pyrophosphatasephosphodiesterase 2 (autotaxin) /FL=gb:L35594.1		
218379_at		NM_016090	gb:NM_016090.1 /DEF=Homo sapiens RNA binding motif protein 7 (RBM7), mRNA. /FEA=mRNA /GEN=RBM7 /PROD=RNA binding motif protein 7 /DB_XREF=gi:9994184 /UG=Hs.5887 RNA binding motif protein 7 /FL=gb:AF156098.1 gb:NM_016090.1		

218478_s_at		NM_017612	gb:NM_017612.1 /DEF=Homo sapiens hypothetical protein DKFZp434E2220 (DKFZp434E2220), mRNA. /FEA=mRNA /GEN=DKFZp434E2220 /PROD=hypothetical protein DKFZp434E2220 /DB_XREF=gi:8922133 /UG=Hs.37706 hypothetical protein DKFZp434E2220 /FL=gb:NM_017612.1		
218757_s_at		NM_023010	gb:NM_023010.1 /DEF=Homo sapiens similar to yeast Upf3, variant B (UPF3B), mRNA. /FEA=mRNA /GEN=UPF3B /PROD=similar to yeast Upf3, variant B /DB_XREF=gi:12711673 /UG=Hs.103832 similar to yeast Upf3, variant B /FL=gb:AY013251.1 gb:NM_023010.1		

210367_s_at		AF010316	gb:AF010316.1 /DEF=Homo sapiens Pig12 (PIG12) mRNA, complete cds. /FEA=mRNA /GEN=PIG12 /PROD=Pig12 /DB_XREF=gi:2415307 /UG=Hs.146688 prostaglandin E synthase /FL=gb:AF010316.1		
209814_at		BC004421	gb:BC004421.1 /DEF=Homo sapiens, nucleolar cysteine-rich protein, clone MGC:1452, mRNA, complete cds. /FEA=mRNA /PROD=nucleolar cysteine-rich protein /DB_XREF=gi:13325205 /UG=Hs.120766 nucleolar cysteine-rich protein /FL=gb:BC004421.1 gb:NM_014487.2		
218461_at		NM_016301	gb:NM_016301.1 /DEF=Homo sapiens protein x 0004 (LOC51184), mRNA. /FEA=mRNA /GEN=LOC51184 /PROD=protein x 0004 /DB_XREF=gi:9994188 /UG=Hs.284164 protein x 0004 /FL=gb:AF117229.1 gb:NM_016301.1		

212643_at	MISS	AI671747	likely ortholog of mouse MAPK-interacting and spindle-stabilizing protein		Hs.388281
219449_s_at		NM_017866	gb:NM_017866.1 /DEF=Homo sapiens hypothetical protein FLJ20533 (FLJ20533), mRNA. /FEA=mRNA /GEN=FLJ20533 /PROD=hypothetical protein FLJ20533 /DB_XREF=gi:8923499 /UG=Hs.106650 hypothetical protein FLJ20533 /FL=gb:BC002748.1 gb:NM_017866.1		
212757_s_at	CAMK2G	BF111268	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma		Hs.153406
219092_s_at		NM_022755	gb:NM_022755.1 /DEF=Homo sapiens hypothetical protein FLJ13163 (FLJ13163), mRNA. /FEA=mRNA /GEN=FLJ13163 /PROD=hypothetical protein FLJ13163 /DB_XREF=gi:12232422 /UG=Hs.16603 hypothetical protein FLJ13163 /FL=gb:NM_022755.1		

209894_at		U50748	gb:U50748.1 /DEF=Homo sapiens leptin receptor short form (db) mRNA, complete cds. /FEA=mRNA /GEN=db /PROD=leptin receptor /DB_XREF=gi:3236285 /UG=Hs.226627 leptin receptor /FL=gb:U50748.1		
210034_s_at	RPL5	AA582460	ribosomal protein L5		Hs.180946
201920_at		NM_005415	gb:NM_005415.2 /DEF=Homo sapiens solute carrier family 20 (phosphate transporter), member 1 (SLC20A1), mRNA. /FEA=mRNA /GEN=SLC20A1 /PROD=solute carrier family 20 (phosphatetransporter), member 1 /DB_XREF=gi:7382462 /UG=Hs.78452 solute carrier family 20 (phosphate transporter), member 1 /FL=gb:L20859.1 gb:NM_005415.2		

204066_s_at		NM_014914	gb:NM_014914.1 /DEF=Homo sapiens KIAA1099 protein (KIAA1099), mRNA. /FEA=mRNA /GEN=KIAA1099 /PROD=KIAA1099 protein /DB_XREF=gi:7662483 /UG=Hs.159377 KIAA1099 protein /FL=gb:AB029022.1 gb:NM_014914.1		
222357_at		AW974823	ESTs		Hs.389296
201770_at		NM_004596	gb:NM_004596.1 /DEF=Homo sapiens small nuclear ribonucleoprotein polypeptide A (SNRPA), mRNA. /FEA=mRNA /GEN=SNRPA /PROD=small nuclear ribonucleoprotein polypeptide A /DB_XREF=gi:4759155 /UG=Hs.173255 small nuclear ribonucleoprotein polypeptide A /FL=gb:BC000405.1 gb:NM_004596.1		
215718_s_at	PHF3	AI949220	PHD finger protein 3		Hs.78893
213876_x_at	U2AF1RS2	AW089584	U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 2		Hs.171909

215452_x_at		AL031133	includes gb:AL031133 /DEF=Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains... /FEA=mRNA_2 /DB_XREF=gi:3676189 /UG=Hs.113293 Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and		
203833_s_at	TGOLN2	BF061845	trans-golgi network protein 2		Hs.14894

203851_at		NM_002178	gb:NM_002178.1 /DEF=Homo sapiens insulin-like growth factor binding protein 6 (IGFBP6), mRNA. /FEA=mRNA /GEN=IGFBP6 /PROD=insulin-like growth factor binding protein 6 /DB_XREF=gi:11321592 /UG=Hs.274313 insulin-like growth factor binding protein 6 /FL=gb:NM_002178.1 gb:BC003507.1 gb:BC005007.1 gb:M62402.1		
201933_at		NM_002768	gb:NM_002768.1 /DEF=Homo sapiens procollagen (type III) N-endopeptidase (PCOLN3), mRNA. /FEA=mRNA /GEN=PCOLN3 /PROD=procollagen (type III) N-endopeptidase /DB_XREF=gi:4506138 /UG=Hs.183138 procollagen (type III) N-endopeptidase /FL=gb:U58048.1 gb:NM_002768.1 gb:AF281063.1		

201976_s_at		NM_012334	gb:NM_012334.1 /DEF=Homo sapiens myosin X (MYO10), mRNA. /FEA=mRNA /GEN=MYO10 /PROD=myosin X /DB_XREF=gi:11037056 /UG=Hs.61638 myosin X /FL=gb:NM_012334.1 gb:AF234532.1 gb:AF247457.2		
217994_x_at		NM_017871	gb:NM_017871.1 /DEF=Homo sapiens hypothetical protein FLJ20542 (FLJ20542), mRNA. /FEA=mRNA /GEN=FLJ20542 /PROD=hypothetical protein FLJ20542 /DB_XREF=gi:8923511 /UG=Hs.6449 hypothetical protein FLJ20542 /FL=gb:AL136813.1 gb:NM_017871.1		

218231_at		NM_017567	gb:NM_017567.1 /DEF=Homo sapiens N-Acetylglucosamine kinase (HSA242910), mRNA. /FEA=mRNA /GEN=HSA242910 /PROD=N-Acetylglucosamine kinase /DB_XREF=gi:8923736 /UG=Hs.7036 N-Acetylglucosamine kinase /FL=gb:BC001029.1 gb:BC005371.1 gb:NM_017567.1		
201711_x_at	RANBP2	AI681120	RAN binding protein 2		Hs.179825
32811_at	MYO1C	X98507	myosin IC	NM_033375	Hs.409112
204256_at		NM_024090	gb:NM_024090.1 /DEF=Homo sapiens hypothetical protein MGC5487 (MGC5487), mRNA. /FEA=mRNA /GEN=MGC5487 /PROD=hypothetical protein MGC5487 /DB_XREF=gi:13129087 /UG=Hs.211556 hypothetical protein MGC5487 /FL=gb:NM_024090.1		
204571_x_at	PIN4	BE797213	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)		Hs.11774

204211_x_at		NM_002759	gb:NM_002759.1 /DEF=Homo sapiens protein kinase, interferon-inducible double stranded RNA dependent (PRKR), mRNA. /FEA=mRNA /GEN=PRKR /PROD=protein kinase, interferon-inducible doublestranded RNA dependent /DB_XREF=gi:4506102 /UG=Hs.274382 protein kinase, interferon-inducible double stranded RNA dependent /FL=gb:M35663.1 gb:M85294.1 gb:NM_002759.1		
214359_s_at	HSPCB	AI218219	heat shock 90kDa protein 1, beta		Hs.74335
214224_s_at	PIN4	BE674061	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)		Hs.11774
203082_at		NM_014753	gb:NM_014753.1 /DEF=Homo sapiens KIAA0187 gene product (KIAA0187), mRNA. /FEA=mRNA /GEN=KIAA0187 /PROD=KIAA0187 gene product /DB_XREF=gi:7661979 /UG=Hs.10848 KIAA0187 gene product /FL=gb:D80009.1 gb:NM_014753.1		
214172_x_at	RYK	BG032035	RYK receptor-like tyrosine kinase		Hs.79350

221599_at		BC002752	gb:BC002752.1 /DEF=Homo sapiens, Similar to PTD015 protein, clone MGC:3367, mRNA, complete cds. /FEA=mRNA /PROD=Similar to PTD015 protein /DB_XREF=gi:12803822 /UG=Hs.95870 PTD015 protein /FL=gb:BC002752.1		
203493_s_at	KIAA0092	AI123527	KIAA0092 gene product		Hs.151791
203721_s_at		NM_016001	gb:NM_016001.1 /DEF=Homo sapiens CGI-48 protein (LOC51096), mRNA. /FEA=mRNA /GEN=LOC51096 /PROD=CGI-48 protein /DB_XREF=gi:7705764 /UG=Hs.6153 CGI-48 protein /FL=gb:AF151806.1 gb:NM_016001.1		
215143_at		AL049437	Consensus includes gb:AL049437.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586E1120 (from clone DKFZp586E1120). /FEA=mRNA /DB_XREF=gi:4500220 /UG=Hs.100292 Homo sapiens mRNA; cDNA DKFZp586E1120 (from clone DKFZp586E1120)		

202272_s_at		NM_015176	gb:NM_015176.1 /DEF=Homo sapiens KIAA0483 protein (KIAA0483), mRNA. /FEA=mRNA /GEN=KIAA0483 /PROD=KIAA0483 protein /DB_XREF=gi:7662157 /UG=Hs.64691 KIAA0483 protein /FL=gb:NM_015176.1		
203788_s_at	SEMA3C	AI962897	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C		Hs.171921
221185_s_at		NM_025111	gb:NM_025111.1 /DEF=Homo sapiens hypothetical protein FLJ23571 (FLJ23571), mRNA. /FEA=mRNA /GEN=FLJ23571 /PROD=hypothetical protein FLJ23571 /DB_XREF=gi:13376682 /UG=Hs.288693 hypothetical protein FLJ23571 /FL=gb:NM_025111.1		
214801_at		W88821	ESTs, Weakly similar to hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]		Hs.408958

217792_at		NM_014426	gb:NM_014426.1 /DEF=Homo sapiens sorting nexin 5 (SNX5), mRNA. /FEA=mRNA /GEN=SNX5 /PROD=sorting nexin 5 /DB_XREF=gi:7657598 /UG=Hs.13794 sorting nexin 5 /FL=gb:BC000100.1 gb:AF121855.1 gb:NM_014426.1		
201025_at		NM_015904	Consensus includes gb:AB018284.1 /DEF=Homo sapiens mRNA for KIAA0741 protein, complete cds. /FEA=mRNA /GEN=KIAA0741 /PROD=KIAA0741 protein /DB_XREF=gi:3882202 /UG=Hs.158688 KIAA0741 gene product /FL=gb:AB018284.1 gb:AF078035.1 gb:NM_015904.1		
217717_s_at	GW128	BF246499	GW128 protein		Hs.182238

207135_at		NM_000621	gb:NM_000621.1 /DEF=Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA. /FEA=mRNA /GEN=HTR2A /PROD=5-hydroxytryptamine (serotonin) receptor 2A /DB_XREF=gi:10835174 /UG=Hs.298623 5-hydroxytryptamine (serotonin) receptor 2A /FL=gb:NM_000621.1		
217645_at		AW088547	ESTs, Weakly similar to hypothetical protein FLJ20378 [Homo sapiens] [H.sapiens]		Hs.390733
206818_s_at		NM_017649	gb:NM_017649.1 /DEF=Homo sapiens hypothetical protein FLJ20064 (FLJ20064), mRNA. /FEA=mRNA /GEN=FLJ20064 /PROD=hypothetical protein FLJ20064 /DB_XREF=gi:8923070 /UG=Hs.271221 hypothetical protein FLJ20064 /FL=gb:NM_017649.1		
61732_r_at	CMG1	AI610355	capillary morphogenesis protein 1		Hs.288617

205839_s_at		NM_004758	gb:NM_004758.1 /DEF=Homo sapiens peripheral benzodiazepine receptor-associated protein 1 (PRAX-1), mRNA. /FEA=mRNA /GEN=PRAX-1 /PROD=peripheral benzodiazepine receptor-associatedprotein 1 /DB_XREF=gi:4758955 /UG=Hs.112499 peripheral benzodiazepine receptor-associated protein 1 /FL=gb:AF039571.1 gb:NM_004758.1		
213164_at		AI867198	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal - human (fragments) [H.sapiens]		Hs.389698
200803_s_at		AF033095	gb:AF033095.1 /DEF=Homo sapiens testis enhanced gene transcript protein (TEGT) mRNA, complete cds. /FEA=mRNA /GEN=TEGT /PROD=testis enhanced gene transcript protein /DB_XREF=gi:2645728 /UG=Hs.74637 testis enhanced gene transcript (BAX inhibitor 1) /FL=gb:BC000916.1 gb:AF033095.1 gb:NM_003217.1		

217790_s_at		NM_007107	gb:NM_007107.1 /DEF=Homo sapiens signal sequence receptor, gamma (translocon-associated protein gamma) (SSR3), mRNA. /FEA=mRNA /GEN=SSR3 /PROD=signal sequence receptor, gamma(translocon-associated protein gamma) /DB_XREF=gi:6005883 /UG=Hs.28707 signal sequence receptor, gamma (translocon-associated protein gamma) /FL=gb:AF110647.1 gb:NM_007107.1		
213503_x_at	ANXA2	BE908217	annexin A2		Hs.217493
37549_g_at	B1	U87408	PTH-responsive osteosarcoma B1 protein	NM_014451	Hs.79340
217042_at		AL096716	Consensus includes gb:AL096716.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564M1462 (from clone DKFZp564M1462); partial cds. /FEA=mRNA /GEN=DKFZp564M1462 /PROD=hypothetical protein /DB_XREF=gi:5419850 /UG=Hs.226007 DKFZP564M1462 protein		

201348_at		NM_002084	gb:NM_002084.2 /DEF=Homo sapiens glutathione peroxidase 3 (plasma) (GPX3), mRNA. /FEA=mRNA /GEN=GPX3 /PROD=plasma glutathione peroxidase 3 precursor /DB_XREF=gi:6006000 /UG=Hs.172153 glutathione peroxidase 3 (plasma) /FL=gb:D00632.1 gb:NM_002084.2 gb:AF217787.1		

204675_at		NM_001047	gb:NM_001047.1 /DEF=Homo sapiens steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1) (SRD5A1), mRNA. /FEA=mRNA /GEN=SRD5A1 /PROD=steroid-5-alpha-reductase, alpha polypeptide 1(3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1) /DB_XREF=gi:4507200 /UG=Hs.552 steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1) /FL=gb:M32313.1 gb:AF052126.1 gb:NM_001047.1		
207724_s_at		NM_014946	gb:NM_014946.2 /DEF=Homo sapiens spastic paraplegia 4 (autosomal dominant; spastin) (SPG4), mRNA. /FEA=mRNA /GEN=SPG4 /PROD=spastin /DB_XREF=gi:11875210 /UG=Hs.26334 spastic paraplegia 4 (autosomal dominant; spastin) /FL=gb:NM_014946.2		

201618_x_at		NM_003801	gb:NM_003801.2 /DEF=Homo sapiens anchor attachment protein 1 (Gaa1p, yeast) homolog (GPAA1), mRNA. /FEA=mRNA /GEN=GPAA1 /PROD=anchor attachment protein 1 /DB_XREF=gi:6031166 /UG=Hs.4742 anchor attachment protein 1 (Gaa1p, yeast) homolog /FL=gb:BC003171.1 gb:BC004129.1 gb:AB006969.1 gb:AB002135.1 gb:NM_003801.2		
204771_s_at	TTF1	AI632304	transcription termination factor, RNA polymerase I		Hs.54780
201601_x_at		NM_003641	gb:NM_003641.1 /DEF=Homo sapiens interferon induced transmembrane protein 1 (9-27) (IFITM1), mRNA. /FEA=mRNA /GEN=IFITM1 /PROD=interferon induced transmembrane protein 1(9-27) /DB_XREF=gi:4504580 /UG=Hs.146360 interferon induced transmembrane protein 1 (9-27) /FL=gb:BC000897.1 gb:J04164.1 gb:NM_003641.1		

216870_x_at		AF264787	Consensus includes gb:AF264787.1 /DEF=Homo sapiens BCMS-upstream neighbor (BCMSUN) mRNA, partial sequence. /FEA=mRNA /DB_XREF=gi:11141510 /UG=Hs.43628 deleted in lymphocytic leukemia, 2		
217918_at		NM_014183	gb:NM_014183.1 /DEF=Homo sapiens HSPC162 protein (HSPC162), mRNA. /FEA=mRNA /GEN=HSPC162 /PROD=HSPC162 protein /DB_XREF=gi:7661821 /UG=Hs.100002 HSPC162 protein /FL=gb:BC002481.1 gb:AY026513.1 gb:AF161511.1 gb:NM_014183.1 gb:AF165516.1		

201189_s_at		NM_002224	gb:NM_002224.1 /DEF=Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3), mRNA. /FEA=mRNA /GEN=ITPR3 /PROD=inositol 1,4,5-triphosphate receptor, type 3 /DB_XREF=gi:4504794 /UG=Hs.77515 inositol 1,4,5-triphosphate receptor, type 3 /FL=gb:D26351.1 gb:NM_002224.1 gb:U01062.1		
205236_x_at		NM_003102	gb:NM_003102.1 /DEF=Homo sapiens superoxide dismutase 3, extracellular (SOD3), mRNA. /FEA=mRNA /GEN=SOD3 /PROD=superoxide dismutase 3, extracellular /DB_XREF=gi:4507150 /UG=Hs.2420 superoxide dismutase 3, extracellular /FL=gb:J02947.1 gb:NM_003102.1		

201162_at		NM_001553	gb:NM_001553.1 /DEF=Homo sapiens insulin-like growth factor binding protein 7 (IGFBP7), mRNA. /FEA=mRNA /GEN=IGFBP7 /PROD=insulin-like growth factor binding protein 7 /DB_XREF=gi:4504618 /UG=Hs.119206 insulin-like growth factor binding protein 7 /FL=gb:L19182.1 gb:NM_001553.1		
200618_at		NM_006148	gb:NM_006148.1 /DEF=Homo sapiens LIM and SH3 protein 1 (LASP1), mRNA. /FEA=mRNA /GEN=LASP1 /PROD=LIM and SH3 protein 1 /DB_XREF=gi:5453709 /UG=Hs.75080 LIM and SH3 protein 1 /FL=gb:NM_006148.1		

205070_at		NM_019071	gb:NM_019071.1 /DEF=Homo sapiens inhibitor of growth family, member 3 (ING3), mRNA. /FEA=mRNA /GEN=ING3 /PROD=inhibitor of growth family, member 3 /DB_XREF=gi:9506658 /UG=Hs.143198 inhibitor of growth family, member 3 /FL=gb:AF074968.1 gb:AY007790.1 gb:NM_019071.1		
200654_at		J02783	gb:J02783.1 /DEF=Human thyroid hormone binding protein (p55) mRNA, complete cds. /FEA=mRNA /GEN=P4HB /DB_XREF=gi:339646 /UG=Hs.75655 procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) /FL=gb:J02783.1 gb:NM_000918.1		

217832_at		NM_006372	Consensus includes gb:BE672181 /FEA=EST /DB_XREF=gi:10032712 /DB_XREF=est:7b51c08.x1 /CLONE=IMAGE:3231758 /UG=Hs.155489 NS1-associated protein 1 /FL=gb:AF155568.1 gb:NM_006372.1		
214305_s_at	SF3B1	AW003030	splicing factor 3b, subunit 1, 155kDa		Hs.334826
200617_at		NM_014730	gb:NM_014730.1 /DEF=Homo sapiens KIAA0152 gene product (KIAA0152), mRNA. /FEA=mRNA /GEN=KIAA0152 /PROD=KIAA0152 gene product /DB_XREF=gi:7661947 /UG=Hs.181418 KIAA0152 gene product /FL=gb:BC000371.1 gb:D63486.1 gb:NM_014730.1		

212268_at		NM_030666	Consensus includes gb:NM_030666.1 /DEF=Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1 (SERPINB1), mRNA. /FEA=CDS /GEN=SERPINB1 /PROD=serine (or cysteine) proteinase inhibitor, cladeB (ovalbumin), member 1 /DB_XREF=gi:13489086 /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1 /FL=gb:NM_030666.1		
211779_x_at		BC006155	gb:BC006155.1 /DEF=Homo sapiens, clone MGC:13188, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:13188) /DB_XREF=gi:13544040 /FL=gb:BC006155.1		

212264_s_at		D87450	Consensus includes gb:BE645850 /FEA=EST /DB_XREF=gi:9970161 /DB_XREF=est:7e77c03.x1 /CLONE=IMAGE:3288484 /UG=Hs.154978 KIAA0261 protein		
209869_at		AF284095	gb:AF284095.1 /DEF=Homo sapiens alpha-2A adrenergic receptor mRNA, complete cds. /FEA=mRNA /PROD=alpha-2A adrenergic receptor /DB_XREF=gi:13447750 /UG=Hs.249159 adrenergic, alpha-2A-, receptor /FL=gb:AF284095.1 gb:NM_000681.1		
211929_at		BE867771	Homo sapiens BX1 mRNA, partial cds		Hs.249247
201628_s_at		NM_006570	gb:NM_006570.1 /DEF=Homo sapiens Ras-related GTP-binding protein (RAGA), mRNA. /FEA=mRNA /GEN=RAGA /PROD=Ras-related GTP-binding protein /DB_XREF=gi:5729998 /UG=Hs.57304 Ras-related GTP-binding protein /FL=gb:U41654.1 gb:NM_006570.1		

212288_at		AB011126	Consensus includes gb:AB011126.1 /DEF=Homo sapiens mRNA for KIAA0554 protein, partial cds. /FEA=mRNA /GEN=KIAA0554 /PROD=KIAA0554 protein /DB_XREF=gi:3043631 /UG=Hs.301763 KIAA0554 protein		
201196_s_at		M21154	gb:M21154.1 /DEF=Human S-adenosylmethionine decarboxylase mRNA, complete cds. /FEA=mRNA /GEN=AMD2 /DB_XREF=gi:178517 /UG=Hs.262476 S-adenosylmethionine decarboxylase 1 /FL=gb:BC000171.2 gb:M21154.1 gb:NM_001634.3		
209539_at		D25304	Consensus includes gb:D25304.1 /DEF=Human mRNA for KIAA0006 gene, partial cds. /FEA=mRNA /GEN=KIAA0006 /DB_XREF=gi:435445 /UG=Hs.79307 RacCdc42 guanine exchange factor (GEF) 6 /FL=gb:D13631.1		

214902_x_at		AL080232	Consensus includes gb:AL080232.1 /DEF=Homo sapiens mRNA; cDNA DKFZp586A061 (from clone DKFZp586A061). /FEA=mRNA /DB_XREF=gi:5262725 /UG=Hs.220696 Homo sapiens mRNA; cDNA DKFZp586A061 (from clone DKFZp586A061)		
202560_s_at		NM_015607	gb:NM_015607.1 /DEF=Homo sapiens DKFZP547E1010 protein (DKFZP547E1010), mRNA. /FEA=mRNA /GEN=DKFZP547E1010 /PROD=DKFZP547E1010 protein /DB_XREF=gi:7661589 /UG=Hs.323817 DKFZP547E1010 protein /FL=gb:NM_015607.1		
201018_at	EIF1A	BE542684	eukaryotic translation initiation factor 1A		Hs.4310

203991_s_at		NM_021140	gb:NM_021140.1 /DEF=Homo sapiens ubiquitously transcribed tetratricopeptide repeat gene, X chromosome (UTX), mRNA. /FEA=mRNA /GEN=UTX /PROD=ubiquitously transcribed tetratricopeptiderepeat gene, X chromosome /DB_XREF=gi:10863942 /UG=Hs.13980 ubiquitously transcribed tetratricopeptide repeat gene, X chromosome /FL=gb:NM_021140.1 gb:AF000992.1 gb:AF000993.1		
205191_at		NM_006915	gb:NM_006915.1 /DEF=Homo sapiens retinitis pigmentosa 2 (X-linked recessive) (RP2), mRNA. /FEA=mRNA /GEN=RP2 /PROD=XRP2 protein /DB_XREF=gi:5902059 /UG=Hs.44766 retinitis pigmentosa 2 (X-linked recessive) /FL=gb:NM_006915.1		
221498_at		BF939727	ESTs, Weakly similar to hypothetical protein FLJ20378 [Homo sapiens] [H.sapiens]		Hs.409278

208706_s_at		AL080102	Consensus includes gb:AK026933.1 /DEF=Homo sapiens cDNA: FLJ23280 fis, clone HEP07194. /FEA=mRNA /DB_XREF=gi:10439907 /UG=Hs.286236 eukaryotic translation initiation factor 5 /FL=gb:AL080102.1		
220173_at		NM_025057	gb:NM_025057.1 /DEF=Homo sapiens hypothetical protein FLJ23189 (FLJ23189), mRNA. /FEA=mRNA /GEN=FLJ23189 /PROD=hypothetical protein FLJ23189 /DB_XREF=gi:13376590 /UG=Hs.287733 hypothetical protein FLJ23189 /FL=gb:NM_025057.1		
208677_s_at	BSG	AL550657	basigin (OK blood group)		Hs.74631

220044_x_at		NM_016424	gb:NM_016424.1 /DEF=Homo sapiens cisplatin resistance-associated overexpressed protein (LUC7A), mRNA. /FEA=mRNA /GEN=LUC7A /PROD=cisplatin resistance-associated overexpressedprotein /DB_XREF=gi:7706534 /UG=Hs.3688 cisplatin resistance-associated overexpressed protein /FL=gb:NM_016424.1		
203694_s_at		NM_003587	gb:NM_003587.2 /DEF=Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide 16 (DDX16), mRNA. /FEA=mRNA /GEN=DDX16 /PROD=DEADH (Asp-Glu-Ala-AspHis) box polypeptide 16 /DB_XREF=gi:13787201 /UG=Hs.12797 DEADH (Asp-Glu-Ala-AspHis) box polypeptide 16 /FL=gb:NM_003587.2 gb:AB011149.1 gb:AB001601.1		

203315_at		BC000103	gb:BC000103.1 /DEF=Homo sapiens, NCK adaptor protein 2, clone MGC:1698, mRNA, complete cds. /FEA=mRNA /PROD=NCK adaptor protein 2 /DB_XREF=gi:12652708 /UG=Hs.101695 NCK adaptor protein 2 /FL=gb:BC000103.1 gb:AF043119.1 gb:AF047487.1 gb:NM_003581.1		
204151_x_at		NM_001353	/DEF=Homo sapiens aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase) (AKR1C1), mRNA. /FEA=mRNA /GEN=AKR1C1 /PROD=aldo-keto reductase family 1, member C1(dihydrodiol dehydrogenase 1; 20-alpha(3-alpha)-hydroxysteroid dehydrogenase) /DB_XREF=gi:5453542 /UG=Hs.306098 aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase) /FL=gb:U05684.1		

202065_s_at		NM_003626	Consensus includes gb:BG033593 /FEA=EST /DB_XREF=gi:12426042 /DB_XREF=est:602301717F1 /CLONE=IMAGE:4403212 /UG=Hs.183648 protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 /FL=gb:NM_003626.1 gb:U22816.1		
208250_s_at		NM_004406	gb:NM_004406.1 /DEF=Homo sapiens deleted in malignant brain tumors 1 (DMBT1), transcript variant 1, mRNA. /FEA=mRNA /GEN=DMBT1 /PROD=deleted in malignant brain tumors 1 isoform aprecursor /DB_XREF=gi:4758169 /UG=Hs.279611 deleted in malignant brain tumors 1 /FL=gb:NM_004406.1		

212956_at		AB020689	Consensus includes gb:AI348094 /FEA=EST /DB_XREF=gi:4085300 /DB_XREF=est:qp61g12.x1 /CLONE=IMAGE:1927558 /UG=Hs.90419 KIAA0882 protein		
39313_at	PRKWNK1	AB002342	protein kinase, lysine deficient 1	NM_018979	Hs.184592
209943_at		AF176699	gb:AF176699.1 /DEF=Homo sapiens F-box protein FBL4 mRNA, complete cds. /FEA=mRNA /PROD=F-box protein FBL4 /DB_XREF=gi:6103636 /UG=Hs.49526 f-box and leucine-rich repeat protein 4 /FL=gb:AF176699.1 gb:AF199355.1 gb:NM_012160.1		
204754_at	HLF	AI810712	hepatic leukemia factor		Hs.250692

206467_x_at		NM_003823	gb:NM_003823.1 /DEF=Homo sapiens tumor necrosis factor receptor superfamily, member 6b, decoy (TNFRSF6B), mRNA. /FEA=mRNA /GEN=TNFRSF6B /PROD=decoy receptor 3 /DB_XREF=gi:4507584 /UG=Hs.278556 tumor necrosis factor receptor superfamily, member 6b, decoy /FL=gb:AF104419.1 gb:NM_003823.1 gb:AF134240.1 gb:AF217794.1		
823_at	CX3CL1	U84487	chemokine (C-X3-C motif) ligand 1	NM_002996	Hs.80420
220319_s_at		NM_013262	gb:NM_013262.2 /DEF=Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA. /FEA=mRNA /GEN=MIR /PROD=myosin regulatory light chain interactingprotein /DB_XREF=gi:10880121 /UG=Hs.20072 myosin regulatory light chain interacting protein /FL=gb:AF187016.2 gb:NM_013262.2 gb:BC002860.1		
215854_at		AU146050	ESTs		Hs.287459

220272_at		NM_017637	gb:NM_017637.1 /DEF=Homo sapiens hypothetical protein FLJ20043 (FLJ20043), mRNA. /FEA=mRNA /GEN=FLJ20043 /PROD=hypothetical protein FLJ20043 /DB_XREF=gi:8923050 /UG=Hs.103853 hypothetical protein FLJ20043 /FL=gb:NM_017637.1		
216595_at		AL049983	Consensus includes gb:AL049983.1 /DEF=Homo sapiens mRNA; cDNA DKFZp564D042 (from clone DKFZp564D042). /FEA=mRNA /DB_XREF=gi:4884234 /UG=Hs.240136 Homo sapiens mRNA; cDNA DKFZp564D042 (from clone DKFZp564D042)		

207554_x_at		NM_001060	gb:NM_001060.1 /DEF=Homo sapiens thromboxane A2 receptor (TBXA2R), mRNA. /FEA=mRNA /GEN=TBXA2R /PROD=thromboxane A2 receptor /DB_XREF=gi:4507380 /UG=Hs.89887 thromboxane A2 receptor /FL=gb:NM_001060.1 gb:D38081.1 gb:U27325.1		
47560_at	FLJ11939	AI525402	hypothetical protein FLJ11939		Hs.94229
203797_at		AF039555	gb:AF039555.1 /DEF=Homo sapiens visinin-like protein 1 (VSNL1) mRNA, complete cds. /FEA=mRNA /GEN=VSNL1 /PROD=visinin-like protein 1 /DB_XREF=gi:4104813 /UG=Hs.2288 visinin-like 1 /FL=gb:AF039555.1 gb:NM_003385.1 gb:AB001104.1 gb:U14747.1		

219263_at		NM_024539	gb:NM_024539.1 /DEF=Homo sapiens hypothetical protein FLJ23516 (FLJ23516), mRNA. /FEA=mRNA /GEN=FLJ23516 /PROD=hypothetical protein FLJ23516 /DB_XREF=gi:13375696 /UG=Hs.9238 hypothetical protein FLJ23516 /FL=gb:NM_024539.1		
213393_at		U79290	Consensus includes gb:AI767210 /FEA=EST /DB_XREF=gi:5233719 /DB_XREF=est:wi94d05.x1 /CLONE=IMAGE:2400969 /UG=Hs.90449 Human clone 23908 mRNA sequence		
202756_s_at		NM_002081	gb:NM_002081.1 /DEF=Homo sapiens glypican 1 (GPC1), mRNA. /FEA=mRNA /GEN=GPC1 /PROD=glypican 1 precursor /DB_XREF=gi:4504080 /UG=Hs.2699 glypican 1 /FL=gb:NM_002081.1		

203337_x_at		NM_004763	gb:NM_004763.1 /DEF=Homo sapiens integrin cytoplasmic domain-associated protein 1 (ICAP-1A), transcript variant 1, mRNA. /FEA=mRNA /GEN=ICAP-1A /PROD=integrin cytoplasmic domain-associated protein1, isoform 1 /DB_XREF=gi:4758577 /UG=Hs.173274 integrin cytoplasmic domain-associated protein 1 /FL=gb:AF012023.1 gb:NM_004763.1		
214277_at	COX11	AI376724	COX11 homolog, cytochrome c oxidase assembly protein (yeast)		Hs.241515
215695_s_at		U94357	Consensus includes gb:U94357.1 /DEF=Homo sapiens glycogenin-2 delta (glycogenin-2) mRNA, partial cds. /FEA=mRNA /GEN=glycogenin-2 /PROD=glycogenin-2 delta /DB_XREF=gi:2618756 /UG=Hs.58589 glycogenin 2		

201140_s_at		NM_004583	gb:NM_004583.1 /DEF=Homo sapiens RAB5C, member RAS oncogene family (RAB5C), mRNA. /FEA=mRNA /GEN=RAB5C /PROD=RAB5C, member RAS oncogene family /DB_XREF=gi:4759019 /UG=Hs.479 RAB5C, member RAS oncogene family /FL=gb:NM_004583.1 gb:U11293.1 gb:U18420.1 gb:AF141304.1		
213359_at	HNRPD	W74620	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)		Hs.303627
218575_at		NM_022662	gb:NM_022662.1 /DEF=Homo sapiens meiotic checkpoint regulator (MCPR), mRNA. /FEA=mRNA /GEN=MCPR /PROD=meiotic checkpoint regulator /DB_XREF=gi:12056970 /UG=Hs.40137 anaphase-promoting complex 1; meiotic checkpoint regulator /FL=gb:NM_022662.1		

220399_at		NM_024796	gb:NM_024796.1 /DEF=Homo sapiens hypothetical protein FLJ22639 (FLJ22639), mRNA. /FEA=mRNA /GEN=FLJ22639 /PROD=hypothetical protein FLJ22639 /DB_XREF=gi:13376167 /UG=Hs.157184 hypothetical protein FLJ22639 /FL=gb:NM_024796.1		
207941_s_at		NM_004902	gb:NM_004902.1 /DEF=Homo sapiens splicing factor (CC1.3) (CC1.3), mRNA. /FEA=mRNA /GEN=CC1.3 /PROD=splicing factor (CC1.3) /DB_XREF=gi:4757925 /UG=Hs.145696 splicing factor (CC1.3) /FL=gb:L10910.1 gb:NM_004902.1		

207969_x_at		NM_020109	gb:NM_020109.1 /DEF=Homo sapiens acrosomal vesicle protein 1 (ACRV1), transcript variant 5, mRNA. /FEA=mRNA /GEN=ACRV1 /PROD=acrosomal vesicle protein 1, isoform eprecursor /DB_XREF=gi:9955932 /UG=Hs.169222 acrosomal vesicle protein 1 /FL=gb:NM_020109.1		
216565_x_at	dJ781L3.1	AL121994	dJ781L3.1 (similar to IFITM3 (interferon induced transmembrane protein 3 (1-8U))) match: proteins: Sw:Q01628 Sw:Q01629 Tr:Q9R175 Tr:Q9R176 Sw:Q91499 Sw:P26376 Tr:O88728 Sw:P13164; Human DNA sequence from clone RP4-781L3 on chromosome 1p34.3-36.11 Contains a pseudogene similar to IFITM3 (interferon inducedntransmembrane protein 3 (1-8U)), STSs and GSSs, complete sequence.		

213083_at		AJ005866	Consensus includes gb:AJ005866.1 /DEF=Homo sapiens mRNA for putative Sqv-7-like protein, partial. /FEA=mRNA /PROD=Sqv-7-like protein /DB_XREF=gi:4008516 /UG=Hs.90078 nucleotide-sugar transporter similar to C. elegans sqv-7		
207332_s_at		NM_003234	gb:NM_003234.1 /DEF=Homo sapiens transferrin receptor (p90, CD71) (TFRC), mRNA. /FEA=mRNA /GEN=TFRC /PROD=transferrin receptor (p90, CD71) /DB_XREF=gi:4507456 /UG=Hs.77356 transferrin receptor (p90, CD71) /FL=gb:NM_003234.1		
71933_at	WNT6	AI218134	wingless-type MMTV integration site family, member 6		Hs.29764

204875_s_at		NM_001500	gb:NM_001500.1 /DEF=Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA. /FEA=mRNA /GEN=GMDS /PROD=GDP-mannose 4,6-dehydratase /DB_XREF=gi:4504030 /UG=Hs.105435 GDP-mannose 4,6-dehydratase /FL=gb:BC000117.1 gb:AF042377.1 gb:NM_001500.1		
212062_at		AB014511	Consensus includes gb:AB014511.1 /DEF=Homo sapiens mRNA for KIAA0611 protein, partial cds. /FEA=mRNA /GEN=KIAA0611 /PROD=KIAA0611 protein /DB_XREF=gi:3327035 /UG=Hs.70604 ATPase, Class II, type 9A		
208772_at	FLJ20288	AU160676	FLJ20288 protein		Hs.84045
216399_s_at		AK025663	Consensus includes gb:AK025663.1 /DEF=Homo sapiens cDNA: FLJ22010 fis, clone HEP07134. /FEA=mRNA /DB_XREF=gi:10438253 /UG=Hs.285848 KIAA1454 protein		

212168_at		AB018308	Consensus includes gb:AL514547 /FEA=EST /DB_XREF=gi:12778041 /DB_XREF=est:AL514547 /CLONE=CL0BB004ZC07 (3 prime) /UG=Hs.180895 putative brain nuclearly-targeted protein		
216268_s_at		U77914	Consensus includes gb:U77914.1 /DEF=Human soluble protein Jagged mRNA, partial cds. /FEA=mRNA /PROD=soluble protein Jagged /DB_XREF=gi:1684889 /UG=Hs.91143 jagged 1 (Alagille syndrome)		
200009_at		NM_001494	gb:NM_001494.2 /DEF=Homo sapiens GDP dissociation inhibitor 2 (GDI2), mRNA. /FEA=mRNA /GEN=GDI2 /PROD=GDP dissociation inhibitor 2 /DB_XREF=gi:6598322 /UG=Hs.56845 GDP dissociation inhibitor 2 /FL=gb:BC005145.1 gb:D13988.1 gb:NM_001494.2		

218351_at		NM_017845	gb:NM_017845.1 /DEF=Homo sapiens hypothetical protein FLJ20502 (FLJ20502), mRNA. /FEA=mRNA /GEN=FLJ20502 /PROD=hypothetical protein FLJ20502 /DB_XREF=gi:8923457 /UG=Hs.23956 hypothetical protein FLJ20502 /FL=gb:AF182421.1 gb:NM_017845.1		
219378_at		NM_024561	gb:NM_024561.1 /DEF=Homo sapiens hypothetical protein FLJ22054 (FLJ22054), mRNA. /FEA=mRNA /GEN=FLJ22054 /PROD=hypothetical protein FLJ22054 /DB_XREF=gi:13375728 /UG=Hs.13277 hypothetical protein FLJ22054 /FL=gb:NM_024561.1		
201626_at	INSIG1	BE300521	insulin induced gene 1		Hs.56205
213300_at	KIAA0404	AW168132	KIAA0404 protein		Hs.105850
201160_s_at	CSDA	AL556190	cold shock domain protein A		Hs.198726

208328_s_at		NM_005587	gb:NM_005587.1 /DEF=Homo sapiens MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A) (MEF2A), mRNA. /FEA=mRNA /GEN=MEF2A /PROD=MADS box transcription enhancer factor 2,polypeptide A (myocyte enhancer factor 2A) /DB_XREF=gi:5031906 /UG=Hs.182280 MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A) /FL=gb:NM_005587.1		
219467_at		NM_017676	gb:NM_017676.1 /DEF=Homo sapiens hypothetical protein FLJ20125 (FLJ20125), mRNA. /FEA=mRNA /GEN=FLJ20125 /PROD=hypothetical protein FLJ20125 /DB_XREF=gi:8923123 /UG=Hs.24088 hypothetical protein FLJ20125 /FL=gb:NM_017676.1		
200920_s_at	BTG1	AL535380	B-cell translocation gene 1, anti-proliferative		Hs.77054

218631_at		NM_021732	gb:NM_021732.1 /DEF=Homo sapiens hypothetical protein PP5395 (PP5395), mRNA. /FEA=mRNA /GEN=PP5395 /PROD=hypothetical protein PP5395 /DB_XREF=gi:11119427 /UG=Hs.23918 hypothetical protein PP5395 /FL=gb:NM_021732.1 gb:AF241786.1 gb:BC000877.1		
208655_at	CCNI	BG530368	cyclin I		Hs.79933
208615_s_at	PTP4A2	BF795101	protein tyrosine phosphatase type IVA, member 2		Hs.82911
213366_x_at	ATP5C1	AV711183	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1		Hs.155433
208611_s_at		U83867	gb:U83867.1 /DEF=Human alpha II spectrin mRNA, complete cds. /FEA=mRNA /PROD=alpha II spectrin /DB_XREF=gi:1805279 /UG=Hs.77196 spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) /FL=gb:J05243.1 gb:U83867.1 gb:NM_003127.1		

219443_at		NM_017714	gb:NM_017714.1 /DEF=Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA. /FEA=mRNA /GEN=FLJ20212 /PROD=hypothetical protein FLJ20212 /DB_XREF=gi:8923201 /UG=Hs.88367 hypothetical protein FLJ20212 /FL=gb:NM_017714.1		
213322_at		AL031778	includes gb:AL031778 /DEF=Human DNA sequence from clone 34B21 on chromosome 6p12.1-21.1. Contains part of a gene for a novel protein with ZU5 domain similar to part of Tight Junction Protein ZO1 (TJP1) and UNC5 Homologs, the gene for a novel BZRP (peripheral benzodiazapine... /FEA=mRNA_2 /DB_XREF=gi:4153958 /UG=Hs.183056 Human DNA sequence from clone 34B21 on chromosome 6p12.1-21.1. Contains part of a gene for a novel protein with ZU5 domain similar to		

217730_at		NM_022152	gb:NM_022152.1 /DEF=Homo sapiens PP1201 protein (PP1201), mRNA. /FEA=mRNA /GEN=PP1201 /PROD=PP1201 protein /DB_XREF=gi:11545897 /UG=Hs.184052 PP1201 protein /FL=gb:NM_022152.1		
212331_at		NM_005611	Consensus includes gb:X76061.1 /DEF=H.sapiens p130 mRNA for 130K protein. /FEA=mRNA /GEN=p130 /PROD=130K protein /DB_XREF=gi:416030 /UG=Hs.79362 retinoblastoma-like 2 (p130) /FL=gb:NM_005611.1		
213140_s_at		AB014593	Consensus includes gb:AB014593.1 /DEF=Homo sapiens mRNA for KIAA0693 protein, partial cds. /FEA=mRNA /GEN=KIAA0693 /PROD=KIAA0693 protein /DB_XREF=gi:3327199 /UG=Hs.154429 KIAA0693 protein		
213133_s_at		BE908931	ESTs, Highly similar to GCHUH glycine cleavage system protein H precursor - human [H.sapiens]		Hs.356054

200789_at		NM_001398	gb:NM_001398.1 /DEF=Homo sapiens enoyl Coenzyme A hydratase 1, peroxisomal (ECH1), mRNA. /FEA=mRNA /GEN=ECH1 /PROD=peroxisomal enoyl-coenzyme A hydratase-likeprotein /DB_XREF=gi:4503446 /UG=Hs.196176 enoyl Coenzyme A hydratase 1, peroxisomal /FL=gb:NM_001398.1 gb:U16660.1		
217168_s_at		AF217990	Consensus includes gb:AF217990.1 /DEF=Homo sapiens clone PP1722 unknown mRNA. /FEA=mRNA /PROD=unknown /DB_XREF=gi:10441910 /UG=Hs.146393 homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1		

211168_s_at		D86988	gb:D86988.1 /DEF=Human mRNA for KIAA0221 gene, complete cds. /FEA=mRNA /GEN=KIAA0221 /PROD=KIAA0221 /DB_XREF=gi:1944406 /UG=Hs.12719 regulator of nonsense transcripts 1 /FL=gb:D86988.1		
201200_at		NM_003851	gb:NM_003851.1 /DEF=Homo sapiens cellular repressor of E1A-stimulated genes (CREG), mRNA. /FEA=mRNA /GEN=CREG /PROD=cellular repressor of E1A-stimulated genes /DB_XREF=gi:4503036 /UG=Hs.5710 cellular repressor of E1A-stimulated genes /FL=gb:AF084523.1 gb:NM_003851.1		
211378_x_at		BC001224	gb:BC001224.1 /DEF=Homo sapiens, clone MGC:982, mRNA, complete cds. /FEA=mRNA /PROD=Unknown (protein for MGC:982) /DB_XREF=gi:12654762 /UG=Hs.267690 KIAA1228 protein /FL=gb:BC001224.1		

205911_at		NM_000316	gb:NM_000316.1 /DEF=Homo sapiens parathyroid hormone receptor 1 (PTHR1), mRNA. /FEA=mRNA /GEN=PTHR1 /PROD=parathyroid hormone receptor 1 /DB_XREF=gi:4506270 /UG=Hs.1019 parathyroid hormone receptor 1 /FL=gb:L04308.1 gb:NM_000316.1 gb:U17418.1		
204908_s_at		NM_005178	gb:NM_005178.1 /DEF=Homo sapiens B-cell CLLlymphoma 3 (BCL3), mRNA. /FEA=mRNA /GEN=BCL3 /PROD=B-cell CLLlymphoma 3 /DB_XREF=gi:4885086 /UG=Hs.31210 B-cell CLLlymphoma 3 /FL=gb:M31732.1 gb:NM_005178.1		

202990_at		NM_002863	gb:NM_002863.1 /DEF=Homo sapiens phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) (PYGL), mRNA. /FEA=mRNA /GEN=PYGL /PROD=phosphorylase, glycogen; liver (Hers disease,glycogen storage disease type VI) /DB_XREF=gi:4506352 /UG=Hs.771 phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) /FL=gb:M14636.1 gb:AF066858.1 gb:AF046785.1 gb:NM_002863.1		
202450_s_at		NM_000396	gb:NM_000396.1 /DEF=Homo sapiens cathepsin K (pycnodysostosis) (CTSK), mRNA. /FEA=mRNA /GEN=CTSK /PROD=cathepsin K (pycnodysostosis) /DB_XREF=gi:4503150 /UG=Hs.83942 cathepsin K (pycnodysostosis) /FL=gb:NM_000396.1 gb:U13665.1		

214790_at		AK001406	Consensus includes gb:AK001406.1 /DEF=Homo sapiens cDNA FLJ10544 fis, clone NT2RP2001601, highly similar to Homo sapiens mRNA for KIAA0797 protein. /FEA=mRNA /DB_XREF=gi:7022642 /UG=Hs.27197 SUMO-1-specific protease		
209695_at		BC003105	gb:BC003105.1 /DEF=Homo sapiens, Similar to protein tyrosine phosphatase type IVA, member 3, clone MGC:1950, mRNA, complete cds. /FEA=mRNA /PROD=Similar to protein tyrosine phosphatase typeIVA, member 3 /DB_XREF=gi:13111874 /UG=Hs.43666 protein tyrosine phosphatase type IVA, member 3 /FL=gb:BC003105.1		
212847_at	FUBP1	AL036840	far upstream element (FUSE) binding protein 1		Hs.118962
214022_s_at	IFITM1	AA749101	interferon induced transmembrane protein 1 (9-27)		Hs.146360

202393_s_at		NM_005655	gb:NM_005655.1 /DEF=Homo sapiens TGFB inducible early growth response (TIEG), mRNA. /FEA=mRNA /GEN=TIEG /PROD=TGFB inducible early growth response /DB_XREF=gi:5032176 /UG=Hs.82173 TGFB inducible early growth response /FL=gb:U21847.1 gb:NM_005655.1		
203786_s_at		NM_003287	gb:NM_003287.1 /DEF=Homo sapiens tumor protein D52-like 1 (TPD52L1), mRNA. /FEA=mRNA /GEN=TPD52L1 /PROD=tumor protein D52-like 1 /DB_XREF=gi:4507640 /UG=Hs.16611 tumor protein D52-like 1 /FL=gb:U44427.1 gb:NM_003287.1		

218152_at		NM_018200	gb:NM_018200.1 /DEF=Homo sapiens high-mobility group 20A (HMG20A), mRNA. /FEA=mRNA /GEN=HMG20A /PROD=high-mobility group 20A /DB_XREF=gi:8922632 /UG=Hs.69594 high-mobility group 20A /FL=gb:AF146222.1 gb:NM_018200.1		
221626_at		AL136548	gb:AL136548.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761G18121 (from clone DKFZp761G18121); complete cds. /FEA=mRNA /GEN=DKFZp761G18121 /PROD=hypothetical protein /DB_XREF=gi:12052731 /UG=Hs.260180 Homo sapiens mRNA; cDNA DKFZp761G18121 (from clone DKFZp761G18121); complete cds /FL=gb:AL136548.1		

214582_at		NM_000753	Consensus includes gb:NM_000753.1 /DEF=Homo sapiens 2,3-cyclic nucleotide 3 phosphodiesterase (CNP), mRNA. /FEA=CDS /GEN=CNP /PROD=2,3-cyclic nucleotide 3 phosphodiesterase /DB_XREF=gi:4502924 /UG=Hs.150741 2,3-cyclic nucleotide 3 phosphodiesterase /FL=gb:NM_000753.1		
214657_s_at		AU134977	Human clone 137308 mRNA, partial cds		Hs.408944
218140_x_at		NM_021203	gb:NM_021203.1 /DEF=Homo sapiens APMCF1 protein (APMCF1), mRNA. /FEA=mRNA /GEN=APMCF1 /PROD=APMCF1 protein /DB_XREF=gi:10864014 /UG=Hs.12152 APMCF1 protein /FL=gb:NM_021203.1 gb:AF141882.1		

202843_at		NM_012328	gb:NM_012328.1 /DEF=Homo sapiens microvascular endothelial differentiation gene 1 (MDG1), mRNA. /FEA=mRNA /GEN=MDG1 /PROD=microvascular endothelial differentiation gene1 /DB_XREF=gi:9558754 /UG=Hs.6790 DnaJ (Hsp40) homolog, subfamily B, member 9 /FL=gb:AF083247.1 gb:AL080081.1 gb:AB026908.1 gb:NM_012328.1		
221480_at	HNRPD	BG180941	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)		Hs.303627
202634_at	POLR2K	AL558030	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa		Hs.351475

202667_s_at		NM_006979	gb:NM_006979.1 /DEF=Homo sapiens HLA class II region expressed gene KE4 (HKE4), mRNA. /FEA=mRNA /GEN=HKE4 /PROD=HLA class II region expressed gene KE4 /DB_XREF=gi:5901935 /UG=Hs.278721 HLA class II region expressed gene KE4 /FL=gb:D82060.1 gb:NM_006979.1		
202677_at		NM_002890	gb:NM_002890.1 /DEF=Homo sapiens RAS p21 protein activator (GTPase activating protein) 1 (RASA1), transcript variant 1, mRNA. /FEA=mRNA /GEN=RASA1 /PROD=RAS p21 protein activator 1, isoform 1 /DB_XREF=gi:4506430 /UG=Hs.758 RAS p21 protein activator (GTPase activating protein) 1 /FL=gb:M23379.1 gb:NM_002890.1		
212579_at	KIAA0650	AA868754	KIAA0650 protein		Hs.8118

221435_x_at		NM_031207	gb:NM_031207.1 /DEF=Homo sapiens hypothetical protein HT036 (HT036), mRNA. /FEA=CDS /GEN=HT036 /PROD=hypothetical protein HT036 /DB_XREF=gi:13654271 /FL=gb:NM_031207.1		
203404_at		NM_014782	gb:NM_014782.1 /DEF=Homo sapiens KIAA0512 gene product (KIAA0512), mRNA. /FEA=mRNA /GEN=KIAA0512 /PROD=KIAA0512 gene product /DB_XREF=gi:7662161 /UG=Hs.48924 KIAA0512 gene product; ALEX2 /FL=gb:AB011084.1 gb:NM_014782.1		
221778_at	KIAA1718	BE217882	KIAA1718 protein		Hs.222707
209430_at		AJ001017	Consensus includes gb:AJ001017.2 /DEF=Homo sapiens partial mRNA for TBP-associated factor 170 (TAFII170). /FEA=mRNA /GEN=TAFII170 /PROD=TBP associated factor /DB_XREF=gi:7018281 /UG=Hs.180930 TBP-associated factor 172 /FL=gb:AF038362.1		

210172_at		D26121	gb:D26121.1 /DEF=Human mRNA for ZFM1 protein alternatively spliced product, complete cds. /FEA=mRNA /PROD=ZFM1 protein, alternatively spliced product /DB_XREF=gi:785998 /UG=Hs.169303 Human mRNA for ZFM1 protein alternatively spliced product, complete cds /FL=gb:D26121.1		
201984_s_at		NM_005228	gb:NM_005228.1 /DEF=Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA. /FEA=mRNA /GEN=EGFR /PROD=epidermal growth factor receptor (avianerythroblastic leukemia viral (v-erb-b) oncogene homolog) /DB_XREF=gi:4885198 /UG=Hs.77432 epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) /FL=gb:NM_005228.1		

212434_at	HMGE	AL542571	GrpE-like protein cochaperone		Hs.151903
204345_at		NM_001856	gb:NM_001856.1 /DEF=Homo sapiens collagen, type XVI, alpha 1 (COL16A1), mRNA. /FEA=mRNA /GEN=COL16A1 /PROD=collagen, type XVI, alpha 1 /DB_XREF=gi:11386158 /UG=Hs.26208 collagen, type XVI, alpha 1 /FL=gb:NM_001856.1 gb:M92642.1		
208829_at		AF029750	gb:AF029750.1 /DEF=Homo sapiens tapasin (NGS-17) mRNA, complete cds. /FEA=mRNA /GEN=NGS-17 /PROD=tapasin /DB_XREF=gi:2587057 /UG=Hs.179600 TAP binding protein (tapasin) /FL=gb:AF314222.1 gb:AF009510.1 gb:AF029750.1 gb:AB010639.1 gb:NM_003190.1		
208863_s_at		M72709	gb:M72709.1 /DEF=Human alternative splicing factor mRNA, complete cds. /FEA=mRNA /DB_XREF=gi:179073 /UG=Hs.73737 splicing factor, arginineserine-rich 1 (splicing factor 2, alternate splicing factor) /FL=gb:M72709.1		

219034_at		NM_017851	gb:NM_017851.1 /DEF=Homo sapiens hypothetical protein FLJ20509 (FLJ20509), mRNA. /FEA=mRNA /GEN=FLJ20509 /PROD=hypothetical protein FLJ20509 /DB_XREF=gi:8923470 /UG=Hs.30634 hypothetical protein FLJ20509 /FL=gb:NM_017851.1		
204379_s_at		NM_000142	gb:NM_000142.2 /DEF=Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3), transcript variant 1, mRNA. /FEA=mRNA /GEN=FGFR3 /PROD=fibroblast growth factor receptor 3, isoform 1precursor /DB_XREF=gi:13112046 /UG=Hs.1420 fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) /FL=gb:NM_000142.2 gb:M58051.1		

201887_at		NM_001560	gb:NM_001560.1 /DEF=Homo sapiens interleukin 13 receptor, alpha 1 (IL13RA1), mRNA. /FEA=mRNA /GEN=IL13RA1 /PROD=interleukin 13 receptor, alpha 1 /DB_XREF=gi:4504646 /UG=Hs.285115 interleukin 13 receptor, alpha 1 /FL=gb:NM_001560.1 gb:U81379.3		
209200_at	MEF2C	N22468	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)		Hs.78995
218205_s_at		NM_017572	gb:NM_017572.1 /DEF=Homo sapiens G protein-coupled receptor kinase 7 (GPRK7), mRNA. /FEA=mRNA /GEN=GPRK7 /PROD=G protein-coupled receptor kinase 7 /DB_XREF=gi:9994196 /UG=Hs.261828 G protein-coupled receptor kinase 7 /FL=gb:AF237776.1 gb:AF125532.1 gb:NM_017572.1		
222279_at	HLA-F	AI669379	major histocompatibility complex, class I, F		Hs.377850

215191_at		AW836210	ESTs, Moderately similar to hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]		Hs.387947
219073_s_at		NM_017784	gb:NM_017784.1 /DEF=Homo sapiens hypothetical protein FLJ20363 (FLJ20363), mRNA. /FEA=mRNA /GEN=FLJ20363 /PROD=hypothetical protein FLJ20363 /DB_XREF=gi:8923336 /UG=Hs.321622 hypothetical protein FLJ20363 /FL=gb:BC003168.1 gb:NM_017784.1		
208962_s_at	FADS1	BE540552	fatty acid desaturase 1		Hs.132898
218807_at		NM_006113	gb:NM_006113.2 /DEF=Homo sapiens vav 3 oncogene (VAV3), mRNA. /FEA=mRNA /GEN=VAV3 /PROD=vav 3 oncogene /DB_XREF=gi:7262390 /UG=Hs.267659 vav 3 oncogene /FL=gb:AF067817.1 gb:AF118887.1 gb:NM_006113.2		

202225_at		NM_016823	Consensus includes gb:AW612311 /FEA=EST /DB_XREF=gi:7317497 /DB_XREF=est:hg95e07.x1 /CLONE=IMAGE:2953380 /UG=Hs.306088 v-crk avian sarcoma virus CT10 oncogene homolog /FL=gb:D10656.1 gb:NM_016823.1		
209896_s_at		AF119855	gb:AF119855.1 /DEF=Homo sapiens PRO1847 mRNA, complete cds. /FEA=mRNA /PROD=PRO1847 /DB_XREF=gi:7770146 /UG=Hs.285196 hypothetical protein PRO1847 /FL=gb:AF119855.1		
202103_at	BRD4	BF718610	bromodomain containing 4		Hs.278675
203791_at		NM_005509	gb:NM_005509.2 /DEF=Homo sapiens Dmx-like 1 (DMXL1), mRNA. /FEA=mRNA /GEN=DMXL1 /PROD=Dmx-like 1 /DB_XREF=gi:9961348 /UG=Hs.181042 Dmx-like 1 /FL=gb:NM_005509.2		
214130_s_at	PDE4DIP	AI821791	phosphodiesterase 4D interacting protein (myomegalin)		Hs.265848

DEMANDE OU BREVET VOLUMINEUX

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