(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
16 September 2004 (16.09.2004)

PCT

(10) International Publication Number
WO 2004/079014 A2

(51) International Patent Classification⁷: C12Q 1/68, G01N 33/574

(21) International Application Number: PCT/US2004/006736

(22) International Filing Date: 4 March 2004 (04.03.2004)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/451,942 4 March 2003 (04.03.2003) US

(71) Applicant (for all designated States except US): ARCTURUS BIOSCIENCE, INC.; 400 Logue Avenue, Mountain View, CA 94043-4019 (US).

(72) Inventors; and
(75) Inventors/Applicants (for US only): ERLANDER, Mark, G. [—/US]; 442 Hillcrest Drive, Encinitas, CA (US). MA, Xiao-Jun [—/US]; 4482 Calle Mar De Armonia, San Diego, CA 92130 (US). WANG, Wei [—/US]; San Marcos, CA (US). WITTLIFF, James, L. [—/US]; 1011 Glenbrook Road, Louisville, KY 40223-2211 (US).

(74) Agent: KAWAI, Lau; Townsend and Townsend and Crew LLP, Two Embarcadero Center, 8th Floor, San Francisco, CA 94111 (US).

(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *without international search report and to be republished upon receipt of that report*

(54) Title: SIGNATURES OF ER STATUS IN BREAST CANCER

(57) Abstract: The invention relates to the identification and use of gene expression profiles, or patterns, suitable for identification of populations that are positive and negative for estrogen receptor expression. The gene expression profiles may be embodied in nucleic acid expression, protein expression, or other expression formats, and may be used in the study and/or diagnosis of cells and tissue in breast cancer as well as for the study and/or determination of prognosis of a patient, including breast cancer survival.

WO 2004/079014 A2

Signatures of ER Status in Breast Cancer

RELATED APPLICATIONS

This application claims benefit of priority from U.S. Provisional Patent application 60/451,942, filed March 4, 2003, which is hereby incorporated by reference in its entirety as if fully set forth.

FIELD OF THE INVENTION

The invention relates to the identification and use of gene expression profiles, or patterns, involved in breast cancer survival. In particular, the invention provides the identities of genes that may be used to identify populations that are positive and negative for estrogen receptor expression. The gene expression profiles, whether embodied in nucleic acid expression, protein expression, or other expression formats, are used in the study and/or diagnosis of cells and tissue in breast cancer as well as for the study and/or determination of prognosis of a patient. The profiles may also be used in methods of diagnosis or prognosis.

BACKGROUND OF THE INVENTION

Breast cancer is by far the most common cancer among women. Each year, more than 180,000 and 1 million women in the U.S. and worldwide, respectively, are diagnosed with breast cancer. Breast cancer is the leading cause of death for women between ages 50-55, and is the most common non-preventable malignancy in women in the Western Hemisphere. An estimated 2,167,000 women in the United States are currently living with the disease (National Cancer Institute, Surveillance Epidemiology and End Results (NCI SEER) program, *Cancer Statistics Review (CSR)*, www-seer.ims.nci.nih.gov/Publications/CSR1973 (1998)). Based on cancer rates from 1995 through 1997, a report from the National Cancer Institute (NCI) estimates that about 1 in 8 women in the United States (approximately 12.8 percent) will develop breast cancer during her lifetime (NCI's Surveillance, Epidemiology, and End Results Program (SEER) publication *SEER Cancer Statistics Review 1973-1997).*

Breast cancer is the second most common form of cancer, after skin cancer, among women in the United States. An estimated 250,100 new cases of breast cancer are expected to be diagnosed in the United States in 2001. Of these, 192,200 new cases of more advanced (invasive) breast cancer are expected to occur among women (an increase of 5% over last year), 46,400 new cases of early stage (*in situ*) breast cancer are expected to occur among women (up 9% from last year), and about 1,500 new cases of breast cancer are expected to be diagnosed in men (Cancer Facts & Figures 2001 American Cancer Society). An estimated 40,600 deaths (40,300 women, 400 men) from breast cancer are expected in 2001. Breast cancer ranks second only to lung cancer among causes of cancer deaths in women. Nearly 86% of women who are diagnosed with breast cancer are likely to still be alive five years later, though 24% of them will die of breast cancer after 10 years, and nearly half (47%) will die of breast cancer after 20 years.

Every woman is at risk for breast cancer. Over 70 percent of breast cancers occur in women who have no identifiable risk factors other than age (U.S. General Accounting Office. Breast Cancer, 1971-1991: Prevention, Treatment and Research. GAO/PEMD-92-12; 1991). Only 5 to 10% of breast cancers are linked to a family history of breast cancer (Henderson IC, Breast Cancer. In: Murphy GP, Lawrence WL, Lenhard RE (eds). *Clinical Oncology*. Atlanta, GA: American Cancer Society; 1995:198-219).

Each breast has 15 to 20 sections called lobes. Within each lobe are many smaller lobules. Lobules end in dozens of tiny bulbs that can produce milk. The lobes, lobules, and bulbs are all linked by thin tubes called ducts. These ducts lead to the nipple in the center of a dark area of skin called the areola. Fat surrounds the lobules and ducts. There are no muscles in the breast, but muscles lie under each breast and cover the ribs. Each breast also contains blood vessels and lymph vessels. The lymph vessels carry colorless fluid called lymph, and lead to the lymph nodes. Clusters of lymph nodes are found near the breast in the axilla (under the arm), above the collarbone, and in the chest.

Breast tumors can be either benign or malignant. Benign tumors are not cancerous, they do not spread to other parts of the body, and are not a threat to life.

They can usually be removed, and in most cases, do not come back. Malignant tumors are cancerous, and can invade and damage nearby tissues and organs. Malignant tumor cells may metastasize, entering the bloodstream or lymphatic system. When breast cancer cells metastasize outside the breast, they are often found in the lymph nodes under the arm (axillary lymph nodes). If the cancer has reached these nodes, it means that cancer cells may have spread to other lymph nodes or other organs, such as bones, liver, or lungs.

Major and intensive research has been focussed on early detection, treatment and prevention. This has included an emphasis on determining the presence of precancerous or cancerous ductal epithelial cells. These cells are analyzed, for example, for cell morphology, for protein markers, for nucleic acid markers, for chromosomal abnormalities, for biochemical markers, and for other characteristic changes that would signal the presence of cancerous or precancerous cells. This has led to various molecular alterations that have been reported in breast cancer, few of which have been well characterized in human clinical breast specimens. Molecular alterations include presence/absence of estrogen and progesterone steroid receptors, HER-2 expression/amplification (Mark HF, et al. HER-2/neu gene amplification in stages I-IV breast cancer detected by fluorescent in situ hybridization. Genet Med; 1(3):98-103 1999), Ki-67 (an antigen that is present in all stages of the cell cycle except G0 and used as a marker for tumor cell proliferation, and prognostic markers (including oncogenes, tumor suppressor genes, and angiogenesis markers) like p53, p27, Cathepsin D, pS2, multi-drug resistance (MDR) gene, and CD31.

Estrogen receptor (ER) status has been of particular interest because it has been correlated with prognosis and treatment regimens. Generally speaking, patients identified as having ER positive breast cancer biopsies have a better overall survival expectation while patients with ER negative biopsies are treated more aggressively, such as with immediate chemotherapy after surgical intervention, because of a poor prognosis.

Citation of documents herein is not intended as an admission that any is pertinent prior art. All statements as to the date or representation as to the contents of documents is based on the information available to the applicant and does not constitute any admission as to the correctness of the dates or contents of the documents.

SUMMARY OF THE INVENTION

The present invention relates to the identification and use of gene expression patterns (or profiles or "signatures") which are correlated with (and thus able to discriminate between) cells that are positive or negative for estrogen receptor (ER) expression in breast cancer specimens. The patterns may thus serve as a supplement to assays for ER status in breast cancer samples or used as a substitute for known assays for ER status. The patterns may thus be used in diagnostic or prognostic methods or assays in the clinic to determine the course of treatment following identification of the presence of breast cancer or subsequent surgical removal thereof.

The patterns also provide the identity of genes that may be the focus of therapeutic efforts to identify agents and treatment methods to alleviate the severity of breast cancer, improve the chances for surviving breast cancer, and/or decrease the chances of breast cancer recurrence or metastases. Such agents and methods may be used to increase or decrease the expression of one or more genes of the patterns to restore cells to a less cancerous state or a state with a better prognosis for the patient. The patterns may also be used to identify cellular mechanisms or pathways, as well as the components of such mechanisms or pathways, to be altered or modulated in the treatment of breast cancer.

The present invention provides a non-subjective means for the identification of ER status in breast cancer samples by assaying for the expression patterns associated with ER status. Thus subjective interpretation is necessary and a more accurate assessment of ER status, and breast cancer status and prognosis, is provided. Furthermore, the expression patterns can also be used as a means to assay small, node negative tumors that are not readily assayed by other means.

The gene expression patterns comprise one or more than one gene capable of discriminating between breast cancer that is ER positive or ER negative with significant accuracy. The gene(s) are identified as correlated with ER expression status in breast cancer such that the levels of their expression are relevant to a determination of ER status in breast cancer of a cell. Thus in one aspect, the invention provides a method to determine the ER status of breast cancer of a subject afflicted with, or suspected of having, breast cancer by assaying a cell containing sample from said subject for expression of one or more than one gene disclosed herein as correlated with ER status in breast cancer.

Gene expression patterns of the invention are identified by analysis of gene expression in multiple samples of ER positive and ER negative samples from breast cancer biopsies. The overall gene expression profile of a sample is obtained through quantifying the expression levels of mRNA corresponding to multiple genes to identify genes that are positively, or negatively, correlated, with ER positive and ER negative sample.

A profile of genes that are highly correlated with ER status may be used to assay an sample from a subject afflicted with, or suspected of having, breast cancer to identify the ER status of breast cancer to which the sample belongs. This may be done in combination with, or separate from a direct assay for ER expression. Such assays may be used as part of a method to determine the therapeutic treatment for said subject based upon the ER status identified. The present invention also provides for the advantageous ability to determine ER status in combination with other information to provide more detailed information in diagnosing and treating breast cancer.

The correlated genes may be used singly with significant accuracy or in combination to increase the ability to accurately identify ER status. The present invention thus provides means for correlating a molecular expression phenotype with ER expression and thus a physiological (cellular) state. This correlation also provides a way to molecularly diagnose and/or monitor a cell's status. Additional uses of the correlated gene(s) are in the classification of cells and tissues; determination of diagnosis and/or prognosis; and determination and/or alteration of therapy.

An assay of the invention may utilize a means related to the expression level of the sequences disclosed herein as long as the assay reflects, quantitatively or qualitatively, expression of the sequence. Preferably, however, a quantitative assay means is preferred. The ability to discriminate is conferred by the identification of expression of the individual genes as relevant and not by the form of the assay used to determine the actual level of expression. An assay may utilize any identifying feature of an identified individual gene as disclosed herein as long as the assay reflects, quantitatively or qualitatively, expression of the gene. Identifying features include, but are not limited to, unique nucleic acid sequences used to encode (DNA), or express (RNA), said gene or epitopes specific to, or activities of, a protein encoded by said gene. Alternative means include detection of nucleic acid amplification as indicative of increased expression levels and nucleic acid inactivation, deletion, or methylation, as indicative of decreased expression levels. Stated differently, the invention may be practiced by assaying one or more aspect of the DNA template(s) underlying the expression of the disclosed sequence(s), of the RNA used as an intermediate to express the sequence(s), or of the proteinaceous product expressed by the sequence(s), as well as proteolytic fragments of such products. As such, the detection of the presence of, amount of, stability of, or degradation (including rate) of, such DNA, RNA and proteinaceous molecules may be used in the practice of the invention. As such, all that is required is the identity of the gene(s) necessary to discriminate between ER positive and negative samples and an appropriate cell containing sample for use in an expression assay.

In one aspect, the invention provides for the identification of the gene expression patterns by analyzing global, or near global, gene expression from single cells or homogenous cell populations which have been dissected away from, or otherwise isolated or purified from, contaminating cells beyond that possible by a simple biopsy. Because the expression of numerous genes fluctuate between cells from different patients as well as between cells from the same patient sample, the expression of multiple individual genes may be analyzed to for the best the ability to discriminate ER positive and negative samples.

In a further aspect, the gene(s) capable of discriminating between ER positive and negative samples may be used to identify ER status of an unknown sample of cell(s) from the breast. Preferably, the sample is isolated via non-invasive means. The expression of said gene(s) in said unknown sample may be determined and compared to the expression of said gene(s) in reference data of gene expression patterns from ER positive and/or negative samples. Alternatively, the expression level may be compared to expression levels in normal or non-cancerous cells, preferably from the same sample or subject. In embodiments of the invention utilizing quantitative PCR, the expression level may be compared to expression levels of reference genes in the same sample or a ratio of expression levels may be used. The invention provides for ratios of the expression level of a sequence that is underexpressed to the expression level of a sequence that is overexpressed as a indicator of ER positive or ER negative status. The use of a ratio can reduce comparisons with normal or non-cancerous cells.

One advantage provided by the present invention is that contaminating, non-breast cells (such as infiltrating lymphocytes or other immune system cells) are not present to possibly affect the genes identified or the subsequent analysis of gene expression to identify the status of suspected breast cancer cells. Such contamination is present where a biopsy is used to generate gene expression profiles.

While the present invention has been described mainly in the context of human breast cancer, it may be practiced in the context of breast cancer of any animal known to be potentially afflicted by breast cancer. Preferred animals for the application of the present invention are mammals, particularly those important to agricultural applications (such as, but not limited to, cattle, sheep, horses, and other "farm animals") and for human companionship (such as, but not limited to, dogs and cats).

DETAILED DESCRIPTION OF THE SPECIFIC EMBODIMENTS

Definitions of terms as used herein:

A gene expression "pattern" or "profile" or "signature" refers to the relative expression of a gene between ER positive and negative cells which expression is correlated with being able to distinguish between ER positive and negative cells.

A "gene" is a polynucleotide that encodes a discrete product, whether RNA or proteinaceous in nature. It is appreciated that more than one polynucleotide may be capable of encoding a discrete product. The term includes alleles and polymorphisms of a gene that encodes the same product, or a functionally associated (including gain, loss, or modulation of function) analog thereof, based upon chromosomal location and ability to recombine during normal mitosis.

A "sequence" or "gene sequence" as used herein is a nucleic acid molecule or polynucleotide composed of a discrete order of nucleotide bases. The term includes the ordering of bases that encodes a discrete product (i.e. "coding region"), whether RNA or proteinaceous in nature, as well as the ordered bases that precede or follow a "coding region". Non-limiting examples of the latter include 5' and 3' untranslated regions of a gene. It is appreciated that more than one polynucleotide may be capable of encoding a discrete product. It is also appreciated that alleles and polymorphisms of the disclosed sequences may exist and may be used in the practice of the invention to identify the expression level(s) of the disclosed sequences or the allele or polymorphism. Identification of an allele or polymorphism depends in part upon chromosomal location and ability to recombine during mitosis.

The terms "correlate" or "correlation" or equivalents thereof refer to an association between expression of one or more genes and the ER status of a breast cancer cell and/or a breast cancer patient. A gene may be expressed at higher or lower levels and still be correlated with ER status and thus breast cancer survival or outcome. The invention provides for the correlation between increases, as well as decreases, in expression of gene sequences and ER positive or negative status. Increases and decreases may be readily expressed in the form of a ratio between expression in a non-normal cell and a normal cell such that a ratio of one (1) indicates no difference while ratios of two (2) and one-half indicate twice as much, and half as much, expression in the non-normal cell versus the normal cell, respectively. Expression levels can be readily determined by quantitative methods as described below.

For example, increases in gene expression can be indicated by ratios of or about 1.1, of or about 1.2, of or about 1.3, of or about 1.4, of or about 1.5, of or about 1.6, of or about 1.7, of or about 1.8, of or about 1.9, of or about 2, of or about 2.5, of or about 3, of or about 3.5, of or about 4, of or about 4.5, of or about 5, of or about 5.5, of or about 6, of or about 6.5, of or about 7, of or about 7.5, of or about 8, of or about 8.5, of or about 9, of or about 9.5, of or about 10, of or about 15, of or about 20, of or about 30, of or about 40, of or about 50, of or about 60, of or about 70, of or about 80, of or about 90, of or about 100, of or about 150, of or about 200, of or about 300, of or about 400, of or about 500, of or about 600, of or about 700, of or about 800, of or about 900, or of or about 1000. A ratio of 2 is a 100% (or a two-fold) increase in expression. Decreases in gene expression can be indicated by ratios of or about 0.9, of or about 0.8, of or about 0.7, of or about 0.6, of or about 0.5, of or about 0.4, of or about 0.3, of or about 0.2, of or about 0.1, of or about 0.05, of or about 0.01, of or about 0.005, of or about 0.001, of or about 0.0005, of or about 0.0001, of or about 0.00005, of or about 0.00001, of or about 0.000005, or of or about 0.000001.

For a given phenotype, a ratio of the expression of a gene sequence expressed at increased levels in correlation with an ER status to the expression of a gene sequence expressed at decreased levels in correlation with the ER status may also be used as an indicator of the phenotype. As a non-limiting example, the ER positive status may be correlated with increased expression of a gene sequence overexpressed in ER positive cells as well as decreased expression of a gene sequence underexpressed in ER positive cells. Therefore, a ratio of the expression levels of the underexpressed sequence to the expression levels of the overexpressed sequence may be used as an indicator of ER status. Ratios comprising gene sequences that are differentially expressed in ER negative cells may also be used.

A “polynucleotide” is a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. This term refers only to the primary structure of the molecule. Thus, this term includes double- and single-stranded DNA and RNA. It also includes known types of modifications including labels known in the art, methylation, “caps”, substitution of one or more of the naturally occurring nucleotides with an analog, and internucleotide modifications such as uncharged linkages (e.g., phosphorothioates, phosphorodithioates, etc.), as well as unmodified forms of the polynucleotide.

The term “amplify” is used in the broad sense to mean creating an amplification product can be made enzymatically with DNA or RNA polymerases. “Amplification,” as used herein, generally refers to the process of producing multiple copies of a desired sequence, particularly those of a sample. "Multiple copies" mean at least 2 copies. A "copy" does not necessarily mean perfect sequence complementarity or identity to the template sequence.

By corresponding is meant that a nucleic acid molecule shares a substantial amount of sequence identity with another nucleic acid molecule. Substantial amount means at least 95%, usually at least 98% and more usually at least 99%, and sequence identity is determined using the BLAST algorithm, as described in Altschul et al. (1990), J. Mol. Biol. 215:403-410 (using the published default setting, i.e. parameters w=4, t=17). Methods for amplifying mRNA are generally known in the art, and include reverse transcription PCR (RT-PCR) and those described in U.S. Patent Application 10/062,857 (filed on October 25, 2001), as well as U.S. Provisional Patent Applications 60/298,847 (filed June 15, 2001) and 60/257,801 (filed December 22, 2000), all of which are hereby incorporated by reference in their entireties as if fully set forth. Another method which may be used is quantitative PCR (or Q-PCR). Alternatively, RNA may be directly labeled as the corresponding cDNA by methods known in the art.

A "microarray" is a linear or two-dimensional array of preferably discrete regions, each having a defined area, formed on the surface of a solid support such as, but not limited to, glass, plastic, or synthetic membrane. The density of the discrete regions on a microarray is determined by the total numbers of immobilized polynucleotides to be detected on the surface of a single solid phase support, preferably at least about $50/cm^2$, more preferably at least about $100/cm^2$, even more preferably at least about $500/cm^2$, but preferably below about $1,000/cm^2$. Preferably, the arrays contain less than about 500, about 1000, about 1500, about 2000, about 2500, or about 3000 immobilized polynucleotides in total. As used herein, a DNA microarray is an array of oligonucleotides or polynucleotides placed on a chip or other surfaces used to hybridize to amplified or cloned polynucleotides from a sample. Since the position of each particular group of primers in the array is known, the identities of a sample polynucleotides can be determined based on their binding to a particular position in the microarray.

Because the invention relies upon the identification of genes that are over- or under-expressed, one embodiment of the invention involves determining expression by hybridization of mRNA, or an amplified or cloned version thereof, of a sample cell to a polynucleotide that is unique to a particular gene sequence. Preferred polynucleotides of this type contain at least about 20, at least about 22, at least about 24, at least about 26, at least about 28, at least about 30, or at least about 32 consecutive basepairs of a gene sequence that is not found in other gene sequences. The term "about" as used in the previous sentence refers to an increase or decrease of 1 from the stated numerical value. Even more preferred are polynucleotides of at least or about 50, at least or about 100, at least about or 150, at least or about 200, at least or about 250, at least or about 300, at least or about 350, or at least or about 400 basepairs of a gene sequence that is not found in other gene sequences. The term "about" as used in the preceding sentence refers to an increase or decrease of 10% from the stated numerical value. Such polynucleotides may also be referred to as polynucleotide probes that are capable of hybridizing to sequences of the genes, or unique portions thereof, described herein. Preferably, the sequences are those of mRNA encoded by the genes, the corresponding cDNA to such mRNAs, and/or amplified versions of such sequences. In preferred embodiments of the invention, the polynucleotide probes are immobilized on an array, other devices, or in individual spots that localize the probes.

In another embodiment of the invention, all or part of a disclosed sequence may be amplified and detected by methods such as the polymerase chain reaction (PCR) and variations thereof, such as, but not limited to, quantitative PCR (Q-PCR), reverse transcription PCR (RT-PCR), and real-time PCR (including as a means of measuring the initial amounts of mRNA copies for each sequence in a sample), optionally real-time RT-PCR or real-time Q-PCR. Such methods would utilize one or two primers that are complementary to portions of a disclosed sequence, where the primers are used to prime nucleic acid synthesis. The newly synthesized nucleic acids are optionally labeled and may be detected directly or by hybridization to a polynucleotide of the invention. The newly synthesized nucleic acids may be contacted with polynucleotides (containing sequences) of the invention under conditions which allow for their hybridization. Additional methods to detect the expression of expressed nucleic acids include RNAse protection assays, including liquid phase hybridizations, and *in situ* hybridization of cells.

Alternatively, and in yet another embodiment of the invention, gene expression may be determined by analysis of expressed protein in a cell sample of interest by use of one or more antibodies specific for one or more epitopes of individual gene products (proteins), or proteolytic fragments thereof, in said cell sample or in a bodily fluid of a subject. The cell sample may be one of breast cancer epithelial cells enriched from the blood of a subject, such as by use of labeled antibodies against cell surface markers followed by fluorescence activated cell sorting (FACS). Such antibodies are preferably labeled to permit their easy detection after binding to the gene product. Detection methodologies suitable for use in the practice of the invention include, but are not limited to, immunohistochemistry of cell containing samples or tissue, enzyme linked immunosorbent assays (ELISAs) including antibody sandwich assays of cell containing tissues or blood samples, mass spectroscopy, and immuno-PCR.

The term "label" refers to a composition capable of producing a detectable signal indicative of the presence of the labeled molecule. Suitable labels include radioisotopes, nucleotide chromophores, enzymes, substrates, fluorescent molecules, chemiluminescent moieties, magnetic particles, bioluminescent moieties, and the like. As such, a label is any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means.

The term "support" refers to conventional supports such as beads, particles, dipsticks, fibers, filters, membranes and silane or silicate supports such as glass slides.

As used herein, a "breast tissue sample" or "breast cell sample" refers to a sample of breast tissue or fluid isolated from an individual suspected of being afflicted with, or at risk of developing, breast cancer. Such samples are primary isolates (in contrast to cultured cells) and may be collected by any non-invasive means, including, but not limited to, ductal lavage, fine needle aspiration, needle biopsy, the devices and methods described in U.S. Patent 6,328,709, or any other suitable means recognized in the art. Alternatively, the "sample" may be collected by an invasive method, including, but not limited to, surgical biopsy. A sample of the invention may also be one that has been formalin fixed and paraffin embedded (FFPE).

"Expression" and "gene expression" include transcription and/or translation of nucleic acid material.

As used herein, the term "comprising" and its cognates are used in their inclusive sense; that is, equivalent to the term "including" and its corresponding cognates.

Conditions that "allow" an event to occur or conditions that are "suitable" for an event to occur, such as hybridization, strand extension, and the like, or "suitable" conditions are conditions that do not prevent such events from occurring. Thus, these conditions permit, enhance, facilitate, and/or are conducive to the event. Such conditions, known in the art and described herein, depend upon, for example, the nature of the nucleotide sequence, temperature, and buffer conditions. These conditions also depend on what event is desired, such as hybridization, cleavage, strand extension or transcription.

Sequence "mutation," as used herein, refers to any sequence alteration in the sequence of a gene disclosed herein interest in comparison to a reference sequence. A sequence mutation includes single nucleotide changes, or alterations of more than one nucleotide in a sequence, due to mechanisms such as substitution, deletion or insertion. Single nucleotide polymorphism (SNP) is also a sequence mutation as used herein. Because the present invention is based on the relative level of gene expression, mutations in non-coding regions of genes as disclosed herein may also be assayed in the practice of the invention.

"Detection" includes any means of detecting, including direct and indirect detection of gene expression and changes therein. For example, "detectably less" products may be observed directly or indirectly, and the term indicates any reduction (including the absence of detectable signal). Similarly, "detectably more" product means any increase, whether observed directly or indirectly.

Increases and decreases in expression of the disclosed sequences are defined in the following terms based upon percent or fold changes over expression in normal cells. Increases may be of 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, or 200% relative to expression levels in normal cells. Alternatively, fold increases may be of 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, or 10 fold over expression levels in normal cells. Decreases may be of 10, 20, 30, 40, 50, 55, 60, 65, 70, 75, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 99 or 100% relative to expression levels in normal cells.

Unless defined otherwise all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs.

Specific Embodiments

The present invention relates to the identification and use of gene expression patterns (or profiles or "signatures") which discriminate between (or are correlated with) breast cancer cells that are ER positive or negative, preferably ERα positive or negative. Because the overall gene expression profile differs from person to person, cancer to cancer, and cancer cell to cancer cell, correlations between genes expressed or underexpressed in ER positive and negative cells are capable of identifying ER status. ER status has been used as a factor in determinations of therapeutic treatment of patients with breast cancer. For example, ER positive status has been used as an indicator of responsiveness to treatment with tamoxifen and other selective estrogen receptor modulators (SERMs).

The present invention may be practiced with any subset of the genes disclosed herein. Gene expression in cells of breast cancer biopsies were used to identify thousands of genes capable of discriminating between ER positive and negative breast cancer cells as described in the following Example. The identification may be made by using expression profiles of various homogenous breast cancer cell populations, which are optionally isolated by microdissection, such as, but not limited to, laser capture microdissection (LCM) of 100-1000 cells.

Genes that are identified as being expressed differently between ER positive and ER negative cells may be analyzed by standard statistical analysis, such as the t-test, to assign a value for the significance of the difference. Genes with a significance above a particular threshold may be included in a pattern that segregates breast cancer based on ER status.

The expression of other genes in a breast cancer cell would be relatively unable to provide information concerning, and thus assist in the discrimination of, ER status in breast cancer.

To determine the (increased or decreased) expression levels of genes in the practice of the present invention, any method known in the art may be utilized. In one preferred embodiment of the invention, expression based on detection of RNA which hybridizes to the genes identified and disclosed herein is used. This is readily performed by any RNA detection or amplification+detection method known or recognized as equivalent in the art such as, but not limited to, reverse transcription-PCR, the methods disclosed in U.S. Patent Application 10/062,857 (filed on October 25, 2001) as well as U.S. Provisional Patent Applications 60/298,847 (filed June 15, 2001) and 60/257,801 (filed December 22, 2000), and methods to detect the presence, or absence, of RNA stabilizing or destabilizing sequences.

Alternatively, expression based on detection of DNA status may be used. Detection of the DNA of an identified gene as methylated or deleted may be used for genes that have decreased expression in correlation with ER status. This may be readily performed by PCR based methods known in the art, including, but not limited to, quantitative PCR (Q-PCR). Conversely, detection of the DNA of an identified gene as amplified may be used for genes that have increased expression in correlation with ER status. This may be readily performed by PCR based, fluorescent *in situ* hybridization (FISH) and chromosome in situ hybridization (CISH) methods known in the art.

Expression based on detection of a presence, increase, or decrease in protein levels or activity may also be used. Detection may be performed by any immunohistochemistry (IHC) based, blood based (especially for secreted proteins), antibody (including autoantibodies against the protein) based, ex foliate cell (from the cancer) based, mass spectroscopy based, and image (including used of labeled ligand) based method known in the art and recognized as appropriate for the detection of the protein. Antibody and image based methods are additionally useful for the localization of tumors after determination of cancer by use of cells obtained by a non-invasive procedure (such as ductal lavage or fine needle aspiration), where the source of the cancerous cells is not known. A labeled antibody or ligand may be used to localize the carcinoma(s) within a patient.

A preferred embodiment using a nucleic acid based assay to determine expression is by immobilization of one or more sequences of the genes identified herein on a solid support, including, but not limited to, a solid substrate as an array or to beads or bead based technology as known in the art. Alternatively, solution based expression assays known in the art may also be used. The immobilized gene(s) may be in the form of polynucleotides that are unique or otherwise specific to the gene(s) such that the polynucleotide would be capable of hybridizing to a DNA or RNA corresponding to the gene(s). These polynucleotides may be the full length of the gene(s) or be short sequences of the genes (up to one nucleotide shorter than the full length sequence known in the art by deletion from the 5' or 3' end of the sequence) that are optionally minimally interrupted (such as by mismatches or inserted non-complementary basepairs) such that hybridization with a DNA or RNA corresponding to the gene(s) is not affected. Preferably, the polynucleotides used are from the 3' end of the gene, such as within about 350, about 300, about 250, about 200, about 150, about 100, or about 50 nucleotides from the polyadenylation signal or polyadenylation site of a gene or expressed sequence. Polynucleotides containing mutations relative to the sequences of the disclosed genes may also be used so long as the presence of the mutations still allows hybridization to produce a detectable signal.

Alternatively, amplification of such sequences from the 3' end of genes by methods such as quantitative PCR may be used to determine the expression levels of the sequences. The Ct values generated by such methods may be used to generate the ratios of expression levels as described herein.

The immobilized gene(s) may be used to determine the state of nucleic acid samples prepared from sample breast cell(s) for which the ER status is not known or for confirmation of a status that is already assigned to the sample breast cell(s). Without limiting the invention, such a cell may be from a patient suspected of being afflicted with, or at risk of developing, breast cancer. The immobilized polynucleotide(s) need only be sufficient to specifically hybridize, optionally under stringent conditions, to the corresponding nucleic acid molecules derived from the sample. While even a single correlated gene sequence may to able to provide adequate accuracy in discriminating between ER status, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, or eleven or more of the genes identified herein may be used as a subset capable of discriminating may be used in combination to increase the accuracy of the method. The invention specifically contemplates the selection of more than one, two or more, three or more, four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, or eleven or more of the genes disclosed in the tables and figures herein for use as a subset in the identification of whether a breast cancer sample is ER positive or negative.

Of course 15 or more, 20 or more, 30 or more, 40 or more, 50 or more, 60 or more, 70 or more, 80 or more, 90 or more, 100 or more, 150 or more, 200 or more, 250 or more, 300 or more, 350 or more, 400 or more, 450 or more, 500 or more, 600 or more, 700 or more, 800 or more, 900 or more, 1000 or more, or all the genes provided in Table 1 or 2 below may be used. Additionally, genes that identify ER positive and ER negative may be used together to permit differential identification of a test sample as being ER positive or ER negative.

In embodiments where only one or a few genes are to be analyzed, the nucleic acid derived from the sample breast cancer cell(s) may be preferentially amplified by use of appropriate primers such that only the genes to be analyzed are amplified to reduce contaminating background signals from other genes expressed in the breast cell. Alternatively, and where multiple genes are to be analyzed or where very few cells (or one cell) is used, the nucleic acid from the sample may be globally amplified before hybridization to the immobilized polynucleotides. Of course RNA, or the cDNA counterpart thereof may be directly labeled and used, without amplification, by methods known in the art.

The invention is preferably practiced with unique sequences present within the gene sequences disclosed herein. The uniqueness of a disclosed gene sequence refers to the portions or entireties of the sequences which are found in each gene to the exclusion of other genes. Such unique sequences include those found at the 3' untranslated portion of the genes. Preferred unique sequences for the practice of the invention are those which contribute to the consensus sequences for each gene such that the unique sequences will be useful in detecting expression in a variety of individuals rather than being specific for a polymorphism present in some individuals. Alternatively, sequences unique to an individual or a subpopulation may be used. The preferred unique sequences are preferably of the lengths of polynucleotides of the invention as discussed herein.

In particularly preferred embodiments of the invention, polynucleotides having sequences present in the 3' untranslated and/or non-coding regions of the disclosed gene sequences are used to detect expression levels in breast cells. Such polynucleotides may optionally contain sequences found in the 3' portions of the coding regions of the disclosed sequences. Polynucleotides containing a combination of sequences from the coding and 3' non-coding regions preferably have the sequences arranged contiguously, with no intervening heterologous sequence(s).

Alternatively, the invention may be practiced with polynucleotides having sequences present in the 5' untranslated and/or non-coding regions of gene sequences in breast cells to detect their levels of expression. Such polynucleotides may optionally contain sequences found in the 5' portions of the coding regions. Polynucleotides containing a combination of sequences from the coding and 5' non-coding regions preferably have the sequences arranged contiguously, with no intervening heterologous sequence(s). The invention may also be practiced with sequences present in the coding regions of disclosed sequences.

Preferred polynucleotides contain sequences from 3' or 5' untranslated and/or non-coding regions of at least about 16, at least about 18, at least about 20, at least about 22, at least about 24, at least about 26, at least about 28, at least about 30, at least about 32, at least about 34, at least about 36, at least about 38, at least about 40, at least about 42, at least about 44, or at least about 46 consecutive nucleotides. The term "about" as used in the previous sentence refers to an increase or decrease of 1 from the stated numerical value. Even more preferred are polynucleotides containing sequences of at least or about 50, at least or about 100, at least about or 150, at least or about 200, at least or about 250, at least or about 300, at least or about 350, or at least or about 400 consecutive nucleotides. The term "about" as used in the preceding sentence refers to an increase or decrease of 10% from the stated numerical value.

Sequences from the 3' or 5' end of the above described coding regions as found in polynucleotides of the invention are of the same lengths as those described above, except that they would naturally be limited by the length of the coding region. The 3' end of a coding region may include sequences up to the 3' half of the coding region. Conversely, the 5' end of a coding region may include sequences up the 5' half of the coding region. Of course the above described sequences, or the coding regions and polynucleotides containing portions thereof, may be used in their entireties.

Polynucleotides combining the sequences from a 3' untranslated and/or non-coding region and the associated 3' end of the coding region are preferably at least or about 100, at least about or 150, at least or about 200, at least or about 250, at least or about 300, at least or about 350, or at least or about 400 consecutive nucleotides. Preferably, the polynucleotides used are from the 3' end of the gene, such as within about 350, about 300, about 250, about 200, about 150, about 100, or about 50 nucleotides from the polyadenylation signal or polyadenylation site of a gene or expressed sequence. Polynucleotides containing mutations relative to the sequences of the disclosed genes may also be used so long as the presence of the mutations still allows hybridization to produce a detectable signal.

In another embodiment of the invention, polynucleotides containing deletions of nucleotides from the 5' and/or 3' end of the above disclosed sequences may be used. The deletions are preferably of 1-5, 5-10, 10-15, 15-20, 20-25, 25-30, 30-35, 35-40, 40-45, 45-50, 50-60, 60-70, 70-80, 80-90, 90-100, 100-125, 125-150, 150-175, or 175-200 nucleotides from the 5' and/or 3' end, although the extent of the deletions would naturally be limited by the length of the disclosed sequences and the need to be able to use the polynucleotides for the detection of expression levels.

Other polynucleotides of the invention from the 3' end of the above disclosed sequences include those of primers and optional probes for quantitative PCR. Preferably, the primers and probes are those which amplify a region less than about

350, less than about 300, less than about 250, less than about 200, less than about 150, less than about 100, or less than about 50 nucleotides from the from the polyadenylation signal or polyadenylation site of a gene or expressed sequence.

In yet another embodiment of the invention, polynucleotides containing portions of the above disclosed sequences including the 3' end may be used in the practice of the invention. Such polynucleotides would contain at least or about 50, at least or about 100, at least about or 150, at least or about 200, at least or about 250, at least or about 300, at least or about 350, or at least or about 400 consecutive nucleotides from the 3' end of the disclosed sequences.

The above assay embodiments may be used in a number of different ways to identify or detect ER status in a breast cancer cell sample from a patient. In many cases, this may reflect a secondary screen for the patient, who may have already undergone mammography or physical exam as a primary screen. If positive, the subsequent needle biopsy, ductal lavage, fine needle aspiration, or other analogous methods may provide the sample for use in the above assay embodiments. The present invention is particularly useful in combination with non-invasive protocols, such as ductal lavage or fine needle aspiration, to prepare a breast cell sample.

The present invention provides an objective set of criteria, in the form of gene expression profiles of a discrete set of genes, to discriminate (or delineate) between ER positive and negative breast cancer cells.

In one embodiment of the invention, the isolation and analysis of a breast cancer cell sample may be performed as follows:

(1) Ductal lavage or other non-invasive procedure is performed on a patient to obtain a sample.

(2) Sample is prepared and coated onto a microscope slide. Note that ductal lavage results in clusters of cells that are cytologically examined as stated above.

(3) Pathologist or image analysis software scans the sample for the presence of non-normal and/or atypical cells.

(4) If non-normal and/or atypical cells are observed, those cells are harvested (e.g. by microdissection such as LCM).

(5) RNA is extracted from the harvested cells.

(6) RNA is purified, amplified, and labeled.

(7) Labeled nucleic acid is contacted with a microarray containing polynucleotides of the genes identified herein as correlated to discriminations between ER status under hybridization conditions to allow hybridization to occur, then processed and scanned to obtain a pattern of intensities of each spot (relative to a control for general gene expression in cells) which determine the level of expression of the gene(s) in the cells.

(8) The pattern of intensities is analyzed by comparison to the expression patterns of the genes in known samples of ER positive and negative breast cancer cells (relative to the same control).

A specific example of the above method would be performing ductal lavage following a primary screen, observing and collecting non-normal and/or atypical cells for analysis. The comparison to known expression patterns, such as that made possible by a model based on the disclosed genes and patterns, identifies the cells as being ER positive or negative.

Alternatively, the sample may permit the collection of both normal as well as non-normal and/or atypical cells for analysis. The gene expression patterns for each of these two samples will be compared to each other as well as the model and the normal versus individual abnormal comparisons therein based upon the reference data set. This approach can be significantly more powerful that the non-normal and/or atypical cells only approach because it utilizes significantly more information from the normal cells and the differences between normal and non-normal/atypical cells (in both the sample and reference data sets) to determine the status of the non-normal and/or atypical cells from the sample.

With use of the present invention, skilled physicians may prescribe treatments based on non-invasive samples that they would have prescribed for a patient which had previously received a diagnosis via a solid tissue biopsy.

The above discussion is also applicable where a palpable lesion is detected followed by fine needle aspiration or needle biopsy of cells from the breast. The cells are plated and reviewed by a pathologist or automated imaging system which selects cells for analysis as described above.

The present invention may also be used, however, with solid tissue biopsies. For example, a solid biopsy may be collected and prepared for visualization followed by determination of expression of one or more genes identified herein to determine ER status in breast cancer. One preferred means is by use of *in situ* hybridization with polynucleotide or protein identifying probe(s) for assaying expression of said gene(s).

In an alternative method, the solid tissue biopsy may be used to extract molecules followed by analysis for expression of one or more gene(s). This provides the ability to leave out the need for visualization and collection of only those cells suspected of being non-normal and/or atypical. This method may of course be modified such that only cells suspected of being non-normal and/or atypical are collected and used to extract molecules for analysis. This would require visualization and selection as an prerequisite to gene expression analysis.

In a further modification of the above, both normal cells and cells suspected of being non-normal and/or atypical are collected and used to extract molecules for analysis of gene expression. The approach, benefits and results are as described above using non-invasive sampling.

The genes identified herein may be used to generate a model capable of predicting the breast cancer ER statis of an unknown breast cell sample based on the expression of the identified genes in the sample.

The detection of gene expression from the samples may be by use of a single microarray able to assay gene expression of the genes disclosed herein, whether correlated with ER positive or negative status.

Other uses of the present invention include providing the ability to identify breast cancer cell samples as being those of ER positive or negative for further research or study. This provides a particular advantage in many contexts requiring the identification of breast cancer ER status based on objective genetic or molecular criteria.

The materials for use in the methods of the present invention are ideally suited for preparation of kits produced in accordance with well known procedures. The invention thus provides kits comprising agents for the detection of expression of the disclosed genes for identifying breast cancer ER status. Such kits optionally comprising the agent with an identifying description or label or instructions relating to their use in the methods of the present invention, is provided. Such a kit may comprise containers, each with one or more of the various reagents (typically in concentrated form) utilized in the methods, including, for example, pre-fabricated microarrays, buffers, the appropriate nucleotide triphosphates (e.g., dATP, dCTP, dGTP and dTTP; or rATP, rCTP, rGTP and UTP), reverse transcriptase, DNA polymerase, RNA polymerase, and one or more primer complexes of the present invention (e.g., appropriate length poly(T) or random primers linked to a promoter reactive with the RNA polymerase). A set of instructions will also typically be included.

The methods provided by the present invention may also be automated in whole or in part. All aspects of the present invention may also be practiced such that they consist essentially of a subset of the disclosed genes to the exclusion of material irrelevant to the identification of ER status.

The present invention also provides for the use of the gene product of one or more of the disclosed gene in the identification of agents that increase or decrease the expression of, or the activity of, said gene product. Methods of identifying such agents are preferably used to identify agents that will return the expression of, or the activity of, a gene product to a more normal level as opposed to the level seen in ER positive or negative cell. Most preferred is the return of an ER negative cell to normalcy in light of the poor prognosis for patients with ER negative status.

Such methods may be used to identify agents that decrease the expression of, or the activity of, a gene product encoded by a gene that is overexpressed in ER positive or ER negative cells. Alternatively, such methods may be used to identify agents that increase the expression of, or the activity of, a gene product encoded by a gene that is underexpressed in ER positive or ER negative cells.

The following tables set forth the genes of the invention. For example, Tables 1 and 3 include the ESR1 (estrogen receptor alpha) gene. "CloneID" as used in the context of the present invention refers to the IMAGE Consortium clone ID number of each gene, the sequences of which are hereby incorporated by reference in their entireties as they are available from the Consortium at image.llnl.gov as accessed on the filing date of the present application. "GeneID" as used in the context of the Tables herein as well as the present invention refers to the GenBank accession number of a sequence of each gene, the sequences of which are hereby incorporated by reference in their entireties as they are available from GenBank as accessed on the filing date of the present application.

P value refers to values assigned as described in the Example below. The indications of "E-xx" where "xx" is a two digit number refers to alternative notation for exponential figures where "E-xx" is "10^{-xx}". Thus in combination with the numbers to the left of "E-xx", the value being represented is the numbers to the left times 10^{-xx}. Chromosome Location refers to the human chromosome to which the gene has been assigned. Description provides a brief identifier of what the gene encodes/expresses.

Table 5 provides non-limiting examples of the corresponding GenBank accession number, clone ID number, and Unigene (cluster) ID numbers for exemplary sequences disclosed herein. The sequences of the invention may thus be identified by any of these identifiers. The identification of other corresponding numbers (GenBank accession number, clone ID number, and/or Unigene (cluster) ID numbers) for sequences disclosed herein can be made as a matter of routine from public information sources and without undue experimentation.

Table 1. Genes that are overexpressed in ER positive cells, and underexpressed in ER negative cells

Clone_ID	P_value	Gene_Description
2308409	0.001730688	KIAA1077 | KIAA1077 protein
1569878	0.016682884	ESTs
757220	6.59E-06	FUS1 | lung cancer candidate
1570414	0.001162673	DKFZP434J037 | hypothetical protein DKFZp434J037
1459742	2.71E-09	MAP-1 | modulator of apoptosis 1
455025	1.04E-05	CGR19 | cell growth regulatory with ring finger domain
767784	0.001891407	JUND | jun D proto-oncogene
1637767	1.80E-12	CS2 | calsyntenin-2
242778	2.42E-19	CEGP1 | CEGP1 protein
897446	3.60E-05	ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]
50577	2.20E-05	MGC16028 | MGC16028 similar to RIKEN cDNA 1700019E19 gene
566106	6.95E-05	Homo sapiens cDNA FLJ31200 fis, clone KIDNE2000574, weakly similar to Staphylococcus epidermidis putative cell-surface adhesin SdrF gene
785710	5.12E-05	KIAA1025 | KIAA1025 protein
866702	0.034946932	PTPN13 | protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)
431505	0.000107772	HS1-2 | putative transmembrane protein
809876	7.98E-06	ATP5G2 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2
2321113	1.80E-12	AGR2 | anterior gradient 2 (Xenepus laevis) homolog
1910426	0.016882187	BM-009 | hypothetical protein
49249	0.000289664	Homo sapiens, clone MGC:10039 IMAGE:3889701, mRNA, complete cds
241043	0.009801049	Human clone 137308 mRNA, partial cds
111389	3.62E-12	ESTs
1866068	0.006067385	ESTs
590310	1.45E-10	Homo sapiens, clone MGC:17393 IMAGE:3914851, mRNA, complete cds
366966	0.004146925	Homo sapiens cDNA: FLJ21333 fis, clone COL02535
840506	0.021449552	3-Apr | apoptosis related protein APR-3
1620396	0.04743837	ESTs

307740	0.001654163	ESTs
1492780	0.040280641	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
845453	0.016037507	ARL3 | ADP-ribosylation factor-like 3
682817	0.01385764	MDM2 | mouse double minute 2, human homolog of; p53-binding protein
773286	1.40E-08	SLC9A3R1 | solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1
144029	0.007899024	EST
197775	3.62E-05	ESTs
796152	0.014513254	Homo sapiens cDNA FLJ11685 fis, clone HEMBA1004934
809892	1.77E-12	SEMA3B | sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B
740941	4.14E-08	APM2 | adipose specific 2
84965	0.000389422	C5orf3 | chromosome 5 open reading frame 3
785732	2.50E-05	BM036 | uncharacterized bone marrow protein BM036
417884	0.007045683	Homo sapiens cDNA FLJ12052 fis, clone HEMBB1002042, moderately similar to CYTOCHROME P450 4C1 (EC 1.14.14.1)
67988	5.65E-05	SNRPD2 | small nuclear ribonucleoprotein D2 polypeptide (16.5kD)
342378	9.49E-06	DUSP5 | dual specificity phosphatase 5
138550	0.006400652	FLJ11137 | hypothetical protein FLJ11137
162753	0.043575209	DD5 | progestin induced protein
1881469	9.79E-05	OCLN | occludin
136954	1.57E-07	ESTs, Weakly similar to YEX0_YEAST HYPOTHETICAL 64.8 KDA PROTEIN IN GDI1-COX15 INTERGENIC REGION [S.cerevisiae]
320456	0.00177597	FLJ10300 | hypothetical protein FLJ10300
134270	0.02511167	Human hbc647 mRNA sequence
840524	0.011860244	GOLGB1 | golgi autoantigen, golgin subfamily b, macrogolgin (with transmembrane signal), 1
1681520	0.005746627	FLJ11068 | hypothetical protein FLJ11068
31225	0.01680194	BCRP2 | Breakpoint cluster region protein, uterine leiomyoma, 2
1518845	7.98E-08	ESTs
590338	0.001677738	LOC51065 | 40S ribosomal protein S27 isoform
491706	0.017583577	Homo sapiens mRNA; cDNA DKFZp434F1622 (from clone DKFZp434F1622)
812042	0.000429178	TSC1 | tuberous sclerosis 1
296702	0.01747597	DIO1 | deiodinase, iodothyronine, type I
785745	1.15E-06	DXS1283E | GS2 gene

279720	5.88E-07	Homo sapiens, Similar to RIKEN cDNA 1700008D07 gene, clone MGC:9830 IMAGE:3863323, mRNA, complete cds
239877	5.74E-07	HDAC3 | histone deacetylase 3
49273	0.030979591	SLC27A4 | solute carrier family 27 (fatty acid transporter), member 4
758206	4.62E-06	PMS2L2 | postmeiotic segregation increased 2-like 2
810446	0.011693351	KIAA1522 | KIAA1522 protein
135220	0.007130449	MGC12981 | hypothetical protein MGC12981
284261	0.001705915	MDS030 | uncharacterized hematopoietic stem/progenitor cells protein MDS030
594627	0.000265791	FLJ11164 | hypothetical protein FLJ11164
487831	0.007143248	Homo sapiens cDNA FLJ14059 fis, clone HEMBB1000573
127063	0.000920217	ESTs
1323448	3.15E-07	CRIP1 | cysteine-rich protein 1 (intestinal)
742565	0.000443835	MYG1 | MYG1 protein
2017756	0.005004126	MOG1 | homolog of yeast MOG1
2171616	0.004755604	ITGB5 | integrin, beta 5
490778	0.003255264	QP-C | low molecular mass ubiquinone-binding protein (9.5kD)
359781	0.004382798	SPTB | spectrin, beta, erythrocytic (includes spherocytosis, clinical type I)
268234	2.81E-06	DMXL1 | Dmx-like 1
1609616	7.68E-06	ESTs
135238	4.44E-05	ESTs
2016022	0.022592867	p25 | brain-specific protein p25 alpha
741919	0.001246921	TJP3 | tight junction protein 3 (zona occludens 3)
22428	0.03083658	ESTs
2017769	0.005529556	EIF4EBP1 | eukaryotic translation initiation factor 4E binding protein 1
289505	1.89E-09	ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
731073	0.041342882	LOC51126 | N-terminal acetyltransferase complex ard1subunit
785766	0.004538178	LOC51321 | hypothetical protein
251936	0.02996845	NSF | N-ethylmaleimide-sensitive factor
810463	0.003602021	DKFZp566O084 | DKFZP566O084 protein
1554430	7.94E-13	Homo sapiens cDNA FLJ10561 fis, clone NT2RP2002672
251938	0.016335389	CA14 | carbonic anhydrase XIV
1032762	0.027468511	Homo sapiens mRNA; cDNA DKFZp434G2127 (from clone DKFZp434G2127)

705274	0.027821949	DGKD | diacylglycerol kinase, delta (130kD)
268240	0.019288575	FXC1 | fracture callus 1 (rat) homolog
50915	0.030739747	MGC2752 | hypothetical protein MGC2752
1535851	0.001352198	COX15 | COX15 (yeast) homolog, cytochrome c oxidase assembly protein
429284	0.023974067	ZNF226 | zinc finger protein 226
124824	1.26E-05	RPL10A | ribosomal protein L10a
24032	0.001081701	CRADD | CASP2 and RIPK1 domain containing adaptor with death domain
788185-2	4.38E-06	TNFRSF10B | tumor necrosis factor receptor superfamily, member 10b
1517136	0.002531495	RBM8A | RNA binding motif protein 8A
343731-2	0.012232736	KLF2 | Kruppel-like factor 2 (lung)
111721	0.020116819	LOC51141 | insulin induced protein 2
71101	3.59E-07	PROCR | protein C receptor, endothelial (EPCR)
530197	0.004873141	Homo sapiens, clone MGC:5522 IMAGE:3454199, mRNA, complete cds
261706	0.010699069	Homo sapiens cDNA FLJ32056 fis, clone NTONG2001619
122147	0.040911534	ELMO2 | engulfment and cell motility 2 (ced-12 homolog, C. elegans)
773617	0.038655611	UBE2D2 | ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC4/5)
279752	0.038399841	DC8 | DKFZP566O1646 protein
838285	7.61E-05	LOC51092 | CGI-40 protein
277074	0.042882678	UNC5C | unc5 (C.elegans homolog) c
2492422	0.019925171	SERPINI2 | serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 2
2009904	0.015782601	FLJ11230 | hypothetical protein FLJ11230
175103	7.33E-06	CELSR2 | cadherin, EGF LAG seven-pass G-type receptor 2, flamingo (Drosophila) homolog
795543	0.02996845	PRDX4 | peroxiredoxin 4
130845-2	0.004607159	PWP1 | nuclear phosphoprotein similar to S. cerevisiae PWP1
137940	3.89E-07	GSTM3 | glutathione S-transferase M3 (brain)
810486	0.014811257	EST
767069	0.012408476	Homo sapiens cDNA: FLJ21930 fis, clone HEP04301, highly similar to HSU90916 Human clone 23815 mRNA sequence
143426	1.35E-08	ARHB | ras homolog gene family, member B
826133	1.99E-08	BTBD2 | BTB (POZ) domain containing 2
301122	0.016918654	ECM1 | extracellular matrix protein 1
26736	0.000107772	Homo sapiens cDNA FLJ30872 fis, clone FEBRA2004293

826138	3.22E-09	GAMT | guanidinoacetate N-methyltransferase
1909163	1.63E-06	B3GNT6 | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6
788334	2.20E-06	MRPL23 | mitochondrial ribosomal protein L23
1518890	4.42E-08	MTL5 | metallothionein-like 5, testis-specific (tesmin)
1703339	0.000289561	STXBP2 | syntaxin binding protein 2
120561	0.025636692	KIDINS220 | likely homolog of rat kinase D-interacting substance of 220 kDa
785795	4.55E-15	FLJ12910 | hypothetical protein FLJ12910
2012854	0.000522332	Homo sapiens cDNA FLJ13137 fis, clone NT2RP3003150
321455	7.33E-07	SARM | sterile alpha and HEAT/Armadillo motif protein, ortholog of Drosophila
179403	0.035275484	CYP2E | cytochrome P450, subfamily IIE (ethanol-inducible)
126455	0.025654559	RAB5B | RAB5B, member RAS oncogene family
44387	1.24E-05	ELOVL2 | elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2
590390	0.013880919	MADP-1 | MADP-1 protein
487882	0.01198186	DKFZP761D0211 | hypothetical protein DKFZp761D0211
342720	0.00238904	KIAA0096 | KIAA0096 protein
75415	5.47E-09	HINT | histidine triad nucleotide-binding protein
415550	7.94E-07	Homo sapiens cDNA FLJ13598 fis, clone PLACE1009921
741954	0.016770876	Homo sapiens cDNA FLJ14656 fis, clone NT2RP2002439
759200	0.000754507	MGC4238 | hypothetical protein MGC4238
1657385	0.005619887	EST
626208	0.000852377	Homo sapiens cDNA: FLJ21904 fis, clone HEP03585
1709233	0.006870641	SLC1A4 | solute carrier family 1 (glutamate/neutral amino acid transporter), member 4
758266	0.01526361	THBS4 | thrombospondin 4
753321	1.76E-05	KIAA0232 | KIAA0232 gene product
1455842	3.72E-06	Homo sapiens cDNA: FLJ22448 fis, clone HRC09541
2028515	0.028548635	SMARCA1 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1
1932725	0.00620659	ZNF281 | zinc finger protein 281
1517171	1.50E-10	IL2RA | interleukin 2 receptor, alpha
1910800	0.022735296	ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
2018758	0.033107716	PEX7 | peroxisomal biogenesis factor 7
469172	0.001026742	SEC22C | vesicle trafficking protein

814792	0.011398824	USP10 | ubiquitin specific protease 10
415564	0.000103761	Homo sapiens, clone MGC:20208 IMAGE:3936339, mRNA, complete cds
31299	0.002342367	Homo sapiens mRNA; cDNA DKFZp761I1912 (from clone DKFZp761I1912)
1882481	6.16E-05	ESTs
1035359	0.012284709	FLJ22593 | hypothetical protein FLJ22593
139573	0.024069066	RNPEP | arginyl aminopeptidase (aminopeptidase B)
79712	0.024734713	IGF2R | insulin-like growth factor 2 receptor
177827	0.005854823	SYT7 | synaptotagmin VII
121533	0.043542397	WHSC1L1 | Wolf-Hirschhorn syndrome candidate 1-like 1
49630	8.03E-10	CACNA1D | calcium channel, voltage-dependent, L type, alpha 1D subunit
741977	0.030962737	BF | B-factor, properdin
1584577	0.019525111	ESTs
1566937	0.012408476	Homo sapiens cDNA FLJ32325 fis, clone PROST2003922
726597	0.000877702	Homo sapiens cDNA FLJ32642 fis, clone SYNOV2001144
277403	0.019916149	Homo sapiens mRNA; cDNA DKFZp586D0918 (from clone DKFZp586D0918)
42018	0.000140658	KIAA1468 | KIAA1468 protein
823912	0.005767924	UBL3 | ubiquitin-like 3
79726	1.98E-06	ESTs, Moderately similar to T46395 hypothetical protein DKFZp434I1120.1 [H.sapiens]
971212	0.002192731	HIVEP2 | human immunodeficiency virus type I enhancer-binding protein 2
1507713	0.030416081	CHAD | chondroadherin
418129	0.000216424	IL18BP | interleukin 18 binding protein
299332	1.25E-10	KIAA0575 | KIAA0575 gene product
70500	1.01E-05	TBX3 | T-box 3 (ulnar mammary syndrome)
741988	0.000741391	ACY1 | aminoacylase 1
769796	2.23E-08	MGC17330 | hypothetical protein MGC17330
1731860	2.65E-05	GADD45B | growth arrest and DNA-damage-inducible, beta
219929	0.000438842	KIAA1415 | KIAA1415 protein
773674	0.005209931	RRAS2 | related RAS viral (r-ras) oncogene homolog 2
712848	0.018338006	MADD | MAP-kinase activating death domain
782497	1.22E-05	BC008967 | hypothetical gene BC008967
843163	8.73E-06	LCP | host cell factor homolog
1707667	1.78E-08	Homo sapiens cDNA FLJ31065 fis, clone HSYRA2001142

2325804	2.47E-05	KIAA0661 | 95 kDa retinoblastoma protein binding protein
131318	0.000194501	LOC55971 | insulin receptor tyrosine kinase substrate
823928	0.009945291	GSTT2 | glutathione S-transferase theta 2
824588	0.000600627	Homo sapiens cDNA FLJ32203 fis, clone PLACE6003038, weakly similar to ZINC FINGER PROTEIN 84
2049813	0.042566514	LOC51063 | hypothetical protein
768068	1.40E-08	DKFZP761E2110 | hypothetical protein DKFZp761E2110
726901	0.037164505	Homo sapiens cDNA FLJ33095 fis, clone TRACH2000708
826194	1.45E-10	SYTL2 | synaptotagmin-like 2
1690739	0.000152094	HSPA4 | heat shock 70kD protein 4
108864	0.000132671	OASIS | old astrocyte specifically induced substance
23454	0.036615517	HRLP5 | H-rev107-like protein 5
1884404	0.001613372	KIAA0285 | KIAA0285 gene product
200954	0.001076393	EST
1556401	0.023586705	EST
2029503	0.041795601	ESTs
2027900	4.84E-09	Homo sapiens cDNA FLJ12187 fis, clone MAMMA1000831
278093	0.000144715	BRAP | BRCA1 associated protein
823940	3.40E-05	TOB1 | transducer of ERBB2, 1
809507	6.95E-05	FLJ20568 | hypothetical protein FLJ20568
504763	0.019901982	SDC4 | syndecan 4 (amphiglycan, ryudocan)
84295	0.004226757	IL1RN | interleukin 1 receptor antagonist
262739	9.25E-05	P125 | Sec23-interacting protein p125
725978	0.016317028	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
714472	0.019175238	KIAA0397 | KIAA0397 gene product
854691	0.028565804	Homo sapiens, clone MGC:17299 IMAGE:3845811, mRNA, complete cds
288948	0.040000458	GTF2H3 | general transcription factor IIH, polypeptide 3 (34kD subunit)
356835	0.010661105	MGC10500 | hypothetical protein MGC10500
2016410	0.046542451	HIVEP3 | human immunodeficiency virus type I enhancer-binding protein 3
343731	0.012195178	KLF2 | Kruppel-like factor 2 (lung)
815794	1.67E-05	NUCB2 | nucleobindin 2
1575008	0.000123427	WBP1 | WW domain binding protein 1

857243	4.97E-07	RPS13 | ribosomal protein S13
296030	0.027904683	Homo sapiens cDNA: FLJ20944 fis, clone ADSE01780
1882823	0.041142646	ESTs
139912	0.010208539	ESTs
202577	0.003099407	HNMT | histamine N-methyltransferase
502096	0.000365845	Homo sapiens mRNA; cDNA DKFZp761K2024 (from clone DKFZp761K2024)
1404841	0.000764648	ZNF175 | zinc finger protein 175
809521	0.003132437	HMT-1 | beta-1,4 mannosyltransferase
666128	2.10E-05	DF | D component of complement (adipsin)
770377	0.0445364	ATP6N1A | ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD)
1860909	8.46E-08	Homo sapiens cDNA FLJ31136 fis, clone IMR322001029
27769	0.001838545	Homo sapiens cDNA FLJ32051 fis, clone NTONG2001428
257135	0.018649252	SLC22A4 | solute carrier family 22 (organic cation transporter), member 4
83653	0.015480089	HSPC128 | HSPC128 protein
345348	0.024128019	PRDM2 | PR domain containing 2, with ZNF domain
1908593	0.01198186	ESTs
811803	0.001032481	SHFM3 | split hand/foot malformation (ectrodactyly) type 3
813408	0.032712756	PSK-1 | type I transmembrane receptor (seizure-related protein)
1568597	0.000166213	FLJ21939 | hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2
39136	0.008152393	ESTs
135640	1.11E-08	STX3A | syntaxin 3A
277463	8.33E-05	C18orf1 | chromosome 18 open reading frame 1
827171	1.92E-05	LRRC2 | leucine-rich repeat-containing 2
303109	0.028556348	P2Y5 | purinergic receptor (family A group 5)
666138	0.002192122	DKFZp761J1523 | hypothetical protein DKFZp761J1523
79782	0.002399976	ZNF161 | zinc finger protein 161
824916	0.038531356	FLJ14511 | hypothetical protein FLJ14511
788714	0.009823852	E46L | like mouse brain protein E46
124143	1.91E-05	DKFZP761H1710 | hypothetical protein DKFZp761H1710
2028597	0.009457359	Homo sapiens cDNA FLJ30306 fis, clone BRACE2003319
815017	2.20E-05	Homo sapiens HSPC337 mRNA, partial cds

491053	0.000490828	ARIH2 | ariadne (Drosophila) homolog 2
796598	0.031676644	LCMT | leucine carboxyl methyltransferase
810873	0.014436416	SCNN1A | sodium channel, nonvoltage-gated 1 alpha
752752	0.005021691	ESTs
809541	0.026417563	BCL2L2 | BCL2-like 2
33267	1.26E-05	EST
813424	0.000140667	PPID | peptidylprolyl isomerase D (cyclophilin D)
80338	9.63E-06	SELENBP1 | selenium binding protein 1
627248	0.000251776	SBBI31 | SBBI31 protein
755301	0.001147972	PRKCD | protein kinase C, delta
52933	5.32E-10	LIV-1 | LIV-1 protein, estrogen regulated
269606	0.025359903	MPG | N-methylpurine-DNA glycosylase
109863	2.63E-06	EMP2 | epithelial membrane protein 2
1592021	1.16E-06	HFL1 | H factor (complement)-like 1
263727	1.73E-05	D5S346 | DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis
295410	0.015532036	PVT1 | pvt-1 (murine) oncogene homolog, MYC activator
814095	0.015960541	LTA4H | leukotriene A4 hydrolase
2014856	0.007182327	HLALS | major histocompatibility complex, class I-like sequence
782851	0.039199758	FLJ12799 | hypothetical protein FLJ12799
2011515	0.000180794	DKFZP586B0923 | DKFZP586B0923 protein
1751466	0.000262724	Homo sapiens, Similar to C-terminal modulator protein, clone MGC:29636 IMAGE:4870462, mRNA, complete cds
278430	0.0220126	KIF5C | kinesin family member 5C
767475	0.046030837	PCANAP7 | prostate cancer associated protein 7
767477	2.38E-09	ANKRA2 | ankyrin repeat, family A (RFXANK-like), 2
179804	1.77E-06	PWP2H | PWP2 (periodic tryptophan protein, yeast) homolog
126851	7.99E-08	FLJ11160 | hypothetical protein FLJ11160
754376	0.034945258	ESTs, Weakly similar to Z195_HUMAN ZINC FINGER PROTEIN 195 [H.sapiens]
1592039	0.001012294	COL4A5 | collagen, type IV, alpha 5 (Alport syndrome)
811843	8.82E-08	SUOX | sulfite oxidase
143661-2	3.51E-07	NTN4 | netrin 4
1947826	0.006003565	ITGAL | integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha

		polypeptide)
1492468	4.10E-08	KIAA0452 | DEME-6 protein
684890	0.000308434	FLJ20274 | hypothetical protein FLJ20274
143846	0.000133999	LRP2 | low density lipoprotein-related protein 2
135688	0.016682884	GATA2 | GATA-binding protein 2
23819	7.73E-09	ABCG1 | ATP-binding cassette, sub-family G (WHITE), member 1
415962	5.02E-06	PACE4 | paired basic amino acid cleaving system 4
149735	2.37E-08	CSNK1G3 | casein kinase 1, gamma 3
71545	3.96E-05	MAP4K1 | mitogen-activated protein kinase kinase kinase kinase 1
1900362	0.005096825	Homo sapiens chromosome 17 open reading frame 26 (C17orf26) mRNA, complete cds
325079	0.002196708	SRA1 | steroid receptor RNA activator 1
767495	2.38E-09	GLI3 | GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome)
897153	0.005755017	PTD009 | PTD009 protein
589479	0.009372382	HPCL2 | 2-hydroxyphytanoyl-CoA lyase
42408	0.004066019	MGC4604 | hypothetical protein MGC4604
744917	4.06E-06	NINJ1 | ninjurin 1
2239290	0.047401567	SDF1 | stromal cell-derived factor 1
2018084	0.000879242	SPAK | Ste-20 related kinase
1700429	2.65E-09	GFRA1 | GDNF family receptor alpha 1
810124	0.009454178	PAFAH1B3 | platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit (29kD)
470121	6.56E-06	TCTA | T-cell leukemia translocation altered gene
155227	4.49E-06	Homo sapiens clone 25194 mRNA sequence
781145	0.029514943	NT5M | 5' nucleotidase, mitochondrial
127821	0.018649252	ACP5 | acid phosphatase 5, tartrate resistant
2818432	0.004788915	EST
897164	0.013650395	CTNNA1 | catenin (cadherin-associated protein), alpha 1 (102kD)
753743	0.000185264	IL6ST | interleukin 6 signal transducer (gp130, oncostatin M receptor)
1630942	0.002517943	CRN | crooked neck protein (crn)
1700436	1.41E-11	ESTs
1877281	0.028655076	SGCG | sarcoglycan, gamma (35kD dystrophin-associated glycoprotein)
810131	0.021198683	KRT19 | keratin 19
22895	0.004091636	INSM1 | insulinoma-associated 1

882467	1.44E-07	EST
768452	0.026097881	Homo sapiens EST from clone 491476, full insert
786096	0.048422373	APC7 | anaphase-promoting complex subunit 7
768454	0.001618599	KIAA1673 | KIAA1673
239568	4.44E-11	ANXA9 | annexin A9
1325816	0.000370005	POLR2L | polymerase (RNA) II (DNA directed) polypeptide L (7.6kD)
266312	8.82E-07	ATP7B | ATPase, Cu++ transporting, beta polypeptide (Wilson disease)
128493	0.028655076	MLH1 | mutL (E. coli) homolog 1 (colon cancer, nonpolyposis type 2)
814423	0.003013488	CNNM4 | cyclin M4
68636	0.036880506	MGC2477 | hypothetical protein MGC2477
69293	0.004896866	PSG6 | pregnancy specific beta-1-glycoprotein 6
2413337	0.00254811	SORL1 | sortilin-related receptor, L(DLR class) A repeats-containing
148022	0.000123978	Homo sapiens clone Z'3-1 placenta expressed mRNA from chromosome X
1159963	0.017851437	IRF7 | interferon regulatory factor 7
46716	2.46E-07	CBX4 | chromobox homolog 4 (Drosophila Pc class)
470144	4.55E-06	EST
701751	0.046183854	CUTL1 | cut (Drosophila)-like 1 (CCAAT displacement protein)
43090	0.002358408	H-L(3)MBT | lethal (3) malignant brain tumor l(3)mbt protein (Drosophila) homolog
1860990	0.003691973	Homo sapiens cDNA FLJ32269 fis, clone PROST1000526
85624	0.025579525	C4BPA | complement component 4-binding protein, alpha
592728	0.021741547	LOC51205 | LPAP for lysophosphatidic acid phosphatase
1569902	7.55E-08	KIAA0556 | KIAA0556 protein
744944	0.017120553	MYO6 | myosin VI
132381	0.028459057	ENDOFIN | endosome-associated FYVE-domain protein
1658777	0.032434932	MY038 | hypothetical brain protein my038
882484	0.028227375	CCT7 | chaperonin containing TCP1, subunit 7 (eta)
725284	0.044510834	PHKG2 | phosphorylase kinase, gamma 2 (testis)
1568967	0.000127809	ESTs
1571106	4.93E-06	KIAA0876 | KIAA0876 protein
767819	0.02727988	KIAA0763 | KIAA0763 gene product
73188	0.001353778	FLJ20259 | hypothetical protein FLJ20259
2303214	0.017204034	NPPB | natriuretic peptide precursor B

145491	0.021270804	PCDH1 | protocadherin 1 (cadherin-like 1)
283315	0.016037507	PGAM2 | phosphoglycerate mutase 2 (muscle)
842925	0.006759973	MGC13064 | hypothetical protein MGC13064
809904	0.014055609	EST
2975668	4.56E-07	RAG2 | recombination activating gene 2
1848168	0.003247172	ZAK | sterile-alpha motif and leucine zipper containing kinase AZK
460395	0.000805296	FLJ22625 | hypothetical protein FLJ22625
1086070	0.013113828	RPH3AL | rabphilin 3A-like (without C2 domains)
773308	0.032700759	Homo sapiens, clone MGC:20276 IMAGE:3844806, mRNA, complete cds
842933	0.046030837	LOC51143 | dynein light chain-A
898147	1.07E-07	FLJ20417 | hypothetical protein FLJ20417
50615	1.84E-06	HSPA1L | heat shock 70kD protein-like 1
1456160	0.039135747	AZGP1 | alpha-2-glycoprotein 1, zinc
1929165	0.043830461	ESTs, Highly similar to HXB3_HUMAN HOMEOBOX PROTEIN HOX-B3 [H.sapiens]
277848	6.68E-06	Homo sapiens cDNA FLJ13900 fis, clone THYRO1001746
743224	0.011593805	Homo sapiens cDNA FLJ11344 fis, clone PLACE1010870, moderately similar to ZINC FINGER PROTEIN 91
302549	0.000135733	BTEB1 | basic transcription element binding protein 1
1603446	0.002762432	ESTs, Weakly similar to unknown [H.sapiens]
2307514	0.00207763	MLC1 | KIAA0027 protein
415229	5.28E-05	VAV3 | vav 3 oncogene
75886	0.00958954	ESTs, Weakly similar to E54024 protein kinase [H.sapiens]
1601845	0.016882187	CAPRI | Ca2+-promoted Ras inactivator
308437	7.30E-08	FUCA1 | fucosidase, alpha-L- 1, tissue
186301	7.86E-05	Homo sapiens cDNA FLJ12924 fis, clone NT2RP2004709
2524445	0.030973781	NPAS1 | neuronal PAS domain protein 1
703383	3.54E-05	ESTs
129478	0.010814891	ESTs
230385	0.006373505	PIP5K2B | phosphatidylinositol-4-phosphate 5-kinase, type II, beta
1915416	0.002066945	CDK7 | cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)
489169	0.000415287	ESTs, Moderately similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]
796986	1.44E-06	SIG11 | putative secreted protein

811121	3.47E-05	Homo sapiens mRNA; cDNA DKFZp586B1922 (from clone DKFZp586B1922)
782147	0.011517902	KIAA0544 | KIAA0544 protein
1637829	1.21E-12	ESTs
898162	0.047678928	C9orf5 | chromosome 9 open reading frame 5
1500542	6.03E-08	RGS11 | regulator of G-protein signalling 11
760224	0.004693782	XRCC1 | X-ray repair complementing defective repair in Chinese hamster cells 1
770785	0.004763371	HMIC | 1,2-alpha-mannosidase IC
488516	0.002192122	Homo sapiens, clone IMAGE:3875012, mRNA
290567	0.002138612	KBRAS1 | I-kappa-B-interacting Ras-like protein 1
813813	0.017612	Homo sapiens cDNA FLJ31638 fis, clone NT2RI2003556
82322	6.98E-08	RBSK | ribokinase
809939	0.001725113	MAPK3 | mitogen-activated protein kinase 3
430623	2.33E-05	ESTs
49303	0.033476578	PPP2R2B | protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform
796996	1.40E-06	IGBP1 | immunoglobulin (CD79A) binding protein 1
431286	4.10E-08	PTD002 | PTD002 protein
773332	0.00185329	ITGAE | integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)
866488	4.10E-08	ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
2048524	0.005767924	JAK2 | Janus kinase 2 (a protein tyrosine kinase)
61061	0.018883013	FNBP3 | formin-binding protein 3
357120	0.000238959	Homo sapiens, clone IMAGE:3538007, mRNA, partial cds
1560723	0.029910221	HOXB3 | homeo box B3
1412344	0.007631302	GP2 | glycoprotein 2 (zymogen granule membrane)
809944	0.00289345	KIAA0310 | KIAA0310 gene product
1607755	7.06E-05	HSPC141 | HSPC141 protein
1460075	0.042644552	PIN1 | protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1
120271	0.004728263	MGC4692 | hypothetical protein MGC4692
1637843	0.001725113	HSPA5 | heat shock 70kD protein 5 (glucose-regulated protein, 78kD)
501868	0.000425258	RAI2 | retinoic acid induced 2
308466	6.75E-05	LOC51128 | GTP-binding protein Sara
362755	0.005875967	PRKAG1 | protein kinase, AMP-activated, gamma 1 non-catalytic subunit
362756	0.020883314	KIAA1164 | hypothetical protein KIAA1164

1604423	0.013359346	ESTs
243800	0.017125244	RYBP | RING1 and YY1 binding protein
731104	3.25E-07	ESTs
266389	8.87E-09	SLC16A6 | solute carrier family 16 (monocarboxylic acid transporters), member 6
502818	2.33E-06	ARHA | ras homolog gene family, member A
1636111	0.019413865	HNRPU | heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
1570502	0.017495868	Homo sapiens cDNA FLJ12936 fis, clone NT2RP2005018
251682	1.50E-06	TINF2 | TERF1 (TRF1)-interacting nuclear factor 2
773353	0.026514552	Homo sapiens cDNA FLJ31753 fis, clone NT2RI2007468
111469	5.71E-05	Homo sapiens clone IMAGE:111469 mRNA sequence
40100	0.029910221	Homo sapiens, clone MGC:18084 IMAGE:4150952, mRNA, complete cds
454173	0.003570072	WDR7 | WD repeat domain 7
842980	1.87E-06	DRG1 | developmentally regulated GTP-binding protein 1
454175	0.009321073	HIT-17 | PKCI-1-related HIT protein
1609372	0.008647658	RIPK3 | receptor-interacting serine-threonine kinase 3
302591	3.97E-10	ARHH | ras homolog gene family, member H
66317	0.029073646	H1F2 | H1 histone family, member 2
201282	0.030274401	DKFZP434N126 | DKFZP434N126 protein
472103	0.005357267	SHOC2 | soc-2 (suppressor of clear, C.elegans) homolog
795288	0.017376841	USP4 | ubiquitin specific protease 4 (proto-oncogene)
2016869	0.006544656	KIAA1131 | KIAA1131 protein
811162	0.024982615	FMOD | fibromodulin
1910516	0.000122585	ESTs
491486	0.000923428	LOC51578 | adrenal gland protein AD-004
1558473	0.020974589	ESTs
1947144	0.028543112	ESTs
757327	0.01394813	LOC51249 | hypothetical protein
429322	0.008351255	Homo sapiens, clone IMAGE:3447394, mRNA, partial cds
868400	0.013032007	QARS | glutaminyl-tRNA synthetase
50675	2.78E-08	KIAA0423 | KIAA0423 protein
143169	4.17E-06	Homo sapiens, clone IMAGE:3881549, mRNA
823615	0.014557615	Homo sapiens cDNA: FLJ21245 fis, clone COL01184

1917063	0.00188129	Homo sapiens, clone MGC:15400 IMAGE:4040570, mRNA, complete cds
1455566	0.000327751	ADORA3 | adenosine A3 receptor
813854	0.028548635	PURA | purine-rich element binding protein A
795296	6.64E-07	CCNH | cyclin H
725649	3.06E-05	NFATC4 | nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4
49344	0.000860578	KIAA0350 | KIAA0350 protein
415287	0.023418315	ESTs
149058	0.042155684	Homo sapiens cDNA FLJ10174 fis, clone HEMBA1003959
2306919	4.44E-05	SLC35A3 | solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3
2072768	0.044848397	NCOA3 | nuclear receptor coactivator 3
757337	6.19E-07	ESTs
1686547	0.039985007	ESTs
74119-2	0.002954849	SNRPN | small nuclear ribonucleoprotein polypeptide N
489509	0.031251603	Homo sapiens mRNA; cDNA DKFZp564L0822 (from clone DKFZp564L0822)
1870049	0.005305054	DDO | D-aspartate oxidase
683569	0.000182323	ITPR1 | inositol 1,4,5-triphosphate receptor, type 1
50685	0.048777689	KIAA1414 | KIAA1414 protein
611239	0.000438876	Homo sapiens cDNA: FLJ22361 fis, clone HRC06524, highly similar to HSU15426 Human anonymous mRNA sequence with CCA repeat region
261472	0.017638942	ORF1-FL49 | putative nuclear protein ORF1-FL49
279800	5.50E-05	SLMAP | sarcolemma associated protein
49351	0.004160342	HSSEXGENE | SEX gene
49354	1.84E-06	ANK2 | ankyrin 2, neuronal
773381	0.000877702	NAPA | N-ethylmaleimide-sensitive factor attachment protein, alpha
714159	0.030468197	Homo sapiens cDNA FLJ32185 fis, clone PLACE6001925
754002	0.040830931	DKK3 | dickkopf (Xenopus laevis) homolog 3
51631	6.17E-07	DKFZP586B1621 | DKFZP586B1621 protein
289287	0.017659789	Homo sapiens mRNA; cDNA DKFZp586J101 (from clone DKFZp586J101)
301963	0.001486067	SNX11 | sorting nexin 11
742641	0.017924982	MGC5540 | hypothetical protein MGC5540
823634	0.000159834	ESTs
564621	0.011672024	SERPINI1 | serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1

814815	0.00048204	EST
796255	6.94E-06	MRPS14 | mitochondrial ribosomal protein S14
344073	7.94E-08	Homo sapiens cDNA FLJ31763 fis, clone NT2RI2007827
1557841	0.001309802	ESTs
2020772	0.000172997	TM7SF2 | transmembrane 7 superfamily member 2
1637893	1.84E-06	Homo sapiens, clone MGC:9575 IMAGE:3879368, mRNA, complete cds
753071	0.005767924	Homo sapiens cDNA: FLJ22528 fis, clone HRC12825
42827	0.003388822	Homo sapiens cDNA FLJ31604 fis, clone NT2RI2002699
22500	0.000613835	ESTs
841287	0.001159126	GNPAT | glyceronephosphate O-acyltransferase
301976	0.000553787	PPP3CC | protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma)
785840	0.028503208	SEC24D | SEC24 (S. cerevisiae) related gene family, member D
814826	0.000212133	ESTs
725672	0.030333035	Homo sapiens, Similar to transducin (beta)-like 3, clone MGC:8613 IMAGE:2961321, mRNA, complete cds
784105	0.03689826	ESTs
812143	0.009962681	FLRT3 | fibronectin leucine rich transmembrane protein 3
1948122	0.0285188	FLJ10450 | hypothetical protein FLJ10450
1877697	0.000466212	ESTs
1901735	0.004586404	RPP14 | ribonuclease P (14kD)
454503	1.11E-05	Homo sapiens, clone IMAGE:3346451, mRNA, partial cds
80798	0.002033157	ITM2B | integral membrane protein 2B
594724	0.001075123	YR-29 | hypothetical protein
681992	0.038338214	Homo sapiens cDNA FLJ13384 fis, clone PLACE1001062, highly similar to Homo sapiens mRNA for lysine-ketoglutarate reductase/saccharopine dehydrogenase
487932	5.59E-09	SYTL2 | synaptotagmin-like 2
868441	0.003083769	FLJ20727 | hypothetical protein FLJ20727
729964	0.004902138	SMPD1 | sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)
345034	0.017833089	SCYB14 | small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK)
884480	0.022202501	COX7C | cytochrome c oxidase subunit VIIc
823655	3.25E-08	AD036 | AD036 protein
823659	1.46E-06	FYCO1 | FYVE and coiled-coil domain containing 1

298417	1.30E-14	TFF3 | trefoil factor 3 (intestinal)
2063982	2.33E-07	KCNK6 | potassium channel, subfamily K, member 6 (TWIK-2)
44443	0.042068695	SCYE1 | small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)
838366	1.25E-05	HMGCL | 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)
754033	7.67E-06	LZTFL1 | leucine zipper transcription factor-like 1
754034	0.001228195	THPO | thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)
897593	1.41E-06	KIAA1548 | KIAA1548 protein
770074	0.00038924	PRRG2 | proline-rich Gla (G-carboxyglutamic acid) polypeptide 2
753092	1.98E-06	EST
1631238	0.007429314	KIAA1483 | KIAA1483 protein
415610	0.000498483	FLJ22402 | hypothetical protein FLJ22402
2018808	0.038787441	PRCP | prolylcarboxypeptidase (angiotensinase C)
823661	0.000706071	Homo sapiens cDNA FLJ31768 fis, clone NT2RI2007891, moderately similar to DMR-N9 PROTEIN
486208	0.000218364	TGFB3 | transforming growth factor, beta 3
487948	0.000529233	Homo sapiens cDNA: FLJ22566 fis, clone HSI01980
67318	0.012702024	Homo sapiens, Similar to RIKEN cDNA 0610039G24 gene, clone MGC:15403 IMAGE:4126342, mRNA, complete cds
83358	1.39E-11	ESTs
1583673	2.86E-06	ESTs, Weakly similar to KIAA0351 [H.sapiens]
784126	0.009372382	TST | thiosulfate sulfurtransferase (rhodanese)
366315	0.024091716	Homo sapiens, clone MGC:20500 IMAGE:4053084, mRNA, complete cds
2366057	0.000958877	CDH12 | cadherin 12, type 2 (N-cadherin 2)
47795	0.01192016	ZNF161 | zinc finger protein 161
51672	9.79E-05	ARRB1 | arrestin, beta 1
124922	0.000642521	SZF1 | KRAB-zinc finger protein SZF1-1
193916	0.030979591	RHBG | Rhesus blood group, B glycoprotein
1925280	5.88E-07	NPR2L | homologous to yeast nitrogen permease (candidate tumor suppressor)
266747	0.034115322	Homo sapiens, Similar to RIKEN cDNA 2010001O09 gene, clone MGC:21387 IMAGE:4471592, mRNA, complete cds
429387	0.001030569	CHN2 | chimerin (chimaerin) 2
345055	9.76E-05	ESTs, Highly similar to LB4D_HUMAN NADP-DEPENDENT LEUKOTRIENE B4 12-

		HYDROXYDEHYDROGENASE [H.sapiens]
345056	0.000129022	KIAA1404 | KIAA1404 protein
258589	0.000383745	REL | v-rel avian reticuloendotheliosis viral oncogene homolog
190295	2.00E-05	FLJ23590 | hypothetical protein FLJ23590
782537	0.045949613	Homo sapiens cDNA FLJ30428 fis, clone BRACE2008941
1554549	1.10E-06	HAGH | hydroxyacyl glutathione hydrolase
143519	0.023557456	FKBP2 | FK506-binding protein 2 (13kD)
838389	1.40E-08	UNC119 | unc119 (C.elegans) homolog
184022	0.010544493	APBB1 | amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65)
840664	0.000657157	EST
203240	3.98E-06	DAB2 | disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein)
300271	0.003251584	SAS10 | disrupter of silencing 10
131070	0.00841697	KIAA0670 | KIAA0670 protein/acinus
196189	1.68E-07	CYB5 | cytochrome b-5
453599	0.001069723	DKFZP564F1123 | DKFZP564F1123 protein
823682	0.026331677	KIAA0710 | KIAA0710 gene product
784140	0.003891255	WDR11 | WD40 repeat domain 11 protein
31366	0.011252089	MYT1 | myelin transcription factor 1
1558832	0.003860708	MAT2B | methionine adenosyltransferase II, beta
742695	3.48E-07	Homo sapiens cDNA FLJ31534 fis, clone NT2RI2000671
726658	8.52E-08	NME3 | non-metastatic cells 3, protein expressed in
823688	0.045171023	MAN1A1 | mannosidase, alpha, class 1A, member 1
2322223	2.50E-05	SNRPA | small nuclear ribonucleoprotein polypeptide A
866874	8.19E-08	HNRPH2 | heterogeneous nuclear ribonucleoprotein H2 (H')
250313	0.000892123	ESTs
685516	2.07E-10	GPCR150 | putative G protein-coupled receptor
288683	0.00367697	ESTs
461761	1.58E-05	ANG | angiogenin, ribonuclease, RNase A family, 5
758347	6.94E-05	SLC2A10 | solute carrier family 2 (facilitated glucose transporter), member 10
1650927	0.004105721	DKFZp547E052 | hypothetical protein DKFZp547E052
128143	2.88E-06	PON1 | paraoxonase 1
753404	0.037494688	KIAA0887 | KIAA0887 protein

214751	0.000487816	Homo sapiens, clone MGC:12617 IMAGE:2964706, mRNA, complete cds
1694775	0.000354216	EST
277185	0.000614717	PRO0461 | PRO0461 protein
2432360	0.006342148	BSN | bassoon (presynaptic cytomatrix protein)
1609748	2.16E-06	MGC10882 | hypothetical protein MGC10882
1915824	0.003398986	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
2067500	4.36E-11	LDB3 | LIM domain binding 3
823691	4.27E-08	CCNG2 | cyclin G2
1895664	0.026431801	PRO2198 | hypothetical protein PRO2198
243100	1.01E-06	ACADSB | acyl-Coenzyme A dehydrogenase, short/branched chain
784150	3.38E-10	RAB31 | RAB31, member RAS oncogene family
785890	0.032434657	Homo sapiens cDNA FLJ14030 fis, clone HEMBA1004086
784154	0.014124729	ESTs, Highly similar to unnamed protein product [H.sapiens]
767170	0.026562375	LOC51606 | CGI-11 protein
767171	5.14E-05	FLJ20015 | hypothetical protein
812196	0.000269329	UGCG | UDP-glucose ceramide glucosyltransferase
145132	0.017780719	MPDU1 | mannose-P-dolichol utilization defect 1
767176	0.003072281	TNFSF13 | tumor necrosis factor (ligand) superfamily, member 13
855385	0.008682257	CLN2 | ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease)
843224	1.13E-05	DSCR2 | Down syndrome critical region gene 2
283751	0.032429761	CORT | cortistatin
233349	0.000116838	FLJ10761 | hypothetical protein FLJ10761
1536925	6.56E-06	PDPK1 | 3-phosphoinositide dependent protein kinase-1
771058	1.40E-08	CISH | cytokine inducible SH2-containing protein
1323591	1.62E-07	SERPINA5 | serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5
826245	1.66E-05	LOC54505 | hypothetical protein
1895672	9.67E-05	ESTs, Weakly similar to S57447 HPBRII-7 protein [H.sapiens]
840687	0.004816698	MUC1 | mucin 1, transmembrane
80050	0.036628745	FLJ23153 | likely ortholog of mouse tumor necrosis-alpha-induced adipose-related protein
82738	2.39E-09	DNASE1L3 | deoxyribonuclease I-like 3
503866	0.011391526	SPA17 | sperm autoantigenic protein 17

1027283	0.009413465	ESTs
147826	0.003162135	ESTs
38213	0.000167261	FLJ22174 | hypothetical protein FLJ22174
1502566	1.61E-05	ESTs, Weakly similar to T21437 hypothetical protein F26H9.4 - Caenorhabditis elegans [C.elegans]
754080	0.012652328	ICAM3 | intercellular adhesion molecule 3
267725	5.65E-05	BC-2 | putative breast adenocarcinoma marker (32kD)
1703455	0.004124332	EDG2 | endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2
344432	0.001735764	MGST2 | microsomal glutathione S-transferase 2
2015517	6.88E-09	FLJ22237 | hypothetical protein FLJ22237
813154	0.046806631	NFIA | nuclear factor I/A
322511	4.76E-08	Homo sapiens mRNA; cDNA DKFZp564D1462 (from clone DKFZp564D1462)
814899	0.001468215	BNIP3L | BCL2/adenovirus E1B 19kD-interacting protein 3-like
160532	0.004538178	ESTs, Weakly similar to JX0331 laurate omega-hydroxylase [H.sapiens]
784178	1.98E-06	Homo sapiens mRNA; cDNA DKFZp586M0723 (from clone DKFZp586M0723)
1536941	0.000449552	ESTs, Moderately similar to ALU2_HUMAN ALU SUBFAMILY SB SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
841641	4.35E-06	CCND1 | cyclin D1 (PRAD1: parathyroid adenomatosis 1)
843248	0.001755052	VAMP3 | vesicle-associated membrane protein 3 (cellubrevin)
127519	2.29E-08	POH1 | 26S proteasome-associated pad1 homolog
43849	0.001286711	ESTs
815847	0.038913997	C11orf5 | chromosome 11 open reading frame 5
261852	0.001941321	ESTs
2306221	1.79E-12	WNT10B | wingless-type MMTV integration site family, member 10B
813165	0.003482886	PGRMC2 | progesterone receptor membrane component 2
811565	1.51E-05	KIAA1694 | KIAA1694 protein
726699	4.73E-07	Homo sapiens, clone MGC:9889 IMAGE:3868330, mRNA, complete cds
1555536	3.04E-06	LGP1 | likely ortholog of mouse D11lgp1
771084	0.000459658	BECN1 | beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)
526757	1.84E-05	CCND1 | cyclin D1 (PRAD1: parathyroid adenomatosis 1)
42118	8.31E-05	P2RX4 | purinergic receptor P2X, ligand-gated ion channel, 4
28475	0.001063475	CRYZ | crystallin, zeta (quinone reductase)
841655	1.97E-05	RBBP2 | retinoblastoma-binding protein 2

1632247	0.001096449	FLJ23436 | hypothetical protein FLJ23436
753447	0.014351752	DDB2 | damage-specific DNA binding protein 2 (48kD)
280444	0.000352001	KIAA0608 | KIAA0608 protein
745289	0.029910221	PNAS-127 | PNAS-127 protein
502153	0.005704405	Homo sapiens, clone MGC:16377 IMAGE:3936171, mRNA, complete cds
378824	0.000177644	HSPC009 | HSPC009 protein
784190	0.000123726	Homo sapiens, Similar to RIKEN cDNA 5530601I19 gene, clone MGC:9743 IMAGE:3854028, mRNA, complete cds
70606	0.022570057	ESTs
854763	9.74E-07	MGC20702 | hypothetical protein MGC20702
2284473	0.01376248	ZK1 | Kruppel-type zinc finger (C2H2)
1588973	0.000173284	IMAGE3451454 | hypothetical protein IMAGE3451454
26883	1.17E-07	PKIB | protein kinase (cAMP-dependent, catalytic) inhibitor beta
796643	0.012443564	NEBL | nebulette
877636	2.16E-05	DCTN4 | dynactin 4 (p62)
2017144	0.002872765	LOC51093 | CGI-41 protein
1048586	0.009471574	BMI1 | murine leukemia viral (bmi-1) oncogene homolog
813183	0.01280152	AZU1 | azurocidin 1 (cationic antimicrobial protein 37)
486288	0.012126378	Homo sapiens clone CDABP0028 mRNA sequence
811582	1.35E-07	GOLPH2 | golgi phosphoprotein 2
838732	1.49E-05	LOC51596 | divalent cation tolerant protein CUTA
813189	2.96E-05	EST
811585	0.000116498	HD | huntingtin (Huntington disease)
1558895	0.041918884	PGAM2 | phosphoglycerate mutase 2 (muscle)
208531	5.51E-06	FLJ20551 | hypothetical protein FLJ20551
150003	1.31E-07	FLJ13187 | phafin 2
293569	9.71E-05	C1orf21 | chromosome 1 open reading frame 21
25154	0.004517557	PLAT | plasminogen activator, tissue
824692	4.04E-06	SEL1L | sel-1 (suppressor of lin-12, C.elegans)-like
841679	0.00456714	SIP2-28 | calcium and integrin binding protein (DNA-dependent protein kinase interacting protein)
1908666	0.018949143	ZNF79 | zinc finger protein 79 (pT7)
1558108	0.000693345	ABCC8 | ATP-binding cassette, sub-family C (CFTR/MRP), member 8

810937	0.001309095	TPST2 | tyrosylprotein sulfotransferase 2
1473914	0.000225716	C21orf15 | chromosome 21 open reading frame 15
897971	0.001037841	COPB | coatomer protein complex, subunit beta
489922	0.006100942	AKAP10 | A kinase (PRKA) anchor protein 10
754417	0.038568449	Homo sapiens mRNA; cDNA DKFZp586H021 (from clone DKFZp586H021)
1456937	0.000129703	OVGP1 | oviductal glycoprotein 1, 120kD (mucin 9, oviductin)
841685	0.03461124	SID6-306 | inorganic pyrophosphatase
796663	0.002337587	DRIP78 | dopamine receptor interacting protein
267778	0.004321341	ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]
1896676	1.24E-06	Homo sapiens cDNA: FLJ22113 fis, clone HEP18418
814145	2.06E-05	JTB | jumping translocation breakpoint
1637504	0.017405243	EST
296123	0.009311435	Homo sapiens PRO1851 mRNA, complete cds
48033	9.67E-07	ESTs
810947	0.006557959	NUDE1 | LIS1-interacting protein NUDE1, rat homolog
810948	0.001616352	TRAP240 | thyroid hormone receptor-associated protein, 240 kDa subunit
454908	0.000286005	CGA | glycoprotein hormones, alpha polypeptide
283023	0.010085994	CX3CR1 | chemokine (C-X3-C) receptor 1
897982	0.009962681	EIF3S8 | eukaryotic translation initiation factor 3, subunit 8 (110kD)
380057	0.000839497	APPBP2 | amyloid beta precursor protein (cytoplasmic tail)-binding protein 2
179572	3.91E-10	Homo sapiens cDNA FLJ14227 fis, clone NT2RP3004095
841695	0.008164837	CG018 | hypothetical gene CG018
30793	0.002706225	PEX11B | peroxisomal biogenesis factor 11B
23579	0.010974699	Homo sapiens clone 23579 mRNA sequence
1914168	0.045350687	FLJ20558 | hypothetical protein FLJ20558
1637516	0.009609456	GS2NA | nuclear autoantigen
1635913	0.041470052	LNX | multi-PDZ-domain-containing protein
502198	0.00087773	PPP1R3C | protein phosphatase 1, regulatory (inhibitor) subunit 3C
1520559	0.031251603	ESTs
294537	2.82E-08	RAB17 | RAB17, member RAS oncogene family
1899230	0.047956858	H.sapiens mRNA for metallothionein isoform 1R
488202	6.46E-07	Homo sapiens cDNA FLJ31235 fis, clone KIDNE2004681, moderately similar to Mus musculus

		peroxisomal long chain acyl-CoA thioesterase Ib (Pte1b) gene
271670	0.012020011	TNFSF12 | tumor necrosis factor (ligand) superfamily, member 12
430318	0.00244659	PVALB | parvalbumin
2284803	0.002768702	SCAMP1 | secretory carrier membrane protein 1
470964	1.58E-07	GALNT6 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)
196570	0.000194501	MGC2747 | hypothetical protein MGC2747
754443	0.023018366	Homo sapiens cDNA FLJ13771 fis, clone PLACE4000270
1536215	0.008360311	GALNAC4S-6ST | B cell RAG associated protein
700836	0.001618877	ZNF19 | zinc finger protein 19 (KOX 12)
1553996	2.38E-05	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
50339	1.99E-07	ESTs, Moderately similar to hypothetical protein [H.sapiens]
2103000	0.019869834	ESTs
25194	0.000197727	Homo sapiens clone 25194 mRNA sequence
1523116	0.000863455	NESH | NESH protein
1593849	0.013132955	PDE4A | phosphodiesterase 4A, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2)
813518	0.001929727	ESTs
2138030	0.0247432	KCNS3 | potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3
66787	0.037494688	TRIP3 | thyroid hormone receptor interactor 3
215000	1.30E-06	VIPR1 | vasoactive intestinal peptide receptor 1
197525	0.009040685	FMO5 | flavin containing monooxygenase 5
826622	1.28E-06	KIAA0430 | KIAA0430 gene product
291216	0.011893765	CETN2 | centrin, EF-hand protein, 2
2460159	0.040000458	TNK1 | tyrosine kinase, non-receptor, 1
1410444	0.002729944	AREG | amphiregulin (schwannoma-derived growth factor)
882511	0.000981881	M17S2 | membrane component, chromosome 17, surface marker 2 (ovarian carcinoma antigen CA125)
214068	4.60E-25	GATA3 | GATA-binding protein 3
417637	0.02117967	KIAA1276 | KIAA1276 protein
111150	0.008720987	LNX | multi-PDZ-domain-containing protein
1558151	3.27E-06	BATF | basic leucine zipper transcription factor, ATF-like
2052113	6.56E-06	FLJ10903 | hypothetical protein FLJ10903

321945	0.000909807	ESTs
810987	1.62E-06	MBC3205 | hypothetical protein MBC3205
26152	0.011314426	KIAA1557 | KIAA1557 protein
1534633	0.019925171	MGC2479 | hypothetical protein MGC2479
788832	9.78E-06	PLAB | prostate differentiation factor
725321	1.53E-22	ESR1 | estrogen receptor 1
85384	0.000225058	ATP11 | hypothetical protein FLJ22351
2018158	0.019146124	ESTs
814191	0.04385949	KIAA0295 | KIAA0295 protein
487297	0.001907323	CAP2 | adenylyl cyclase-associated protein 2
730942	0.002682409	DECR2 | 2,4-dienoyl CoA reductase 2, peroxisomal
502518	0.000152832	LAMB2 | laminin, beta 2 (laminin S)
811937	0.015875339	SNX9 | sorting nexin 9
278531	7.09E-07	COX6C | cytochrome c oxidase subunit VIc
1558166	1.96E-07	ESTs, Moderately similar to AF072733 1 putative secreted protein [H.sapiens]
137370	0.007518112	ESTs
704062	5.44E-05	SIRT3 | sirtuin (silent mating type information regulation 2, S.cerevisiae, homolog) 3
593431	8.35E-13	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1287006
595037	0.008509083	RAI3 | retinoic acid induced 3
240966	0.012397017	PCBP2 | poly(rC)-binding protein 2
754474	0.016470796	ESTs
344820	0.021127692	KIF3A | kinesin family member 3A
486641	0.000140204	MOCS2 | molybdenum cofactor synthesis 2
1898619	7.34E-10	MGC15737 | hypothetical protein MGC15737
450673	7.31E-05	SPATA2 | spermatogenesis associated 2
1917837	0.034946932	FLJ11838 | hypothetical protein FLJ11838
85394	0.01312499	PPAP2B | phosphatidic acid phosphatase type 2B
345487	0.035143688	Homo sapiens, clone MGC:23280 IMAGE:4637504, mRNA, complete cds
811944	0.045490722	ESTs
786169	0.003709448	FLJ11088 | hypothetical protein FLJ11088
376516	7.09E-07	LRBA | vesicle trafficking, beach and anchor containing
70692	0.025359903	SERPINB2 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2

147147	0.005871121	ESTs
1563792	0.001655476	LOC51333 | mesenchymal stem cell protein DSC43
1687976	0.005209931	SIL1 | endoplasmic reticulum chaperone SIL1, homolog of yeast
1898625	0.00480123	ANKTM1 | ankyrin-like with transmembrane domains 1
130845	0.016285335	PWP1 | nuclear phosphoprotein similar to S. cerevisiae PWP1
1947933	0.032222366	FLJ12800 | hypothetical protein FLJ12800
296190	0.000356685	KIAA0321 | KIAA0321 protein
588915	0.001292252	IFI27 | interferon, alpha-inducible protein 27
50383	0.019695801	KIAA1598 | KIAA1598 protein
2346188	0.037722909	PNKP | polynucleotide kinase 3'-phosphatase
41569	2.04E-09	FLJ12650 | hypothetical protein FLJ12650
868119	0.000560528	LOC57117 | hypothetical nuclear factor SBBI22
815167	0.001112368	PLEKHA3 | pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 3
342164	0.037052367	FLJ14486 | hypothetical protein FLJ14486
377193	0.024734713	LOC54505 | hypothetical protein
1492587	0.01198186	Homo sapiens, Similar to RAB37, member of RAS oncogene family, clone MGC:21391 IMAGE:4520191, mRNA, complete cds
276962	0.000184101	LOC57149 | hypothetical protein A-211C6.1
143966	0.044999609	2-Sep | septin 6
1707078	0.023623028	LOC51646 | CGI-127 protein
108265	0.027824136	Homo sapiens, clone MGC:21518 IMAGE:3900532, mRNA, complete cds
785535	0.029849385	DDXBP1 | DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1
1415720	0.032290985	EST
243549	1.35E-05	MYB | v-myb avian myeloblastosis viral oncogene homolog
1031592	9.21E-07	KIF9 | kinesin family member 9
1460110	0.026915103	PSMB5 | proteasome (prosome, macropain) subunit, beta type, 5
285798	1.41E-06	ESTs, Weakly similar to S65824 reverse transcriptase homolog [H.sapiens]
176606	0.032429761	NELL2 | nel (chicken)-like 2
272694	0.037494688	C1orf9 | chromosome 1 open reading frame 9
814528	4.69E-05	p53DINP1 | p53-inducible p53DINP1
342181	1.41E-11	BCL2 | B-cell CLL/lymphoma 2

813584	0.028503208	PA26 | p53 regulated PA26 nuclear protein
813585	0.004222762	XAP4 | HBV associated factor
2011660	0.005969978	DKFZp434K1210 | hypothetical protein DKFZp434K1210
248499	0.010004815	AF5Q31 | ALL1 fused gene from 5q31
898221	5.65E-05	NR4A2 | nuclear receptor subfamily 4, group A, member 2
898222	0.000898114	ATP12 | homolog of yeast ATP12
770840	0.012755509	AVIL | advillin
1640821	3.60E-08	Homo sapiens, clone IMAGE:3899073, mRNA, partial cds
470249	0.000754806	ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
491486-2	0.002434509	LOC51578 | adrenal gland protein AD-004
143989	0.020286058	KIAA1340 | KIAA1340 protein
665658	0.000136335	MSX2 | msh (Drosophila) homeo box homolog 2
1762326	4.41E-05	ESTs
74223	0.00021037	HTPAP | HTPAP protein
344988-2	2.10E-05	EST
768570	3.26E-12	FLJ11280 | hypothetical protein FLJ11280
858387	0.000198568	MGC4767 | hypothetical protein MGC4767
1030953	0.007749864	LOC80298 | transcription termination factor-like protein
365060	0.000392359	RAB11A | RAB11A, member RAS oncogene family
283413	0.004226861	LRDD | leucine-rich and death domain containing
1709786	0.026592724	TRPS1 | trichorhinophalangeal syndrome I
143995	0.025539645	Homo sapiens mRNA from chromosome 5q21-22, clone:FBR89
1526826	4.26E-06	HOXB2 | homeo box B2
140655	0.004076409	dJ453C12.4.1 | similar to RIKEN cDNA 2610042O14 gene (M. musculus)
322160-2	0.023425543	PTEN | phosphatase and tensin homolog (mutated in multiple advanced cancers 1)
814546	0.019909138	ESTs, Highly similar to PCD1_HUMAN CYTOHESIN 1 [H.sapiens]
130895	8.00E-10	Homo sapiens cDNA: FLJ22930 fis, clone KAT07255
725394	0.005095011	CLPX | ClpX (caseinolytic protease X, E. coli) homolog
504187	4.31E-05	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
725395	0.037816121	UBE2L6 | ubiquitin-conjugating enzyme E2L 6
502585	0.001007942	RAB18 | RAB18, member RAS oncogene family

782385-2	0.011252089	DKFZP566D193 | DKFZP566D193 protein
132381-2	1.73E-05	ENDOFIN | endosome-associated FYVE-domain protein
154707	0.02165445	MPV17 | MpV17 transgene, murine homolog, glomerulosclerosis
163528	0.000751027	PALM | paralemmin
306924	6.86E-07	KIAA0222 | KIAA0222 gene product
296529	0.027905446	KIAA1504 | KIAA1504 protein
470261	7.82E-05	SMA5 | SMA5
1709791	9.70E-08	BAIAP1 | BAI1-associated protein 1
110578	0.000133284	ESTs
1457205	4.94E-05	Homo sapiens cDNA FLJ20525 fis, clone KAT10610
1708055	0.026818494	GOV | glioblastoma overexpressed
358936	4.04E-06	ESTs, Weakly similar to T2D3_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT [H.sapiens]
1626409	0.005619887	AP2A1 | adaptor-related protein complex 2, alpha 1 subunit
770866	0.042071414	Homo sapiens, clone MGC:9709 IMAGE:3850147, mRNA, complete cds
347434	0.000306027	SC65 | nucleolar autoantigen (55kD) similar to rat synaptonemal complex protein
795330	0.043246672	NR1D1 | nuclear receptor subfamily 1, group D, member 1
347436	0.000531118	GSTTLp28 | glutathione-S-transferase like; glutathione transferase omega
357996	0.024330122	FLJ20156 | hypothetical protein FLJ20156
770869	0.002110844	MGC2592 | hypothetical protein MGC2592
126229	0.007870589	MGC12760 | hypothetical protein MGC12760
130104	0.025309814	Homo sapiens, clone IMAGE:3352566, mRNA, partial cds
269788	0.001755224	SEDLP | spondyloepiphyseal dysplasia, late, pseudogene
785571	0.000352444	DNAJL1 | hypothetical protein similar to mouse Dnajl1
325515	2.23E-08	FLJ10980 | hypothetical protein FLJ10980
868168	6.52E-05	SPRR2A | small proline-rich protein 2A
785574	0.000174826	SNX1 | sorting nexin 1
199505	0.000661388	SENP7 | sentrin/SUMO-specific protease
46843	0.012102208	SLI | neuronal Shc adaptor homolog
898251	0.020270563	FLJ20727 | hypothetical protein FLJ20727
1950130	0.009056557	Homo sapiens cDNA FLJ14115 fis, clone MAMMA1001760
739450	0.002041876	LASS2 | longevity assurance (LAG1, S. cerevisiae) homolog 2

781295	0.004349202	SCAD-SRL | peroxisomal short-chain alcohol dehydrogenase
127970	0.029073646	Homo sapiens cDNA FLJ13557 fis, clone PLACE1007737
772477	0.008407492	Homo sapiens, clone MGC:19570 IMAGE:3942960, mRNA, complete cds
241988	7.09E-06	WDR6 | WD repeat domain 6
795342	0.026143501	ESTs
753897	3.10E-07	AMFR | autocrine motility factor receptor
786525	0.020146808	KIAA1917 | KIAA1917 protein
812968	0.00014351	PTPRN2 | protein tyrosine phosphatase, receptor type, N polypeptide 2
1559198	0.000278805	Homo sapiens cDNA FLJ14923 fis, clone PLACE1008244, weakly similar to VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1
141623	0.037935139	LOC51056 | leucine aminopeptidase
366039	2.23E-05	ESTs, Weakly similar to ABP2_HUMAN ENDOTHELIAL ACTIN-BINDING PROTEIN [H.sapiens]
2054896	0.007810967	FLJ21669 | hypothetical protein FLJ21669
969495	0.001699546	TIGA1 | TIGA1
786530	0.001147277	FLJ23027 | hypothetical protein FLJ23027
82421	0.010334304	CD44 | CD44 antigen (homing function and Indian blood group system)
1892025	0.019936342	MGC13170 | hypothetical protein MGC13170
343174	1.92E-05	Homo sapiens cDNA FLJ31204 fis, clone KIDNE2003305, weakly similar to PUTATIVE AMIDASE AF1954 (EC 3.5.1.4)
769552	0.001219419	LENG4 | leukocyte receptor cluster (LRC) member 4
1409509	0.007517038	TNNT1 | troponin T1, skeletal, slow
785595	0.033081925	STE | sulfotransferase, estrogen-preferring
139354	8.04E-09	HSPC195 | hypothetical protein
1493596	0.018150022	VLGR1 | very large G protein-coupled receptor 1
898276	0.000107772	HSMNP1 | uncharacterized hypothalamus protein HSMNP1
788141	0.000137025	XPA | xeroderma pigmentosum, complementation group A
3208314	0.017495868	GPR27 | G protein-coupled receptor 27
2164248	0.041777908	HMG20B | high-mobility group 20B
502909	0.000155359	KIAA0326 | KIAA0326 protein
812989	0.039337098	DJ1141E15.2 | hypothetical protein dJ1141E15.2
1556957	0.013797398	Homo sapiens cDNA FLJ32647 fis, clone SYNOV2001374, moderately similar to ZINC FINGER PROTEIN 134

897625	0.024870477	KIAA0532 | KIAA0532 protein
701112	0.000600597	XPC | xeroderma pigmentosum, complementation group C
179212	4.11E-11	ESTs, Moderately similar to T12539 hypothetical protein DKFZp434J154.1 [H.sapiens]
1539977	0.001651449	SLC27A1 | solute carrier family 27 (fatty acid transporter), member 1
824354	0.004173726	GRLF1 | glucocorticoid receptor DNA binding factor 1
327150	0.033503623	DOCK1 | dedicator of cyto-kinesis 1
487697	0.001175473	CROT | carnitine O-octanoyltransferase
1603583	3.02E-05	SH3BGRL | SH3 domain binding glutamic acid-rich protein like
769571	0.000117954	SREBF1 | sterol regulatory element binding transcription factor 1
510794	0.00135873	MYCBP | c-myc binding protein
712622	0.000806331	GTF2H2 | general transcription factor IIH, polypeptide 2 (44kD subunit)
1573946	7.33E-06	MRPS30 | mitochondrial ribosomal protein S30
51700	8.17E-09	ESTs
854444	9.48E-13	HLA-DQB1 | major histocompatibility complex, class II, DQ beta 1
712624	0.030232568	Homo sapiens mRNA; cDNA DKFZp564C1216 (from clone DKFZp564C1216)
2054122	6.11E-07	SLC11A3 | solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3
1698784	0.038568449	Human glucose transporter pseudogene
163579	0.006154605	RAB3A | RAB3A, member RAS oncogene family
1641837	0.002757371	Homo sapiens putative ion channel protein CATSPER2 (CATSPER2), mRNA
1472638	0.010481096	FLJ14117 | hypothetical protein FLJ14117
1592530	0.010585978	IP6K2 | mammalian inositol hexakisphosphate kinase 2
364469	0.007213754	NDUFA7 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (14.5kD, B14.5a)
591157	0.01978301	NET-7 | transmembrane 4 superfamily member (tetraspan NET-7)
67070	0.00152487	SLU7 | step II splicing factor SLU7
795382	0.000206162	EPAC | Rap1 guanine-nucleotide-exchange factor directly activated by cAMP
786562	0.009803386	ZNF43 | zinc finger protein 43 (HTF6)
180561	0.001401571	GSTM1 | glutathione S-transferase M1
263159	4.66E-06	PL6 | PL6 protein
73638	1.57E-05	PTP4A2 | protein tyrosine phosphatase type IVA, member 2
156363	0.009457359	FLJ12934 | likely ortholog of mouse actin-related protein 8 homolog (S. cerevisiae)
810017-2	0.001130048	PLAUR | plasminogen activator, urokinase receptor
1697055	0.022652474	EST

1031963	1.29E-08	Homo sapiens mRNA; cDNA DKFZp586A0618 (from clone DKFZp586A0618)
306982	0.006503031	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
1952866	0.004498241	Homo sapiens chromosome 9, P1 clone 11659
46896	1.52E-05	PRO1331 | hypothetical protein PRO1331
27516	0.012811838	CAMLG | calcium modulating ligand
796330	0.005722733	FLJ14888 | hypothetical protein FLJ14888
32050	1.89E-09	Homo sapiens mRNA; cDNA DKFZp586P1124 (from clone DKFZp586P1124)
2017917	0.016701054	Homo sapiens cDNA: FLJ23371 fis, clone HEP16068, highly similar to HSTFIISH Homo sapiens mRNA for transcription elongation factor TFIIS
823719	0.000166213	ESTs
1585327	0.007304469	AXIN2 | axin 2 (conductin, axil)
84068	0.000831262	CL25084 | hypothetical protein
1902462	0.048261732	AF038169 | hypothetical protein
1733262	1.95E-11	BLu | BLu protein
950836	2.86E-08	DDB1 | damage-specific DNA binding protein 1 (127kD)
839081	3.95E-05	HELO1 | homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2
757435	0.014952072	NKX3A | NK homeobox (Drosophila), family 3, A
161993	0.022731389	CEBPB | CCAAT/enhancer binding protein (C/EBP), beta
756490	5.64E-05	BCAT2 | branched chain aminotransferase 2, mitochondrial
250069	0.001412816	DUSP8 | dual specificity phosphatase 8
809939-2	0.000350689	MAPK3 | mitogen-activated protein kinase 3
825323	0.004670589	CKAP1 | cytoskeleton-associated protein 1
2018581	1.22E-05	IL6ST | interleukin 6 signal transducer (gp130, oncostatin M receptor)
788180	0.011295686	AMACR | alpha-methylacyl-CoA racemase
741790	0.000210007	FLJ20080 | hypothetical protein FLJ20080
193736-2	0.035288396	BRCA2 | breast cancer 2, early onset
344168	0.003024674	POLL | polymerase (DNA directed), lambda
812227	0.017120553	SLC9A1 | solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na+/H+, amiloride sensitive)
741795	6.69E-06	RALGPS1A | Ral guanine nucleotide exchange factor RalGPS1A
246194	0.000395219	ESTs

565379	0.001699546	GRB10 | growth factor receptor-bound protein 10
325583	3.88E-05	EST
73659	0.022122876	Homo sapiens, clone IMAGE:3463399, mRNA, partial cds
47853	0.037258896	ALDH4A1 | aldehyde dehydrogenase 4 family, member A1
198917	0.001513766	Homo sapiens cDNA FLJ32847 fis, clone TESTI2003376
358217	0.027049095	GPC4 | glypican 4
450301	0.00677521	MLH3 | mutL (E. coli) homolog 3
127243	0.009413465	ESTs
194638	0.011615484	ESTs, Weakly similar to alternatively spliced product using exon 13A [H.sapiens]
726703	4.06E-10	Homo sapiens clone 23736 mRNA sequence
814913	2.00E-07	C11orf15 | chromosome 11 open reading frame 15
1569306	0.019052814	FLJ14225 | hypothetical protein FLJ14225
112541	5.78E-07	Homo sapiens cDNA FLJ30580 fis, clone BRAWH2006996
108667	0.001139656	SF3A1 | splicing factor 3a, subunit 1, 120kD
813973	0.044951328	VPS11 | vacuolar protein sorting 11 (yeast homolog)
340974	3.20E-05	Homo sapiens cDNA: FLJ23270 fis, clone COL10309, highly similar to HSU33271 Human normal keratinocyte mRNA
1901824	0.001796004	HSPC207 | hypothetical protein
1636251	0.001241866	BAG1 | BCL2-associated athanogene
700500	0.000197697	PCTK2 | PCTAIRE protein kinase 2
51741	0.000159834	RHO6 | GTP-binding protein
789147	0.007583738	ENO2 | enolase 2, (gamma, neuronal)
265874	0.030801508	NFIC | nuclear factor I/C (CCAAT-binding transcription factor)
769901	0.006350535	CDIPT | CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)
785941	0.00543149	ZNF278 | zinc finger protein 278
172721	0.006694279	Homo sapiens cDNA FLJ31795 fis, clone NT2RI2008812
1908378	0.002044263	MPP3 | membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)
70332	0.036594925	ACP2 | acid phosphatase 2, lysosomal
731257	8.33E-05	UNC13 | UNC13 (C. elegans)-like
825350	0.034288184	KIAA1040 | KIAA1040 protein
841393	0.003180363	PRO0149 | PRO0149 protein
360518	0.019741126	GNGT1 | guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1

784212	4.52E-09	FLJ20152 | hypothetical protein
49481	1.04E-06	FLJ14800 | hypothetical protein FLJ14800
49482	0.000459287	ESTs
767236	0.008346481	CGI-51 | CGI-51 protein
1570663	1.29E-05	FKBP4 | FK506-binding protein 4 (59kD)
1871127	0.005023894	ESTs
745314	0.008936352	HIRIP5 | HIRA-interacting protein 5
611373	0.043542397	PROSC | proline synthetase co-transcribed (bacterial homolog)
744374	0.032359098	DKFZP564D166 | putative ankyrin-repeat containing protein
23282	0.027026711	IK | IK cytokine, down-regulator of HLA II
1738537	0.027971153	ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]
1605539	4.91E-07	IDUA | iduronidase, alpha-L-
416374	0.007441554	NET-6 | tetraspan NET-6 protein
884599	3.77E-06	FLJ10579 | hypothetical protein FLJ10579
687990	0.026614804	ARHGEF6 | Rac/Cdc42 guanine exchange factor (GEF) 6
2013685	0.025604814	PTDSS2 | phosphatidylserine synthase 2
502988	1.97E-05	ZNF20 | zinc finger protein 20 (KOX 13)
51774	0.005356389	ESTs
277266	0.000518693	ESTs, Highly similar to T46303 hypothetical protein DKFZp434N1710.1 [H.sapiens]
138788	0.000130376	PRLR | prolactin receptor
265103	0.000987968	MMEL2 | membrane metallo-endopeptidase-like 2
489657	0.001447974	WRB | tryptophan rich basic protein
34795	0.003683559	DAZAP2 | DAZ associated protein 2
183170	0.003453647	Homo sapiens cDNA: FLJ23199 fis, clone REC01091
511012	1.21E-07	AGPS | alkylglycerone phosphate synthase
814951	0.023784403	Homo sapiens, RIKEN cDNA 2310005G07 gene, clone MGC:10049 IMAGE:3890955, mRNA, complete cds
788518	0.026818494	PXMP3 | peroxisomal membrane protein 3 (35kD, Zellweger syndrome)
360539	0.014513254	PPP3CB | protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta)
795738	0.013722183	GNG10 | guanine nucleotide binding protein 10
810671	1.19E-06	FLJ22269 | hypothetical protein FLJ22269
589232	8.03E-05	FLJ11506 | hypothetical protein FLJ11506

309591	0.049912405	EP300 | E1A binding protein p300
198960	2.65E-05	LOC51604 | CGI-06 protein
713647	0.040280641	TSPAN-3 | tetraspan 3
2273013	0.001241866	TESK2 | testis-specific kinase 2
1554646	0.034592388	CPT1A | carnitine palmitoyltransferase I, liver
1609836	0.000260109	GLUL | glutamate-ammonia ligase (glutamine synthase)
79592	7.09E-05	AKR7A2 | aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)
745339	1.79E-05	KIAA0419 | KIAA0419 gene product
1499864	0.009095192	ESTs
76252	0.000627204	HSPC134 | HSPC134 protein
840768	0.007517578	ATP6L | ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD
1916575	0.011828437	BIK | BCL2-interacting killer (apoptosis-inducing)
1582050	0.000266243	IMPDH2 | IMP (inosine monophosphate) dehydrogenase 2
730633	0.019761169	OA48-18 | acid-inducible phosphoprotein
2011308	0.030221619	DKFZP564O0463 | DKFZP564O0463 protein
278222	0.010334304	Homo sapiens, clone MGC:10083 IMAGE:3897118, mRNA, complete cds
1559596	1.29E-05	ESTs, Highly similar to AF175283 1 zinc metalloendopeptidase [H.sapiens]
767268	2.03E-06	DPP7 | dipeptidylpeptidase 7
1556259	4.63E-09	ALAD | aminolevulinate, delta-, dehydratase
1635649	0.000560777	CDS2 | CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2
772888	0.011513725	KIAA1012 | KIAA1012 protein
1551317	0.045171023	EST
203350	0.01354434	KIAA0561 | KIAA0561 protein
814971	0.001470365	Homo sapiens cDNA FLJ10046 fis, clone HEMBA1001133
859761	0.000282387	PVRL2 | poliovirus receptor-related 2 (herpesvirus entry mediator B)
1584746	0.00604339	FLJ22283 | hypothetical protein FLJ22283
162211	1.71E-05	ABCD3 | ATP-binding cassette, sub-family D (ALD), member 3
1733625	0.023369612	ESTs
279970	0.038137895	ADORA2A | adenosine A2a receptor
685626	0.007916953	ATP2B1 | ATPase, Ca++ transporting, plasma membrane 1
625458	6.02E-05	MGC3234 | hypothetical protein MGC3234
855487	4.99E-06	ASAH | N-acylsphingosine amidohydrolase (acid ceramidase)

1900149	0.000390804	SBB103 | hypothetical SBBI03 protein
1470333	2.37E-05	APBB2 | amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)
192306	8.94E-05	MPP2 | membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)
86035	1.21E-05	LOC51015 | CGI-111 protein
1573251	2.47E-05	ZAP128 | peroxisomal long-chain acyl-coA thioesterase
2021882	0.000110404	SCNN1D | sodium channel, nonvoltage-gated 1, delta
376214	6.82E-06	MRPL43 | mitochondrial ribosomal protein L43
74677	4.70E-06	Homo sapiens, Similar to RIKEN cDNA A430107J06 gene, clone MGC:21416 IMAGE:4452699, mRNA, complete cds
726779	0.021235222	CNN1 | calponin 1, basic, smooth muscle
1870512	0.000932203	TNFRSF14 | tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)
1504268	0.002697689	ESTs, Highly similar to dJ25J6.2 [H.sapiens]
43933	0.007274143	MAOA | monoamine oxidase A
1941742	0.015997677	GSA7 | ubiquitin activating enzyme E1-like protein
700571	0.02055268	CDC14A | CDC14 (cell division cycle 14, S. cerevisiae) homolog A
745363	0.006742484	ESTs
380898	0.000625106	AWP1 | protein associated with PRK1
1895781	0.000806373	ESTs, Highly similar to AC004836 1 similar to cadherin and Drosophila Fat protein [H.sapiens]
2018958	0.015480089	Homo sapiens cDNA FLJ31025 fis, clone HLUNG2000501
505575	0.000134468	FLJ10116 | hypothetical protein FLJ10116
647397	2.31E-09	MAPT | microtubule-associated protein tau
149539	0.007870589	MKP-7 | MAPK phosphatase-7
47142	0.000743442	PEX12 | peroxisomal biogenesis factor 12
838807	0.019798041	MGC11308 | hypothetical protein MGC11308
1492276	1.60E-06	EST
240680	6.30E-05	BIG1 | brefeldin A-inhibited guanine nucleotide-exchange protein 1
2314197	0.006926366	FLJ12671 | hypothetical protein FLJ12671
487301	5.30E-08	FBXL5 | f-box and leucine-rich repeat protein 5
360778-2	1.36E-11	ATM | ataxia telangiectasia mutated (includes complementation groups A, C and D)
364865	1.95E-05	FLJ21062 | hypothetical protein FLJ21062
813261	0.021270804	Homo sapiens clone 23645 mRNA sequence
814209	0.000165303	ESTs

1883630	2.71E-11	KIAA1547 | KIAA1547 protein
324225	1.89E-05	RARRES3 | retinoic acid receptor responder (tazarotene induced) 3
229596	0.001770222	TIC | SEC7 homolog
1694113	0.030227648	FLJ21031 | hypothetical protein FLJ21031
1635681	3.06E-05	NDUFA2 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8)
782688	4.97E-07	P28 | dynein, axonemal, light intermediate polypeptide
143661	1.59E-05	NTN4 | netrin 4
825715	0.019909138	IFI41 | interferon-induced protein 41, 30kD
271721	0.011868489	EST
30850	0.001756144	MMP17 | matrix metalloproteinase 17 (membrane-inserted)
814214	0.001725113	D8S2298E | reproduction 8
796739	1.69E-06	MGC10924 | hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5
486374	0.00241838	MGC4645 | hypothetical protein MGC4645
855800	0.000428278	PREP | prolyl endopeptidase
120006	0.000302823	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
490251	0.014632388	PPP1R2 | protein phosphatase 1, regulatory (inhibitor) subunit 2
270786	1.17E-05	Homo sapiens cDNA FLJ30436 fis, clone BRACE2009037
813279	4.41E-05	APEH | N-acylaminoacyl-peptide hydrolase
160656	3.25E-08	LU | Lutheran blood group (Auberger b antigen included)
1850224	0.000270348	ESTs
788580	0.008853088	CCNDBP1 | cyclin D-type binding-protein 1
82871	0.014746648	SHBG | sex hormone-binding globulin
813281	5.45E-13	WWP1 | WW domain-containing protein 1
547058	0.014177292	CCNG1 | cyclin G1
1416092	0.016682884	CHDH | choline dehydrogenase
854874	0.000592334	KIAA0212 | KIAA0212 gene product
1631701	0.000187841	JFC1 | NADPH oxidase-related, C2 domain-containing protein
854879	0.001309802	SPHK2 | sphingosine kinase type 2 isoform
752903	1.78E-08	KIAA0303 | KIAA0303 protein
45578	1.91E-05	MAP2K6 | mitogen-activated protein kinase kinase 6
51056	0.010636427	CNIL | cornichon-like
43977	0.014632388	KIAA0182 | KIAA0182 protein

301380	0.002812591	UGTREL7 | UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter
814232	0.043182465	C21orf59 | chromosome 21 open reading frame 59
796754	0.00150122	DREV1 | CGI-81 protein
824792	0.001312689	BM045 | uncharacterized bone marrow protein BM045
814234	3.88E-05	SUCLG2 | succinate-CoA ligase, GDP-forming, beta subunit
1915982	0.00065014	Homo sapiens cDNA FLJ32488 fis, clone SKNSH1000086
229901	0.049474849	CTSO | cathepsin O
503214	9.28E-09	KIAA1243 | KIAA1243 protein
796757	0.037697334	AP3S1 | adaptor-related protein complex 3, sigma 1 subunit
1917588	0.048777689	DNASE2 | deoxyribonuclease II, lysosomal
271748	6.83E-06	RBMS1 | RNA binding motif, single stranded interacting protein 1
49860	9.02E-05	PDK2 | pyruvate dehydrogenase kinase, isoenzyme 2
504959	7.12E-10	Homo sapiens mRNA; cDNA DKFZp586G0321 (from clone DKFZp586G0321)
1602284	1.87E-07	EST
687289	0.004049154	Homo sapiens, clone MGC:3245 IMAGE:3505639, mRNA, complete cds
150118	0.017865847	DKFZp434F054 | hypothetical protein DKFZp434F054
140354	0.013770597	Homo sapiens, Similar to secretory carrier membrane protein 4, clone MGC:19661 IMAGE:3161979, mRNA, complete cds
786202	0.002899676	Homo sapiens cDNA FLJ13553 fis, clone PLACE1007454
361565	6.41E-05	GLUD1 | glutamate dehydrogenase 1
512045	0.042758148	JM1 | JM1 protein
591597	0.011216747	TNNI3 | troponin I, cardiac
1574252	0.03289313	DKFZP586D0623 | DKFZP586D0623 protein
740476	0.002102096	IRF1 | interferon regulatory factor 1
951125	1.70E-05	PECI | peroxisomal D3,D2-enoyl-CoA isomerase
1636669	0.001613372	FLJ21939 | hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2
283124	4.09E-07	Homo sapiens, clone IMAGE:3917549, mRNA, partial cds
79960	0.006425318	RRP40 | exosome component Rrp40
25274	2.51E-09	LOC51161 | g20 protein
261204	2.66E-16	ESTs, Highly similar to JC5931 high mobility group I HMGI chromosomal protein isoform C-alpha [H.sapiens]
949938	2.51E-07	CST3 | cystatin C (amyloid angiopathy and cerebral hemorrhage)

49883	0.016175391	SYT13 | synaptotagmin XIII
155072	8.66E-16	ESTs
502297	0.000223246	POLI | polymerase (DNA directed) iota
150137	0.040830931	DKFZP564O123 | DKFZP564O123 protein
85450	8.06E-09	ACOX2 | acyl-Coenzyme A oxidase 2, branched chain
212542	0.000127809	Homo sapiens mRNA; cDNA DKFZp586J2118 (from clone DKFZp586J2118)
813603	5.67E-06	KIAA1075 | KIAA1075 protein
361587	4.46E-05	KIAA1789 | KIAA1789 protein
742094	0.003398986	FLJ20950 | hypothetical protein FLJ20950
156023	0.019869669	MGC3123 | hypothetical protein MGC3123
1558233	8.16E-12	ESTs
229937	5.99E-05	DDX30 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 30
1469084	0.019869669	KIAA0804 | KIAA0804 protein
362532	0.002943504	C12orf22 | chromosome 12 open reading frame 22
51093	0.003245464	ZNFN2A1 | zinc finger protein, subfamily 2A (FYVE domain containing) , 1
1631746	5.44E-05	POLM | polymerase (DNA directed), mu
51097	1.98E-05	BAIAP3 | BAI1-associated protein 3
2108048	8.16E-07	DNB5 | DNB5
342181-2	8.94E-21	BCL2 | B-cell CLL/lymphoma 2
785293	3.42E-07	HREV107 | similar to rat HREV107
1741884	0.001594038	ESTs, Highly similar to IRX3_HUMAN IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-3 [H.sapiens]
48167	0.001837947	FLJ10483 | hypothetical protein FLJ10483
155094	0.010881395	DNAJB12 | DnaJ (Hsp40) homolog, subfamily B, member 12
842762	0.014914359	FLJ20363 | hypothetical protein FLJ20363
1685363	0.003881514	GLRB | glycine receptor, beta
1840803	0.032260939	FLJ20686 | hypothetical protein FLJ20686
825785	1.01E-05	KIAA0435 | KIAA0435 gene product
2016644	0.009775018	LIMD1 | LIM domains containing 1
255754	2.24E-06	LOC51297 | LUNX protein; PLUNC (palate lung and nasal epithelium clone); tracheal epithelium enriched protein
159380	0.000970624	FLJ23462 | duodenal cytochrome b
159381	1.10E-06	RARA | retinoic acid receptor, alpha

1517749	0.012504399	ESTs
712314	3.40E-05	MIR | myosin regulatory light chain interacting protein
2284924	1.10E-14	KIAA0882 | KIAA0882 protein
1475662	0.000802641	AXUD1 | AXIN1 up-regulated
1637647	7.42E-05	ESTs
878744	0.012204566	TSG101 | tumor susceptibility gene 101
824052	0.031302263	C6orf1 | chromosome 6 open reading frame 1
40695	0.044959539	NAPB | N-ethylmaleimide-sensitive factor attachment protein, beta
773152	0.001310908	ESTs
289057	0.004505214	HT021 | HT021
120271-2	0.015988127	MGC4692 | hypothetical protein MGC4692
744010	7.00E-05	Homo sapiens mRNA; cDNA DKFZp586K1318 (from clone DKFZp586K1318)
79216	0.008448199	AHNAK | AHNAK nucleoprotein (desmoyokin)
842785	0.011581406	LRPAP1 | low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1)
41647	1.11E-06	PTPRT | protein tyrosine phosphatase, receptor type, T
549016	0.019299231	BTBD1 | BTB (POZ) domain containing 1
705110	0.001790158	CASP9 | caspase 9, apoptosis-related cysteine protease
2313921	0.001677464	NDUFB3 | NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3 (12kD, B12)
810305	0.002373538	Homo sapiens cDNA FLJ30463 fis, clone BRACE2009517
289060	0.000990298	HSPA4 | heat shock 70kD protein 4
262996	0.02908529	CHD1 | chromodomain helicase DNA binding protein 1
687638	0.006365847	ESTs
1670688	0.006338445	BACH2 | BTB and CNC homology 1, basic leucine zipper transcription factor 2
154466	5.44E-05	STUB1 | STIP1 homology and U-Box containing protein 1
52071	0.026442939	ESTs, Highly similar to AC004836 1 similar to cadherin and Drosophila Fat protein [H.sapiens]
301740	0.018221151	Homo sapiens cDNA FLJ30298 fis, clone BRACE2003172
52076	0.000531118	OLFM1 | olfactomedin 1
34439	0.000548494	FUS2 | putative tumor suppressor
428184	8.50E-10	Homo sapiens, clone MGC:18216 IMAGE:4156235, mRNA, complete cds
743081	0.048000809	NDUFA3 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3 (9kD, B9)
565062	0.023268805	Homo sapiens clone 24812 mRNA sequence

31893	0.010529568	LOC84548 | hypothetical protein from Xq28
646057	0.010403382	Homo sapiens cDNA: FLJ21897 fis, clone HEP03447, highly similar to AF052178 Homo sapiens clone 24523 mRNA sequence
809779	8.13E-08	KIAA0239 | KIAA0239 protein
1575263	0.005751783	DKFZP586N0721 | DKFZP586N0721 protein
773170	2.17E-06	TPBG | trophoblast glycoprotein
853506	0.002203842	PISD | phosphatidylserine decarboxylase
757135	2.60E-05	DKFZP564J0123 | DKFZP564J0123 protein
381166	3.78E-06	MORF | histone acetyltransferase
361922	0.040228151	ZMPSTE24 | zinc metalloproteinase, STE24 (yeast, homolog)
50484	2.41E-05	CCRK | cell cycle related kinase
281590	0.026213959	FLJ10656 | hypothetical protein FLJ10656
1700621	0.001782567	EGFL4 | EGF-like-domain, multiple 4
26289	0.041064782	FLJ12879 | hypothetical protein FLJ12879
565075	0.000170815	STC1 | stanniocalcin 1
1568056	0.005442251	ESTs, Moderately similar to I78885 serine/threonine-specific protein kinase [H.sapiens]
252453	0.00590112	LOC51635 | CGI-86 protein
810325	2.48E-05	IVD | isovaleryl Coenzyme A dehydrogenase
1469425	0.00010497	SOX22 | SRY (sex determining region Y)-box 22
781342	2.74E-05	MGC11115 | hypothetical protein MGC11115
154482	1.29E-05	SERPINB1 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1
845352	0.000586706	NUDT9 | nudix (nucleoside diphosphate linked moiety X)-type motif 9
266500	2.03E-08	ESTs
773185	0.008673574	ESTs
136845	0.024067407	Homo sapiens, clone IMAGE:3915000, mRNA
1870938	0.007988734	CDS1 | CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1
310584	7.42E-05	ARL1 | ADP-ribosylation factor-like 1
1585040	1.45E-08	TCEB1L | transcription elongation factor B (SIII), polypeptide 1-like
1916225	0.005767924	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens]
26294	2.07E-09	RNB6 | RNB6
416042	0.000488136	Homo sapiens cDNA FLJ31053 fis, clone HSYRA2000640, highly similar to Homo sapiens FRG1 mRNA
248583	0.036283521	NFX1 | nuclear transcription factor, X-box binding 1

344959	2.38E-09	HSA250839 | gene for serine/threonine protein kinase
2010012	0.004201172	P37NB | 37 kDa leucine-rich repeat (LRR) protein
71763	0.001262603	SIP | Siah-interacting protein
154493	0.015871	IFI41 | interferon-induced protein 41, 30kD
2054945	0.000649145	SLC23A2 | solute carrier family 23 (nucleobase transporters), member 2
797000	0.011811432	TERE1 | transitional epithelia response protein
594517	0.036288061	SFRS6 | splicing factor, arginine/serine-rich 6
206341	0.011625517	ESTs, Weakly similar to A49364 59 protein, brain [H.sapiens]
280950	4.51E-05	SRI | sorcin
109316	0.006324487	SERPINA3 | serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3
203003	0.002285045	NME4 | non-metastatic cells 4, protein expressed in
503602	0.000403283	PRO1489 | hypothetical protein PRO1489
769600	0.013770597	UNG2 | uracil-DNA glycosylase 2
1968246	1.12E-05	FUT8 | fucosyltransferase 8 (alpha (1,6) fucosyltransferase)
432093	2.37E-06	IL18BP | interleukin 18 binding protein
1879094	0.002741302	FLJ23392 | hypothetical protein FLJ23392
782306	3.08E-06	FLJ13110 | hypothetical protein FLJ13110
1635307	4.84E-05	Homo sapiens, clone IMAGE:3833472, mRNA
1420370	0.036288061	BLVRB | biliverdin reductase B (flavin reductase (NADPH))
284160	3.04E-08	CACNA2D2 | calcium channel, voltage-dependent, alpha 2/delta subunit 2
595181	0.000601881	MIR | myosin regulatory light chain interacting protein
470348	0.001309802	ESTs
1926007	0.00216623	EST
33817	7.74E-06	ESTs
1456348	0.020321818	SAS | N-acetylneuraminic acid phosphate synthase; sialic acid synthase
1056172	0.002436429	NMES1 | normal mucosa of esophagus specific 1
84880	0.000162089	LOC51004 | CGI-10 protein
491612	0.000816756	Homo sapiens cDNA FLJ11752 fis, clone HEMBA1005582, weakly similar to TROPOMYOSIN 1, NON-MUSCLE ISOFORM
344970	0.009457359	ITGA4 | integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)
796079	0.001202428	MGC4171 | hypothetical protein MGC4171

504279	0.016946636	TBL1 | transducin (beta)-like 1
898333	0.04010901	ESTs
950574	0.013952573	H3F3B | H3 histone, family 3B (H3.3B)
250883	0.010544493	UBE1L | ubiquitin-activating enzyme E1-like
230560	0.003417271	ESTs
666707	0.002506551	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
825060	0.012784217	DUT | dUTP pyrophosphatase
1690262	0.032703827	Homo sapiens cDNA FLJ20763 fis, clone COL09911
788208	7.66E-07	FLJ10659 | hypothetical protein FLJ10659
265592	0.019761169	Homo sapiens, activated RNA polymerase II transcription cofactor 4, clone MGC:21503 IMAGE:3881373, mRNA, complete cds
291399	0.000155359	HMG2 | high-mobility group (nonhistone chromosomal) protein 2
262251	0.000333214	CLCN7 | chloride channel 7
786607	0.000772083	TCEAL1 | transcription elongation factor A (SII)-like 1
108395	1.56E-05	DLG5 | discs, large (Drosophila) homolog 5
245273	0.019521612	LOC57020 | hypothetical protein
626861	0.009420842	EIF4G2 | eukaryotic translation initiation factor 4 gamma, 2
1323361	0.008588081	NR2F6 | nuclear receptor subfamily 2, group F, member 6
489351	0.00010205	DKFZP566J2046 | hypothetical protein DKFZp566J2046
2054977	0.000148287	KIAA0373 | KIAA0373 gene product
26617	0.000316752	ALCAM | activated leucocyte cell adhesion molecule
268148	0.000875061	TRIM4 | tripartite motif-containing 4
665774	0.049423242	EIF4E | eukaryotic translation initiation factor 4E
797038	0.011982092	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1502032
1652310	0.017604138	Homo sapiens cDNA FLJ30306 fis, clone BRACE2003319
562867	0.044978437	RRS1 | homolog of yeast ribosome biogenesis regulatory protein RRS1
1880743	0.008335378	ESTs
38781	0.03544066	ATP9B | ATPase, Class II, type 9B
1609538	3.46E-05	KIAA1324 | KIAA1324 protein
487761	0.034130662	TAF2S | TATA box binding protein (TBP)-associated factor, RNA polymerase II, S, 150kD
36491-2	0.00247482	ESTs
755599	0.023780533	IFITM1 | interferon induced transmembrane protein 1 (9-27)

2017684	0.000107787	LOC51644 | CGI-120 protein
244637	0.000498127	CRI1 | CREBBP/EP300 inhibitory protein 1
156437-2	0.001309095	ATP1A2 | ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide
2222453	0.028657358	EHD2 | EH-domain containing 2
53092	0.008880977	KIAA0436 | putative L-type neutral amino acid transporter
841415	4.94E-05	EPLIN | epithelial protein lost in neoplasm beta
770983	0.010403382	FLJ11730 | hypothetical protein FLJ11730
363590	0.00042623	ARNT2 | aryl hydrocarbon receptor nuclear translocator 2
1586043	0.018119429	ESTs
2709505	4.45E-08	LPHB | lipophilin B (uteroglobin family member), prostatein-like
204790	2.03E-09	FLJ20273 | hypothetical protein
1897065	0.017531828	SMUG1 | single-strand selective monofunctional uracil DNA glycosylase
487777	0.02848343	RB1 | retinoblastoma 1 (including osteosarcoma)
263229	0.001149746	LAF4 | lymphoid nuclear protein related to AF4
1911343	3.74E-12	RAB26 | RAB26, member RAS oncogene family
1558642	1.95E-11	MLPH | melanophilin
60602	3.22E-06	CSH1 | chorionic somatomammotropin hormone 1 (placental lactogen)
156437	0.036072406	ATP1A2 | ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide
730346	0.003570072	HEBP1 | heme binding protein 1
143332	0.005649342	NPY1R | neuropeptide Y receptor Y1
32122	2.31E-09	FLJ10210 | hypothetical protein FLJ10210
195346	7.13E-06	FLJ00005 | FLJ00005 protein
786640	0.005990788	VEZATIN | transmembrane protein vezatin
109379	0.003007609	HMGCR | 3-hydroxy-3-methylglutaryl-Coenzyme A reductase
590298	0.023157899	MRPL45 | mitochondrial ribosomal protein L45
645485	0.005375632	TERF1 | telomeric repeat binding factor (NIMA-interacting) 1
134523	5.65E-05	EMAP-2 | microtubule-associated protein like echinoderm EMAP
134525	0.013501077	CUL3 | cullin 3
44292	0.027304029	Homo sapiens mRNA; cDNA DKFZp434C107 (from clone DKFZp434C107)
140008	0.018500323	EBNA1BP2 | EBNA1-binding protein 2
511831	3.46E-05	MGC12936 | hypothetical protein MGC12936
2014373	0.0330879	HNK-1ST | HNK-1 sulfotransferase

928315	0.014172516	CARKL | carbohydrate kinase-like
172495	0.002069329	KIAA0028 | leucyl-tRNA synthetase, mitochondrial
724888	4.45E-05	CYP4B1 | cytochrome P450, subfamily IVB, polypeptide 1
296679	0.0002926	Homo sapiens clone TCCCTA00151 mRNA sequence
357344	0.035245897	KCNQ1 | potassium voltage-gated channel, KQT-like subfamily, member 1
843046	0.009533011	GPRK7 | G protein-coupled receptor kinase 7
789204	0.001843366	TLOC1 | translocation protein 1
183200	0.012787936	FAH | fumarylacetoacetate hydrolase (fumarylacetoacetase)
744417	0.006558294	CRAT | carnitine acetyltransferase
812300	0.003557075	FLJ20265 | hypothetical protein FLJ20265
418019	0.001030569	KIAA0542 | KIAA0542 gene product
1569096	0.022893459	ESTs
79629-2	0.014086588	CXCR4 | chemokine (C-X-C motif), receptor 4 (fusin)
782385	0.031219133	DKFZP566D193 | DKFZP566D193 protein
897745	0.002311826	FLJ13868 | hypothetical protein FLJ13868
843054	0.004353571	KIAA1533 | KIAA1533 protein
826070	0.017970183	ZFP91 | zinc finger protein homologous to Zfp91 in mouse
1608928	0.028565804	CYP4F11 | cytochrome P450, subfamily IVF, polypeptide 11
564801	0.006100942	Homo sapiens cDNA: FLJ21409 fis, clone COL03924
826077	0.000373482	PDHB | pyruvate dehydrogenase (lipoamide) beta
177737	0.014789221	PURA | purine-rich element binding protein A
823819	0.001641999	EST
83508	0.026147968	B9 | B9 protein
795498	0.001139656	HS1-2 | putative transmembrane protein
505299	0.000389422	BBP | beta-amyloid binding protein precursor
49546	0.02081588	P29 | GCIP-interacting protein p29
2028440	0.001074094	ESTs
346942	0.0003267	PIGQ | phosphatidylinositol glycan, class Q
34849	0.017962259	EEF2 | eukaryotic translation elongation factor 2
247230	0.011626312	Homo sapiens cDNA FLJ30532 fis, clone BRAWH2001129, weakly similar to OCCLUDIN
50888	0.000228763	PRDX3 | peroxiredoxin 3
754998	0.039096645	SRP19 | signal recognition particle 19kD

2168667	0.002032038	POLR2H | polymerase (RNA) II (DNA directed) polypeptide H
724112	0.001610749	ESTs, Weakly similar to B34087 hypothetical protein [H.sapiens]
741891	2.17E-05	RAB2L | RAB2, member RAS oncogene family-like
130276	0.027971153	Homo sapiens mRNA; cDNA DKFZp586H0324 (from clone DKFZp586H0324)
66535	0.000646325	OAZ2 | ornithine decarboxylase antizyme 2
1500000	0.000577003	H2BFB | H2B histone family, member B
1049330	0.000116235	SSPN | sarcospan (Kras oncogene-associated gene)
1683411	0.000739744	ESTs
611443	0.000106149	MB | myoglobin
591281	0.021583844	MVP | major vault protein
504657	0.013710873	KIAA0438 | KIAA0438 gene product
810734	6.48E-09	POLD4 | polymerase (DNA-directed), delta 4
2297394	0.022064191	FLJ13612 | hypothetical protein FLJ13612
1901924	0.014853485	ESTs, Weakly similar to T21364 hypothetical protein F25H5.6 - Caenorhabditis elegans [C.elegans]
1553766	0.000795582	FLJ10283 | hypothetical protein FLJ10283
267571	2.41E-06	SNAPC2 | small nuclear RNA activating complex, polypeptide 2, 45kD
1588791	0.02123298	MGMT | O-6-methylguanine-DNA methyltransferase
1049346	1.26E-05	FOXP1 | forkhead box P1
121470	0.030626	BCCIP | BRCA2 and CDKN1A-interacting protein
298603	0.005015434	KIAA1474 | KIAA1474 protein
1569418	2.89E-07	Homo sapiens cDNA FLJ11385 fis, clone HEMBA1000520
782700	0.000804231	CLASP2 | CLIP-associating protein 2
884677	3.02E-05	Homo sapiens, clone IMAGE:3611719, mRNA, partial cds
782702	8.52E-08	LOC56270 | hypothetical protein 628
108425-2	0.006209446	ESTs, Weakly similar to JC5314 CDC28/cdc2-like kinase associating arginine-serine cyclophilin [H.sapiens]
154103	0.000352444	SCN1B | sodium channel, voltage-gated, type I, beta polypeptide
759163	2.95E-13	MFAP4 | microfibrillar-associated protein 4
1566877	0.020116819	C11orf2 | chromosome 11 open reading frame2
1635705	0.016769168	ESTs, Highly similar to T46422 hypothetical protein DKFZp434M2023.1 [H.sapiens]
35812	0.022973459	PCLO | piccolo (presynaptic cytomatrix protein)
51851	0.004091636	ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]

1839935	2.36E-06	ESTs
2169632	0.022764168	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 42138
669359	0.00497373	Homo sapiens clone 24405 mRNA sequence
1625945	0.004424523	NDRG3 | N-myc downstream-regulated gene 3
682058	0.00167005	SPOP | speckle-type POZ protein
752625	0.00014539	Homo sapiens mRNA; cDNA DKFZp667D095 (from clone DKFZp667D095)
843094	0.046423899	UBL1 | ubiquitin-like 1 (sentrin)
298610	0.007478622	Homo sapiens cDNA FLJ13927 fis, clone Y79AA1000627, moderately similar to Homo sapiens zinc finger protein (ZF5128) mRNA
299274	0.033282881	Homo sapiens cDNA FLJ32430 fis, clone SKMUS2001129, weakly similar to NAD-DEPENDENT METHANOL DEHYDROGENASE (EC 1.1.1.244)
41302	0.002068339	KIAA0643 | KIAA0643 protein
682063	0.001692383	ZNF189 | zinc finger protein 189
824802	1.92E-05	HTGN29 | HTGN29 protein
35828	0.024474794	DTR | diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)
283919	0.046763683	H2AFL | H2A histone family, member L
868652	4.71E-08	C4B | complement component 4B
1668067	7.31E-05	DKFZP434D146 | DKFZP434D146 protein
345247	0.007295582	ESTs, Moderately similar to T03094 A-kinase anchor protein DAKAP550 - fruit fly [D.melanogaster]
823867	0.005767924	ESTs
2455403	0.000513257	ZNF91 | zinc finger protein 91 (HPF7, HTF10)
366511	0.003874401	ACTA1 | actin, alpha 1, skeletal muscle
767346	0.017970183	C14orf4 | chromosome 14 open reading frame 4
241474-2	0.000122034	BRCA1 | breast cancer 1, early onset
772962	0.00014351	Homo sapiens cDNA FLJ31149 fis, clone IMR322001491, moderately similar to Rattus norvegicus tricarboxylate carrier-like protein mRNA
855559	2.45E-10	SAS | sarcoma amplified sequence
36491	0.01049982	ESTs
669379	0.031219133	Homo sapiens, clone IMAGE:3463399, mRNA, partial cds
36493	0.015997677	NAGA | N-acetylgalactosaminidase, alpha-
282980	0.001343272	ESTs
752643	1.91E-05	PLA2G12 | group XII secreted phospholipase A2

69124	0.000606588	CIRBP | cold inducible RNA-binding protein
566466	0.01931096	HSU93850 | elongation factor-2 kinase
510170	0.000277083	PAIP2 | PABP-interacting protein 2
855563	5.61E-05	ERBB3 | v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3
139835	7.14E-08	UGDH | UDP-glucose dehydrogenase
154138	0.024566797	Homo sapiens cDNA FLJ32174 fis, clone PLACE6001064
2284619	0.011581406	ZNF132 | zinc finger protein 132 (clone pHZ-12)
460218	0.018807962	EST
488025	0.000960715	ZNF226 | zinc finger protein 226
745437	0.003016551	ESTs
208387	0.000636782	KIAA1407 | KIAA1407 protein
1843843	0.025604134	SRGAP1 | KIAA1304 protein
258790	0.006397727	CCK | cholecystokinin
205049	0.000551716	H11 | protein kinase H11
490306	0.000487266	TM9SF1 | transmembrane 9 superfamily member 1
773922	0.004876463	BZAP45 | basic leucine-zipper protein BZAP45
66599	1.39E-11	NAT1 | N-acetyltransferase 1 (arylamine N-acetyltransferase)
280602	0.000362169	ESTs
488033	0.002117729	DNAJB9 | DnaJ (Hsp40) homolog, subfamily B, member 9
1860836	0.007295582	Homo sapiens cDNA FLJ30927 fis, clone FEBRA2006736
726860	0.011916108	C11orf14 | chromosome 11 open reading frame 14
840878	0.000600849	DHCR24 | 24-dehydrocholesterol reductase
1702695	0.003491873	MRPL53 | mitochondrial ribosomal protein L53
289830	0.024964587	KIAA0329 | KIAA0329 gene product
1569465	0.027305675	IGHMBP2 | immunoglobulin mu binding protein 2
2367226	0.001193191	HRC | histidine-rich calcium-binding protein
2048040	0.002874419	Homo sapiens cDNA FLJ32130 fis, clone PEBLM2000248, weakly similar to ZINC FINGER PROTEIN 157
810791	0.006604078	MNAT1 | menage a trois 1 (CAK assembly factor)
810795	1.05E-05	FLJ21940 | hypothetical protein FLJ21940
1561981	7.62E-05	EST
28643	5.46E-05	DKFZP564D1378 | hypothetical protein DKFZp564D1378

665405	4.33E-05	MYO5C | myosin 5C
1518402	1.68E-09	KIAA1361 | KIAA1361 protein
283956	6.52E-05	Homo sapiens cDNA FLJ13155 fis, clone NT2RP3003433
840882	1.48E-06	NBP | nucleotide binding protein
742115	1.20E-06	DCI | dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
809464	0.015509308	FGFR2 | fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)
85195	0.00013313	GADD45G | growth arrest and DNA-damage-inducible, gamma
1521341	8.51E-05	HIRIP3 | HIRA-interacting protein 3
768324	0.010220908	KIAA0107 | KIAA0107 gene product
210688	1.39E-12	ADCY9 | adenylate cyclase 9
1557318	0.028091838	ESTs
1636707	0.010283446	EIF3S3 | eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD)
837953	1.10E-05	NEDD4L | neural precursor cell expressed, developmentally down-regulated 4-like
429906	0.009533011	PIGN | phosphatidylinositol glycan, class N
530814	0.000234182	SEPP1 | selenoprotein P, plasma, 1
258026	0.000719645	EST
41356	0.035107908	PPP2R5A | protein phosphatase 2, regulatory subunit B (B56), alpha isoform
1631487	0.001988084	ESTs
752688	1.73E-05	ESTs
565849	0.000900648	C3IP1 | kelch-like protein C3IP1
1699142	3.36E-05	AP1G2 | adaptor-related protein complex 1, gamma 2 subunit
253884	0.043335326	Homo sapiens, clone IMAGE:3625286, mRNA, partial cds
810017	0.000594167	PLAUR | plasminogen activator, urokinase receptor
1422723	0.02727988	IFI35 | interferon-induced protein 35
1868349	0.023383495	PLA2G4B | phospholipase A2, group IVB (cytosolic)
730768	9.62E-05	Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245)
1537001	0.012963093	ESTs
470261-2	0.000165604	SMA5 | SMA5
712049	0.01747597	IL24 | interleukin 24
526945	0.013261832	FABGL | FabG (beta-ketoacyl-[acyl-carrier-protein] reductase, E coli) like
814306	0.020168182	TPD52 | tumor protein D52

726890	0.00099919	MGC4643 | hypothetical protein MGC4643
1572710	0.008888435	FLJ21213 | hypothetical protein FLJ21213
809488	0.007951698	RAI17 | retinoic acid induced 17
502349	2.77E-06	CAB56184 | hypothetical protein CAB56184
781046	0.000438842	ERBB2IP | erbb2-interacting protein ERBIN
782787	2.14E-05	FLJ21347 | hypothetical protein FLJ21347
365919	6.59E-07	STAU | staufen (Drosophila, RNA-binding protein)
1898442	0.001557478	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens]
1908840	1.16E-05	ZNF174 | zinc finger protein 174
2298710	0.012030871	TRIM16 | tripartite motif-containing 16
1560279	0.02187025	Homo sapiens clone CDABP0155 mRNA sequence
743880	0.014144736	KIAA0263 | KIAA0263 gene product
824879	5.97E-08	MGC11275 | hypothetical protein MGC11275
270883	0.001399452	CNNM3 | cyclin M3
341316	2.88E-07	HTATSF1 | HIV TAT specific factor 1
1910040	2.37E-06	LOC51701 | nemo-like kinase
81229	0.00100873	FTL | ferritin, light polypeptide
811774	5.01E-08	LOC51097 | CGI-49 protein
1521375	8.48E-06	Homo sapiens cDNA FLJ13542 fis, clone PLACE1006779
839583	0.01394813	ESTs, Moderately similar to T46386 hypothetical protein DKFZp434P011.1 [H.sapiens]
214205	9.59E-12	Homo sapiens, clone MGC:17687 IMAGE:3865868, mRNA, complete cds
825822	0.000681333	DJ167A19.1 | hypothetical protein
1762111	0.000300738	NPR3 | natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)
487425	0.001309802	CETN3 | centrin, EF-hand protein, 3 (CDC31 yeast homolog)
195786	0.000395849	EST
2298723	0.014679158	KIAA0708 | KIAA0708 protein
66931	0.023818015	FLJ20307 | hypothetical protein FLJ20307
490360	0.018119429	MGC5560 | hypothetical protein MGC5560
767706	3.86E-05	ESTs
1732033	0.00024242	FLJ14427 | hypothetical protein FLJ14427
234537	0.039367559	Homo sapiens, clone IMAGE:3869590, mRNA, partial cds
1631807	0.013415846	GMPPB | GDP-mannose pyrophosphorylase B

2017352	0.003753263	B4GALT7 | xylosylprotein beta1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)
361659	0.023660933	DKFZP434D146 | DKFZP434D146 protein
66946	0.017962259	U2AF1RS2 | U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 2
1610546	2.73E-11	HNF3A | hepatocyte nuclear factor 3, alpha
811790	0.024330122	DKFZP564G0222 | DKFZP564G0222 protein
951216	0.001063475	NDUFB10 | NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10 (22kD, PDSW)
811792	0.00199207	GSS | glutathione synthetase
813396	0.006131911	KIAA1204 | KIAA1204 protein
242706	0.033985397	HSPC274 | HSPC274 protein
173878	0.005539042	MGC14327 | hypothetical protein MGC14327
52103	3.48E-05	FLJ23045 | hypothetical protein FLJ23045
450810	0.031458387	FLJ12154 | hypothetical protein FLJ12154
592630	0.002077599	MINPP1 | multiple inositol polyphosphate histidine phosphatase, 1
1156538	4.81E-16	ESTs
487444	0.015004486	ARPP-19 | cyclic AMP phosphoprotein, 19 kD
273454	0.016029967	ESTs
2296063	0.010400431	KIAA0528 | KIAA0528 gene product
120138	0.000909767	JDP1 | J domain containing protein 1
810063	0.016542848	GFER | growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)
1635022	0.007124761	DDAH2 | dimethylarginine dimethylaminohydrolase 2
144740	6.16E-11	SDCCAG28 | serologically defined colon cancer antigen 28
470061	8.03E-07	SIAH2 | seven in absentia (Drosophila) homolog 2
1631820	0.038581914	ESTs
1456060	0.004330191	ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]
230271	0.000257296	AD-017 | glycosyltransferase AD-017
138189	4.90E-09	WFS1 | Wolfram syndrome 1 (wolframin)
842838	0.02024356	TADA3L | transcriptional adaptor 3 (ADA3, yeast homolog)-like (PCAF histone acetylase complex)
2028876	7.96E-05	SFRS5 | splicing factor, arginine/serine-rich 5
1632487	0.02848343	WISP2 | WNT1 inducible signaling pathway protein 2
530875	0.001185188	TKT | transketolase (Wernicke-Korsakoff syndrome)
814350	0.010880033	IDE | insulin-degrading enzyme
432108	0.001273848	I-1 | imidazoline receptor candidate

<table>
<tr><td>814353</td><td>0.012831119</td><td>PMAIP1 | phorbol-12-myristate-13-acetate-induced protein 1</td></tr>
<tr><td>726147</td><td>0.024330122</td><td>MAP2K4 | mitogen-activated protein kinase kinase 4</td></tr>
<tr><td>23776</td><td>3.95E-07</td><td>QDPR | quinoid dihydropteridine reductase</td></tr>
<tr><td>503338</td><td>0.000584849</td><td>WT1 | Wilms tumor 1</td></tr>
<tr><td>156117</td><td>0.033291452</td><td>Homo sapiens, clone IMAGE:3884331, mRNA, partial cds</td></tr>
<tr><td>768395</td><td>0.013459172</td><td>ESTs</td></tr>
<tr><td>898058</td><td>0.001034397</td><td>ESTs</td></tr>
<tr><td>1854648</td><td>0.000117862</td><td>HPX | hemopexin</td></tr>
<tr><td>35147</td><td>2.97E-07</td><td>ESTs, Weakly similar to UOG1_HUMAN UOG-1 PROTEIN [H.sapiens]</td></tr>
<tr><td>2388571</td><td>0.001899953</td><td>AKAP8 | A kinase (PRKA) anchor protein 8</td></tr>
<tr><td>809828</td><td>1.10E-13</td><td>E2F5 | E2F transcription factor 5, p130-binding</td></tr>
<tr><td>811024</td><td>7.03E-05</td><td>BST2 | bone marrow stromal cell antigen 2</td></tr>
<tr><td>625923</td><td>0.015565633</td><td>PCK2 | phosphoenolpyruvate carboxykinase 2 (mitochondrial)</td></tr>
<tr><td>1882051</td><td>0.014745604</td><td>FLJ20080 | hypothetical protein FLJ20080</td></tr>
<tr><td>121898</td><td>2.79E-06</td><td>Homo sapiens mRNA; cDNA DKFZp586J0720 (from clone DKFZp586J0720)</td></tr>
<tr><td>1583198</td><td>1.28E-06</td><td>ESTs, Weakly similar to S65824 reverse transcriptase homolog [H.sapiens]</td></tr>
<tr><td>1031727</td><td>0.012784217</td><td>SIRT2 | sirtuin (silent mating type information regulation 2, S.cerevisiae, homolog) 2</td></tr>
<tr><td>810088</td><td>0.025874177</td><td>FLJ20258 | hypothetical protein FLJ20258</td></tr>
<tr><td>241798</td><td>0.03154152</td><td>Homo sapiens cDNA FLJ30407 fis, clone BRACE2008553</td></tr>
<tr><td>85561</td><td>4.23E-05</td><td>CYP2A7 | cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7</td></tr>
<tr><td>809838</td><td>0.032429761</td><td>EST</td></tr>
<tr><td>743146</td><td>7.92E-05</td><td>FLJ23403 | hypothetical protein FLJ23403</td></tr>
<tr><td>489079</td><td>0.003602021</td><td>IL2RB | interleukin 2 receptor, beta</td></tr>
<tr><td>361698</td><td>0.002131744</td><td>LIPE | lipase, hormone-sensitive</td></tr>
<tr><td>49204</td><td>0.00050472</td><td>Homo sapiens mRNA; cDNA DKFZp566A1046 (from clone DKFZp566A1046)</td></tr>
<tr><td>811038</td><td>0.016882187</td><td>LOC51238 | hypothetical protein</td></tr>
<tr><td>2012454</td><td>0.045950427</td><td>Homo sapiens, clone IMAGE:4391536, mRNA</td></tr>
<tr><td>155197</td><td>3.41E-06</td><td>ESTs</td></tr>
<tr><td>470092</td><td>0.001366354</td><td>LARGE | like-glycosyltransferase</td></tr>
<tr><td>1412245</td><td>0.016770876</td><td>CPA2 | carboxypeptidase A2 (pancreatic)</td></tr>
<tr><td>488422</td><td>0.028019793</td><td>HMG20B | high-mobility group 20B</td></tr>
<tr><td>1635059</td><td>2.23E-09</td><td>Homo sapiens, clone MGC:16638 IMAGE:4121964, mRNA, complete cds</td></tr>
</table>

345663	0.002436388	RAMP3 | receptor (calcitonin) activity modifying protein 3
42389	0.002362537	ESTs, Weakly similar to Z195_HUMAN ZINC FINGER PROTEIN 195 [H.sapiens]
203846	0.037582255	FLJ22060 | hypothetical protein FLJ22060
1894519	0.000251134	FLJ12085 | hypothetical protein FLJ12085
74070	0.000230079	ENSA | endosulfine alpha
627542	6.23E-06	BLVRA | biliverdin reductase A
773240	0.02515722	ALG5 | Alg5, S. cerevisiae, homolog of
1562231	0.007588458	SETBP1 | SET binding protein 1
1635062	9.01E-06	DKFZP586A011 | DKFZP586A011 protein
773248	0.000803586	Homo sapiens cDNA FLJ31373 fis, clone NB9N42000342
898083	0.041184366	HBOA | histone acetyltransferase
291426	0.001816883	KIAA1846 | similar to acetyl-coenzyme A synthetase
123802	1.92E-06	MFAP1 | microfibrillar-associated protein 1
177419	9.51E-05	SH3GLB2 | SH3-domain, GRB2-like, endophilin B2
309316	0.040000458	LOC58498 | myosin light chain 2a
627555	0.001343272	MGC3020 | hypothetical protein MGC3020
1637751	0.001227916	OXA1L | oxidase (cytochrome c) assembly 1-like
49229	0.000209018	GPHN | gephyrin
781418	0.011924329	NPIP | nuclear pore complex interacting protein
767775	0.011293731	LOC51242 | hypothetical protein
48285	0.000352444	PIG11 | p53-induced protein
785701	0.011615484	RAB31 | RAB31, member RAS oncogene family
809869	0.020168182	ESTs
810402	0.002154308	LOC51248 | hypothetical protein
785708	0.044838359	ESTs, Weakly similar to O4HUD1 debrisoquine 4-hydroxylase [H.sapiens]
2306804	1.41E-11	PSMD13 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 13

Table 2. Genes that are overexpressed in ER negative cells, and underexpressed in ER positive cells

Clone_ID	P_value	Gene_Description
1557714	0.000249393	ADAM19 | a disintegrin and metalloproteinase domain 19 (meltrin beta)
340745	0.000173284	Homo sapiens cDNA FLJ31683 fis, clone NT2RI2005353
325365	0.00025078	HRB2 | HIV-1 rev binding protein 2
1467905	0.032429761	NSG-X | brain and nasopharyngeal carcinoma susceptibility protein
757225	0.002362784	SNX3 | sorting nexin 3
140806	0.002900139	PAM | peptidylglycine alpha-amidating monooxygenase
796134	0.000177795	MAP3K7 | mitogen-activated protein kinase kinase kinase 7
842896	0.018473624	DKFZp762L0311 | hypothetical protein DKFZp762L0311
1550894	3.48E-08	ESTs, Highly similar to A46297 beta-1,6-N-acetylglucosaminyltransferase [H.sapiens]
813751	0.028826444	SIAT4C | sialyltransferase 4C (beta-galactosidase alpha-2,3-sialytransferase)
740925	0.012998471	INDO | indoleamine-pyrrole 2,3 dioxygenase
795191	1.39E-05	XPNPEP1 | X-prolyl aminopeptidase (aminopeptidase P) 1, soluble
824179	0.016037507	KIAA0655 | huntingtin interacting protein-1-related
731023	0.020902723	WDR5 | WD repeat domain 5
2016775	4.63E-09	GPRC5B | G protein-coupled receptor, family C, group 5, member B
324712	0.023557456	RPS6KB2 | ribosomal protein S6 kinase, 70kD, polypeptide 2
2326057	0.000136732	MLN51 | MLN51 protein
795197	0.000998067	UBE2E2 | ubiquitin-conjugating enzyme E2E 2 (homologous to yeast UBC4/5)
1570427	0.000231261	MGC4309 | hypothetical protein MGC4309
199367	2.20E-05	TNRC3 | trinucleotide repeat containing 3
40021	0.002599711	HR | hairless (mouse) homolog
884355	0.000576316	WASF3 | WAS protein family, member 3
1257131	2.20E-05	ESTs, Weakly similar to SYN1 MOUSE SYNAPSIN I [M.musculus]
731031	5.77E-06	LOC51622 | CGI-43 protein
415191	1.80E-12	KIAA0161 | KIAA0161 gene product
1637781	0.00021037	EST
1858992	0.004823705	KIAA0615 | KIAA0615 gene product
712454	2.82E-06	Homo sapiens mRNA; cDNA DKFZp434O1317 (from clone DKFZp434O1317)

1911099	0.02187025	SCYA8 | small inducible cytokine subfamily A (Cys-Cys), member 8 (monocyte chemotactic protein 2)
785733	1.41E-05	FLJ12892 | hypothetical protein FLJ12892
2009574	0.000167648	T | T brachyury (mouse) homolog
490753	0.001096449	FLJ20420 | hypothetical protein FLJ20420
502753	0.003728424	ANGPT2 | angiopoietin 2
172517	0.004544404	HPCAL1 | hippocalcin-like 1
731044	0.006043174	GLRX2 | glutaredoxin 2
155532	2.88E-07	ESTs, Highly similar to bK989H11.1 [H.sapiens]
731047	5.13E-08	ESTs
49266	0.001856861	LOC51667 | NEDD8 ultimate buster-1
1723604	0.000868338	MSP | mosaic serine protease
1637791	0.001388783	MGC5350 | hypothetical protein MGC5350
1759290	9.79E-05	FLJ11264 | hypothetical protein FLJ11264
221828	0.003359378	ATSV | axonal transport of synaptic vesicles
291478	1.72E-06	RUNX3 | runt-related transcription factor 3
141495	0.009886773	SULT2B1 | sulfotransferase family, cytosolic, 2B, member 1
1534888	1.05E-06	TNFRSF21 | tumor necrosis factor receptor superfamily, member 21
784005	0.003109725	CARD12 | caspase recruitment domain protein 12
120516	0.004325708	ESTs
812048	5.76E-07	PRNP | prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)
563598	1.56E-09	GABRP | gamma-aminobutyric acid (GABA) A receptor, pi
759948	3.06E-06	S100B | S100 calcium-binding protein, beta (neural)
757265	0.000137487	MGC4399 | hypothetical protein MGC4399
1933324	0.017405243	MPZ | myelin protein zero (Charcot-Marie-Tooth neuropathy 1B)
2027515	0.000231471	SFN | stratifin
1614140	0.018506461	LOC51285 | Ris
526297	0.020076393	NTSR1 | neurotensin receptor 1 (high affinity)
113300	0.000965053	TRIM14 | tripartite motif-containing 14
1587847	0.000486268	MCM6 | minichromosome maintenance deficient (mis5, S. pombe) 6
40056	0.000446292	CSPG4 | chondroitin sulfate proteoglycan 4 (melanoma-associated)
270505	0.019185378	MMP14 | matrix metalloproteinase 14 (membrane-inserted)

2017754	0.015486907	DGSI | DiGeorge syndrome critical region gene DGSI; likely ortholog of mouse expressed sequence 2 embryonic lethal
1522734	0.039850127	Homo sapiens cDNA FLJ31090 fis, clone IMR321000102
784016	0.000332608	FLJ20624 | hypothetical protein FLJ20624
884388	0.017638942	FLJ21103 | hypothetical protein FLJ21103
490772	0.000274015	SNRPA1 | small nuclear ribonucleoprotein polypeptide A'
810454	1.82E-05	BACE2 | beta-site APP-cleaving enzyme 2
490777	0.001468215	EST
49284	2.69E-08	FGF11 | fibroblast growth factor 11
1500815	0.003016551	Homo sapiens cDNA: FLJ22130 fis, clone HEP19632
126413	0.013564319	ITIH2 | inter-alpha (globulin) inhibitor, H2 polypeptide
1631132	2.58E-05	PHT2 | peptide transporter 3
593690	0.000827726	TNFSF13B | tumor necrosis factor (ligand) superfamily, member 13b
133637	0.007572041	PRKDC | protein kinase, DNA-activated, catalytic polypeptide
221846	0.006921653	CHES1 | checkpoint suppressor 1
25763	0.000129642	ANKH | ankylosis, progressive (mouse) homolog
68950	3.39E-09	CCNE1 | cyclin E1
788309	0.035143688	RMP | RPB5-mediating protein
730410	0.001453479	LCK | lymphocyte-specific protein tyrosine kinase
503725	0.010812215	ESTs
346688	0.001091951	MIA | melanoma inhibitory activity
2306860	0.000346451	MAD2L2 | MAD2 (mitotic arrest deficient, yeast, homolog)-like 2
782428	0.044484074	C1orf16 | chromosome 1 open reading frame 16
242037	6.76E-06	FLJ20746 | hypothetical protein
358052	0.005746627	ESTs
1946448	2.88E-05	CAV2 | caveolin 2
2046118	2.22E-06	RAD54L | RAD54 (S.cerevisiae)-like
1471841	0.000169912	ATP1A1 | ATPase, Na+/K+ transporting, alpha 1 polypeptide
824510	0.00041118	LOC51647 | CGI-128 protein
141806	0.002003247	TNFAIP3 | tumor necrosis factor, alpha-induced protein 3
486110	0.004730919	PFN2 | profilin 2
1586124	3.20E-05	FLJ11413 | hypothetical protein FLJ11413

840556	0.00087773	EIF4EL3 | eukaryotic translation initiation factor 4E-like 3
1589468	0.001850652	EMP1 | epithelial membrane protein 1
2019376	0.03681114	MGC2718 | hypothetical protein MGC2718
346696	0.021270804	TEAD4 | TEA domain family member 4
796197	6.83E-06	DMD | dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272
796198	0.004000613	EFNB2 | ephrin-B2
731080	2.98E-05	FLJ12661 | hypothetical protein FLJ12661
324772	0.042068695	LCCP | Leman coiled-coil protein
950690	0.035127941	CCNA2 | cyclin A2
841501	2.51E-07	KIAA0102 | KIAA0102 gene product
1466237	0.002257726	TES | testis derived transcript (3 LIM domains)
1457416	0.004076409	KIAA0728 | KIAA0728 protein
153977	0.00188129	POP4 | POP4 (processing of precursor , S. cerevisiae) homolog
840567	0.000523423	TM4SF1 | transmembrane 4 superfamily member 1
768000	0.000909544	RNASEH1 | ribonuclease H1
341763	0.044284858	CASP5 | caspase 5, apoptosis-related cysteine protease
768007	1.46E-07	CL683 | weakly similar to glutathione peroxidase 2
768008	0.000389422	BAG2 | BCL2-associated athanogene 2
39833	9.83E-05	CPVL | carboxypeptidase, vitellogenic-like
843110	0.0039532	GDI1 | GDP dissociation inhibitor 1
155583	0.034919482	TRAF1 | TNF receptor-associated factor 1
810485	0.000238475	ID1 | inhibitor of DNA binding 1, dominant negative helix-loop-helix protein
767068	4.46E-13	DKFZP586G1517 | DKFZP586G1517 protein
108801	3.53E-05	FLJ20392 | hypothetical protein FLJ20392
290866	1.21E-06	RAF1 | v-raf-1 murine leukemia viral oncogene homolog 1
1604703	0.009410539	HLA-F | major histocompatibility complex, class I, F
1584540	0.000352001	Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022)
1590021	3.88E-07	ETV6 | ets variant gene 6 (TEL oncogene)
204897	6.91E-07	PLCG2 | phospholipase C, gamma 2 (phosphatidylinositol-specific)
769751	2.75E-07	KIAA0095 | KIAA0095 gene product
430928	0.005339331	BARD1 | BRCA1 associated RING domain 1

823598	0.029081002	PSMD12 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
843121	0.000124807	CLIC1 | chloride intracellular channel 1
139558	0.008816	Homo sapiens gastric cancer-related protein GCYS-20 (gcys-20) mRNA, complete cds
843126	0.010510953	SIPL | SIPL protein
753313	0.002864496	LAPTM5 | Lysosomal-associated multispanning membrane protein-5
175123	0.037853387	MAPK7 | mitogen-activated protein kinase 7
824547	0.000238959	MHC2TA | MHC class II transactivator
1592715	1.98E-05	HOMER-3 | Homer, neuronal immediate early gene, 3
272155	0.006067385	SRGAP2 | KIAA0456 protein
1845169	0.006064365	RAB35 | RAB35, member RAS oncogene family
489489	2.07E-07	LBR | lamin B receptor
629542	0.002987142	MYH1 | myosin, heavy polypeptide 1, skeletal muscle, adult
490023	1.39E-05	WNT5B | wingless-type MMTV integration site family, member 5B
2430676	0.039914681	EZFIT | endothelial zinc finger protein induced by tumor necrosis factor alpha
868396	1.13E-05	LOC64148 | 17kD fetal brain protein
782460	0.009363602	Homo sapiens cDNA FLJ10500 fis, clone NT2RP2000369
1948085	0.000313027	CBR3 | carbonyl reductase 3
235938	0.009238649	BAK1 | BCL2-antagonist/killer 1
897822	0.003765884	SYK | spleen tyrosine kinase
586803	7.34E-08	PGF | placental growth factor, vascular endothelial growth factor-related protein
746105	4.10E-05	LTRPC7 | homolog of mouse transient receptor potential-phospholipase C-interacting kinase CHaK; hypothetical protein FLJ20117
2271240	0.001624493	RPS12 | ribosomal protein S12
32231	0.000744224	FLJ12442 | hypothetical protein FLJ12442
1394099	0.000187841	MGC5528 | hypothetical protein MGC5528
202514	0.000114404	DNMT3A | DNA (cytosine-5-)-methyltransferase 3 alpha
788355	0.001475302	STAG3 | stromal antigen 3
815737	3.71E-09	ATP5A1 | ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle
726582	1.36E-05	ARP3BETA | actin-related protein 3-beta
244764	0.001161294	B7-H3 | B7 homolog 3
814798	2.03E-08	ALDH1A3 | aldehyde dehydrogenase 1 family, member A3

854644	0.011182578	NPC2 | Niemann-Pick disease, type C2 gene
2011138	0.001310947	KIAA1036 | KIAA1036 protein
194804	0.0121963	PITPN | phosphotidylinositol transfer protein
209066	0.001333458	STK15 | serine/threonine kinase 15
121530	0.023976232	MGC10966 | hypothetical protein MGC10966
430954	9.12E-06	FLJ22341 | hypothetical protein FLJ22341
687054	0.016868879	RELB | v-rel avian reticuloendotheliosis viral oncogene homolog B (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3)
624627	0.004546557	RRM2 | ribonucleotide reductase M2 polypeptide
357450	0.030931622	MTVR | Mouse Mammary Turmor Virus Receptor homolog
25030	0.006951821	PCMF | potassium channel modulatory factor
756687	0.004407309	CD36L1 | CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1
666879	4.67E-06	ANXA8 | annexin A8
68225	0.036628745	Homo sapiens pTM5 mariner-like transposon mRNA, partial sequence
486175	0.0005382	SLC16A1 | solute carrier family 16 (monocarboxylic acid transporters), member 1
796539	0.000602202	TRIM28 | tripartite motif-containing 28
745189	9.02E-05	DAZAP1 | DAZ associated protein 1
810813	0.001864702	S100A2 | S100 calcium-binding protein A2
486179	0.000858947	NFAT5 | nuclear factor of activated T-cells 5, tonicity-responsive
149355	0.011544468	TRAM | translocating chain-associating membrane protein
1476053	0.03289313	RAD51 | RAD51 (S. cerevisiae) homolog (E coli RecA homolog)
2062507	2.18E-07	KLF5 | Kruppel-like factor 5 (intestinal)
1634832	0.026304968	WSX-1 | class I cytokine receptor
1420842	0.01376248	MALT1 | mucosa associated lymphoid tissue lymphoma translocation gene 1
489805	0.028082851	HSF4 | heat shock transcription factor 4
611532	7.05E-06	TNNI2 | troponin I, skeletal, fast
796542	8.87E-05	ETV5 | ets variant gene 5 (ets-related molecule)
727551	1.40E-08	IRF2 | interferon regulatory factor 2
50987	0.016625494	PABPC4 | poly(A)-binding protein, cytoplasmic 4 (inducible form)
823925	0.001754502	LOC51177 | CK2 interacting protein 1; HQ0024c protein
121551	1.86E-08	LAD1 | ladinin 1
869375	0.003859746	IDH2 | isocitrate dehydrogenase 2 (NADP+), mitochondrial

73852	0.017664041	Homo sapiens cDNA FLJ14388 fis, clone HEMBA1002716
252953	0.019402013	GS3786 | predicted osteoblast protein
2321529	0.026304832	KCNG1 | potassium voltage-gated channel, subfamily G, member 1
1476065	0.000528763	STMN1 | stathmin 1/oncoprotein 18
854678	0.015997677	DKFZP566J091 | hypothetical protein DKFZp566J091
196435	0.00388413	ESTs, Weakly similar to KIAA0738 protein [H.sapiens]
843174	0.001025358	PGM1 | phosphoglucomutase 1
52594	0.036156197	PCDH8 | protocadherin 8
20115	0.021509161	SLC9A6 | solute carrier family 9 (sodium/hydrogen exchanger), isoform 6
669443	0.003570072	HSF2 | heat shock transcription factor 2
770355	0.014696243	LSS | lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)
51947	0.025874177	Homo sapiens, clone MGC:20842 IMAGE:4542449, mRNA, complete cds
809503	0.001947255	ESTs, Weakly similar to AC004858 3 U1 small ribonucleoprotein 1SNRP homolog [H.sapiens]
193106	0.003498139	ATP5G3 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3
1702742	2.07E-07	SLC7A5 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
815781	0.046183854	HSP105B | heat shock 105kD
782800	0.046687885	UQCRFS1 | ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1
68259	0.000734236	RENT2 | regulator of nonsense transcripts 2
121577	1.83E-06	FLJ22393 | hypothetical protein FLJ22393
1912458	1.43E-08	IL12A | interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35)
70533	0.00154863	HPS | Hermansky-Pudlak syndrome
1660666	0.017638942	CA5B | carbonic anhydrase VB, mitochondrial
51950	0.002759641	AQP1 | aquaporin 1 (channel-forming integral protein, 28kD)
291880	2.95E-05	MFAP2 | microfibrillar-associated protein 2
1555478	0.031251603	ST2 | syntenin-2 protein
51955	1.54E-08	FLJ22282 | hypothetical protein FLJ22282
79761	0.038130306	TMPO | thymopoietin
843195	0.005767924	PSPH | phosphoserine phosphatase
292388-2	0.000484852	LOC55977 | hypothetical protein 24636
246704	0.013447399	RAI | RelA-associated inhibitor
782811	6.86E-07	HMGIY | high-mobility group (nonhistone chromosomal) protein isoforms I and Y

271568	0.000866786	ACTR3 | ARP3 (actin-related protein 3, yeast) homolog
2307119	2.37E-06	INPP4A | inositol polyphosphate-4-phosphatase, type I, 107kD
838662	0.010070202	HCNGP | transcriptional regulator protein
810859	0.047573891	NK4 | natural killer cell transcript 4
241481	0.014557615	CASP10 | caspase 10, apoptosis-related cysteine protease
2094232	5.18E-06	EGLN1 | EGL nine (C.elegans) homolog 1
267691	0.007853541	FLJ20360 | hypothetical protein FLJ20360
788705	0.018859374	USF1 | upstream transcription factor 1
592359	0.037494688	HKE4 | HLA class II region expressed gene KE4
2159983	3.25E-08	PORIMIN | pro-oncosis receptor inducing membrane injury gene
2016426	0.009898035	KIAA0664 | KIAA0664 protein
270917	3.65E-08	SFRP1 | secreted frizzled-related protein 1
625623	0.001515188	Homo sapiens mRNA; cDNA DKFZp434F152 (from clone DKFZp434F152)
1492426	0.000486718	C19orf3 | chromosome 19 open reading frame 3
1556433	0.013873827	GRO3 | GRO3 oncogene
2010543	0.000219946	DDX28 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 28
1466621	0.023035247	ATP2C1 | ATPase, Ca++ transporting, type 2C, member 1
299388	1.27E-06	PP15 | nuclear transport factor 2 (placental protein 15)
1469966	0.002597189	DLL3 | delta-like 3 (Drosophila)
771323	6.28E-10	PLOD | procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI)
306444	0.011573645	TAF11 | TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28 kD
382654	0.005845554	PCSK2 | proprotein convertase subtilisin/kexin type 2
544639	1.14E-07	ESTs
306446	0.001825487	C11orf24 | chromosome 11 open reading frame 24
838676	0.017828051	CAPN6 | calpain 6
42070	0.000619438	NT5 | 5' nucleotidase (CD73)
809530	0.009640123	MCM2 | minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin)
754346	2.60E-05	ESTs, Weakly similar to B49647 GTP-binding protein rab8 [H.sapiens]
882402	0.003800629	KIAA0692 | KIAA0692 protein
770388	0.004124332	CLDN4 | claudin 4
815015	0.000124184	TERA | TERA protein

1604005	1.58E-05	SH3KBP1 | SH3-domain kinase binding protein 1
789376	0.02515722	TXNRD1 | thioredoxin reductase 1
814072	0.000473	Homo sapiens, clone MGC:19517 IMAGE:4335816, mRNA, complete cds
504791	0.004943728	GSTA4 | glutathione S-transferase A4
3220641	0.018173943	OR7E24P | olfactory receptor, family 7, subfamily E, member 24 pseudogene
325033	0.016712654	ESTs
814076	0.01354434	NSAP1 | NS1-associated protein 1
811817	0.009457359	FLJ21032 | hypothetical protein FLJ21032
510273	0.030089117	PLEC1 | plectin 1, intermediate filament binding protein, 500kD
377048	0.000173284	MYO1B | myosin IB
1034776	0.000124401	AD037 | AD037 protein
322494	1.89E-05	CBFB | core-binding factor, beta subunit
46367	0.001719417	CHK | choline kinase
1519143	0.000508533	RISC | likely homolog of rat and mouse retinoid-inducible serine carboxypeptidase
789382	0.029514943	NOTCH4 | Notch (Drosophila) homolog 4
263716	0.003686053	COL6A1 | collagen, type VI, alpha 1
823982	0.00726442	TRIM26 | tripartite motif-containing 26
140197	0.004538178	LOC51299 | neuritin
786048	0.000316752	E2F4 | E2F transcription factor 4, p107/p130-binding
1947804	0.014717852	TREX1 | three prime repair exonuclease 1
414999	0.00278887	ETV4 | ets variant gene 4 (E1A enhancer-binding protein, E1AF)
279085	0.012204566	MYO9B | myosin IXB
259842	2.42E-05	PMPCB | peptidase (mitochondrial processing) beta
232697	0.003201006	TIMM10 | translocase of inner mitochondrial membrane 10 (yeast) homolog
809557	0.006003565	MCM3 | minichromosome maintenance deficient (S. cerevisiae) 3
725223	1.33E-05	KIAA0077 | KIAA0077 protein
840978	6.56E-06	CD81 | CD81 antigen (target of antiproliferative antibody 1)
490414	2.13E-08	C2orf2 | chromosome 2 open reading frame 2
786053	0.038091532	Homo sapiens cDNA FLJ30898 fis, clone FEBRA2005572
564981	2.34E-05	Homo sapiens, Similar to RIKEN cDNA 2810433K01 gene, clone MGC:10200 IMAGE:3909951, mRNA, complete cds
810899	9.04E-06	ESTs

288999	0.000887435	SPEC1 | small protein effector 1 of Cdc42
1473876	4.29E-05	KIAA0187 | KIAA0187 gene product
796904	1.58E-05	PLAGL1 | pleiomorphic adenoma gene-like 1
344720	0.001678075	GYPC | glycophorin C (Gerbich blood group)
1534544	0.004653836	PCCX2 | protein containing CXXC domain 2
126858	0.038264032	SOAT1 | sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1
202904	0.00238904	SFRS7 | splicing factor, arginine/serine-rich 7 (35kD)
840984	0.004457062	CAV2 | caveolin 2
138672-2	5.39E-06	ESTs
882439	0.017638691	CPR2 | cell cycle progression 2 protein
2721773	0.027704333	NOG | noggin
786067	8.88E-05	CDC25B | cell division cycle 25B
1575059	0.028270162	TBCC | tubulin-specific chaperone c
1947827	0.01489065	MSTP028 | MSTP028 protein
2390593	4.77E-06	PTPN14 | protein tyrosine phosphatase, non-receptor type 14
767487	5.80E-05	ARIH1 | ariadne (Drosophila) homolog, ubiquitin-conjugating enzyme E2-binding protein, 1
161484	4.46E-05	DGAT2 | diacylglycerol O-acyltransferase homolog 2 (mouse)
2052032	1.96E-07	MYO10 | myosin X
712139	2.31E-09	ARL7 | ADP-ribosylation factor-like 7
770709	0.000831262	KIAA1089 | KIAA1089 protein
2017415	1.21E-05	CENPA | centromere protein A (17kD)
740620	2.38E-05	TPM2 | tropomyosin 2 (beta)
184354	6.99E-07	EST
182750	0.012645421	MSI1 | Musashi (Drosophila) homolog 1
76481	0.024566797	PTK9L | protein tyrosine kinase 9-like (A6-related protein)
785417	0.011581406	NCUBE1 | non-canonical ubquitin conjugating enzyme 1
2313732	0.002401111	PLAA | phospholipase A2-activating protein
1911864	0.005343697	GNG4 | guanine nucleotide binding protein 4
503096	1.97E-05	ESTs
810119	3.53E-05	SNAI1 | snail 1 (drosophila homolog), zinc finger protein
713886	0.018673346	CNN2 | calponin 2
281392	0.005737829	Homo sapiens mRNA; cDNA DKFZp761G02121 (from clone DKFZp761G02121); partial cds

431214	0.005427358	FLJ12484 | hypothetical protein FLJ12484
205185	0.010013706	THBD | thrombomodulin
813460	0.005587928	PCSK7 | proprotein convertase subtilisin/kexin type 7
809588	0.022949968	GGH | gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)
1901310	0.001063475	KIAA1209 | KIAA1209 protein
257197	0.005064867	NRBF-2 | nuclear receptor binding factor-2
502446	0.004574652	DKFZP564A2416 | DKFZP564A2416 protein
156962	0.016124526	ESTs
882459	0.007855578	PPIC | peptidylprolyl isomerase C (cyclophilin C)
588822	0.000420841	COVA1 | cytosolic ovarian carcinoma antigen 1
625683	4.54E-05	NOC4 | neighbor of COX4
470128	2.92E-08	MYO1E | myosin IE
233679	2.38E-05	FLJ22362 | hypothetical protein FLJ22362
683177	0.016770876	MAP4K5 | mitogen-activated protein kinase kinase kinase kinase 5
700792	0.026756579	CDKN3 | cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)
882461	0.001070887	ASS | argininosuccinate synthetase
1518538	0.000295474	MGC4607 | hypothetical protein MGC4607
1517595	2.27E-06	KIAA0175 | likely ortholog of maternal embryonic leucine zipper kinase
950355	0.000138935	ESTs, Weakly similar to TRHY_HUMAN TRICHOHYALI [H.sapiens]
839682	4.07E-06	UBE2N | ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)
625693	0.001165816	MGC10911 | hypothetical protein MGC10911
289978	0.00024508	UBL4 | ubiquitin-like 4
25440	0.003949353	STAU2 | staufen (Drosophila, RNA-binding protein) homolog 2
346360	0.039034227	LAT | linker for activation of T cells
1161155	0.000197727	CDKN2A | cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)
2028949	0.034919482	PRO1855 | hypothetical protein PRO1855
1925939	0.025350497	PLAGL2 | pleiomorphic adenoma gene-like 2
32664	0.04577709	GNAO1 | guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O
1542749	3.27E-08	AMD1 | S-adenosylmethionine decarboxylase 1
2316305	0.000257732	DKFZP566D213 | DKFZP566D213 protein
724615	0.00452876	CHC1 | chromosome condensation 1
951304	0.011615484	KIAA0573 | KIAA0573 protein

75859	4.68E-06	NDRG2 | N-myc downstream-regulated gene 2
950361	0.002582165	EST
898122	0.003101713	C7 | complement component 7
898123	1.31E-05	GART | phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase
1881171	0.00258728	ESTs
594322	0.014086588	PAPSS1 | 3'-phosphoadenosine 5'-phosphosulfate synthase 1
530958	0.000152832	SMOH | smoothened (Drosophila) homolog
813490	7.09E-07	CORO1C | coronin, actin-binding protein, 1C
2308153	0.003570072	ELL | ELL gene (11-19 lysine-rich leukemia gene)
785459	0.001112368	SMTN | smoothelin
767817	7.55E-07	POLR2F | polymerase (RNA) II (DNA directed) polypeptide F
153650	0.001255544	KIAA1140 | KIAA1140 protein
810156	0.007406628	DTYMK | deoxythymidylate kinase (thymidylate kinase)
1035796	0.00021094	ESTs, Weakly similar to T33068 hypothetical protein C35E7.9 - Caenorhabditis elegans [C.elegans]
811897	0.002192122	MKL1 | megakaryoblastic leukemia (translocation) 1
824203	0.018221151	DNCLI2 | dynein, cytoplasmic, light intermediate polypeptide 2
744952	0.024481266	ESTs, Moderately similar to UQHUR7 ubiquitin / ribosomal protein S27a, cytosolic [H.sapiens]
85634	0.000676725	C1S | complement component 1, s subcomponent
132395	0.008012849	SRRM1 | serine/arginine repetitive matrix 1
2012523	6.10E-07	FABP5 | fatty acid binding protein 5 (psoriasis-associated)
773301	3.74E-12	CDH3 | cadherin 3, type 1, P-cadherin (placental)
811108	0.000222819	TRIP6 | thyroid hormone receptor interactor 6
416959	1.42E-08	NFIB | nuclear factor I/B
250699	0.019002987	Homo sapiens, clone IMAGE:3888869, mRNA, partial cds
144849	3.25E-08	CLP | coactosin-like protein
743220	0.000600627	FLJ12517 | hypothetical protein FLJ12517
283328	0.000987968	EST
842939	0.022592867	ADARB1 | adenosine deaminase, RNA-specific, B1 (homolog of rat RED1)
417905	0.00632472	Homo sapiens, Similar to RIKEN cDNA 5730528L13 gene, clone MGC:17337 IMAGE:4213591, mRNA, complete cds
809918	0.000355143	FLJ21047 | hypothetical protein FLJ21047

811116	0.027129738	Homo sapiens, clone IMAGE:3632168, mRNA
2014138	0.003381521	FACL2 | fatty-acid-Coenzyme A ligase, long-chain 2
309092	3.07E-05	APG5L | APG5 (autophagy 5, S. cerevisiae)-like
128811	0.000579172	MGC2452 | hypothetical protein MGC2452
768496	0.011680975	EBI3 | Epstein-Barr virus induced gene 3
772373	0.001284654	Homo sapiens cDNA FLJ30865 fis, clone FEBRA2004099
140574	4.08E-13	SCYD1 | small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)
263013	0.000365845	PLOD2 | procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2
2161427-2	0.000159834	PGR | progesterone receptor
1606790	0.002826291	MGC12217 | hypothetical protein MGC12217
1509761	1.92E-06	KRTHB6 | keratin, hair, basic, 6 (monilethrix)
469924	0.00156327	PCTP | phosphatidylcholine transfer protein
724652	0.000324169	CD8B1 | CD8 antigen, beta polypeptide 1 (p37)
773322	0.001724267	SHOX2 | short stature homeobox 2
773324	0.00075407	FLJ10439 | hypothetical protein FLJ10439
711552	0.004197328	CBR1 | carbonyl reductase 1
773329	0.003063069	KIAA1204 | KIAA1204 protein
1422894	0.01526361	NOTCH2 | Notch (Drosophila) homolog 2
2010949	0.000264549	ME2 | malic enzyme 2, NAD(+)-dependent, mitochondrial
897509	0.000195032	ESTs, Weakly similar to S23650 retrovirus-related hypothetical protein II [H.sapiens]
223176	0.004691656	MAD | MAX dimerization protein
744980	0.029325674	KIAA0304 | KIAA0304 gene product
1518591	0.000137744	EST
784830	0.0001858	D123 | D123 gene product
431280	0.000580358	EST
246041	0.00099919	MRPS35 | mitochondrial ribosomal protein S35
25499	0.031951505	DKFZp564A176 | hypothetical protein DKFZp564A176
505059	0.017104301	HSD11B1 | hydroxysteroid (11-beta) dehydrogenase 1
377441	0.000151691	S100A3 | S100 calcium-binding protein A3
80727	3.81E-05	ROR1 | receptor tyrosine kinase-like orphan receptor 1
814478	0.009751136	BCL2A1 | BCL2-related protein A1
714106	0.003765884	PLAU | plasminogen activator, urokinase

773330	0.000805296	GPNMB | glycoprotein (transmembrane) nmb
343079	0.044429786	Homo sapiens mRNA; cDNA DKFZp761P0114 (from clone DKFZp761P0114)
773331	1.90E-05	ESTs, Weakly similar to YK61_YEAST HYPOTHETICAL 39.6 KDA PROTEIN IN MTD1-NUP133 INTERGENIC REGION [S.cerevisiae]
324492	0.029371795	MMP3 | matrix metalloproteinase 3 (stromelysin 1, progelatinase)
132711	5.39E-08	KLF5 | Kruppel-like factor 5 (intestinal)
841226	0.005177763	NS1-BP | NS1-binding protein
842968	0.000543163	BUB1B | budding uninhibited by benzimidazoles 1 (yeast homolog), beta
795263	0.004420295	FLJ22638 | hypothetical protein FLJ22638
2309141	0.007213754	CD97 | CD97 antigen
950700	0.002257726	PP | pyrophosphatase (inorganic)
725618	0.007582436	Homo sapiens mRNA containing (CAG)4 repeat, clone CZ-CAG-7
1655480	0.00653861	ESTs
377452	0.037494688	LOC55818 | putative zinc finger protein
845513	0.000814278	AP47 | clathrin-associated protein AP47
811149	0.002784531	C9orf3 | chromosome 9 open reading frame 3
160126	0.009121318	COX10 | COX10 (yeast) homolog, cytochrome c oxidase assembly protein (heme A: farnesyltransferase)
144880	8.33E-05	LOC56932 | hypothetical protein from EUROIMAGE 1759349
144881	0.000416861	CALU | calumenin
845519	0.002618542	ATP5C1 | ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
884425	0.01173607	CCT5 | chaperonin containing TCP1, subunit 5 (epsilon)
950710	3.51E-06	PCCA | propionyl Coenzyme A carboxylase, alpha polypeptide
2013515	6.64E-07	SGK | serum/glucocorticoid regulated kinase
1869486	0.001399452	PRKX | protein kinase, X-linked
897531	4.76E-06	MCAM | melanoma cell adhesion molecule
782176	0.001737318	LOC136442 | similar to MRJ gene for a member of the DNAJ protein family (H. sapiens)
703707	8.41E-06	ASPH | aspartate beta-hydroxylase
154657	0.030945971	Homo sapiens cDNA: FLJ21286 fis, clone COL01915
753034	0.006100942	NFIX | nuclear factor I/X (CCAAT-binding transcription factor)
753038	3.93E-06	KIFC3 | kinesin family member C3
795280	0.017638942	ESTs
628602	0.003953106	MYL3 | myosin, light polypeptide 3, alkali; ventricular, skeletal, slow

813841	0.00266223	PLAT | plasminogen activator, tissue
785804	0.000661605	CECR5 | cat eye syndrome chromosome region, candidate 5
73531	2.64E-07	NIFU | nitrogen fixation cluster-like
271219	0.010004815	Homo sapiens cDNA FLJ12566 fis, clone NT2RM4000852
1879255	0.021427151	DPYSL4 | dihydropyrimidinase-like 4
1913855	0.005854823	MRPS17 | mitochondrial ribosomal protein S17
345787	1.23E-05	HEC | highly expressed in cancer, rich in leucine heptad repeats
810504	0.020902723	PLP2 | proteolipid protein 2 (colonic epithelium-enriched)
811161	0.000316188	ABCF1 | ATP-binding cassette, sub-family F (GCN20), member 1
1556872	0.012702024	FLJ12628 | hypothetical protein FLJ12628
897542	9.81E-05	DKFZP564F0522 | DKFZP564F0522 protein
282720	0.02278302	OIP2 | Opa-interacting protein 2
897544	0.02996845	LMNA | lamin A/C
757328	0.002130274	FLJ22678 | hypothetical protein FLJ22678
589869	2.56E-07	TAZ | transcriptional co-activator with PDZ-binding motif (TAZ)
1474149	0.042782235	PVRL1 | poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin)
789012	0.000225033	FBLN2 | fibulin 2
842994	0.002759641	CTSZ | cathepsin Z
249705	0.037596341	DSS1 | Deleted in split-hand/split-foot 1 region
2028238	0.000866786	KIAA0300 | KIAA0300 protein
530237	0.012438932	Homo sapiens cDNA FLJ14208 fis, clone NT2RP3003264
664975	0.008779706	CLDN1 | claudin 1
70201	3.09E-06	LOC51312 | mitochondrial solute carrier
340850	0.0041899	MGC12992 | hypothetical protein MGC12992
191978	5.46E-05	ATP5J2 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2
782193	0.002728134	TXN | thioredoxin
485220	7.62E-05	HSA011916 | hypothetical protein
2019426	3.13E-05	PTPNS1 | protein tyrosine phosphatase, non-receptor type substrate 1
825229	0.001223619	MRPL11 | mitochondrial ribosomal protein L11
809981	7.94E-07	GPX4 | glutathione peroxidase 4 (phospholipid hydroperoxidase)
179163-2	0.029938789	GRIN2C | glutamate receptor, ionotropic, N-methyl D-aspartate 2C
41869	0.034236898	FLJ11017 | hypothetical protein FLJ11017

563673	0.008164837	ALDH7A1 | aldehyde dehydrogenase 7 family, member A1
2714973	8.88E-05	GALNS | galactosamine (N-acetyl)-6-sulfate sulfatase (Morquio syndrome, mucopolysaccharidosis type IVA)
1638827	0.015500819	RFPL3S | ret finger protein-like 3 antisense
295843	0.042020398	CYP27A1 | cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1
156283	0.041270668	ESTs
307843	5.77E-07	PPP2CA | protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
1474164	0.010013706	FLJ12886 | hypothetical protein FLJ12886
289288	0.003697618	ATP2C1 | ATPase, Ca++ transporting, type 2C, member 1
50693	0.000289561	FLJ20232 | hypothetical protein
884462	0.000194201	DSCR1 | Down syndrome critical region gene 1
338599	1.85E-05	NRBP | nuclear receptor binding protein
279810	0.039210986	Homo sapiens mRNA; cDNA DKFZp564O1016 (from clone DKFZp564O1016)
1948119	0.001273848	GRAF | GTPase regulator associated with the focal adhesion kinase pp125
292512	0.001680803	MLL3 | myeloid/lymphoid or mixed-lineage leukemia 3
685182	0.00023067	CCT6A | chaperonin containing TCP1, subunit 6A (zeta 1)
1636156	0.005363775	FLJ21709 | hypothetical protein FLJ21709
1553560	2.41E-06	ESTs, Weakly similar to hyperpolarization-activated cyclic nucleotide-gated channel hHCN2 [H.sapiens]
471196	2.95E-13	ITM3 | integral membrane protein 3
754018	0.000287497	SVIL | supervillin
179163	0.019936342	GRIN2C | glutamate receptor, ionotropic, N-methyl D-aspartate 2C
770059	0.002506551	HSPG2 | heparan sulfate proteoglycan 2 (perlecan)
504461	0.00094691	OPN3 | opsin 3 (encephalopsin, panopsin)
760298	0.018009132	PRSC1 | protease, cysteine, 1 (legumain)
796268	0.010529568	PPP1R1A | protein phosphatase 1, regulatory (inhibitor) subunit 1A
782501	0.000195601	PP1665 | hypothetical protein PP1665
782503	0.015719214	FADS1 | fatty acid desaturase 1
263097	0.000642521	RPIA | ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase)
687875	0.027149103	CTSS | cathepsin S
1733191	0.009227097	ESTs
771004	0.026126878	Homo sapiens, clone IMAGE:3880654, mRNA

1708335	0.005854823	GDF5 | growth differentiation factor 5 (cartilage-derived morphogenetic protein-1)
756708	1.43E-08	KCNN4 | potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4
1636166	0.000160656	KIAA0668 | KIAA0668 protein
684539	0.011902794	Homo sapiens mRNA; cDNA DKFZp761E212 (from clone DKFZp761E212)
712577	0.000236843	HCCS | holocytochrome c synthase (cytochrome c heme-lyase)
754026	1.64E-09	SMURF2 | E3 ubiquitin ligase SMURF2
1161564	9.84E-11	DMN | desmuslin
429368	0.018119429	HOX11 | homeo box 11 (T-cell lymphoma 3-associated breakpoint)
41898	0.005343697	PTGDS | prostaglandin D2 synthase (21kD, brain)
810551	0.000677873	LRP1 | low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)
812159	8.87E-05	FLJ20337 | hypothetical protein FLJ20337
70245	0.011187375	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 50374
138672	7.63E-08	ESTs
1874367	0.019549691	SCYA20 | small inducible cytokine subfamily A (Cys-Cys), member 20
49389	0.000722653	STX1A | syntaxin 1A (brain)
897590	0.036633129	NESP55 | neuroendocrine secretory protein 55
824602	0.014186983	IFI16 | interferon, gamma-inducible protein 16
140951	4.83E-06	ACTN4 | actinin, alpha 4
41108	0.039873583	Homo sapiens clone 25023 mRNA sequence
40164	0.008273187	Homo sapiens clone 23836 mRNA sequence
415613	0.042602065	LOC51304 | DHHC1 protein
180803	0.01441978	INPP1 | inositol polyphosphate-1-phosphatase
823665	0.000516552	PBEF | pre-B-cell colony-enhancing factor
122238	0.013397185	KIAA0669 | KIAA0669 gene product
502880	0.003571882	MGC11352 | hypothetical protein MGC11352
812164	0.006694394	384D8-2 | hypothetical protein 384D8_6
784129	0.003286809	YWHAG | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide
812167	0.045013394	GGA3 | ADP-ribosylation factor-binding protein GGA3
810567	0.007408045	ARHGEF2 | rho/rac guanine nucleotide exchange factor (GEF) 2
593001	4.44E-05	WHSC1 | Wolf-Hirschhorn syndrome candidate 1
285323	0.000245162	ESTs, Weakly similar to A28996 proline-rich protein M14 precursor - mouse [M.musculus]

754040	6.62E-06	Homo sapiens cDNA FLJ31626 fis, clone NT2RI2003317
364716	0.000137407	MSH6 | mutS (E. coli) homolog 6
193913	4.65E-09	LYN | v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
205913	4.76E-05	FLJ10955 | hypothetical protein FLJ10955
489553	0.014887446	ESRRA | estrogen-related receptor alpha
122241	0.000328148	PSMB2 | proteasome (prosome, macropain) subunit, beta type, 2
360436	0.002697689	COPEB | core promoter element binding protein
1584623	0.000523143	CCNC | cyclin C
1914863	3.34E-10	DYSF | dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive)
2244561	0.026955181	CROC4 | transcriptional activator of the c-fos promoter
742685	0.000245162	DAB2 | disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein)
289615	0.008351255	LAMP2 | lysosomal-associated membrane protein 2
1576468	0.001426413	HSD17B2 | hydroxysteroid (17-beta) dehydrogenase 2
145112	0.009363602	ICAM1 | intercellular adhesion molecule 1 (CD54), human rhinovirus receptor
756731	0.022873245	MAP3K3 | mitogen-activated protein kinase kinase kinase 3
624390	0.000380341	DC13 | DC13 protein
35642	0.007213754	FLJ10826 | hypothetical protein FLJ10826
310034	5.32E-10	PRKY | protein kinase, Y-linked
1846982	0.016285335	INHBC | inhibin, beta C
825284	0.028295772	MGC5508 | hypothetical protein MGC5508
868472	4.10E-08	CLIC4 | chloride intracellular channel 4
327425	0.019017794	ESTs
2237353	0.021840957	GAL | galanin
1911531	0.000758456	SH3GLB1 | SH3-domain, GRB2-like, endophilin B1
345069	3.99E-06	NFE2L3 | nuclear factor (erythroid-derived 2)-like 3
767164	2.48E-07	Homo sapiens cDNA FLJ32401 fis, clone SKMUS2000339
812187	0.029639799	MGC3279 | hypothetical protein MGC3279 similar to collectins
758343	0.000196981	PPIF | peptidylprolyl isomerase F (cyclophilin F)
780947	0.02676531	POLD1 | polymerase (DNA directed), delta 1, catalytic subunit (125kD)
593023	0.008498512	DTNB | dystrobrevin, beta
209066-2	0.000805479	STK15 | serine/threonine kinase 15
209137	3.88E-07	GABRE | gamma-aminobutyric acid (GABA) A receptor, epsilon

1588924	0.001432315	HHGP | HHGP protein
292567	0.000125692	MCPR | anaphase-promoting complex 1; meiotic checkpoint regulator
44477	0.008204839	VCAM1 | vascular cell adhesion molecule 1
1721076	3.74E-05	ZNF136 | zinc finger protein 136 (clone pHZ-20)
825293	0.031216746	KIAA0082 | KIAA0082 protein
840677	0.004604961	IGKC | immunoglobulin kappa constant
768111	0.008346481	Homo sapiens mRNA; cDNA DKFZp586L0120 (from clone DKFZp586L0120)
769857	0.002264658	CBS | cystathionine-beta-synthase
841620	0.000244327	DPYSL2 | dihydropyrimidinase-like 2
855389	0.04294858	TACC1 | transforming, acidic coiled-coil containing protein 1
28444	0.045698004	CRSP2 | cofactor required for Sp1 transcriptional activation, subunit 2 (150kD)
43828	0.002262746	Homo sapiens, clone MGC:5564, mRNA, complete cds
42880	2.84E-07	CDK8 | cyclin-dependent kinase 8
896978	0.00231445	FLJ12810 | hypothetical protein FLJ12810
767180	0.000175172	C1orf6 | chromosome 1 open reading frame 6
43833	0.001478693	DGKG | diacylglycerol kinase, gamma (90kD)
207550	0.004415317	KIAA0057 | TRAM-like protein
188335	0.016029967	EMR2 | egf-like module containing, mucin-like, hormone receptor-like sequence 2
276547	0.01022325	DNMT1 | DNA (cytosine-5-)-methyltransferase 1
744605	0.000194318	FLJ10297 | hypothetical protein FLJ10297
756769	0.000566667	CHAF1B | chromatin assembly factor 1, subunit B (p60)
753428	0.016749826	Homo sapiens, Similar to RIKEN cDNA 1110014B07 gene, clone MGC:20766 IMAGE:4586039, mRNA, complete cds
344430	0.008499295	BMP7 | bone morphogenetic protein 7 (osteogenic protein 1)
345090	0.006154605	GL004 | GL004 protein
1622465	0.026837772	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
1917449	0.000329467	SAA4 | serum amyloid A4, constitutive
76182	0.000472307	DKFZP761F241 | hypothetical protein DKFZp761F241
254625	0.010898804	KIAA0229 | KIAA0229 protein
840697	0.040193056	FKBP9 | FK506-binding protein 9 (63 kD)
255285	5.16E-09	ESTs

813157	7.60E-08	DKFZp547A023 | hypothetical protein DKFZp547A023
259842-2	1.51E-06	PMPCB | peptidase (mitochondrial processing) beta
782575	0.000103262	HSJ001348 | cDNA for differentially expressed CO16 gene
612274	0.000642521	TUBA1 | tubulin, alpha 1 (testis specific)
28469	0.015871	OXCT | 3-oxoacid CoA transferase
1630639	0.043830461	ATP1A3 | ATPase, Na+/K+ transporting, alpha 3 polypeptide
302996	0.022945273	CLIC3 | chloride intracellular channel 3
378813	5.00E-10	SLPI | secretory leukocyte protease inhibitor (antileukoproteinase)
782581	1.03E-05	KIAA0996 | KIAA0996 protein
471568	8.73E-06	HN1 | hematological and neurological expressed 1
877621	0.013066696	AF9Q34 | nGAP-like protein
746229	1.17E-13	MAP4K4 | mitogen-activated protein kinase kinase kinase kinase 4
265060	0.000287204	KIT | v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
1632248	0.019761169	Homo sapiens cDNA FLJ14181 fis, clone NT2RP2004300
488956	0.002056402	CUGBP2 | CUG triplet repeat, RNA-binding protein 2
591465	0.032429761	Homo sapiens, clone MGC:2908 IMAGE:3029644, mRNA, complete cds
2163910	0.021936941	CSPG3 | chondroitin sulfate proteoglycan 3 (neurocan)
814117	0.01403347	DDX21 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21
769890	0.000279148	NP | nucleoside phosphorylase
234325	0.006737438	CUL4A | cullin 4A
45464	6.10E-07	AK2 | adenylate kinase 2
284734	0.044838359	WASF1 | WAS protein family, member 1
843263	0.005565298	MRPL37 | mitochondrial ribosomal protein L37
897956	0.000566151	PRAME | preferentially expressed antigen in melanoma
282051	0.007261049	ESTs, Highly similar to I38945 melanoma ubiquitous mutated protein [H.sapiens]
744632	5.13E-08	EST
43865	1.57E-05	DNCI1 | dynein, cytoplasmic, intermediate polypeptide 1
841663	3.62E-05	NARF | nuclear prelamin A recognition factor
1525461	0.001442019	RIPK2 | receptor-interacting serine-threonine kinase 2
826286	0.002032859	IMP13 | importin 13
1470278	0.000152832	FLJ21841 | hypothetical protein FLJ21841
796646	6.57E-07	ODC1 | ornithine decarboxylase 1

502161	0.001298549	APPBP1 | amyloid beta precursor protein-binding protein 1, 59kD
1610338	0.021681051	FLJ22324 | hypothetical protein FLJ22324
146123	0.003881514	PTPRK | protein tyrosine phosphatase, receptor type, K
153340	0.009064405	GRO2 | GRO2 oncogene
243155	0.048299748	FLJ12549 | hypothetical protein FLJ12549
897963	6.59E-06	PPAP2A | phosphatidic acid phosphatase type 2A
304908	1.10E-05	E2F3 | E2F transcription factor 3
2701197	0.019362001	C11orf9 | chromosome 11open reading frame 9
119384	0.000965202	CHIT1 | chitinase 1 (chitotriosidase)
877644	0.001738247	PRCC | papillary renal cell carcinoma (translocation-associated)
220293	0.010938828	Homo sapiens cDNA: FLJ21800 fis, clone HEP00618
1732922	0.001365668	Homo sapiens mRNA; cDNA DKFZp762H106 (from clone DKFZp762H106)
470930	2.82E-05	DDX11 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase)
701460	0.001790158	CHFR | checkpoint with forkhead and ring finger domains
269374	0.000195253	KIAA0301 | KIAA0301 protein
825641	3.34E-06	B4GALT5 | UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5
531608	0.002759613	HMGIC | high-mobility group (nonhistone chromosomal) protein isoform I-C
300632	0.042347323	FLJ21044 | hypothetical protein FLJ21044 similar to Rbig1
266037	0.00106935	MAFG | v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein G
1585650	0.01494333	FLJ10781 | hypothetical protein FLJ10781
841689	0.018506257	ATP6S1 | ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1
1461477	1.32E-05	Homo sapiens mRNA; cDNA DKFZp586I0324 (from clone DKFZp586I0324)
784504	0.000195601	MBTPS1 | membrane-bound transcription factor protease, site 1
1493160	0.001295674	SCYB10 | small inducible cytokine subfamily B (Cys-X-Cys), member 10
47096	0.014632388	FUSIP2 | FUS-interacting protein (serine-arginine rich) 2
770462	0.000758456	CPZ | carboxypeptidase Z
745606	0.014811257	PP591 | hypothetical protein PP591
268727	0.001267014	MUTYH | mutY (E. coli) homolog
787851	0.042347323	Homo sapiens PRO2893 mRNA, complete cds
825659	0.006087414	NDRG1 | N-myc downstream regulated
22917	0.013187912	Homo sapiens mRNA; cDNA DKFZp761M0111 (from clone DKFZp761M0111)
1593829	0.044484074	TIA1 | TIA1 cytotoxic granule-associated RNA-binding protein

111120	7.01E-06	KIAA0063 | KIAA0063 gene product
810958	0.004710677	CPNE1 | copine I
950096	0.004536135	ARCN1 | archain 1
853066	0.003225295	CNAP1 | chromosome condensation-related SMC-associated protein 1
292936	4.65E-06	FLJ10468 | hypothetical protein FLJ10468
701481	0.003482886	MX2 | myxovirus (influenza) resistance 2, homolog of murine
897997	0.04142324	SMC1L1 | SMC1 (structural maintenance of chromosomes 1, yeast)-like 1
136399	3.96E-05	DKFZP586F2423 | hypothetical protein DKFZp586F2423
752837	4.76E-08	Homo sapiens mRNA for FLJ00074 protein, partial cds
278650-2	0.015052222	PPP1R8 | protein phosphatase 1, regulatory (inhibitor) subunit 8
809627	0.000137744	NRIP1 | nuclear receptor interacting protein 1
787860	2.92E-08	ESTs
183468	7.58E-08	EGFR | epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)
416676	2.51E-09	PELI1 | pellino (Drosophila) homolog 1
323522	8.66E-06	NRBP | nuclear receptor binding protein
49794	0.005649538	LOC51700 | cytochrome b5 reductase b5R.2
278504	0.036283521	KIAA0607 | neurochondrin
951048	0.009825328	DKFZP434K046 | hypothetical protein DKFZp434K046
460403	0.006497654	LAMC2 | laminin, gamma 2 (nicein (100kD), kalinin (105kD), BM600 (100kD), Herlitz junctional epidermolysis bullosa))
124246	0.044429786	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C WARNING ENTRY !!! [H.sapiens]
505836	0.00219195	ESTs, Moderately similar to reduced expression in cancer [H.sapiens]
796694	0.00244749	BIRC5 | baculoviral IAP repeat-containing 5 (survivin)
811918	0.002709516	KIAA0952 | KIAA0952 protein
1556545	0.012132745	Homo sapiens, Similar to RIKEN cDNA 2600001B17 gene, clone IMAGE:2822298, mRNA, partial cds
704045	4.14E-09	MGC4126 | hypothetical protein MGC4126
1856063	0.013677014	TTYH1 | tweety (Drosophila) homolog 1
276915	1.29E-05	DNMT3B | DNA (cytosine-5-)-methyltransferase 3 beta
211800	0.005621271	KIAA0833 | KIAA0833 protein
232789	0.021224486	POLR2J | polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)
277579	0.008167816	ESTs
813520	0.000287377	EPHB3 | EphB3

486626	0.0454965	Homo sapiens, clone IMAGE:4332938, mRNA
882515	0.001000384	EIF3S9 | eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD)
429799	0.031044349	FLJ21939 | hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2
1569658	0.006181327	ESTs
1474900	0.043509438	KRT15 | keratin 15
810983	0.001630467	DKFZP434H132 | DKFZP434H132 protein
308163	0.018779849	ESTs, Weakly similar to TRHY_HUMAN TRICHOHYALI [H.sapiens]
839736	7.03E-08	CRYAB | crystallin, alpha B
1899263	0.04697029	FLJ20113 | hypothetical protein FLJ20113
1536236	1.53E-14	FLJ13154 | hypothetical protein FLJ13154
124261	0.010467742	SNRP70 | small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen)
2018154	4.91E-07	ETFB | electron-transfer-flavoprotein, beta polypeptide
67741	0.000180391	PP2135 | PP2135 protein
266085	0.0003394	KHSRP | KH-type splicing regulatory protein (FUSE binding protein 2)
825695	0.004394757	HSPC111 | hypothetical protein
809657	0.013236102	Homo sapiens cDNA FLJ31373 fis, clone NB9N42000342
110507	0.000223108	ESTs, Weakly similar to T46471 hypothetical protein DKFZp434L0130.1 [H.sapiens]
724387	0.012976841	SNRPC | small nuclear ribonucleoprotein polypeptide C
855786	0.002192122	WARS | tryptophanyl-tRNA synthetase
259950	1.91E-05	CML66 | chronic myelogenous leukemia tumor antigen 66
1899274	0.00024151	EGLN2 | EGL nine (C.elegans) homolog 2
23903	0.020116819	Homo sapiens clone 23903 mRNA sequence
302292	0.005746627	EXT2 | exostoses (multiple) 2
815142	0.000812059	SACS | spastic ataxia of Charlevoix-Saguenay (sacsin)
505864	0.000602202	RGL | RalGDS-like gene
325160	1.02E-11	NP25 | neuronal protein
1868534	3.65E-05	MGC2408 | hypothetical protein MGC2408
376515	0.00998974	FLJ10416 | similar to constitutive photomorphogenic protein 1 (Arabidopsis)
136722	1.06E-05	ATP1B3 | ATPase, Na+/K+ transporting, beta 3 polypeptide
284022	0.001908121	ARHGEF10 | Rho guanine nucleotide exchange factor (GEF) 10
2010684	0.009238649	KIAA0640 | SWAP-70 protein
1739821	0.022220862	LOC83690 | CocoaCrisp

<table>
<tr><td>1618987</td><td>0.008755709</td><td>RLBP1 | retinaldehyde-binding protein 1</td></tr>
<tr><td>282428</td><td>0.003858041</td><td>Homo sapiens, Similar to RIKEN cDNA 9030409E16 gene, clone MGC:26939 IMAGE:4796761, mRNA, complete cds</td></tr>
<tr><td>1607482</td><td>5.44E-05</td><td>CEBPG | CCAAT/enhancer binding protein (C/EBP), gamma</td></tr>
<tr><td>123627</td><td>0.012829341</td><td>P5 | protein disulfide isomerase-related protein</td></tr>
<tr><td>1606829</td><td>0.005336709</td><td>HDAC4 | histone deacetylase 4</td></tr>
<tr><td>81409</td><td>0.016588172</td><td>GABARAPL1 | GABA(A) receptor-associated protein like 1</td></tr>
<tr><td>340558</td><td>0.000227672</td><td>ARPC5 | actin related protein 2/3 complex, subunit 5 (16 kD)</td></tr>
<tr><td>1635970</td><td>1.87E-07</td><td>MFHAS1 | malignant fibrous histiocytoma amplified sequence 1</td></tr>
<tr><td>454970</td><td>7.09E-05</td><td>HAIK1 | type I intermediate filament cytokeratin</td></tr>
<tr><td>198509</td><td>0.034037336</td><td>NUDEL | LIS1-interacting protein NUDEL; endooligopeptidase A</td></tr>
<tr><td>51328</td><td>0.000752302</td><td>CDC34 | cell division cycle 34</td></tr>
<tr><td>41565</td><td>0.004757679</td><td>MYCN | v-myc avian myelocytomatosis viral related oncogene, neuroblastoma derived</td></tr>
<tr><td>1691868</td><td>0.000858947</td><td>PTX3 | pentaxin-related gene, rapidly induced by IL-1 beta</td></tr>
<tr><td>505881</td><td>0.006498381</td><td>ADA | adenosine deaminase</td></tr>
<tr><td>813560</td><td>0.002137013</td><td>TRN-SR | transportin-SR</td></tr>
<tr><td>505882</td><td>0.023035247</td><td>FLJ20550 | hypothetical protein FLJ20550</td></tr>
<tr><td>469686</td><td>5.61E-06</td><td>RIT | Ric (Drosophila)-like, expressed in many tissues</td></tr>
<tr><td>1493527</td><td>2.33E-05</td><td>ASNS | asparagine synthetase</td></tr>
<tr><td>325182</td><td>0.027251157</td><td>CDH2 | cadherin 2, type 1, N-cadherin (neuronal)</td></tr>
<tr><td>784589</td><td>0.008673574</td><td>MMP15 | matrix metalloproteinase 15 (membrane-inserted)</td></tr>
<tr><td>2579848</td><td>0.016470796</td><td>CHRAC1 | chromatin accessibility complex 1</td></tr>
<tr><td>854079</td><td>0.024580007</td><td>ACTN1 | actinin, alpha 1</td></tr>
<tr><td>344854</td><td>2.86E-06</td><td>ANKRD3 | ankyrin repeat domain 3</td></tr>
<tr><td>809696</td><td>0.0324664</td><td>DDX38 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 38</td></tr>
<tr><td>725365</td><td>0.015956866</td><td>GAS1 | growth arrest-specific 1</td></tr>
<tr><td>713202</td><td>0.00119998</td><td>HSU79252 | hypothetical protein</td></tr>
<tr><td>1723400</td><td>0.000511825</td><td>ESTs</td></tr>
<tr><td>950451</td><td>0.015225688</td><td>MGC10818 | hypothetical protein MGC10818</td></tr>
<tr><td>844601</td><td>0.00263797</td><td>CCKBR | cholecystokinin B receptor</td></tr>
<tr><td>502558</td><td>0.010898808</td><td>Homo sapiens, Similar to RIKEN cDNA 1110060O18 gene, clone MGC:17236 IMAGE:3864137, mRNA, complete cds</td></tr>
</table>

811976	0.002743023	Homo sapiens cDNA FLJ10071 fis, clone HEMBA1001702
587992	0.000692211	MGC5350 | hypothetical protein MGC5350
795309	1.99E-05	SOD3 | superoxide dismutase 3, extracellular
486683	0.001570786	Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323)
768561	0.006003565	SCYA2 | small inducible cytokine A2 (monocyte chemotactic protein 1, homologous to mouse Sig-je)
756401	0.008336499	RHEB2 | Ras homolog enriched in brain 2
756405	0.014632388	ID3 | inhibitor of DNA binding 3, dominant negative helix-loop-helix protein
144924	0.001209009	C6orf5 | chromosome 6 open reading frame 5
768569	0.038661233	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1517766
1688953	1.02E-07	ESTs
144926	0.012004594	MGC3133 | hypothetical protein MGC3133
594428	0.038751321	SEC3 | Sec3-like
770848	0.00619877	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
429065	0.00025476	ANKH | ankylosis, progressive (mouse) homolog
1933127	4.99E-05	CX46.6 | connexin46.6
1551675	0.002246831	Homo sapiens cDNA FLJ13903 fis, clone THYRO1001854
30093	3.59E-07	RANBP1 | RAN binding protein 1
768571	2.06E-05	SOX8 | SRY (sex determining region Y)-box 8
252382	0.004755604	TM4SF6 | transmembrane 4 superfamily member 6
1493557	0.014557615	PRP18 | pre-mRNA processing factor 18
144932	6.88E-09	CDK2AP1 | CDK2-associated protein 1
705064	0.028746951	TACC3 | transforming, acidic coiled-coil containing protein 3
391949	7.81E-05	SH2D2A | SH2 domain protein 2A
1688965	0.016029967	Homo sapiens mRNA for putative NSE1 protein
361861	0.000352001	PCBP4 | poly(rC)-binding protein 4
142259	0.001096449	FIP2 | tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains; Huntingtin interacting protein L; transcrption factor IIIA-interacting protein
131839	0.000190493	FOLR1 | folate receptor 1 (adult)
130892	0.000109361	EHD3 | EH-domain containing 3
2252417	0.004138974	RPS10 | ribosomal protein S10
298122	0.003448915	FZD7 | frizzled (Drosophila) homolog 7

725390	2.24E-09	GSTP1 | glutathione S-transferase pi
2308263	0.015071436	FDXR | ferredoxin reductase
153760	4.24E-05	EPHB1 | EphB1
713238	0.000107772	MONDOA | KIAA0867 protein
250797	0.034063029	FLJ20038 | hypothetical protein FLJ20038
126221	0.001359734	TPD52L2 | tumor protein D52-like 2
898249	0.001409555	ESTs
129569	0.000115962	HSPC049 | HSPC049 protein
2115545	7.00E-05	ADCY7 | adenylate cyclase 7
269787	0.027049095	L1CAM | L1 cell adhesion molecule (hydrocephalus, stenosis of aqueduct of Sylvius 1, MASA (mental retardation, aphasia, shuffling gait and adducted thumbs) syndrome, spastic paraplegia 1)
246120	0.008472265	HRMT1L2 | HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2
415326	0.023366836	ESTs
868169	0.000993361	LPL | lipoprotein lipase
1903066	7.49E-07	KRTHB1 | keratin, hair, basic, 1
306933	0.036825	Homo sapiens clone 25012 mRNA sequence
773419	0.002212104	ESTs
758037	0.001366354	HIVEP1 | human immunodeficiency virus type I enhancer-binding protein 1
308539	0.001531987	Homo sapiens cDNA FLJ12777 fis, clone NT2RP2001720
1469377	9.20E-06	LHFPL2 | lipoma HMGIC fusion partner-like 2
898258	0.014789221	CHN1 | chimerin (chimaerin) 1
841308	2.88E-07	MYLK | myosin, light polypeptide kinase
815501	2.47E-08	MGC2721 | hypothetical protein MGC2721
208969	0.000183624	EST
814562	0.003359378	ABT1 | TATA-binding protein-binding protein
204686	0.015480089	FXYD1 | FXYD domain-containing ion transport regulator 1 (phospholemman)
491545	0.001014724	KIAA0965 | KIAA0965 protein
261518	2.50E-06	FLJ20287 | hypothetical protein FLJ20287
154720	0.04010901	ARD1 | N-acetyltransferase, homolog of S. cerevisiae ARD1
859359	5.91E-05	PIG3 | quinone oxidoreductase homolog
2306682	0.028235912	AKAP9 | A kinase (PRKA) anchor protein (yotiao) 9
756442	0.000637212	POR | P450 (cytochrome) oxidoreductase

1388395	0.013736819	ELK1 | ELK1, member of ETS oncogene family
770880	0.000953714	PRIM2A | primase, polypeptide 2A (58kD)
770884	0.00070891	TIP-1 | Tax interaction protein 1
788136	0.026617009	PDE4B | phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)
1639531	0.000121707	RAB27A | RAB27A, member RAS oncogene family
248829	0.000127033	LOX | lysyl oxidase
28140	0.009335762	Homo sapiens mRNA; cDNA DKFZp586F2224 (from clone DKFZp586F2224)
50743	0.038854573	TXNL2 | thioredoxin-like 2
884511	0.024982068	COX7B | cytochrome c oxidase subunit VIIb
41929	0.015950143	PICALM | phosphatidylinositol binding clathrin assembly protein
82434	0.021226526	EEF1G | eukaryotic translation elongation factor 1 gamma
1574594	0.000255461	MDK | midkine (neurite growth-promoting factor 2)
1031940	0.001333654	CAMP | cathelicidin antimicrobial peptide
898281	8.51E-05	FLNA | filamin A, alpha (actin-binding protein-280)
287749	9.83E-05	CDC7L1 | CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1
701115	1.56E-08	PRO2013 | hypothetical protein PRO2013
283461	0.009028782	FLJ13910 | hypothetical protein FLJ13910
188036	0.000166323	BPAG1 | bullous pemphigoid antigen 1 (230/240kD)
196992	0.00144083	AKR1C1 | aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)
150466	0.043662375	Homo sapiens cDNA FLJ14885 fis, clone PLACE1003711
760344	0.000228463	UMPS | uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)
841338	0.000233667	PRNPIP | prion protein interacting protein
509458	0.029325674	LOC57228 | hypothetical protein from clone 643
132828	0.004269143	DSCR1L2 | Down syndrome critical region gene 1-like 2
2015212	0.007053992	MRPS25 | mitochondrial ribosomal protein S25
742707	1.36E-05	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PRECURSOR [H.sapiens]
815534	0.000247752	ICAP-1A | integrin cytoplasmic domain-associated protein 1
344134	0.00261847	IGLL1 | immunoglobulin lambda-like polypeptide 1
795371	0.004029813	LSM5 | U6 snRNA-associated Sm-like protein
261541	2.09E-09	PRKCN | protein kinase C, nu

24958	1.98E-06	Homo sapiens mRNA; cDNA DKFZp434C2016 (from clone DKFZp434C2016)
66406	4.34E-09	ESTs, Highly similar to T47163 hypothetical protein DKFZp762E1312.1 [H.sapiens]
2316471	1.76E-05	DEDD | death effector domain-containing
22278	3.17E-05	FLJ20511 | hypothetical protein FLJ20511
844680	0.01394813	TRD@ | T cell receptor delta locus
1716265	0.001534143	WDR3 | WD repeat domain 3
278938	0.009614286	LOC51144 | steroid dehydrogenase homolog
177621	0.04563828	RXRB | retinoid X receptor, beta
1642496	0.00087773	MGC11266 | hypothetical protein MGC11266
796323	0.00106935	ADD3 | adducin 3 (gamma)
50768	6.93E-06	DKFZp667O2416 | hypothetical protein DKFZp667O2416
26566	1.26E-06	POMT1 | protein-O-mannosyltransferase 1
1461138	0.029910221	H4FG | H4 histone family, member G
130153	5.61E-06	SUPT5H | suppressor of Ty (S.cerevisiae) 5 homolog
190325	0.000121317	Homo sapiens mRNA; cDNA DKFZp434E235 (from clone DKFZp434E235)
2149968	8.36E-07	FZD9 | frizzled (Drosophila) homolog 9
767982	9.30E-07	Homo sapiens, clone IMAGE:4134852, mRNA, partial cds
51710	5.76E-07	Homo sapiens, clone IMAGE:3605655, mRNA
153025	0.00010788	LIF | leukemia inhibitory factor (cholinergic differentiation factor)
773469	0.037388104	PTGFRN | prostaglandin F2 receptor negative regulator
758088	8.07E-05	CALD1 | caldesmon 1
823715	0.035143688	TRIP-Br2 | transcriptional regulator interacting with the PHS-bromodomain 2
26578	0.012675854	PES1 | pescadillo (zebrafish) homolog 1, containing BRCT domain
815556	0.003550049	FLJ10430 | hypothetical protein FLJ10430
810612	0.013015797	S100A11 | S100 calcium-binding protein A11 (calgizzarin)
795395	0.037638089	MGC5306 | hypothetical protein MGC5306
182177	0.031563977	ADAM17 | a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)
155717	0.002588609	CD79B | CD79B antigen (immunoglobulin-associated beta)
897650	0.000154041	PUS1 | pseudouridylate synthase 1
825320	0.031634717	Homo sapiens, clone IMAGE:3355383, mRNA, partial cds
1705861	0.003557075	KLK1 | kallikrein 1, renal/pancreas/salivary

2055888	0.040566492	CENTG3 | centaurin, gamma 3
161998	0.017117327	FLJ23138 | hypothetical protein FLJ23138
265853	0.001192546	TEM8 | tumor endothelial marker 8
2325609	0.001089545	MCM7 | minichromosome maintenance deficient (S. cerevisiae) 7
774420	0.011363913	LMAN1 | lectin, mannose-binding, 1
324927	0.00185329	KIAA0375 | KIAA0375 gene product
151449	9.30E-05	PTPN21 | protein tyrosine phosphatase, non-receptor type 21
753162	0.005108161	KIAA0603 | KIAA0603 gene product
897669	0.025225569	PRKCSH | protein kinase C substrate 80K-H
2017930	0.020336469	KIP2 | DNA-dependent protein kinase catalytic subunit-interacting protein 2
50794	0.011154216	ZNF133 | zinc finger protein 133 (clone pHZ-13)
530359	0.013769878	FNTA | farnesyltransferase, CAAX box, alpha
785933	0.003257805	SRPX | sushi-repeat-containing protein, X chromosome
731241	0.01978529	MPST | mercaptopyruvate sulfurtransferase
61500	1.32E-08	HLF | hepatic leukemia factor
248886	0.020116819	RAB3-GAP150 | rab3 GTPase-activating protein, non-catalytic subunit (150kD)
1416782	0.015739275	CKB | creatine kinase, brain
154790	0.038568449	NGFR | nerve growth factor receptor (TNFR superfamily, member 16)
969843	2.51E-09	ESTs, Weakly similar to LKHU proteoglycan link protein precursor [H.sapiens]
2062329	1.54E-08	TTK | TTK protein kinase
1323636	0.001297059	MGAT1 | mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
27544	4.45E-11	PROML1 | prominin (mouse)-like 1
825343	0.015128158	Homo sapiens, clone MGC:15887 IMAGE:3530481, mRNA, complete cds
41987	3.24E-06	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 966164
812244	0.00582367	CKLF1 | chemokine-like factor 1
2321341	5.72E-06	PGC | progastricsin (pepsinogen C)
1698036	0.030089117	UBE2V1 | ubiquitin-conjugating enzyme E2 variant 1
855438	0.013975654	ATP6S14 | ATPase, vacuolar, 14 kD
774446	0.000137487	ADM | adrenomedullin
626068	0.025636692	XPOT | exportin, tRNA (nuclear export receptor for tRNAs)
36374	0.008011127	CCNB1 | cyclin B1
69002	0.000262283	ANGPTL4 | angiopoietin-like 4

531319	6.30E-08	STK12 | serine/threonine kinase 12
1704155	0.046542451	IER5 | immediate early response 5
753184	0.003943783	SOX9 | SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal)
2032251	0.000446292	ESTs
34778	0.001089665	VEGF | vascular endothelial growth factor
264146	0.008936352	FLJ13194 | hypothetical protein FLJ13194
812256	0.01030915	Homo sapiens cDNA: FLJ21693 fis, clone COL09609
509800	0.008621514	CASK | calcium/calmodulin-dependent serine protein kinase (MAGUK family)
712683	0.000116468	NCK1 | NCK adaptor protein 1
2020898	0.012093702	PLOD3 | procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3
1597813	0.001549458	PP1044 | hypothetical protein PP1044
359982	0.008864958	BNIP3 | BCL2/adenovirus E1B 19kD-interacting protein 3
1674521	0.026617009	EST
41208	3.23E-05	BMP1 | bone morphogenetic protein 1
486304	5.01E-05	RASAL2 | RAS protein activator like 2
2017960	0.001121595	PP1201 | PP1201 protein
788507	0.046423899	ESTs, Weakly similar to LIN1_HUMAN LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]
327506	0.000554961	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 327506
753198	4.39E-09	JPO1 | c-Myc target JPO1
769921	6.30E-05	UBE2C | ubiquitin-conjugating enzyme E2C
201727	0.000831262	BCL6 | B-cell CLL/lymphoma 6 (zinc finger protein 51)
2262296	0.012689251	MUC6 | mucin 6, gastric
1568391	4.48E-10	PLS3 | plastin 3 (T isoform)
785963	0.00019309	KIAA0191 | KIAA0191 protein
431759	0.043544579	TEAD3 | TEA domain family member 3
785967	0.001744131	EPB41L2 | erythrocyte membrane protein band 4.1-like 2
731279	0.015827676	HRB | HIV-1 Rev binding protein
28510	0.000923428	CNTN2 | contactin 2 (axonal)
838478	0.000657157	NCALD | neurocalcin delta
36393	0.003553426	ACAT2 | acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)
788511	0.022786019	RPS6KA1 | ribosomal protein S6 kinase, 90kD, polypeptide 1
259627	4.41E-05	KIAA1126 | KIAA1126 protein

840753	0.00460254	SCYA5 | small inducible cytokine A5 (RANTES)
795730	0.000182825	EFS2 | signal transduction protein (SH3 containing)
281145	0.006338467	AOC2 | amine oxidase, copper containing 2 (retina-specific)
1894005	0.044484074	FLJ12615 | hypothetical protein FLJ12615 similar to membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 5)
823775	0.000549733	GNAI3 | guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3
774471	0.000851455	LAMB1 | laminin, beta 1
454632	7.14E-08	KIAA0481 | KIAA0481 gene product
323238	3.88E-05	GRO1 | GRO1 oncogene (melanoma growth stimulating activity, alpha)
950897	0.001851412	Homo sapiens mRNA; cDNA DKFZp586G1922 (from clone DKFZp586G1922)
878330	0.037388104	Homo sapiens cDNA: FLJ22044 fis, clone HEP09141
755891	0.002132318	KIAA0317 | KIAA0317 gene product
3172883	0.002068426	ESTs, Weakly similar to S24195 dopamine receptor D4 [H.sapiens]
358267	4.15E-05	ESTs, Moderately similar to AF119917 63 PRO2831 [H.sapiens]
230882	1.51E-06	PAX6 | paired box gene 6 (aniridia, keratitis)
754157	3.44E-05	Homo sapiens mRNA; cDNA DKFZp434K2172 (from clone DKFZp434K2172)
1915913	0.006354505	CLIC2 | chloride intracellular channel 2
788524	0.040583119	HSPC156 | HSPC156 protein
282895	0.025901698	FLJ20048 | hypothetical protein FLJ20048
795746	0.036395976	Homo sapiens cDNA FLJ33167 fis, clone UTERU2000569
1608898	1.20E-08	JRKL | jerky (mouse) homolog-like
71312	0.000227672	UACA | uveal autoantigen with coiled-coil domains and ankyrin repeats
162208	0.004091636	ARPC2 | actin related protein 2/3 complex, subunit 2 (34 kD)
160609	0.000448621	ESTs, Weakly similar to ALUA_HUMAN !!!! ALU CLASS A WARNING ENTRY !!! [H.sapiens]
136409	0.000809442	DKFZp547A023 | hypothetical protein DKFZp547A023
1572298	0.046169524	CD3Z | CD3Z antigen, zeta polypeptide (TiT3 complex)
460126	8.06E-07	KIAA0819 | KIAA0819 protein
1049291	0.004674543	OR7E47P | olfactory receptor, family 7, subfamily E, member 47 pseudogene
489677	0.000218116	UP | uridine phosphorylase
814970	0.000351004	ELOVL1 | elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1
795757	6.07E-05	FLJ11896 | hypothetical protein FLJ11896
795758	0.001312689	DKFZP434B044 | hypothetical protein DKFZp434B044

1486770	0.001073614	FLJ10569 | hypothetical protein FLJ10569
812294	0.001477658	ESTs
784257	0.001547684	KIF3C | kinesin family member 3C
769959	2.17E-06	COL4A2 | collagen, type IV, alpha 2
843321	2.31E-05	KRT7 | keratin 7
1350439	1.82E-11	KIAA0015 | KIAA0015 gene product
767277	1.69E-05	PPIH | peptidyl prolyl isomerase H (cyclophilin H)
2018941	2.34E-06	D21S2056E | DNA segment on chromosome 21 (unique) 2056 expressed sequence
1755555	0.001985435	MAP3K6 | mitogen-activated protein kinase kinase kinase 6
840788	0.008900276	TMSB10 | thymosin, beta 10
814989	0.001107206	PPM1G | protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform
172785	0.001708977	LOC51754 | NAG-5 protein
1608120	0.0041899	AIB3 | nuclear receptor coactivator RAP250; peroxisome proliferator-activated receptor interacting protein; thyroid hormone receptor binding protein
767289	0.038751321	KIAA1001 | KIAA1001 protein
1926364	0.000305567	RBM9 | RNA binding motif protein 9
346134	0.024280742	CRHSP-24 | calcium-regulated heat-stable protein (24kD)
824753	0.000389422	FLJ22624 | hypothetical protein FLJ22624
212198	3.41E-06	TP53BP2 | tumor protein p53-binding protein, 2
813256	5.48E-07	ABCB1 | ATP-binding cassette, sub-family B (MDR/TAP), member 1
1902841	0.001271788	SLC16A7 | solute carrier family 16 (monocarboxylic acid transporters), member 7
415766	8.23E-06	KIAA1357 | KIAA1357 protein
562409	0.022876597	NDUFS5 | NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase)
48886	0.037983017	MRC1 | mannose receptor, C type 1
713685	1.49E-06	PRSS2 | protease, serine, 2 (trypsin 2)
233464	2.63E-06	EVA1 | epithelial V-like antigen 1
2010393	0.001127212	FTSJ1 | FtsJ homolog 1 (E. coli)
826363	3.96E-05	LYPLA2 | lysophospholipase II
726791	0.016588172	EST00098 | hypothetical protein EST00098
788568	0.003344334	ARHGEF7 | Rho guanine nucleotide exchange factor (GEF) 7
813265	4.16E-05	Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone DKFZp564H1916)
289760	0.000134622	ESTs, Highly similar to T00391 hypothetical protein KIAA0612 [H.sapiens]

768246	0.000180794	Homo sapiens cDNA FLJ30869 fis, clone FEBRA2004224
783629	0.002812591	HUMAUANTIG | nucleolar GTPase
2322367	2.80E-05	RTN4 | reticulon 4
837870	0.001262114	PRELP | proline arginine-rich end leucine-rich repeat protein
1690915	0.005767924	ESTs
220372	0.000449552	HS3ST1 | heparan sulfate (glucosamine) 3-O-sulfotransferase 1
140328	0.000370802	ESTs
361539	0.002866566	Homo sapiens sortilin 1 (SORT1), mRNA
84464	0.00852718	FLJ12806 | hypothetical protein FLJ12806
2018976	0.000159096	PTTG1 | pituitary tumor-transforming 1
235080	0.000566403	PDGFRA | platelet-derived growth factor receptor, alpha polypeptide
307255	1.71E-06	ICB-1 | basement membrane-induced gene
154093	8.41E-06	CIR | CBF1 interacting corepressor
138059	0.017914037	FLJ20374 | hypothetical protein FLJ20374
363146	0.002345896	PPP3R1 | protein phosphatase 3 (formerly 2B), regulatory subunit B (19kD), alpha isoform (calcineurin B, type I)
1704527	4.34E-05	BCRP2 | Breakpoint cluster region protein, uterine leiomyoma, 2
150897	7.05E-06	B3GNT3 | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3
504940	0.00048204	ESTs
267859	0.000661605	LOC51256 | hypothetical protein
813280	0.000241441	ADSL | adenylosuccinate lyase
1649746	0.039806156	ESTs
725076	0.002237924	NT5B | 5'-nucleotidase (purine), cytosolic type B
236034	0.036288061	UCP2 | uncoupling protein 2 (mitochondrial, proton carrier)
754509	0.000164308	MET | met proto-oncogene (hepatocyte growth factor receptor)
31818	0.003705111	Homo sapiens clone 23700 mRNA sequence
220395	3.49E-09	FLJ23293 | likely ortholog of mouse ADP-ribosylation-like factor 6 interacting protein 2
796759	0.03681114	VDAC3 | voltage-dependent anion channel 3
768271	7.84E-07	Homo sapiens cDNA FLJ11436 fis, clone HEMBA1001213
951117	0.000316188	SHMT2 | serine hydroxymethyltransferase 2 (mitochondrial)
731648	0.019893343	NFYA | nuclear transcription factor Y, alpha
135811	2.09E-09	DEPP | decidual protein induced by progesterone

1631711	0.000920277	EST
51063	0.002903498	ESTs
824001	0.003653268	FLJ10342 | hypothetical protein FLJ10342
825740	0.043917654	DKFZP434J1813 | DKFZp434J1813 protein
530761	0.007489303	ADSS | adenylosuccinate synthase
266135	0.016029967	ESTs, Highly similar to S21424 nestin [H.sapiens]
1509540	0.003570072	HRH1 | histamine receptor H1
796767	0.00038577	DKFZP564D0764 | DKFZP564D0764 protein
344588	0.004877897	KLK5 | kallikrein 5
155064	0.015807797	USP13 | ubiquitin specific protease 13 (isopeptidase T-3)
592540	0.001362977	KRT5 | keratin 5 (epidermolysis bullosa simplex, Dowling-Meara/Kobner/Weber-Cockayne types)
624867	0.000152832	FLJ20186 | hypothetical protein FLJ20186
214131	0.00084937	NIT2 | Nit protein 2
1854539	5.38E-06	SAM68 | GAP-associated tyrosine phosphoprotein p62 (Sam68)
51078	8.56E-06	ESTs, Weakly similar to JC5314 CDC28/cdc2-like kinase associating arginine-serine cyclophilin [H.sapiens]
1659533	6.94E-09	MATN4 | matrilin 4
42258	0.008593378	ESTs, Weakly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens]
843398	0.042747042	BMP2 | bone morphogenetic protein 2
32493	2.00E-05	ITGA6 | integrin, alpha 6
1671299	0.000270513	HRK | harakiri, BCL2-interacting protein (contains only BH3 domain)
757873	5.86E-06	CDK5R1 | cyclin-dependent kinase 5, regulatory subunit 1 (p35)
770579	0.034946932	CLDN3 | claudin 3
665384	1.40E-09	KIAA1609 | KIAA1609 protein
877772	7.08E-10	MRAS | muscle RAS oncogene homolog
813609	1.83E-05	MP1 | metalloprotease 1 (pitrilysin family)
122739	0.005245158	FLJ21918 | hypothetical protein FLJ21918
783681	0.024373058	UREB1 | upstream regulatory element binding protein 1
289027	0.029539479	Homo sapiens cDNA FLJ31413 fis, clone NT2NE2000259, moderately similar to OOCYTE ZINC FINGER PROTEIN XLCOF6.1
52031	0.005871121	ESTs
243295	0.000174047	DKFZP434J154 | DKFZP434J154 protein

376298	0.008888435	CGI-203 | CGI-203 protein
770588	0.047831695	Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds
815214	7.86E-05	CHI3L2 | chitinase 3-like 2
2016632	0.028295772	ESTs, Moderately similar to T00359 hypothetical protein KIAA0680 [H.sapiens]
131563	4.01E-05	Homo sapiens cDNA FLJ13443 fis, clone PLACE1002853
254004	0.047241769	LOC51639 | CGI-110 protein
814270	0.000160656	PMSCL1 | polymyositis/scleroderma autoantigen 1 (75kD)
1468431	4.32E-05	LOC131601 | seven transmembrane domain orphan receptor
783698	3.71E-07	LPIN1 | lipin 1
504201	0.014811257	Homo sapiens, clone IMAGE:3677194, mRNA, partial cds
248531	4.67E-07	GMPS | guanine monphosphate synthetase
108316	0.004877897	RAB3IL1 | RAB3A interacting protein (rabin3)-like 1
200402	0.001715387	DJ616B8.3 | hypothetical protein dJ616B8.3
1610490	1.12E-05	CSNK1D | casein kinase 1, delta
813629	0.001013874	YME1L1 | YME1 (S.cerevisiae)-like 1
377252	5.60E-06	ADORA2B | adenosine A2b receptor
49117	0.010535254	KIAA0215 | KIAA0215 gene product
377253	0.003016551	FLJ14728 | hypothetical protein FLJ14728
366830	0.006482896	ESTs
855872	0.035143688	NRD1 | nardilysin (N-arginine dibasic convertase)
366834	0.021925399	EVPL | envoplakin
1686314	3.96E-09	Homo sapiens cDNA FLJ31627 fis, clone NT2RI2003338
755506	0.020241721	ANXA4 | annexin A4
756163	0.003928565	BCR | breakpoint cluster region
1642186	0.009231307	DPH2L2 | diptheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)-like 2
1552374	0.000107772	PLSCR3 | phospholipid scramblase 3
428163	0.04294858	ESTs, Weakly similar to NAH6_HUMAN SODIUM/HYDROGEN EXCHANGER 6 [H.sapiens]
1604220	0.000124487	LRPPRC | leucine-rich PPR-motif containing
280907	0.001755052	LOC57209 | Kruppel-type zinc finger protein
815235	0.000153521	RCD-8 | autoantigen
1541958	0.001831779	POU2AF1 | POU domain, class 2, associating factor 1
239724	0.000451254	Homo sapiens mRNA; cDNA DKFZp667B0711 (from clone DKFZp667B0711)

272748	0.001611957	D1S155E | NRAS-related gene
1868626	0.033272185	PFKL | phosphofructokinase, liver
814297	0.002489422	PEPD | peptidase D
768619	0.016678558	Homo sapiens cDNA FLJ32643 fis, clone SYNOV2001212
950516	0.007644628	CNNM4 | cyclin M4
80549	0.02497657	PBX2 | pre-B-cell leukemia transcription factor 2
51408	0.00712188	DSCR1L1 | Down syndrome critical region gene 1-like 1
366848	3.47E-08	ESTs
825005	1.29E-05	IPLA2(GAMMA) | intracellular membrane-associated calcium-independent phospholipase A2 gamma
739193	0.002561152	CRABP1 | cellular retinoic acid-binding protein 1
301735	0.039966603	TGM3 | transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase)
358689	0.039496567	EPHB2 | EphB2
2030301	0.017481981	SLIT3 | slit (Drosophila) homolog 3
1550783	0.009173647	CHORDC1 | cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1
824068	0.047848128	COX5A | cytochrome c oxidase subunit Va
345586	0.003770645	TNFRSF12 | tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein)
813645	0.000248914	FLJ20500 | hypothetical protein
741474	4.08E-06	GPI | glucose phosphate isomerase
502625	0.000483976	FLJ21212 | hypothetical protein FLJ21212
180263	0.005375632	KIAA0537 | KIAA0537 gene product
377275	5.69E-15	TRIM29 | tripartite motif-containing 29
127510-2	7.79E-05	CDC25A | cell division cycle 25A
41650	0.044529607	HGF | hepatocyte growth factor (hepapoietin A; scatter factor)
2019214	0.00105118	CAD | carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase
281580	0.035143688	ESTs
842794	2.57E-05	KIAA1668 | KIAA1668 protein
841057	1.17E-05	MAGE-E1 | MAGE-E1 protein
530036	0.007079545	FLJ13078 | hypothetical protein FLJ13078
813651	0.000139851	ALAS1 | aminolevulinate, delta-, synthase 1
2308314	0.016063781	KIAA1055 | KIAA1055 protein
785616	0.005985046	SSR1 | signal sequence receptor, alpha (translocon-associated protein alpha)

2604635	0.001601276	YAP1 | Yes-associated protein 1, 65 kDa
50483	0.001534143	FBLN5 | fibulin 5
1509904	0.020270563	PTGS2 | prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)
809784	1.53E-05	KLK6 | kallikrein 6 (neurosin, zyme)
725454	0.010208539	CKS2 | CDC28 protein kinase 2
490649	3.45E-05	MCCC1 | methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)
146605	0.012998471	FPRL1 | formyl peptide receptor-like 1
773183	9.02E-05	AF093680 | similar to mouse Glt3 or D. malanogaster transcription factor IIB
845355	0.038531356	CTSC | cathepsin C
1570339	1.02E-06	Homo sapiens, clone IMAGE:3948909, mRNA, partial cds
83120	0.000644819	RBM10 | RNA binding motif protein 10
753946	0.001034397	HKE2 | HLA class II region expressed gene KE2
744047	0.000853947	PLK | polo (Drosophia)-like kinase
814617	0.001106068	MEF2A | MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A)
813671	7.06E-05	ESTs, Weakly similar to T31636 hypothetical protein Y57A10A.n - Caenorhabditis elegans [C.elegans]
815276	0.038667897	NUP62 | nucleoporin 62kD
813673	0.011252089	HDGF | hepatoma-derived growth factor (high-mobility group protein 1-like)
2018297	0.038531356	CTL2 | CTL2 gene
2009477	0.006324566	CD6 | CD6 antigen
2713047	0.000148737	PVR | poliovirus receptor
844703	7.67E-08	T-STAR | Sam68-like phosphotyrosine protein, T-STAR
703541	1.21E-05	KIAA1858 | KIAA1858 protein
2062028	0.001614105	ZNF259 | zinc finger protein 259
770935	0.000827726	7h3 | hypothetical protein FLJ13511
29927	0.012880496	FLJ10737 | hypothetical protein FLJ10737
42627	0.035383143	COCH | coagulation factor C (Limulus polyphemus homolog); cochlin
51448	0.00048184	ATF3 | activating transcription factor 3
133518	0.000238959	MAPRE2 | microtubule-associated protein, RP/EB family, member 2
1455394	2.92E-06	HCS | cytochrome c
1898758	0.011460543	BCE-1 | BCE-1 protein
36393-2	0.005878639	ACAT2 | acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)
815285	0.012980026	ERPROT213-21 | protein with polyglutamine repeat; calcium (ca2+) homeostasis endoplasmic reticulum

		protein
486787	0.001271197	CNN3 | calponin 3, acidic
626841	0.012861341	MET | met proto-oncogene (hepatocyte growth factor receptor)
2308346	0.027141267	CDK2 | cyclin-dependent kinase 2
756502	0.000554935	NUDT1 | nudix (nucleoside diphosphate linked moiety X)-type motif 1
502669	9.98E-06	HDAC2 | histone deacetylase 2
129644	0.003508671	SSH3BP1 | spectrin SH3 domain binding protein 1
898328	6.78E-07	EDR2 | early development regulator 2 (homolog of polyhomeotic 2)
756509	0.041594075	H105E3 | NAD(P) dependent steroid dehydrogenase-like; H105e3
745003	0.002269285	ZNF76 | zinc finger protein 76 (expressed in testis)
590242	0.000669517	ESTs
841091	0.000803586	FAF1 | Fas (TNFRSF6) associated factor 1
841093	0.000742995	CUL1 | cullin 1
345916	0.000621801	Homo sapiens mRNA; cDNA DKFZp564N1063 (from clone DKFZp564N1063)
1460224	0.006815479	ESTs, Weakly similar to I38133 protein kinase [H.sapiens]
379200	0.00041118	IRAK1 | interleukin-1 receptor-associated kinase 1
2009491	0.005321091	LOC51191 | cyclin-E binding protein 1
41698	0.00083009	PGRMC1 | progesterone receptor membrane component 1
2306752	0.000328235	STMN2 | stathmin-like 2
813698	0.009151254	SPRY2 | sprouty (Drosophila) homolog 2
898332	0.001879562	NPR1 | natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A)
856887	0.02806084	ESTs
1570364	0.005587928	FLJ21324 | hypothetical protein FLJ21324
950578	0.000159834	NDUFA5 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kD, B13)
745011	3.47E-05	KIAA1750 | KIAA1750 protein
178324	0.04004725	ESTs
280970	0.00148396	NOL1 | nucleolar protein 1 (120kD)
309161-2	0.001831364	TBX2 | T-box 2
788205	0.001756144	SOX4 | SRY (sex determining region Y)-box 4
755578	7.43E-08	SLC7A5 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
786605	8.78E-05	APG-1 | heat shock protein (hsp110 family)
123774	0.003147591	ESTs

83156	0.003569567	C6orf34 | chromosome 6 open reading frame 34
416075	0.003099407	TCF19 | transcription factor 19 (SC1)
773502	0.018979013	ESTs, Weakly similar to S65824 reverse transcriptase homolog [H.sapiens]
502682	0.037642103	ENIGMA | enigma (LIM domain protein)
502689	0.029859423	Homo sapiens clone HH409 unknown mRNA
309288	0.005363273	RFC4 | replication factor C (activator 1) 4 (37kD)
307687	0.000599469	PRSS16 | protease, serine, 16 (thymus)
44255	6.27E-06	MRPL3 | mitochondrial ribosomal protein L3
1926024	0.004189378	BCL2L12 | BCL2-like 12 (proline rich)
1160723	2.20E-05	LIMK2 | LIM domain kinase 2
85840	0.000112138	NNMT | nicotinamide N-methyltransferase
130201	0.000950305	ICAM2 | intercellular adhesion molecule 2
33837	0.004299371	KIAA1500 | KIAA1500 protein
530093	0.000479617	MPZL1 | myelin protein zero-like 1
1358393	0.0011328	MAP2K3 | mitogen-activated protein kinase kinase 3
282587	0.000754806	CA11 | carbonic anhydrase XI
502690	0.00352586	RPN1 | ribophorin I
626874	9.10E-08	FLJ23399 | hypothetical protein FLJ23399
853562	0.023644346	TRIM28 | tripartite motif-containing 28
782339	8.33E-05	PRKAB1 | protein kinase, AMP-activated, beta 1 non-catalytic subunit
162308-2	0.000128308	CYYR1 | cysteine and tyrosine-rich protein 1
366126	2.91E-05	KIAA0354 | KIAA0354 gene product
703581	0.034266941	PRG1 | proteoglycan 1, secretory granule
741831	0.02005317	PLTP | phospholipid transfer protein
825085	3.88E-07	ST14 | suppression of tumorigenicity 14 (colon carcinoma, matriptase, epithin)
814662	0.016952234	AP4B1 | adaptor-related protein complex 4, beta 1 subunit
1468820	0.004338248	NOS3 | nitric oxide synthase 3 (endothelial cell)
852913	0.033456546	SNRPF | small nuclear ribonucleoprotein polypeptide F
704532	0.000420604	NMI | N-myc (and STAT) interactor
245296	0.049442498	RAD52 | RAD52 (S. cerevisiae) homolog
1880757	0.006991988	MAP3K5 | mitogen-activated protein kinase kinase kinase 5
788234	4.76E-08	ID4 | inhibitor of DNA binding 4, dominant negative helix-loop-helix protein

741841	0.003707205	DDX11 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase)
211216	0.024810654	KLF1 | Kruppel-like factor 1 (erythroid)
360254	0.000831262	CYR61 | cysteine-rich, angiogenic inducer, 61
741842	0.000446292	LOC51690 | U6 snRNA-associated Sm-like protein LSm7
363597	0.000180473	C11orf8 | chromosome 11 open reading frame 8
726464	0.001854106	SPAG9 | sperm associated antigen 9
49502	0.0009273	CYLN2 | cytoplasmic linker 2
47900	0.006683198	KIAA1382 | amino acid transporter 2
529861	1.29E-05	PSMB6 | proteasome (prosome, macropain) subunit, beta type, 6
810391	0.016029967	HYAL1 | hyaluronoglucosaminidase 1
2322038	5.74E-07	COL4A6 | collagen, type IV, alpha 6
2012757	0.000801869	D2S448 | Melanoma associated gene
1632011	0.0039532	NPR2 | natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)
845709	1.35E-05	ESTs
470393	1.08E-05	MMP7 | matrix metalloproteinase 7 (matrilysin, uterine)
132911	0.001603821	PPP1CB | protein phosphatase 1, catalytic subunit, beta isoform
756556	0.008247752	SERPING1 | serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1
1635359	0.031634717	RASD1 | RAS, dexamethasone-induced 1
753215	4.53E-06	GNAI1 | guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1
738916	0.014632388	REV1L | REV1 (yeast homolog)- like
361204	1.64E-06	COL9A3 | collagen, type IX, alpha 3
1536727	0.022064191	MGC11324 | hypothetical protein MGC11324
2096458	4.36E-08	CALU | calumenin
869234	0.005357267	ESTs
739578	0.013280693	C4.4A | GPI-anchored metastasis-associated protein homolog
788247	0.020732026	CUL2 | cullin 2
430834	0.027276602	Homo sapiens, Similar to RIKEN cDNA 2810405F18 gene, clone MGC:22960 IMAGE:4865283, mRNA, complete cds
1639640	0.001388783	EIF5A | eukaryotic translation initiation factor 5A
564492	2.90E-05	MTCH2 | mitochondrial carrier homolog 2
244654	0.001763838	ELAC1 | elaC (E.coli) homolog 1
1574693	0.000601881	SLB | selective LIM binding factor, rat homolog

860013	0.024373058	MGC1136 | hypothetical protein MGC1136
897720	0.000629574	TRO | trophinin
137862	0.028270162	HIP-55 | src homology 3 domain-containing protein HIP-55
1635364	3.42E-06	LSM2 | U6 snRNA-associated Sm-like protein
1551030	0.031216746	CDA | cytidine deaminase
293328	0.000795582	C2orf2 | chromosome 2 open reading frame 2
1404396	0.000304786	PLCB3 | phospholipase C, beta 3 (phosphatidylinositol-specific)
292388	0.004770631	LOC55977 | hypothetical protein 24636
840493	0.006951821	RNASE1 | ribonuclease, RNase A family, 1 (pancreatic)
268188	0.000728707	PRRG1 | proline-rich Gla (G-carboxyglutamic acid) polypeptide 1
503671	2.23E-08	Homo sapiens cDNA FLJ14368 fis, clone HEMBA1001122
645495	0.014557615	BICD1 | Bicaudal D (Drosophila) homolog 1
80946	0.005577147	ABCE1 | ATP-binding cassette, sub-family E (OABP), member 1
1883327	0.015005389	Homo sapiens cDNA FLJ30999 fis, clone HLUNG1000110, weakly similar to PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR
897731	0.014470496	KIAA0786 | latrophilin
897732	5.30E-05	SAD1 | SnRNP assembly defective 1 homolog
1950274	0.025668592	ESTs
753236	0.000420604	ESTs, Weakly similar to S71512 hypothetical protein T2 - mouse [M.musculus]
1055581	0.038751321	DKFZP564K192 | likely ortholog of mouse dysbindin
344243	0.00041118	UMPK | uridine monophosphate kinase
788264	0.023178776	DPAGT1 | dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)
774502	0.031310371	PTPN12 | protein tyrosine phosphatase, non-receptor type 12
49532	8.13E-08	VIM | vimentin
1558675	2.00E-07	SOX10 | SRY (sex determining region Y)-box 10
308682	0.000155359	ABCF2 | ATP-binding cassette, sub-family F (GCN20), member 2
773564	0.000739744	NIN283 | nerve injury gene 283
2719303	0.015247808	SLC18A1 | solute carrier family 18 (vesicular monoamine), member 1
125722	0.003691973	DGUOK | deoxyguanosine kinase
509570	0.015704565	Homo sapiens cDNA: FLJ22656 fis, clone HSI07655
231574	0.048699543	FBI1 | HIV-1 inducer of short transcripts binding protein; lymphoma related factor

301061	0.000176121	COL18A1 | collagen, type XVIII, alpha 1
79629	0.011251927	CXCR4 | chemokine (C-X-C motif), receptor 4 (fusin)
344251	0.012443564	FLJ10783 | hypothetical protein FLJ10783
795499	0.010004815	NDRG4 | NDRG family, member 4
772912	0.02555164	AGS3 | likely ortholog of rat activator of G-protein signaling 3
156473	0.001838545	EPHX2 | epoxide hydrolase 2, cytoplasmic
772913	1.23E-11	Homo sapiens cDNA FLJ31951 fis, clone NT2RP7007177, weakly similar to Homo sapiens multiple membrane spanning receptor TRC8 mRNA
773571	2.09E-06	GTF3C3 | general transcription factor IIIC, polypeptide 3 (102kD)
630013	0.000293426	MSH2 | mutS (E. coli) homolog 2 (colon cancer, nonpolyposis type 1)
856167	8.78E-05	TARS | threonyl-tRNA synthetase
2322079	0.020096884	EST
1472754	0.019822944	COX6B | cytochrome c oxidase subunit VIb
756595	6.16E-05	S100A10 | S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))
50884	0.002936718	DYRK2 | dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2
509589	0.00458557	LOC51122 | HSPC042 protein
884657	0.036349025	TIMM8B | translocase of inner mitochondrial membrane 8 (yeast) homolog B
121454	0.004821899	ALOX12 | arachidonate 12-lipoxygenase
112636	1.36E-05	IL1RAP | interleukin 1 receptor accessory protein
2062415	1.01E-05	GMDS | GDP-mannose 4,6-dehydratase
135503	0.022046067	BRD4 | bromodomain-containing 4
2062418	0.034945258	AIM1 | absent in melanoma 1
843070	4.81E-05	NUP88 | nucleoporin 88kD
1759582	0.000276452	FN14 | type I transmembrane protein Fn14
50892	0.044429786	Homo sapiens, clone MGC:9913 IMAGE:3870821, mRNA, complete cds
566421	0.023116508	PIMT | PRIP-interacting protein with methyltransferase domain
841478	0.000244327	VIT1 | vitiligo-associated protein VIT-1
1860497	0.000102553	Homo sapiens, clone MGC:5352 IMAGE:3048106, mRNA, complete cds
418049	1.52E-06	Homo sapiens cDNA: FLJ21909 fis, clone HEP03834
855521	0.040241164	KRT18 | keratin 18
767312	0.040844999	PLD2 | phospholipase D2
235882	0.001352198	KIAA0709 | endocytic receptor (macrophage mannose receptor family)

306318	3.49E-06	ORC6L | origin recognition complex, subunit 6 (yeast homolog)-like
71087	0.022618851	MAFF | v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein F
840821	0.044848397	SSR4 | signal sequence receptor, delta (translocon-associated protein delta)
525926	6.55E-07	SDC1 | syndecan 1
1686766	9.44E-06	RAGD | Rag D protein
613056	0.005068207	RCN1 | reticulocalbin 1, EF-hand calcium binding domain
79655	0.003417271	MGC2722 | hypothetical protein MGC2722
489729	1.40E-07	ETS1 | v-ets avian erythroblastosis virus E26 oncogene homolog 1
2610539	0.005368978	KRT6B | keratin 6B
795805	0.001440423	KIAA0332 | KIAA0332 protein
841485	0.01354434	Homo sapiens cDNA FLJ31058 fis, clone HSYRA2000828
74713	0.00017506	FLJ20059 | hypothetical protein FLJ20059
753278	1.39E-05	CXCL16 | chemokine (C-X-C motif) ligand 16
796469	0.016508823	HSPC150 | HSPC150 protein similar to ubiquitin-conjugating enzyme
1613496	0.001928041	EST
430894	0.012480222	TLN1 | talin 1
1947381	0.000752302	FLJ22329 | hypothetical protein FLJ22329
2499237	0.000760968	SERPINB5 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5
321708	0.01621547	TFDP1 | transcription factor Dp-1
843091	0.000367291	MGC20533 | similar to RIKEN cDNA 2410004L22 gene (M. musculus)
588368	0.01394813	KIAA0947 | KIAA0947 protein
590640	7.53E-05	PDXK | pyridoxal (pyridoxine, vitamin B6) kinase
1519013	1.16E-06	Homo sapiens, clone IMAGE:3537447, mRNA, partial cds
823850	0.001603821	RAI14 | retinoic acid induced 14
357396	0.038563775	Homo sapiens cDNA: FLJ23137 fis, clone LNG08842
345234	0.002720745	ESTs, Weakly similar to T00705 N-chimerin homolog F25965_3 [H.sapiens]
753285	0.047573891	GYG | glycogenin
566443	6.48E-06	Homo sapiens cDNA FLJ12793 fis, clone NT2RP2002033
796475	2.49E-07	FHL3 | four and a half LIM domains 3
83549	0.000116498	C1R | complement component 1, r subcomponent
1637311	0.003072498	KIAA0036 | KIAA0036 gene product
810753	0.000438842	MRPS10 | mitochondrial ribosomal protein S10

41300	8.52E-05	Homo sapiens clones 24714 and 24715 mRNA sequence
1554727	0.005587928	HSF2 | heat shock transcription factor 2
743810	0.012831119	MGC2577 | hypothetical protein MGC2577
140071	0.011056053	FRZB | frizzled-related protein
726830	0.022786019	FLJ10748 | hypothetical protein FLJ10748
282977	0.039374425	ADCY2 | adenylate cyclase 2 (brain)
884690	0.001462177	CCT8 | chaperonin containing TCP1, subunit 8 (theta)
282978	0.000356685	TGFB2 | transforming growth factor, beta 2
823864	0.005015434	TCN2 | transcobalamin II; macrocytic anemia
415814	0.000792587	LOC56901 | NADH:ubiquinone oxidoreductase MLRQ subunit homolog
511107	0.005854823	CCT4 | chaperonin containing TCP1, subunit 4 (delta)
741139	0.000808096	EYA2 | eyes absent (Drosophila) homolog 2
323322	0.008351255	ESTs
810762	0.018133375	YKT6 | SNARE protein
49595	0.010562779	DKFZP434F091 | DKFZP434F091 protein
1637328	0.000165971	AOX1 | aldehyde oxidase 1
2062453	0.001470365	DKFZP727G051 | DKFZP727G051 protein
703972	0.002002869	KIAA0699 | KIAA0699 protein
669375	6.11E-06	DKK1 | dickkopf (Xenopus laevis) homolog 1
489755	0.001048773	ADAM12 | a disintegrin and metalloproteinase domain 12 (meltrin alpha)
611481	1.40E-06	TCF-3 | HMG-box transcription factor TCF-3
487071	0.000245994	GNRH1 | gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)
417424	0.000622484	ABP/ZF | Alu-binding protein with zinc finger domain
788617	9.28E-09	LOC91689 | hypothetical gene supported by AL449243
825478	0.010722629	ZNF146 | zinc finger protein 146
431869	0.017680318	Homo sapiens, clone IMAGE:3506202, mRNA, partial cds
897011	0.00140216	KIAA0842 | KIAA0842 protein
1910785	0.001443649	ATP11A | ATPase, Class VI, type 11A
813609-2	5.33E-06	MP1 | metalloprotease 1 (pitrilysin family)
284592	5.11E-11	DKFZp762A227 | hypothetical protein DKFZp762A227
788620	4.20E-05	Homo sapiens, clone MGC:17225 IMAGE:4151716, mRNA, complete cds
1837280	0.002741302	EST

504940-2	6.84E-05	ESTs
795841	0.000205324	FLJ14466 | hypothetical protein FLJ14466
345262	0.032131824	PCDHB2 | protocadherin beta 2
162308	0.000536545	CYYR1 | cysteine and tyrosine-rich protein 1
853977	0.000294844	ESTs
1534430	0.012397017	GUCY1B2 | guanylate cyclase 1, soluble, beta 2
450464	0.008351255	ACVR2 | activin A receptor, type II
142788	4.92E-08	SERPINH2 | serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 2
486436	0.002295943	UGP2 | UDP-glucose pyrophosphorylase 2
629839	0.034919482	dJ908M14.2 | hypothetical protein dJ908M14.2
781014	2.92E-05	ST5 | suppression of tumorigenicity 5
241705	0.002362784	PYGL | phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)
782756	1.92E-05	TBPL1 | TBP-like 1
293715	0.047831695	RAB1 | RAB1, member RAS oncogene family
2345302	0.027994066	KIAA0675 | KIAA0675 gene product
509943	0.000400309	DKC1 | dyskeratosis congenita 1, dyskerin
1534440	0.033905314	EST
743851	0.024878213	ESTs, Weakly similar to S55916 ribosomal protein S5, cytosolic [H.sapiens]
1456799	0.019816713	Homo sapiens cDNA FLJ32537 fis, clone SMINT2000400, highly similar to Homo sapiens FRG1 mRNA
415851	6.35E-08	ARHE | ras homolog gene family, member E
248256	2.71E-07	KIAA1691 | KIAA1691 protein
810002	3.90E-05	Homo sapiens, clone MGC:19762 IMAGE:3636045, mRNA, complete cds
626502	4.10E-08	ARPC1B | actin related protein 2/3 complex, subunit 1B (41 kD)
167268	0.047573891	ESTs
781026	0.016470796	Homo sapiens cDNA FLJ11801 fis, clone HEMBA1006253, weakly similar to DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR
462926	0.01888892	NEK2 | NIMA (never in mitosis gene a)-related kinase 2
156270-2	0.004049154	ESTs
44692	0.000993361	CRHR1 | corticotropin releasing hormone receptor 1
753625	0.00994019	Homo sapiens cDNA FLJ14844 fis, clone PLACE1000133, highly similar to TRANSCRIPTION FACTOR BTF3
683059	2.83E-06	CEP3 | Cdc42 effector protein 3

756968	0.015062537	EFNB1 | ephrin-B1
1898426	0.02483948	MGC4268 | hypothetical protein MGC4268
739983	0.0041899	KIAA0042 | KIAA0042 gene product
1473788	0.016370991	TRADD | TNFRSF1A-associated via death domain
66902	0.000352001	Homo sapiens cDNA FLJ32121 fis, clone PEBLM1000083
41358	0.037052367	MEIS2 | Meis (mouse) homolog 2
743866	2.59E-07	FLJ10201 | hypothetical protein FLJ10201
725143	0.040000458	FLJ22418 | hypothetical protein FLJ22418
49920	0.035411663	PTDSS1 | phosphatidylserine synthase 1
260303	4.78E-05	ETS2 | v-ets avian erythroblastosis virus E26 oncogene homolog 2
343695	0.002155839	Homo sapiens cDNA FLJ31668 fis, clone NT2RI2004916
713782	0.000328235	ADAM15 | a disintegrin and metalloproteinase domain 15 (metargidin)
240780	0.000237546	NINJ2 | ninjurin 2
136534	0.003770645	MGC10753 | hypothetical protein MGC10753
462939	0.036642651	Homo sapiens cDNA FLJ31303 fis, clone LIVER1000082
291057	0.024002401	CDKN2C | cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)
417473	0.010898808	GNAS1 | guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1
725152	3.29E-10	DKFZp762A227 | hypothetical protein DKFZp762A227
814309	0.031933058	PIST | PDZ/coiled-coil domain binding partner for the rho-family GTPase TC10
858153	2.72E-07	NFIL3 | nuclear factor, interleukin 3 regulated
772220	7.74E-06	PDIR | for protein disulfide isomerase-related
2057973	0.043575209	CCND3 | cyclin D3
781047	0.000900648	BUB1 | budding uninhibited by benzimidazoles 1 (yeast homolog)
37491	0.000305556	TRIP10 | thyroid hormone receptor interactor 10
134942	0.011506861	FBXL11 | f-box and leucine-rich repeat protein 11
1553054	0.013614879	PRSS12 | protease, serine, 12 (neurotrypsin, motopsin)
208718	1.94E-09	ANXA1 | annexin A1
230235	0.018133375	CRFG | G protein-binding protein CRFG
214990	1.04E-07	GSN | gelsolin (amyloidosis, Finnish type)
418422	9.66E-07	PPBP | pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2)
123441	0.02798739	GALNT2 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2

		(GalNAc-T2)
742143	0.03760007	CD5 | CD5 antigen (p56-62)
69184	0.000101368	SUDD | sudD (suppressor of bimD6, Aspergillus nidulans) homolog
795893	0.010292994	PPP1R15A | protein phosphatase 1, regulatory (inhibitor) subunit 15A
120106	0.018649252	CASP1 | caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)
2919651	0.000222692	PGLYRP | peptidoglycan recognition protein
898010	0.000371143	EST
858167	8.01E-05	FACL4 | fatty-acid-Coenzyme A ligase, long-chain 4
782794	0.001204679	SLC25A19 | solute carrier family 25 (mitochondrial deoxynucleotide carrier), member 19
33500	2.81E-08	Homo sapiens clone 23556 mRNA sequence
133213	0.001335593	FUT4 | fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
1553065	0.010881395	FLJ14993 | hypothetical protein FLJ14993
416833	0.016095957	FKBP5 | FK506-binding protein 5
68534	0.006753838	Homo sapiens cDNA: FLJ22290 fis, clone HRC04405
1574330	7.62E-05	GROS1 | growth suppressor 1
502367	0.027654372	FBLN1 | fibulin 1
502369	3.35E-06	PDCD5 | programmed cell death 5
856575	6.13E-05	APP | amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)
366591	3.53E-05	TIAM2 | T-cell lymphoma invasion and metastasis 2
290422	2.17E-06	ZNF216 | zinc finger protein 216
1534493	1.17E-07	ESTs
280666	0.011314426	SEMA4D | sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D
344672	0.017131408	DKFZp761J139 | hypothetical protein DKFZp761J139
23758	0.005068225	Homo sapiens clone 23758 mRNA sequence
858183	0.001057603	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 684990
629896	0.000370779	MAP1B | microtubule-associated protein 1B
725188	0.027824136	MDH1 | malate dehydrogenase 1, NAD (soluble)
858188	0.042931319	Homo sapiens cDNA FLJ32144 fis, clone PLACE5000105, highly similar to Mus musculus mRNA for heparan sulfate 6-sulfotransferase 2
810057	6.03E-08	CSDA | cold shock domain protein A
2062825	0.001409555	KIAA0964 | KIAA0964 protein

50506	0.000975654	MAPK6 | mitogen-activated protein kinase 6
739235	0.000209372	STK25 | serine/threonine kinase 25 (Ste20, yeast homolog)
345621	0.002744036	CXX1 | CAAX box 1
743113	1.29E-05	KLK13 | kallikrein 13
133236	4.10E-05	RBMX | RNA binding motif protein, X chromosome
814341	0.004173726	DAPP1 | dual adaptor of phosphotyrosine and 3-phosphoinositides
2391494	0.000271971	EFNA4 | ephrin-A4
772261	0.028380323	MAPK14 | mitogen-activated protein kinase 14
704216	2.82E-05	MAP4K2 | mitogen-activating protein kinase kinase kinase kinase 2
293785	0.000141314	ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]
770665	0.000828447	FLJ12750 | hypothetical protein FLJ12750
264640	0.010224986	CLTB | clathrin, light polypeptide (Lcb)
824117	0.01125807	VRK2 | vaccinia related kinase 2
1711877	0.01333655	ESTs
503335	0.002578724	FLJ11196 | hypothetical protein FLJ11196
811013	0.001613372	AMPD2 | adenosine monophosphate deaminase 2 (isoform L)
1475730	0.015717591	CCT6A | chaperonin containing TCP1, subunit 6A (zeta 1)
52120	4.80E-07	DTX1 | deltex (Drosophila) homolog 1
2013094	0.003571882	KIF1C | kinesin family member 1C
768393	0.001209009	FLJ10829 | hypothetical protein FLJ10829
128711	7.44E-05	ANLN | anillin (Drosophila Scraps homolog), actin binding protein
1635032	0.002192122	NOLA1 | nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs)
137535	0.003910158	TIF1 | transcriptional intermediary factor 1
1870684	0.020116819	PCYT1A | phosphate cytidylyltransferase 1, choline, alpha isoform
825861	0.047376087	NUP153 | nucleoporin 153kD
809824	0.000141145	TMEPAI | transmembrane, prostate androgen induced RNA
815303	0.002677229	DARS | aspartyl-tRNA synthetase
842849	0.002998058	POLA2 | polymerase (DNA-directed), alpha (70kD)
22040	0.004853144	MMP9 | matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase)
24729	4.25E-06	CHRM1 | cholinergic receptor, muscarinic 1
159462	9.93E-07	MSE55 | serum constituent protein
811020	1.65E-11	Homo sapiens, clone IMAGE:4278205, mRNA, partial cds

2307420	0.040870882	TUBB | tubulin, beta polypeptide
627521	0.014104273	ESTs, Weakly similar to KIAA1140 protein [H.sapiens]
361688	0.023373299	DPP6 | dipeptidylpeptidase VI
1603358	0.019799335	FAT | FAT tumor suppressor (Drosophila) homolog
1946069	6.72E-08	SPHK1 | sphingosine kinase 1
268946	0.000809644	Homo sapiens cDNA FLJ31861 fis, clone NT2RP7001319
824132	0.00066839	Homo sapiens, Similar to cofactor required for Sp1 transcriptional activation, subunit 8 (34kD), clone MGC:11274 IMAGE:3944264, mRNA, complete cds
266263	0.012980026	ESTs
1710152	0.041184366	SOAT1 | sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1
813714	0.000195754	CFLAR | CASP8 and FADD-like apoptosis regulator
813719	0.000693345	ESTs, Weakly similar to DAP1_HUMAN DEATH-ASSOCIATED PROTEIN 1 [H.sapiens]
712401	0.005587928	PIK3CD | phosphoinositide-3-kinase, catalytic, delta polypeptide
785392	0.036628745	DKFZP434F2021 | DKFZP434F2021 protein
1883008	0.008613382	EST, Weakly similar to T24581 hypothetical protein T06D8.8 - Caenorhabditis elegans [C.elegans]
1637732	5.51E-05	PPAN | peter pan (Drosophila) homolog
1493390	4.71E-06	ILF2 | interleukin enhancer binding factor 2, 45kD
595213	0.027525584	BM-009 | hypothetical protein
842861	0.018460389	HNRPR | heterogeneous nuclear ribonucleoprotein R
878833	1.99E-05	UCHL1 | ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)
1631853	0.000227064	Homo sapiens, Similar to RIKEN cDNA 2410003K15 gene, clone MGC:20424 IMAGE:4646294, mRNA, complete cds
132619	0.003085822	ESTs
502701	1.67E-08	FREQ | frequenin (Drosophila) homolog
504308	3.20E-05	FLJ10540 | hypothetical protein FLJ10540
950600	2.03E-06	Homo sapiens mRNA; cDNA DKFZp586C1019 (from clone DKFZp586C1019)
80633	0.001826411	TLR2 | toll-like receptor 2
784744	0.001112368	MPHOSPH6 | M-phase phosphoprotein 6
811044	1.63E-08	EST
845419	5.05E-05	FANCA | Fanconi anemia, complementation group A
897427	0.018369144	Homo sapiens, clone IMAGE:3638994, mRNA, partial cds
878846	9.96E-12	BRI3 | brain protein I3

345670	2.09E-06	NFYC | nuclear transcription factor Y, gamma
1631868	0.038386276	MGC13061 | hypothetical protein MGC13061
811054	0.019642843	GNA12 | guanine nucleotide binding protein (G protein) alpha 12
839941	1.31E-05	FLJ14590 | hypothetical protein FLJ14590
589751	0.000104128	HTATIP2 | HIV-1 Tat interactive protein 2, 30 kDa
208001	0.000566004	CD59 | CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344)
1637756	0.000324573	ENO1 | enolase 1, (alpha)
755612	9.22E-06	GPR39 | G protein-coupled receptor 39
685045	0.002900139	ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]
306771	1.68E-06	TMSNB | thymosin, beta, identified in neuroblastoma cells
377368	0.001270033	LOC57099 | cell death regulator aven
898092	2.20E-05	CTGF | connective tissue growth factor
1631874	0.020656474	LOC51068 | CGI-07 protein
841149	0.004225448	TGFBR2 | transforming growth factor, beta receptor II (70-80kD)
813742	6.19E-07	PTK7 | PTK7 protein tyrosine kinase 7
785707	0.001862647	PRC1 | protein regulator of cytokinesis 1

Table 3. Genes that are overexpressed in ER positive cells, and underexpressed in ER negative cells

GeneID	P-value	Description
AW473119	$p < 1e-07$	ESR1 | estrogen receptor 1
AF088867	$p < 1e-07$	AGR2 | anterior gradient 2 homolog (Xenepus laevis)
AW015443	$p < 1e-07$	ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
AW137092	$p < 1e-07$	Homo sapiens cDNA FLJ10561 fis, clone NT2RP2002672
BC017859	$p < 1e-07$	TFF3 | trefoil factor 3 (intestinal)
AL137566	$p < 1e-07$	Homo sapiens mRNA; cDNA DKFZp586G0321 (from clone DKFZp586G0321)
NM_004496	$p < 1e-07$	HNF3A | hepatocyte nuclear factor 3, alpha
AW451986	$p < 1e-07$	ESTs

AW207206	p < 1e-07	ESTs
AA412108	p < 1e-07	ESTs
NM_001218	p < 1e-07	CA12 | carbonic anhydrase XII
AI128582	p < 1e-07	ESTs
R41823	p < 1e-07	ESTs
AF356492	p < 1e-07	DACH | dachshund homolog (Drosophila)
BC014962	p < 1e-07	GFRA1 | GDNF family receptor alpha 1
AA688021	p < 1e-07	ESTs
AI200852	p < 1e-07	ESTs
AW086163	p < 1e-07	ESTs
AF007153	p < 1e-07	Homo sapiens clone 23736 mRNA sequence
AI050855	p < 1e-07	ESTs
AA569340	p < 1e-07	CYP2B7 | cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 7
AI125908	p < 1e-07	Homo sapiens cDNA FLJ30555 fis, clone BRAWH2003818
BC013732	p < 1e-07	NAT1 | N-acetyltransferase 1 (arylamine N-acetyltransferase)
AA542898	p < 1e-07	P28 | dynein, axonemal, light intermediate polypeptide
AI820662	p < 1e-07	ESTs
AA846824	p < 1e-07	ESTs
NM_020974	p < 1e-07	CEGP1 | CEGP1 protein
AI373462	p < 1e-07	ESTs
AJ009985	p < 1e-07	ANXA9 | annexin A9
BF433570	p < 1e-07	ESTs
AI377320	p < 1e-07	ESTs
NM_000767	p < 1e-07	CYP2B6 | cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6
AF070632	p < 1e-07	Homo sapiens clone 24405 mRNA sequence
AF131785	p < 1e-07	KIAA0882 | KIAA0882 protein
AW300348	p < 1e-07	Homo sapiens ovarian cancer-related protein 2 (OCR2) mRNA, complete cds
AL512749	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp667D095 (from clone DKFZp667D095)
AI733682	p < 1e-07	ESTs
AW780011	p < 1e-07	ESTs
AW135648	p < 1e-07	ESTs
AI263695	p < 1e-07	NME5 | non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)
NM_000044	p < 1e-07	AR | androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)

AK000158	$p < 1e-07$	FLJ20151 | hypothetical protein FLJ20151
AF176012	$p < 1e-07$	JDP1 | J domain containing protein 1
BC018035	$p < 1e-07$	Homo sapiens, clone IMAGE:4819956, mRNA, partial cds
BC008429	$p < 1e-07$	C20orf114 | chromosome 20 open reading frame 114
BF436400	$p < 1e-07$	EST
BC006496	$p < 1e-07$	PDZK1 | PDZ domain containing 1
BC014659	$p < 1e-07$	NG22 | NG22 protein
AA182477	$p < 1e-07$	ESTs
AI272823	$p < 1e-07$	ESTs
BC010951	$p < 1e-07$	PIP | prolactin-induced protein
BC014948	$p < 1e-07$	MLPH | melanophilin
AI026825	$p < 1e-07$	DNLC2B | dynein light chain 2B
BC015338	$p < 1e-07$	CPB1 | carboxypeptidase B1 (tissue)
AI355477	$p < 1e-07$	ESTs
R60583	$p < 1e-07$	NOVA1 | neuro-oncological ventral antigen 1
AK058158	$p < 1e-07$	Homo sapiens cDNA FLJ25429 fis, clone TST05630
BC014601	$p < 1e-07$	Homo sapiens, Similar to RIKEN cDNA 1700017I11 gene, clone MGC:26847 IMAGE:4821517, mRNA, complete cds
AK024204	$p < 1e-07$	Homo sapiens cDNA FLJ14142 fis, clone MAMMA1002880
AI874215	$p < 1e-07$	KIAA0575 | KIAA0575 gene product
AK027176	$p < 1e-07$	CAPN13 | calpain 13
BC008915	$p < 1e-07$	SERPINA5 | serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5
BC017758	$p < 1e-07$	CYP4B1 | cytochrome P450, subfamily IVB, polypeptide 1
AI871614	$p < 1e-07$	HSA250839 | gene for serine/threonine protein kinase
AA903339	$p < 1e-07$	RET | ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)
AA553710	$p < 1e-07$	EST
BC016861	$p < 1e-07$	Homo sapiens, clone MGC:17393 IMAGE:3914851, mRNA, complete cds
AY009106	$p < 1e-07$	DKFZP434I092 | DKFZP434I092 protein
BC013438	$p < 1e-07$	Homo sapiens, clone IMAGE:3899073, mRNA, partial cds
NM_005518	$p < 1e-07$	HMGCS2 | 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)
AW024203	$p < 1e-07$	Homo sapiens, clone MGC:5522 IMAGE:3454199, mRNA, complete cds
AL133619	$p < 1e-07$	Homo sapiens mRNA; cDNA DKFZp434E2321 (from clone DKFZp434E2321); partial cds
NM_000507	$p < 1e-07$	FBP1 | fructose-1,6-bisphosphatase 1
AF237813	$p < 1e-07$	NPD009 | NPD009 protein

AI828071	p < 1e-07	BCAS1 | breast carcinoma amplified sequence 1
AA557177	p < 1e-07	EST
Z11162	p < 1e-07	AGTR1 | angiotensin receptor 1
NM_007050	p < 1e-07	PTPRT | protein tyrosine phosphatase, receptor type, T
NM_007293	p < 1e-07	C4A | complement component 4A
AK021931	p < 1e-07	Homo sapiens cDNA FLJ11869 fis, clone HEMBA1007002
AA130089	p < 1e-07	ESTs
BC007997	p < 1e-07	RERG | RAS-like, estrogen-regulated, growth-inhibitor
AK055698	p < 1e-07	Homo sapiens cDNA FLJ31136 fis, clone IMR322001029
AI668602	p < 1e-07	ESTs, Weakly similar to JX0331 laurate omega-hydroxylase [H.sapiens]
AW261844	p < 1e-07	ESTs
AI337740	p < 1e-07	FLJ12650 | hypothetical protein FLJ12650
AW073282	p < 1e-07	ESTs
BC000558	p < 1e-07	MAPT | microtubule-associated protein tau
AI498298	p < 1e-07	FACVL1 | fatty-acid-Coenzyme A ligase, very long-chain 1
AI570494	p < 1e-07	ESTs
AF209930	p < 1e-07	CHRD | chordin
AK026756	p < 1e-07	KIAA1603 | KIAA1603 protein
AW070592	p < 1e-07	ESTs
BC014189	p < 1e-07	MGC20702 | hypothetical protein MGC20702
AL117406	p < 1e-07	ABCC11 | ATP-binding cassette, sub-family C (CFTR/MRP), member 11
AI190693	p < 1e-07	ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]
NM_003561	p < 1e-07	PLA2G10 | phospholipase A2, group X
AA513718	p < 1e-07	ESTs
BF591743	p < 1e-07	LPHB | lipophilin B (uteroglobin family member), prostatein-like
AK026958	p < 1e-07	FLJ23305 | hypothetical protein FLJ23305
AW016378	p < 1e-07	ESTs
BC017701	p < 1e-07	AD036 | AD036 protein
AW294316	p < 1e-07	ESTs
BC006793	p < 1e-07	GATA3 | GATA binding protein 3
AK026427	p < 1e-07	FLJ22774 | hypothetical protein FLJ22774
NM_004310	p < 1e-07	ARHH | ras homolog gene family, member H
AK000181	p < 1e-07	FLJ20174 | hypothetical protein FLJ20174
NM_016613	p < 1e-07	LOC51313 | AD021 protein

BC000088	p < 1e-07	GSTM3 | glutathione S-transferase M3 (brain)
BC011721	p < 1e-07	TUBA2 | tubulin, alpha 2
AI631708	p < 1e-07	ESTs, Weakly similar to 1312318A cystatin SA [H.sapiens]
NM_001756	p < 1e-07	SERPINA6 | serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 6
NM_004525	p < 1e-07	LRP2 | low density lipoprotein-related protein 2
BC012613	p < 1e-07	CPA3 | carboxypeptidase A3 (mast cell)
BC011348	p < 1e-07	FLJ12910 | hypothetical protein FLJ12910
NM_001502	p < 1e-07	GP2 | glycoprotein 2 (zymogen granule membrane)
AA807457	p < 1e-07	MYB | v-myb myeloblastosis viral oncogene homolog (avian)
AL157505	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp586P1124 (from clone DKFZp586P1124)
NM_005080	p < 1e-07	XBP1 | X-box binding protein 1
AI277016	p < 1e-07	ESTs
AA648777	p < 1e-07	MS4A7 | membrane-spanning 4-domains, subfamily A, member 7
AL360204	p < 1e-07	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 980547
BE967259	p < 1e-07	BCL2 | B-cell CLL/lymphoma 2
BC012372	p < 1e-07	C4B | complement component 4B
AI797041	p < 1e-07	TRH | thyrotropin-releasing hormone
AI804588	p < 1e-07	BLu | BLu protein
AI309080	p < 1e-07	ESTs
BF725007	p < 1e-07	ADRA2A | adrenergic, alpha-2A-, receptor
AI253198	p < 1e-07	Homo sapiens cDNA FLJ13945 fis, clone Y79AA1000969
AK000373	p < 1e-07	FLJ20366 | hypothetical protein FLJ20366
AI028773	p < 1e-07	ACOX2 | acyl-Coenzyme A oxidase 2, branched chain
AW664923	0.0000002	GRIA2 | glutamate receptor, ionotropic, AMPA 2
BC004518	p < 1e-07	LOC51760 | B/K protein
NM_002145	p < 1e-07	HOXB2 | homeo box B2
NM_000792	p < 1e-07	DIO1 | deiodinase, iodothyronine, type I
AK024872	p < 1e-07	SYTL2 | synaptotagmin-like 2
BC015628	p < 1e-07	ABAT | 4-aminobutyrate aminotransferase
BC000658	p < 1e-07	STC2 | stanniocalcin 2
AL050227	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp586M0723 (from clone DKFZp586M0723)
AK027006	p < 1e-07	TNRC9 | trinucleotide repeat containing 9
AA659816	p < 1e-07	ESTs
AA845338	p < 1e-07	FMO5 | flavin containing monooxygenase 5

BC012625	p < 1e-07	PPP1R3C | protein phosphatase 1, regulatory (inhibitor) subunit 3C
AW015140	p < 1e-07	ESTs
AI992108	p < 1e-07	Homo sapiens cDNA FLJ25333 fis, clone TST00656
R39691	p < 1e-07	SYT1 | synaptotagmin I
BC001665	p < 1e-07	Homo sapiens, Similar to KIAA0843 protein, clone MGC:1835 IMAGE:2988043, mRNA, complete cds
AF403428	p < 1e-07	LRG | leucine-rich alpha-2-glycoprotein
AK057315	p < 1e-07	TSGA2 | testes specific A2 homolog (mouse)
R40824	p < 1e-07	FBXL7 | F-box and leucine-rich repeat protein 7
AI732534	p < 1e-07	MGB1 | mammaglobin 1
BC012375	p < 1e-07	KIAA1001 | KIAA1001 protein
AI587351	0.0000012	CEACAM6 | carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)
BC007681	p < 1e-07	RAB26 | RAB26, member RAS oncogene family
AI694966	p < 1e-07	RAI2 | retinoic acid induced 2
AL136926	p < 1e-07	DKFZP586M1120 | hypothetical protein DKFZp586M1120
AW070746	p < 1e-07	NCAM2 | neural cell adhesion molecule 2
AI432856	p < 1e-07	EST
AF384856	p < 1e-07	PGLYRP | peptidoglycan recognition protein L precursor
AI823785	p < 1e-07	BC008967 | hypothetical gene BC008967
BC014250	p < 1e-07	CHST8 | carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8
R49089	p < 1e-07	ESTs, Moderately similar to T12539 hypothetical protein DKFZp434J154.1 [H.sapiens]
AW134740	p < 1e-07	DCAMKL1 | doublecortin and CaM kinase-like 1
AL390084	p < 1e-07	LOC56964 | hypothetical protein from EUROIMAGE 384293
AI056882	p < 1e-07	KIAA1493 | KIAA1493 protein
AK000532	p < 1e-07	Homo sapiens cDNA FLJ20525 fis, clone KAT10610
N22687	p < 1e-07	ESTs
NM_003770	p < 1e-07	KRTHA7 | keratin, hair, acidic, 7
AK000563	p < 1e-07	HRASLS2 | HRAS-like suppressor 2
AW082090	0.0000001	Homo sapiens cDNA FLJ33105 fis, clone TRACH2000926, weakly similar to PROBABLE OXIDOREDUCTASE EPHD (EC 1.-.-.-)
AA069179	p < 1e-07	INPP4B | inositol polyphosphate-4-phosphatase, type II, 105kD
NM_007210	p < 1e-07	GALNT6 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)
AI826254	p < 1e-07	HPN | hepsin (transmembrane protease, serine 1)
AL080222	p < 1e-07	FLJ13110 | hypothetical protein FLJ13110
AI082272	p < 1e-07	KIAA1467 | KIAA1467 protein

AF257081	p < 1e-07	KCNK15 | potassium channel, subfamily K, member 15 (TASK-5)
AI439798	p < 1e-07	FGD3 | FGD1 family, member 3
AI471793	p < 1e-07	Homo sapiens cDNA FLJ13598 fis, clone PLACE1009921
AI741657	p < 1e-07	ITPR1 | inositol 1,4,5-triphosphate receptor, type 1
AK023655	p < 1e-07	FLJ13593 | hypothetical protein FLJ13593
NM_006763	p < 1e-07	BTG2 | BTG family, member 2
AK001783	p < 1e-07	FLJ10921 | hypothetical protein FLJ10921
BC008814	p < 1e-07	SLC7A4 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 4
BC006526	p < 1e-07	SCNN1A | sodium channel, nonvoltage-gated 1 alpha
AJ224171	p < 1e-07	LPHA | lipophilin A (uteroglobin family member)
AI955511	0.0000003	ESTs
AA255953	p < 1e-07	ACADSB | acyl-Coenzyme A dehydrogenase, short/branched chain
AJ249248	p < 1e-07	GPCR150 | putative G protein-coupled receptor
AI276310	p < 1e-07	EST, Moderately similar to G02666 cysteine-rich protein 1 [H.sapiens]
R60224	0.0000001	ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]
AF224266	p < 1e-07	IL20 | interleukin 20
AJ420562	p < 1e-07	PKIB | protein kinase (cAMP-dependent, catalytic) inhibitor beta
AF052504	p < 1e-07	RNB6 | RNB6
AI420473	p < 1e-07	EST
NM_014599	p < 1e-07	EHD4 | EH-domain containing 4
AL080151	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp434D024 (from clone DKFZp434D024)
BC012727	p < 1e-07	FLJ22593 | hypothetical protein FLJ22593
AA574174	p < 1e-07	CYP2A7 | cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7
AI193043	p < 1e-07	ESTs, Weakly similar to T17226 hypothetical protein DKFZp566G223.1 [H.sapiens]
AF048700	p < 1e-07	SPINK4 | serine protease inhibitor, Kazal type 4
AA860090	p < 1e-07	ESTs
AA904027	p < 1e-07	Homo sapiens cDNA FLJ30147 fis, clone BRACE2000266
NM_012244	p < 1e-07	SLC7A8 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 8
AI151349	p < 1e-07	ENPP1 | ectonucleotide pyrophosphatase/phosphodiesterase 1
BC005395	p < 1e-07	HPX | hemopexin
AI247880	p < 1e-07	F7 | coagulation factor VII (serum prothrombin conversion accelerator)
AW207804	p < 1e-07	ESTs, Weakly similar to A36036 cytochrome P450 2F1 [H.sapiens]
AK025256	p < 1e-07	FLJ21603 | hypothetical protein FLJ21603
BF434467	p < 1e-07	ESTs

AI799887	p < 1e-07	EST
AA804407	p < 1e-07	FLJ10980 | hypothetical protein FLJ10980
AW138427	p < 1e-07	ESTs
BC010626	p < 1e-07	Homo sapiens, clone MGC:17687 IMAGE:3865868, mRNA, complete cds
BC009722	p < 1e-07	Homo sapiens, clone MGC:9575 IMAGE:3879368, mRNA, complete cds
BF129497	p < 1e-07	EST
BC014851	p < 1e-07	LFNG | lunatic fringe homolog (Drosophila)
BF510534	p < 1e-07	UMOD | uromodulin (uromucoid, Tamm-Horsfall glycoprotein)
AA627358	p < 1e-07	ESTs
AA846278	p < 1e-07	ESTs
AA933076	p < 1e-07	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
BC004143	p < 1e-07	BF | B-factor, properdin
BC014607	p < 1e-07	ASP | AKAP-associated sperm protein
AA810085	p < 1e-07	CXorf10 | chromosome X open reading frame 10
AF070604	p < 1e-07	CACNA1H | calcium channel, voltage-dependent, alpha 1H subunit
BC001278	p < 1e-07	SPUVE | protease, serine, 23
AF038191	p < 1e-07	BAIAP3 | BAI1-associated protein 3
BC013430	p < 1e-07	UGDH | UDP-glucose dehydrogenase
BC008962	p < 1e-07	PLAB | prostate differentiation factor
U45975	p < 1e-07	PIB5PA | phosphatidylinositol (4,5) bisphosphate 5-phosphatase, A
BF476394	p < 1e-07	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
BC006428	p < 1e-07	HSPC195 | hypothetical protein
NM_004419	p < 1e-07	DUSP5 | dual specificity phosphatase 5
AL512743	0.0000054	SYT13 | synaptotagmin XIII
BC014213	p < 1e-07	RAB30 | RAB30, member RAS oncogene family
NM_000352	p < 1e-07	ABCC8 | ATP-binding cassette, sub-family C (CFTR/MRP), member 8
X83301	p < 1e-07	SMA5 | SMA5
AL049265	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp564F053 (from clone DKFZp564F053)
AF237905	p < 1e-07	MS4A8B | membrane-spanning 4-domains, subfamily A, member 8B
BC002738	p < 1e-07	CRIP1 | cysteine-rich protein 1 (intestinal)
BF476123	p < 1e-07	ESTs, Weakly similar to S65824 reverse transcriptase homolog [H.sapiens]
AK026912	0.0000001	FLJ23259 | hypothetical protein FLJ23259
AI254131	p < 1e-07	ESTs

AK027159	p < 1e-07	FLJ23506 | hypothetical protein FLJ23506
BC004488	p < 1e-07	GRP | gastrin-releasing peptide
AK021798	p < 1e-07	FLJ11736 | hypothetical protein FLJ11736
AF007170	p < 1e-07	KIAA0452 | DEME-6 protein
BC010607	p < 1e-07	Homo sapiens, clone MGC:18216 IMAGE:4156235, mRNA, complete cds
AK027311	p < 1e-07	KIAA1276 | KIAA1276 protein
NM_057158	p < 1e-07	DUSP4 | dual specificity phosphatase 4
AI198522	p < 1e-07	SLC11A3 | solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3
BC003513	0.0000003	SCYB14 | small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK)
AI352080	p < 1e-07	FLJ14299 | hypothetical protein FLJ14299
NM_002381	p < 1e-07	MATN3 | matrilin 3
L07738	p < 1e-07	CACNG1 | calcium channel, voltage-dependent, gamma subunit 1
AI636974	p < 1e-07	LOC51097 | CGI-49 protein
AF191017	0.0000007	H11 | protein kinase H11
AI620482	p < 1e-07	EST
AW300891	p < 1e-07	FLJ20753 | hypothetical protein FLJ20753
BC005273	p < 1e-07	Homo sapiens, clone MGC:12318 IMAGE:3685423, mRNA, complete cds
AF367473	p < 1e-07	NYD-SP21 | testes development-related NYD-SP21
AL137761	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp586L2424 (from clone DKFZp586L2424)
AI468574	p < 1e-07	ESTs
AW292427	p < 1e-07	Homo sapiens cDNA FLJ13596 fis, clone PLACE1009637
AJ420423	p < 1e-07	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1287006
AI432615	p < 1e-07	DXS1283E | GS2 gene
AW207201	p < 1e-07	CHAD | chondroadherin
BC012900	p < 1e-07	Homo sapiens, clone IMAGE:3881549, mRNA
AI559487	p < 1e-07	SALL2 | sal-like 2 (Drosophila)
AW194426	p < 1e-07	ESTs
NM_003225	p < 1e-07	TFF1 | trefoil factor 1 (breast cancer, estrogen-inducible sequence expressed in)
AW270334	p < 1e-07	ESTs
BC013591	p < 1e-07	NTN4 | netrin 4
NM_004923	p < 1e-07	MTL5 | metallothionein-like 5, testis-specific (tesmin)
AI685841	p < 1e-07	ESTs
AW613732	p < 1e-07	Homo sapiens cDNA FLJ31137 fis, clone IMR322001049
AL133644	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp434P1514 (from clone DKFZp434P1514); partial cds

AY048757	p < 1e-07	ABCG1 | ATP-binding cassette, sub-family G (WHITE), member 1
AW292522	p < 1e-07	ESTs, Highly similar to A55713 inositol 1,4,5-triphosphate receptor type 1 [H.sapiens]
BC001809	p < 1e-07	MGC3771 | hypothetical protein MGC3771
AB038463	p < 1e-07	CAPN9 | calpain 9 (nCL-4)
NM_033380	p < 1e-07	COL4A5 | collagen, type IV, alpha 5 (Alport syndrome)
BC004240	p < 1e-07	CITED1 | Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1
AF435925	p < 1e-07	VLGR1 | very large G protein-coupled receptor 1
AI378647	p < 1e-07	ESTs
AF035408	p < 1e-07	CILP | cartilage intermediate layer protein, nucleotide pyrophosphohydrolase
U11058	p < 1e-07	KCNMA1 | potassium large conductance calcium-activated channel, subfamily M, alpha member 1
AI814187	p < 1e-07	KIAA1061 | KIAA1061 protein
AI399653	p < 1e-07	ESTs
AL050090	p < 1e-07	DKFZP586F1018 | DKFZP586F1018 protein
AY043361	p < 1e-07	WWP1 | WW domain-containing protein 1
AK027241	p < 1e-07	FLJ23588 | hypothetical protein FLJ23588
AK024892	p < 1e-07	SH3BGRL | SH3 domain binding glutamic acid-rich protein like
AI928365	0.0000003	SLC1A1 | solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1
BE675157	p < 1e-07	ESTs
AI669410	p < 1e-07	ESTs
AA826324	p < 1e-07	Homo sapiens cDNA FLJ32320 fis, clone PROST2003537
BC009203	p < 1e-07	LOC90355 | hypothetical gene supported by AF038182; BC009203
AI828600	p < 1e-07	ESTs
AK026141	p < 1e-07	Homo sapiens cDNA: FLJ22488 fis, clone HRC10948, highly similar to HSU79298 Human clone 23803 mRNA
AI208471	0.0000001	HRLP5 | H-rev107-like protein 5
AK000978	p < 1e-07	FLJ10116 | hypothetical protein FLJ10116
AL136579	p < 1e-07	KIAA1415 | KIAA1415 protein
AI479704	p < 1e-07	CYP21A2 | cytochrome P450, subfamily XXIA (steroid 21-hydroxylase, congenital adrenal hyperplasia), polypeptide 2
AW148827	p < 1e-07	SEZ6L | seizure related 6 homolog (mouse)-like
AF220189	0.0000329	BEX1 | brain expressed, X-linked 1
AA557341	p < 1e-07	EST
BC004504	p < 1e-07	MGC11138 | hypothetical protein MGC11138
AI922204	0.0000002	Homo sapiens cDNA FLJ30298 fis, clone BRACE2003172
AI969835	0.0000003	NELL2 | NEL-like 2 (chicken)

NM_000841	0.0000012	GRM4 | glutamate receptor, metabotropic 4
AW205768	0.0000269	THRSP | thyroid hormone responsive (SPOT14 homolog, rat)
AF100759	$p < 1e-07$	NET-6 | tetraspan NET-6 protein
AF121129	$p < 1e-07$	NR2E3 | nuclear receptor subfamily 2, group E, member 3
AI126271	$p < 1e-07$	Homo sapiens cDNA FLJ31235 fis, clone KIDNE2004681, moderately similar to Mus musculus peroxisomal long chain acyl-CoA thioesterase Ib (Pte1b) gene
AI457338	$p < 1e-07$	Homo sapiens cDNA FLJ33115 fis, clone TRACH2001314
BM126815	$p < 1e-07$	Homo sapiens cDNA FLJ11375 fis, clone HEMBA1000411, weakly similar to ANKYRIN
BF002534	$p < 1e-07$	FLJ10244 | hypothetical protein FLJ10244
AA700070	0.0000066	SLC6A4 | solute carrier family 6 (neurotransmitter transporter, serotonin), member 4
BC014913	$p < 1e-07$	Homo sapiens, Similar to synaptotagmin-like 4, clone MGC:17313 IMAGE:3908307, mRNA, complete cds
AF026477	$p < 1e-07$	GALNAC4S-6ST | B cell RAG associated protein
R16838	$p < 1e-07$	ESTs
AF116660	0.0000006	C8orf4 | chromosome 8 open reading frame 4
AI568799	$p < 1e-07$	ENPP5 | ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function)
AA633845	$p < 1e-07$	ESTs
AW265341	$p < 1e-07$	ESTs
AA738043	$p < 1e-07$	SCAP1 | src family associated phosphoprotein 1
AK024999	$p < 1e-07$	Homo sapiens cDNA: FLJ21346 fis, clone COL02705
M76558	$p < 1e-07$	CACNA1D | calcium channel, voltage-dependent, L type, alpha 1D subunit
AW016396	$p < 1e-07$	PACE4 | paired basic amino acid cleaving system 4
H04392	$p < 1e-07$	ESTs
BC000314	0.0000001	RTN1 | reticulon 1
AI823800	0.0000002	GPR54 | G protein-coupled receptor 54
AW135596	$p < 1e-07$	FLJ10058 | hypothetical protein FLJ10058
AI364725	$p < 1e-07$	KIAA0239 | KIAA0239 protein
AI200759	$p < 1e-07$	Homo sapiens cDNA FLJ32802 fis, clone TESTI2002580
NM_005544	$p < 1e-07$	IRS1 | insulin receptor substrate 1
AA580157	$p < 1e-07$	EIF4B | eukaryotic translation initiation factor 4B
AI926614	$p < 1e-07$	EST
NM_006113	$p < 1e-07$	VAV3 | vav 3 oncogene
AW007851	$p < 1e-07$	RAB5EP | rabaptin-5
BC009373	$p < 1e-07$	Homo sapiens, clone MGC:16638 IMAGE:4121964, mRNA, complete cds
AL157499	$p < 1e-07$	Homo sapiens mRNA; cDNA DKFZp434N2412 (from clone DKFZp434N2412)

BC015520	$p < 1e-07$	RNASE4 | ribonuclease, RNase A family, 4
AB050468	$p < 1e-07$	LIG1 | ortholog of mouse integral membrane glycoprotein LIG-1
AI446183	$p < 1e-07$	ESTs, Highly similar to CYA5_HUMAN ADENYLATE CYCLASE, TYPE V [H.sapiens]
AI806109	0.0000003	KIAA1580 | KIAA1580 protein
AI479419	$p < 1e-07$	KIAA1511 | KIAA1511 protein
AL136858	$p < 1e-07$	DKFZp434N2435 | hypothetical protein DKFZp434N2435
BI491333	$p < 1e-07$	Homo sapiens cDNA FLJ13289 fis, clone OVARC1001170
AF035282	$p < 1e-07$	C1orf21 | chromosome 1 open reading frame 21
R36615	$p < 1e-07$	ESTs
AI673455	$p < 1e-07$	ESTs
BC000809	$p < 1e-07$	TCEAL1 | transcription elongation factor A (SII)-like 1
AW450693	$p < 1e-07$	Homo sapiens mRNA, exon 1, 2, 3, 4, clone:RES4-24A
AV646597	$p < 1e-07$	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
AA749341	$p < 1e-07$	KIAA0040 | KIAA0040 gene product
BC000576	$p < 1e-07$	QDPR | quinoid dihydropteridine reductase
BC003559	$p < 1e-07$	SERPINA3 | serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3
BC008940	0.0000051	HOXB5 | homeo box B5
AF057164	$p < 1e-07$	SLC22A5 | solute carrier family 22 (organic cation transporter), member 5
L02785	0.0000373	SLC26A3 | solute carrier family 26, member 3
AF054910	$p < 1e-07$	TEKT2 | tektin 2 (testicular)
NM_002847	$p < 1e-07$	PTPRN2 | protein tyrosine phosphatase, receptor type, N polypeptide 2
AA775255	$p < 1e-07$	ANKHZN | ANKHZN protein
AL080192	$p < 1e-07$	Homo sapiens mRNA; cDNA DKFZp434B102 (from clone DKFZp434B102)
AK027206	$p < 1e-07$	MGC16309 | hypothetical gene MGC16309
BE671061	$p < 1e-07$	C20orf103 | chromosome 20 open reading frame 103
X95097	0.0000007	VIPR2 | vasoactive intestinal peptide receptor 2
M57609	$p < 1e-07$	GLI3 | GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome)
AF248053	$p < 1e-07$	SLC2A10 | solute carrier family 2 (facilitated glucose transporter), member 10
AK022441	$p < 1e-07$	Homo sapiens cDNA FLJ12379 fis, clone MAMMA1002554
AB026707	$p < 1e-07$	NMES1 | normal mucosa of esophagus specific 1
BC005153	$p < 1e-07$	RPH3AL | rabphilin 3A-like (without C2 domains)
AW449824	$p < 1e-07$	ESTs
AW080831	$p < 1e-07$	SEC14L2 | SEC14-like 2 (S. cerevisiae)

AI674226	p < 1e-07	Homo sapiens, Similar to RIKEN cDNA 1700008D07 gene, clone MGC:9830 IMAGE:3863323, mRNA, complete cds
AI382972	p < 1e-07	TPBG | trophoblast glycoprotein
AK025198	0.0000003	Homo sapiens cDNA: FLJ21545 fis, clone COL06195
BC000662	p < 1e-07	MGC2601 | hypothetical protein MGC2601
AL133622	p < 1e-07	KIAA0876 | KIAA0876 protein
R42185	p < 1e-07	Homo sapiens cDNA FLJ32064 fis, clone OCBBF1000080
U62325	p < 1e-07	APBB2 | amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)
BC008317	p < 1e-07	LIV-1 | LIV-1 protein, estrogen regulated
AI825621	0.0000001	KIAA1130 | KIAA1130 protein
M93119	0.0006433	INSM1 | insulinoma-associated 1
BC016018	p < 1e-07	Homo sapiens, clone MGC:27478 IMAGE:4714682, mRNA, complete cds
D89675	p < 1e-07	BMPR1B | bone morphogenetic protein receptor, type IB
AI093769	p < 1e-07	ESTs
NM_006006	0.0000002	ZNF145 | zinc finger protein 145 (Kruppel-like, expressed in promyelocytic leukemia)
AW294857	p < 1e-07	LOC51161 | g20 protein
AK000269	p < 1e-07	FLJ20262 | hypothetical protein FLJ20262
AI674190	p < 1e-07	FLJ13941 | hypothetical protein FLJ13941
AW207696	0.0000453	MGB2 | mammaglobin 2
R41429	p < 1e-07	ATP7B | ATPase, Cu++ transporting, beta polypeptide (Wilson disease)
AF131784	p < 1e-07	Homo sapiens clone 25194 mRNA sequence
BC010963	0.0000002	TNNT1 | troponin T1, skeletal, slow
BC009799	0.0000392	AREG | amphiregulin (schwannoma-derived growth factor)
AJ278018	p < 1e-07	CS2 | calsyntenin-2
BI494440	p < 1e-07	KIAA0222 | KIAA0222 gene product
AF140240	p < 1e-07	TBX3 | T-box 3 (ulnar mammary syndrome)
D50840	p < 1e-07	UGCG | UDP-glucose ceramide glucosyltransferase
AW157331	p < 1e-07	KIAA1246 | KIAA1246 protein
AW074266	p < 1e-07	ESTs
BF110928	p < 1e-07	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
AI961444	p < 1e-07	P37NB | 37 kDa leucine-rich repeat (LRR) protein
AK027251	p < 1e-07	FLJ23598 | hypothetical protein FLJ23598
AF131832	p < 1e-07	DKFZp761F2014 | hypothetical protein DKFZp761F2014
AI866858	0.0000002	MUC1 | mucin 1, transmembrane

AI688494	0.0000005	FLJ13189 | hypothetical protein FLJ13189
AW150267	0.0000037	C21orf9 | chromosome 21 open reading frame 9
AI038082	p < 1e-07	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 receptor (MBR,PBR, PBKS, IBP, Isoquinoline-binding protein)) LIKE protein, the gene for a novel protein similar to part of APOBEC1 (Phorbolin 1, Apolipoprotein B mRNA editing protein), and the NFYA gene for nuclear transcription factor Y, alpha (CCAAT-Binding transcription factor subunit B, CBF-B, CAAT-Box DNA binding protein subunit A). Contains ESTs, STSs, GSSs, two putative CpG islands and a ca repeat polymorphism
AL110139	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp564O1763 (from clone DKFZp564O1763)
BC002471	p < 1e-07	CPLX1 | complexin 1
AB031549	p < 1e-07	PDEF | prostate epithelium-specific Ets transcription factor
U63008	0.0000033	HGD | homogentisate 1,2-dioxygenase (homogentisate oxidase)
AF153330	p < 1e-07	SLC19A2 | solute carrier family 19 (thiamine transporter), member 2
AL136693	p < 1e-07	FLJ23462 | duodenal cytochrome b
BC007339	0.0000001	HEP27 | short-chain alcohol dehydrogenase family member
AF146192	p < 1e-07	MRPS30 | mitochondrial ribosomal protein S30
AL137748	p < 1e-07	NBEA | neurobeachin
AI989600	p < 1e-07	ESTs
AW469017	p < 1e-07	ESTs
U56725	0.0000001	HSPA2 | heat shock 70kD protein 2
AK057601	p < 1e-07	KIAA0303 | KIAA0303 protein
AI147370	p < 1e-07	ESTs
AA497018	p < 1e-07	ADCY1 | adenylate cyclase 1 (brain)
BF510257	0.0000001	PLAC1 | placenta-specific 1
AB028967	0.0000032	KCND2 | potassium voltage-gated channel, Shal-related subfamily, member 2
NM_003221	0.0004633	TFAP2B | transcription factor AP-2 beta (activating enhancer binding protein 2 beta)
AI349306	0.0000004	ESTs
AY029191	0.0000011	ASPN | asporin (LRR class 1)
BG272534	p < 1e-07	ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
AI288717	p < 1e-07	RFX2 | regulatory factor X, 2 (influences HLA class II expression)
AI080649	p < 1e-07	KIAA0938 | KIAA0938 protein
AA177001	p < 1e-07	DKFZP586J0619 | DKFZP586J0619 protein
AW340797	0.0000006	ESTs

N95437	0.000001	ESTs
BC016153	0.0000058	Homo sapiens, Similar to hypothetical protein FLJ10134, clone MGC:13208 IMAGE:3841102, mRNA, complete cds
AL136592	p < 1e-07	DKFZP761I172 | hypothetical protein DKFZp761I172
AI217517	p < 1e-07	KIAA0557 | KIAA0557 protein
AI128331	p < 1e-07	ENDOFIN | endosome-associated FYVE-domain protein
BF446355	p < 1e-07	ESTs
AK000634	p < 1e-07	FLJ20627 | hypothetical protein FLJ20627
AI655104	p < 1e-07	ESTs
AL136901	p < 1e-07	FLJ22944 | hypothetical protein FLJ22944
NM_000909	0.0000001	NPY1R | neuropeptide Y receptor Y1
AI379600	p < 1e-07	FLJ11715 | hypothetical protein FLJ11715
AF098277	p < 1e-07	SLC23A2 | solute carrier family 23 (nucleobase transporters), member 2
AI631667	p < 1e-07	Homo sapiens cDNA FLJ31763 fis, clone NT2RI2007827
AL157484	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp762M127 (from clone DKFZp762M127)
AY040546	0.0001123	Homo sapiens RPE-spondin (RPESP) mRNA, partial cds
AI373939	0.00001	GJA1 | gap junction protein, alpha 1, 43kD (connexin 43)
NM_001322	p < 1e-07	CST2 | cystatin SA
U96136	0.0000023	CTNND2 | catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)
AB038518	p < 1e-07	COLEC12 | collectin sub-family member 12
AI332972	p < 1e-07	Homo sapiens, clone MGC:9889 IMAGE:3868330, mRNA, complete cds
AL161952	p < 1e-07	GLUL | glutamate-ammonia ligase (glutamine synthase)
BE464993	p < 1e-07	Homo sapiens PAC clone RP4-751H13 from 7q35-qter
AI394310	p < 1e-07	GALNT7 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)
AW149773	0.0000001	p25 | brain-specific protein p25 alpha
Y17978	p < 1e-07	FUT8 | fucosyltransferase 8 (alpha (1,6) fucosyltransferase)
AF183421	p < 1e-07	RAB31 | RAB31, member RAS oncogene family
BE676675	p < 1e-07	RIPK3 | receptor-interacting serine-threonine kinase 3
AL096739	p < 1e-07	DKFZp586H0623 | putative UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase T9
R37016	0.0000002	KIAA0534 | KIAA0534 protein
AB018286	0.0000069	NRXN3 | neurexin 3
AK026842	p < 1e-07	FLJ23189 | hypothetical protein FLJ23189
NM_003489	p < 1e-07	NRIP1 | nuclear receptor interacting protein 1
D86322	0.0000004	CLGN | calmegin

AI951144	p < 1e-07	ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]
AA706017	p < 1e-07	ESTs
AA631782	0.0000004	EST
AL117550	p < 1e-07	LOC51643 | CGI-119 protein
AI000682	p < 1e-07	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
AJ420490	0.0000818	IL20RA | interleukin 20 receptor, alpha
AY007114	p < 1e-07	Homo sapiens clone TCCCTA00151 mRNA sequence
AF035299	p < 1e-07	DOK1 | docking protein 1, 62kD (downstream of tyrosine kinase 1)
AI039854	p < 1e-07	SYNCOILIN | intermediate filament protein syncoilin
AW139266	p < 1e-07	FLJ12057 | hypothetical protein FLJ12057
NM_003961	p < 1e-07	RHBDL | rhomboid, veinlet-like 1 (Drosophila)
AI277269	p < 1e-07	KIAA0944 | KIAA0944 protein
AF153605	p < 1e-07	AIG-1 | androgen induced protein
M60445	0.0000066	HDC | histidine decarboxylase
BC002668	p < 1e-07	PECI | peroxisomal D3,D2-enoyl-CoA isomerase
AW296675	p < 1e-07	NUCB2 | nucleobindin 2
BE464662	p < 1e-07	ESTs
AW205080	p < 1e-07	NEURL | neuralized-like (Drosophila)
Y10183	p < 1e-07	ALCAM | activated leucocyte cell adhesion molecule
AL137449	0.0000081	HOXB4 | homeo box B4
AF004222	p < 1e-07	RTN2 | reticulon 2
AK022482	p < 1e-07	Homo sapiens cDNA FLJ12420 fis, clone MAMMA1003049
NM_007069	p < 1e-07	HRASLS3 | HRAS-like suppressor 3
NM_001231	p < 1e-07	CASQ1 | calsequestrin 1 (fast-twitch, skeletal muscle)
AL136760	p < 1e-07	DKFZP434H0115 | hypothetical protein DKFZp434H0115
AI244129	0.0000001	RAMP3 | receptor (calcitonin) activity modifying protein 3
BC000548	0.0000002	RAMP1 | receptor (calcitonin) activity modifying protein 1
BC005257	0.0000724	MSMB | microseminoprotein, beta-
AF116574	p < 1e-07	ASTN2 | astrotactin 2
AA782483	p < 1e-07	REPS2 | RALBP1 associated Eps domain containing 2
AI912086	p < 1e-07	Homo sapiens cDNA FLJ30744 fis, clone FEBRA2000378
U78168	p < 1e-07	EPAC | Rap1 guanine-nucleotide-exchange factor directly activated by cAMP
AA016043	p < 1e-07	SAG | S-antigen; retina and pineal gland (arrestin)

NM_003155	0.0000041	STC1 | stanniocalcin 1
BE672557	p < 1e-07	ESTs
AK026275	p < 1e-07	FLJ22622 | hypothetical protein FLJ22622
AA993573	p < 1e-07	TGFB3 | transforming growth factor, beta 3
BC018043	0.0000003	SERPINI1 | serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1
BC006168	p < 1e-07	KIAA0089 | KIAA0089 protein
AW206445	p < 1e-07	ESTs, Weakly similar to UOG1_HUMAN UOG-1 PROTEIN [H.sapiens]
AA513133	p < 1e-07	ESTs, Weakly similar to 1209280A tropomyosin [H.sapiens]
AL080094	0.0000673	Homo sapiens mRNA; cDNA DKFZp564O1262 (from clone DKFZp564O1262)
BC009211	p < 1e-07	ELP2 | elongator protein 2
BC004161	p < 1e-07	NET-7 | transmembrane 4 superfamily member (tetraspan NET-7)
NM_001094	0.0000052	ACCN1 | amiloride-sensitive cation channel 1, neuronal (degenerin)
AL136539	p < 1e-07	DKFZP761E2110 | hypothetical protein DKFZp761E2110
AA846880	p < 1e-07	MEIS3 | Meis1, myeloid ecotropic viral integration site 1 homolog 3 (mouse)
AF144094	p < 1e-07	MYO15A | myosin XVA
AF159570	0.0000001	RGS5 | regulator of G-protein signalling 5
AW015327	p < 1e-07	IGF1R | insulin-like growth factor 1 receptor
AK021540	p < 1e-07	Homo sapiens cDNA FLJ11478 fis, clone HEMBA1001781
BC007618	0.0000001	MGC15730 | hypothetical protein MGC15730
NM_001899	p < 1e-07	CST4 | cystatin S
R74353	p < 1e-07	HNMT | histamine N-methyltransferase
AI262988	p < 1e-07	KIAA1548 | KIAA1548 protein
AA505938	p < 1e-07	EST
AI866828	0.0000073	COL10A1 | collagen, type X, alpha 1(Schmid metaphyseal chondrodysplasia)
AI076506	0.0000001	RORC | RAR-related orphan receptor C
AJ245503	0.0000001	PXR2b | PXR2b protein
AF217970	p < 1e-07	Homo sapiens clone PP1195 unknown mRNA
AI963850	p < 1e-07	KIAA1324 | KIAA1324 protein
U80811	p < 1e-07	EDG2 | endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2
AA745593	p < 1e-07	BATF | basic leucine zipper transcription factor, ATF-like
AW328488	0.0000002	PTK6 | PTK6 protein tyrosine kinase 6
AA258057	p < 1e-07	ESTs
AW104057	p < 1e-07	ESTs
AK027148	p < 1e-07	FLJ23495 | hypothetical protein FLJ23495

AW070918	p < 1e-07	ESTs, Weakly similar to T2D3_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT [H.sapiens]
AI369214	p < 1e-07	ESTs
BC002591	0.0001249	MMP10 | matrix metalloproteinase 10 (stromelysin 2)
AA431407	0.0000011	MACS1 | medium-chain acyl-CoA synthetase
BC016955	p < 1e-07	Homo sapiens cDNA: FLJ22182 fis, clone HRC00953
AI033912	0.0000003	RLN2 | relaxin 2 (H2)
AA600175	0.0000428	ESTs
AI436323	0.0000487	ROBO2 | roundabout, axon guidance receptor, homolog 2 (Drosophila)
AL136939	p < 1e-07	HELO1 | homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2
AI471839	p < 1e-07	THBD | thrombomodulin
S61953	p < 1e-07	ERBB3 | v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)
AA595802	p < 1e-07	ESTs, Weakly similar to T17279 hypothetical protein DKFZp434F1935.1 [H.sapiens]
AA865325	p < 1e-07	RAMP2 | receptor (calcitonin) activity modifying protein 2
AI866867	0.0000002	SEMA3C | sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C
AI768204	0.000014	CDSN | corneodesmosin
AI200391	0.0000004	ESTs, Weakly similar to S26689 hypothetical protein hc1 - mouse [M.musculus]
AI670779	p < 1e-07	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C WARNING ENTRY !!! [H.sapiens]
BC010924	0.0000001	PRO1073 | PRO1073 protein
NM_006103	0.0000086	WFDC2 | WAP four-disulfide core domain 2
AI955538	p < 1e-07	Homo sapiens cDNA FLJ33142 fis, clone UTERU1000192
BC010522	p < 1e-07	Homo sapiens, clone MGC:18084 IMAGE:4150952, mRNA, complete cds
N89991	p < 1e-07	Homo sapiens cDNA FLJ31149 fis, clone IMR322001491, moderately similar to Rattus norvegicus tricarboxylate carrier-like protein mRNA
AK026813	p < 1e-07	PCANAP1 | prostate cancer associated protein 1
BC003098	p < 1e-07	HSD17B4 | hydroxysteroid (17-beta) dehydrogenase 4
AK027056	0.0000001	FLJ23403 | hypothetical protein FLJ23403
AA582929	0.0000095	SERHL | kraken-like
AV656862	p < 1e-07	Homo sapiens cDNA FLJ13603 fis, clone PLACE1010270
AI686160	p < 1e-07	ESTs
R42732	p < 1e-07	ESTs
AK025000	p < 1e-07	FLJ21347 | hypothetical protein FLJ21347
AW247958	p < 1e-07	SDCCAG28 | serologically defined colon cancer antigen 28
AI804711	p < 1e-07	EST, Moderately similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING

		ENTRY [H.sapiens]
BC010553	0.0000179	TIMP4 | tissue inhibitor of metalloproteinase 4
AK027024	p < 1e-07	Homo sapiens cDNA: FLJ23371 fis, clone HEP16068, highly similar to HSTFIISH Homo sapiens mRNA for transcription elongation factor TFIIS
AL133591	0.0000241	Homo sapiens mRNA; cDNA DKFZp434N079 (from clone DKFZp434N079)
AW513195	p < 1e-07	Homo sapiens cDNA FLJ13524 fis, clone PLACE1006002
AI866286	p < 1e-07	ESTs, Weakly similar to CA13 MOUSE COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [M.musculus]
AL583912	p < 1e-07	KIF13B | kinesin family member 13B
NM_018653	0.0000004	GPRC5C | G protein-coupled receptor, family C, group 5, member C
AI218954	p < 1e-07	KIAA0717 | KIAA0717 protein
AJ420566	p < 1e-07	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1572223
BF447150	0.0000017	ESTs
AK025296	p < 1e-07	FLJ20273 | hypothetical protein
AK025732	p < 1e-07	ASAH | N-acylsphingosine amidohydrolase (acid ceramidase)
AK001648	p < 1e-07	FLJ10786 | hypothetical protein FLJ10786
BC015182	p < 1e-07	CYB5 | cytochrome b-5
R56053	0.0000002	ME3 | malic enzyme 3, NADP(+)-dependent, mitochondrial
AW450080	0.0000018	Human clone 137308 mRNA, partial cds
NM_033014	0.0000032	OGN | osteoglycin (osteoinductive factor, mimecan)
AK026817	p < 1e-07	FLJ23577 | hypothetical protein FLJ23577
R61469	0.0000454	Human (clone CTG-A4) mRNA sequence
BC002619	0.000176	LOC51617 | HMP19 protein
AI150439	p < 1e-07	KIAA1407 | KIAA1407 protein
BC017338	p < 1e-07	FUCA1 | fucosidase, alpha-L- 1, tissue
AF117708	p < 1e-07	KCNK6 | potassium channel, subfamily K, member 6 (TWIK-2)
AW139414	p < 1e-07	PRLR | prolactin receptor
AI559968	p < 1e-07	RGL3 | RalGEF-like protein 3, mouse homolog
AW195539	p < 1e-07	DDO | D-aspartate oxidase
AK024964	p < 1e-07	NFIA | nuclear factor I/A
BC004925	0.0000004	Homo sapiens, Similar to G protein-coupled receptor, family C, group 5, member C, clone MGC:10304 IMAGE:3622005, mRNA, complete cds
AJ420521	0.0000005	SMOC2 | secreted modular calcium-binding protein 2
AF271783	p < 1e-07	FLJ21174 | hypothetical protein FLJ21174
AA883246	0.0000032	Homo sapiens cDNA FLJ30428 fis, clone BRACE2008941

AW050970	0.0000062	DF | D component of complement (adipsin)
BC016615	p < 1e-07	Homo sapiens, Similar to RAB37, member of RAS oncogene family, clone MGC:21391 IMAGE:4520191, mRNA, complete cds
AI972866	p < 1e-07	ESTs
AA554481	0.0000003	ESTs
NM_014279	0.0000094	OLFM1 | olfactomedin 1
AI628869	p < 1e-07	FLJ12953 | hypothetical protein FLJ12953 similar to Mus musculus D3Mm3e
AL133636	p < 1e-07	CIRBP | cold inducible RNA binding protein
AW148329	p < 1e-07	ESTs
AL043469	0.0000007	F13A1 | coagulation factor XIII, A1 polypeptide
BC005989	0.0001701	PNLIPRP2 | pancreatic lipase-related protein 2
AL133033	p < 1e-07	KIAA1025 | KIAA1025 protein
AI536750	0.0000003	ROR2 | receptor tyrosine kinase-like orphan receptor 2
BC001638	0.000447	ASCL1 | achaete-scute complex-like 1 (Drosophila)
BC008185	p < 1e-07	FABGL | FabG (beta-ketoacyl-[acyl-carrier-protein] reductase, E coli) like (E. coli)
AA399226	p < 1e-07	TJP3 | tight junction protein 3 (zona occludens 3)
NM_003979	p < 1e-07	RAI3 | retinoic acid induced 3
AI367233	p < 1e-07	EST
BC018636	p < 1e-07	PLAT | plasminogen activator, tissue
AI565489	p < 1e-07	PDE4A | phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)
AW136191	p < 1e-07	ESTs
AI421708	p < 1e-07	Homo sapiens cDNA FLJ13137 fis, clone NT2RP3003150
AW057705	0.0000003	FLT3 | fms-related tyrosine kinase 3
AA843666	0.0000031	ESTs
BC000232	p < 1e-07	D5S346 | DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis
AB023416	p < 1e-07	ASC | apoptosis-associated speck-like protein containing a CARD
AL049987	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp564F112 (from clone DKFZp564F112)
AF261655	p < 1e-07	HMIC | 1,2-alpha-mannosidase IC
AK025683	0.0000001	Homo sapiens cDNA: FLJ22030 fis, clone HEP08669
AA401311	0.0000002	KIAA1377 | KIAA1377 protein
BF446757	p < 1e-07	ESTs
AW076080	p < 1e-07	Homo sapiens, clone IMAGE:3463399, mRNA, partial cds
BC009778	0.0000007	LOC51207 | protein phosphatase
X13897	0.0000008	CYP2A6 | cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6

AW450142	0.0000002	SLC22A4 | solute carrier family 22 (organic cation transporter), member 4
AA086248	0.0000009	ESTs
AW150018	0.0000001	FMOD | fibromodulin
AA831831	p < 1e-07	MORF | histone acetyltransferase
AL050143	p < 1e-07	DKFZP586B2420 | DKFZP586B2420 protein
AL110252	0.0000155	Homo sapiens mRNA; cDNA DKFZp566A1046 (from clone DKFZp566A1046)
M92432	0.0000243	GUCY2D | guanylate cyclase 2D, membrane (retina-specific)
AI185187	p < 1e-07	LOC51133 | NY-REN-45 antigen
AF094758	p < 1e-07	NESG1 | nasopharyngeal epithelium specific protein 1
BC012541	0.0000005	ALEX2 | armadillo repeat protein ALEX2
AW140108	0.0000121	HOXD8 | homeo box D8
AF212239	0.0000254	RBP5 | retinol binding protein 5, cellular
AK000207	p < 1e-07	FLJ20200 | hypothetical protein FLJ20200
BC002842	0.0000004	H2BFB | H2B histone family, member B
AI263595	0.0000118	ESTs
AL136911	p < 1e-07	EPLIN | epithelial protein lost in neoplasm beta
NM_004694	p < 1e-07	SLC16A6 | solute carrier family 16 (monocarboxylic acid transporters), member 6
BC007323	0.0000001	NDUFC2 | NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b)
AI474354	0.0000155	TSLRP | testis specific leucine rich repeat protein
NM_004430	0.0000026	EGR3 | early growth response 3
BM128958	p < 1e-07	KIAA1643 | KIAA1643 protein
AL360141	p < 1e-07	PEX11A | peroxisomal biogenesis factor 11A
BC000465	p < 1e-07	GADD45G | growth arrest and DNA-damage-inducible, gamma
AI629046	p < 1e-07	EMX1 | empty spiracles homolog 1 (Drosophila)
AF267859	0.0000002	FLJ13153 | hypothetical protein FLJ13153
AA654227	p < 1e-07	BCAS4 | breast carcinoma amplified sequence 4
U38276	p < 1e-07	SEMA3F | sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F
NM_053056	p < 1e-07	CCND1 | cyclin D1 (PRAD1: parathyroid adenomatosis 1)
AL117393	p < 1e-07	KIF5C | kinesin family member 5C
AI921122	0.000001	ESTs, Highly similar to dJ25J6.2 [H.sapiens]
BC009381	0.0000055	STMN3 | stathmin-like 3
AW207140	0.0000101	ARNT2 | aryl-hydrocarbon receptor nuclear translocator 2
AW083384	p < 1e-07	ESTs, Moderately similar to T46395 hypothetical protein DKFZp434I1120.1 [H.sapiens]
AJ420536	p < 1e-07	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 994183

AI561078	p < 1e-07	TSPAN-1 | tetraspan 1
AK000209	p < 1e-07	FLJ20202 | hypothetical protein FLJ20202
AI674472	p < 1e-07	EST
R40176	0.0000412	Homo sapiens cDNA FLJ32051 fis, clone NTONG2001428
NM_003248	0.0000968	THBS4 | thrombospondin 4
AK023243	p < 1e-07	FLJ13181 | hypothetical protein FLJ13181
AB000509	p < 1e-07	TRAF5 | TNF receptor-associated factor 5
AA400069	0.0000004	FLJ13031 | hypothetical protein FLJ13031
AA846684	p < 1e-07	ESTs
AI744756	p < 1e-07	ESTs
AK001889	0.0000002	Homo sapiens cDNA FLJ11027 fis, clone PLACE1004114
AA557345	0.0000009	EST, Weakly similar to 2109260A B cell growth factor [H.sapiens]
NM_012168	0.0000109	FBXO2 | F-box only protein 2
BF475464	p < 1e-07	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
AL050116	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp586A131 (from clone DKFZp586A131)
NM_001089	p < 1e-07	ABCA3 | ATP-binding cassette, sub-family A (ABC1), member 3
BC017586	0.0000002	Homo sapiens, Similar to RIKEN cDNA 1700028N11 gene, clone MGC:26610 IMAGE:4837506, mRNA, complete cds
AW006452	0.0000006	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
AI097387	p < 1e-07	PRO1489 | hypothetical protein PRO1489
AA601573	p < 1e-07	ESTs
AW080826	p < 1e-07	KIAA0984 | KIAA0984 protein
AI809547	0.0000005	ESTs
AJ420459	p < 1e-07	LOC51184 | protein x 0004
BE856073	p < 1e-07	STK39 | serine threonine kinase 39 (STE20/SPS1 homolog, yeast)
AK000416	0.0000062	SLC16A5 | solute carrier family 16 (monocarboxylic acid transporters), member 5
AW291846	p < 1e-07	C21orf15 | chromosome 21 open reading frame 15
AI971681	0.000003	PLCE | phospholipase C, epsilon
AL157455	0.000004	Homo sapiens mRNA; cDNA DKFZp761I1912 (from clone DKFZp761I1912)
AI823660	0.0000048	Homo sapiens cDNA: FLJ22133 fis, clone HEP20529
AF137027	0.0000933	TCL1B | T-cell leukemia/lymphoma 1B
AF161423	p < 1e-07	PTD002 | PTD002 protein
NM_006186	0.0000034	NR4A2 | nuclear receptor subfamily 4, group A, member 2

BC009522	0.0000046	SSTR2 | somatostatin receptor 2
AI783781	0.0002071	EST
AL157492	p < 1e-07	DKFZP434P0111 | hypothetical protein DKFZp434P0111
AK000691	p < 1e-07	FLJ22174 | hypothetical protein FLJ22174
BC004312	0.0000013	IGFBP2 | insulin-like growth factor binding protein 2 (36kD)
AA973836	0.0001602	ESTs
AL049223	p < 1e-07	SCAMP1 | secretory carrier membrane protein 1
AI650407	p < 1e-07	ESTs
AA054983	p < 1e-07	EST
AA643697	0.000009	ESTs
BC000059	0.0000092	CELSR1 | cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)
BC008703	p < 1e-07	MGC15737 | hypothetical protein MGC15737
AK054785	p < 1e-07	Homo sapiens cDNA FLJ30223 fis, clone BRACE2001785
AK025209	p < 1e-07	Homo sapiens cDNA: FLJ21556 fis, clone COL06353
AY033290	p < 1e-07	LABH1 | lung alpha/beta hydrolase 1
AW074143	0.0000002	ESTs
AL137419	0.0001168	C12orf3 | chromosome 12 open reading frame 3
AI031941	p < 1e-07	ESTs, Weakly similar to YEX0_YEAST HYPOTHETICAL 64.8 KDA PROTEIN IN GDI1-COX15 INTERGENIC REGION [S.cerevisiae]
BF511644	p < 1e-07	ESTs, Weakly similar to Z195_HUMAN ZINC FINGER PROTEIN 195 [H.sapiens]
BF436282	p < 1e-07	RBSK | ribokinase
AA854788	p < 1e-07	KAL1 | Kallmann syndrome 1 sequence
H08145	0.0000011	ESTs
NM_000139	0.0000023	MS4A2 | membrane-spanning 4-domains, subfamily A, member 1
NM_000142	0.000013	FGFR3 | fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
AI204186	0.0001851	ESTs
AI341790	p < 1e-07	Homo sapiens, clone MGC:2492 IMAGE:3353520, mRNA, complete cds
AI499814	p < 1e-07	KIAA1372 | KIAA1372 protein
BC014000	p < 1e-07	Homo sapiens, clone MGC:20208 IMAGE:3936339, mRNA, complete cds
AI221721	0.0000001	CBFA2T3 | core-binding factor, runt domain, alpha subunit 2; translocated to, 3
AW139237	0.000015	ESTs
AA910336	0.0000163	ESTs
AK022443	0.0000003	Homo sapiens cDNA FLJ12381 fis, clone MAMMA1002566
AL133030	0.0000029	KIAA1666 | KIAA1666 protein

AK025532	p < 1e-07	FLJ21213 | hypothetical protein FLJ21213
AL119854	0.0000017	KIAA1789 | KIAA1789 protein
AA613425	0.0000152	COMP | cartilage oligomeric matrix protein (pseudoachondroplasia, epiphyseal dysplasia 1, multiple)
AF245044	p < 1e-07	HT023 | hypothetical protein HT023
AI951472	p < 1e-07	FLJ10724 | melanoma antigen recognized by T cells 2
AK026216	p < 1e-07	Homo sapiens cDNA: FLJ22563 fis, clone HSI01928
BC017772	0.0000182	HT021 | HT021
AI810347	p < 1e-07	ESTs, Weakly similar to ABP2_HUMAN ENDOTHELIAL ACTIN-BINDING PROTEIN [H.sapiens]
X86163	0.0000009	BDKRB2 | bradykinin receptor B2
U67784	0.0000164	RDC1 | G protein-coupled receptor
BC013083	p < 1e-07	CST3 | cystatin C (amyloid angiopathy and cerebral hemorrhage)
AK025047	0.0000001	FLJ21394 | hypothetical protein FLJ21394
AF288571	0.0000002	LEF1 | lymphoid enhancer-binding factor 1
BC002865	0.0000004	MGC11242 | hypothetical protein MGC11242
BF061965	0.0000011	KIAA1257 | KIAA1257 protein
H05388	0.0000808	KIAA0844 | KIAA0844 protein
AF243505	0.0002923	OTOR | otoraplin
AL136721	p < 1e-07	DKFZP566K1946 | hypothetical protein DKFZp566K1946
AK024715	p < 1e-07	FLJ21062 | hypothetical protein FLJ21062
W52485	p < 1e-07	MST1 | macrophage stimulating 1 (hepatocyte growth factor-like)
AA398015	0.0006358	CLECSF1 | C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 1 (cartilage-derived)
NM_001771	p < 1e-07	CD22 | CD22 antigen
AW451965	p < 1e-07	ESTs
NM_004425	0.0000213	ECM1 | extracellular matrix protein 1
AA962285	p < 1e-07	KIAA1010 | KIAA1010 protein
BC011806	p < 1e-07	FLJ13187 | phafin 2
AI304875	p < 1e-07	DGKD | diacylglycerol kinase, delta (130kD)
AA406206	0.0000026	EPB41L4 | erythrocyte protein band 4.1-like 4
BC004540	0.0000031	MGC11287 | hypothetical protein MGC11287 similar to ribosomal protein S6 kinase ,
L13773	p < 1e-07	MLLT2 | myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2
AK026698	p < 1e-07	FLJ23045 | hypothetical protein FLJ23045
BC007617	p < 1e-07	G6PT1 | glucose-6-phosphatase, transport (glucose-6-phosphate) protein 1
BF447022	0.0000008	EST

AL080136	0.0005363	SPAG6 | sperm associated antigen 6
BC000691	p < 1e-07	LOC51673 | brain specific protein
BF939249	p < 1e-07	ESTs
AF113212	0.0000001	MSTP032 | MSTP032 protein
AI620139	p < 1e-07	ESTs
BC014336	0.0000002	HHEX | hematopoietically expressed homeobox
AI241077	0.0001517	PAH | phenylalanine hydroxylase
BC015571	p < 1e-07	SLC22A1L | solute carrier family 22 (organic cation transporter), member 1-like
T23696	p < 1e-07	FLJ20015 | hypothetical protein
AW196636	p < 1e-07	ESTs
R38689	0.0000006	PCLO | piccolo (presynaptic cytomatrix protein)
AJ251053	0.0000017	STHM | sialyltransferase
BC002757	0.0000033	COX7A1 | cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)
X59766	0.0000194	AZGP1 | alpha-2-glycoprotein 1, zinc
AK000772	p < 1e-07	BA526D8.4 | KRAB box containing C2H2 type zinc finger bA526D8.4
AW134884	0.0000014	GHRH | growth hormone releasing hormone
AF263545	0.0000217	Homo sapiens HUT11 protein mRNA, partial 3' UTR
AF034996	0.0000879	AMPH | amphiphysin (Stiff-Mann syndrome with breast cancer 128kD autoantigen)
NM_004029	p < 1e-07	IRF7 | interferon regulatory factor 7
AI216751	0.0005965	ESTs
AI350518	p < 1e-07	ESTs
AL049329	p < 1e-07	DKFZP564G196 | DKFZP564G196 protein
AK023757	p < 1e-07	Homo sapiens cDNA FLJ13695 fis, clone PLACE2000124
AI338252	p < 1e-07	LARGE | like-glycosyltransferase
NM_005410	0.0001146	SEPP1 | selenoprotein P, plasma, 1
AK024898	p < 1e-07	Homo sapiens cDNA: FLJ21245 fis, clone COL01184
AW207060	p < 1e-07	DNAJL1 | hypothetical protein similar to mouse Dnajl1
AL136790	p < 1e-07	DKFZp434F1819 | hypothetical protein DKFZp434F1819
AI973194	p < 1e-07	OVGP1 | oviductal glycoprotein 1, 120kD (mucin 9, oviductin)
U01824	0.0000003	SLC1A2 | solute carrier family 1 (glial high affinity glutamate transporter), member 2
AL136789	0.0000006	DKFZp434F1719 | hypothetical protein DKFZp434F1719
BC014277	0.0000017	TIMP3 | tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)
AK024750	0.0000299	C11orf14 | chromosome 11 open reading frame 14
BC000187	0.0000002	COX6C | cytochrome c oxidase subunit VIc

AB025904	p < 1e-07	CA14 | carbonic anhydrase XIV
AW004703	0.0000002	FLJ10916 | hypothetical protein FLJ10916
AK001865	0.0000065	Homo sapiens cDNA FLJ11003 fis, clone PLACE1002851
AK026690	p < 1e-07	Homo sapiens cDNA: FLJ23037 fis, clone LNG02036, highly similar to HSU68019 Homo sapiens mad protein homolog (hMAD-3) mRNA
BC001526	p < 1e-07	Homo sapiens, clone MGC:3245 IMAGE:3505639, mRNA, complete cds
BC014651	0.0000068	HOXB6 | homeo box B6
AF085233	0.0000138	SGKL | serum/glucocorticoid regulated kinase-like
AF000546	0.0000001	P2Y5 | purinergic receptor (family A group 5)
AL109959	p < 1e-07	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1019273
R15800	p < 1e-07	ESTs
AW069800	0.0000002	Homo sapiens cDNA FLJ11685 fis, clone HEMBA1004934
AA906471	0.0000003	ESTs, Weakly similar to A28996 proline-rich protein M14 precursor - mouse [M.musculus]
AA233862	0.0000017	ESTs
AK056155	p < 1e-07	Homo sapiens cDNA FLJ31593 fis, clone NT2RI2002481
AI214383	p < 1e-07	SYNGR1 | synaptogyrin 1
AW070489	p < 1e-07	HOXC6 | homeo box C6
AI401095	p < 1e-07	EST
AK027245	0.0000001	LOC55815 | hypothetical protein
AW732240	0.0000024	ESTs
AF130068	0.0000027	SERPINA1 | serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1
AA766862	p < 1e-07	KIAA0298 | KIAA0298 gene product
AA765256	0.0000004	ESTs, Weakly similar to unnamed protein product [H.sapiens]
AA805317	0.0000038	HOXC4 | homeo box C4
AF119815	0.0000147	GPR74 | G protein-coupled receptor 74
X97881	p < 1e-07	GPRK2L | G protein-coupled receptor kinase 2-like (Drosophila)
BF431989	0.0000001	ESTs
AI939560	p < 1e-07	ESTs, Weakly similar to CIKF_HUMAN VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 [H.sapiens]
AK024106	0.0000006	Homo sapiens cDNA FLJ14044 fis, clone HEMBA1006124
X95715	0.0000013	ABCC6 | ATP-binding cassette, sub-family C (CFTR/MRP), member 6
AJ409065	p < 1e-07	LEAP-2 | liver-expressed antimicrobial peptide 2
AW590215	p < 1e-07	SLC4A8 | solute carrier family 4, sodium bicarbonate cotransporter, member 8
BF508608	0.000066	Homo sapiens cDNA FLJ12993 fis, clone NT2RP3000197
BF508719	0.0006111	CGI-96 | CGI-96 protein

AK023905	p < 1e-07	Homo sapiens cDNA FLJ13843 fis, clone THYRO1000796
AA631898	p < 1e-07	EST
AF030186	0.0001916	GPC4 | glypican 4
AI655416	p < 1e-07	FLJ11756 | hypothetical protein FLJ11756
BI492432	0.0000001	PMP22 | peripheral myelin protein 22
AI273078	0.0000001	ELL2 | ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR
BC011690	p < 1e-07	CORO2A | coronin, actin binding protein, 2A
AI695809	p < 1e-07	A1BG | alpha-1-B glycoprotein
AI753700	p < 1e-07	ESTs
AI567961	0.0000001	Homo sapiens cDNA FLJ13557 fis, clone PLACE1007737
AA053400	0.0000015	ESTs
AF182316	p < 1e-07	FER1L3 | fer-1-like 3, myoferlin (C. elegans)
AI096474	0.0000001	APXL | apical protein-like (Xenopus laevis)
BF475375	0.0000002	EST
AI125473	0.0000075	ESTs
NM_001900	0.0000093	CST5 | cystatin D
AF173081	0.0006871	VELI1 | Vertebrate LIN7 homolog 1, Tax interaction protein 33
AK024733	0.0000009	FLJ21080 | hypothetical protein FLJ21080
AI341378	0.0000025	ESTs, Moderately similar to KIAA0940 protein [H.sapiens]
AF334710	0.0000246	Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence
AW073096	0.0001789	ESTs
AI373912	0.0005046	HABP2 | hyaluronan binding protein 2
BC014949	p < 1e-07	LGP2 | likely ortholog of mouse D11lgp2
AA160784	p < 1e-07	ESTs
AL359558	0.0000013	Homo sapiens mRNA; cDNA DKFZp762O1615 (from clone DKFZp762O1615)
AI335013	0.0000015	Homo sapiens cDNA FLJ12052 fis, clone HEMBB1002042, moderately similar to CYTOCHROME P450 4C1 (EC 1.14.14.1)
AW138839	0.0000113	ESTs
R54824	0.0001665	PCDH19 | protocadherin 19
N52765	0.0002372	CACNA1I | calcium channel, voltage-dependent, alpha 1I subunit
AI571426	0.0006325	SFRP4 | secreted frizzled-related protein 4
AI675370	0.0000005	Homo sapiens cDNA FLJ30279 fis, clone BRACE2002772, moderately similar to HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
AW452172	0.000098	ESTs

BC001356	p < 1e-07	IFI35 | interferon-induced protein 35
AK026642	0.0000001	C20orf35 | chromosome 20 open reading frame 35
AL133102	0.0000012	CGI-142 | CGI-142
AI950985	0.0000045	ESTs
BC002709	p < 1e-07	TP53TG1 | TP53 target gene 1
BE465899	p < 1e-07	ESTs
AA905217	0.0000049	Homo sapiens cDNA FLJ25460 fis, clone TST09046
BC007659	0.0000091	NQO1 | NAD(P)H dehydrogenase, quinone 1
M73481	p < 1e-07	GRPR | gastrin-releasing peptide receptor
AI912080	p < 1e-07	ESTs
AF039698	p < 1e-07	SDCCAG33 | serologically defined colon cancer antigen 33
AI668861	p < 1e-07	C18orf1 | chromosome 18 open reading frame 1
AW139766	p < 1e-07	ESTs
AK000322	0.0000112	FLJ20315 | hypothetical protein FLJ20315
R52665	0.0000001	KIAA0323 | KIAA0323 protein
AY014282	0.0000008	FLJ12476 | hypothetical protein FLJ12476
AF264784	p < 1e-07	TRPS1 | trichorhinophalangeal syndrome I
AF073770	0.0000002	CROT | carnitine O-octanoyltransferase
X08020	0.0000003	GSTM1 | glutathione S-transferase M1
L03785	p < 1e-07	MYL5 | myosin, light polypeptide 5, regulatory
AI651570	p < 1e-07	PCM1 | pericentriolar material 1
AL049949	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp564L0822 (from clone DKFZp564L0822)
AK027191	0.0000008	Homo sapiens cDNA: FLJ23538 fis, clone LNG08010, highly similar to BETA2 Human MEN1 region clone epsilon/beta mRNA
AW450777	0.0000011	FLJ14009 | hypothetical protein FLJ14009
AI027237	0.0000012	CACNA2D2 | calcium channel, voltage-dependent, alpha 2/delta subunit 2
AA668884	0.0000034	ESTs
AL360254	0.0000007	SLI | neuronal Shc adaptor homolog
BC014123	p < 1e-07	FLJ20920 | hypothetical protein FLJ20920
AF334676	0.0001389	TEKT3 | tektin 3
AI123176	p < 1e-07	ESTs
AK026782	p < 1e-07	FLJ23129 | hypothetical protein FLJ23129
AF047033	0.0000008	SLC4A7 | solute carrier family 4, sodium bicarbonate cotransporter, member 7
BF509554	0.0000021	ESTs

NM_001337	0.0003886	CX3CR1 | chemokine (C-X3-C) receptor 1
AL353936	0.0004393	DKFZp761K1423 | hypothetical protein DKFZp761K1423
AF285836	0.0000001	NPDC1 | neural proliferation, differentiation and control, 1
AF038633	0.0000003	UCN | urocortin
AW301079	0.0006045	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
BF432086	0.0006733	LOC63923 | hypothetical protein similar to tenascin-R
T52873	0.0000001	ESTs, Moderately similar to G02075 transcription repressor zinc finger protein 85 [H.sapiens]
AB018303	0.0000147	OAZ | OLF-1/EBF associated zinc finger gene
AA233494	0.000036	ZNF132 | zinc finger protein 132 (clone pHZ-12)
AK057894	0.0000335	Homo sapiens cDNA FLJ25165 fis, clone CBR08421
AF132197	p < 1e-07	PRO1331 | hypothetical protein PRO1331
AL122071	0.0004254	Homo sapiens mRNA; cDNA DKFZp434H1235 (from clone DKFZp434H1235); partial cds
AK054617	0.0006328	Homo sapiens cDNA FLJ30055 fis, clone ADRGL1000165, weakly similar to IMIDAZOLONEPROPIONASE (EC 3.5.2.7)
AK024986	0.0000001	Homo sapiens cDNA: FLJ21333 fis, clone COL02535
L11672	0.0000009	ZNF91 | zinc finger protein 91 (HPF7, HTF10)
AK025583	0.0000089	Homo sapiens cDNA: FLJ21930 fis, clone HEP04301, highly similar to HSU90916 Human clone 23815 mRNA sequence
R92436	0.0000707	ESTs
AF062595	0.0002667	AK5 | adenylate kinase 5
AW575162	0.0000014	ACP5 | acid phosphatase 5, tartrate resistant
AB067468	0.0000552	KIAA1881 | KIAA1881 protein
AF192522	0.0001271	NPC1L1 | NPC1 (Niemann-Pick disease, type C1, gene)-like 1
AI668626	0.0000009	Homo sapiens cDNA FLJ11648 fis, clone HEMBA1004405
NM_017458	p < 1e-07	MVP | major vault protein
AI393709	0.0000001	DFFA | DNA fragmentation factor, 45 kD, alpha polypeptide
BC003667	0.0000003	RPS27L | ribosomal protein S27-like
BE857676	0.0004456	ESTs
AI910755	0.0000002	ESTs
Z48633	0.0000007	H.sapiens mRNA for retrotransposon
AK024192	0.000001	Homo sapiens cDNA FLJ14130 fis, clone MAMMA1002618
L10386	0.0000027	TGM3 | transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase)
BC014105	0.0000005	LOC51015 | CGI-111 protein

H10298	0.000003	ESTs
AI620965	0.0000143	ESTs
BF056618	0.0002275	C20orf39 | chromosome 20 open reading frame 39
AI984359	0.0000002	MAWBP | MAWD binding protein
BC018001	0.0000004	MB | myoglobin
AK026839	0.0000347	FLJ23186 | hypothetical protein FLJ23186
BC012069	p < 1e-07	NUDT4 | nudix (nucleoside diphosphate linked moiety X)-type motif 4
H66199	0.0000002	OR2W3P | olfactory receptor, family 2, subfamily W, member 3 pseudogene
AL080213	0.0000003	Homo sapiens mRNA; cDNA DKFZp586I1823 (from clone DKFZp586I1823)
NM_030761	0.0000204	WNT4 | wingless-type MMTV integration site family, member 4
AF052224	0.0000265	BSN | bassoon (presynaptic cytomatrix protein)
NM_002625	0.0000553	PFKFB1 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1
AI741469	0.0000946	ESTs
AW293219	0.0004089	Homo sapiens cDNA FLJ12280 fis, clone MAMMA1001744
BC002752	0.0000008	PTD015 | PTD015 protein
BC010082	0.0000028	Homo sapiens, Similar to hypothetical protein FLJ10761, clone MGC:19512 IMAGE:4329734, mRNA, complete cds
AI954686	0.0001698	BFSP2 | beaded filament structural protein 2, phakinin
AI620480	0.0003718	EST
AA758546	0.0004796	LOC51086 | putative protein-tyrosine kinase
NM_001873	0.000995	CPE | carboxypeptidase E
BC009789	0.0000001	NPHP1 | nephronophthisis 1 (juvenile)
AF218006	0.0000018	FLJ13612 | hypothetical protein FLJ13612
AA580186	0.0000046	EST
AI247211	0.0000002	ESTs
BC010117	0.0000006	MGC13038 | hypothetical protein MGC13038
X55720	0.0000006	CSF3R | colony stimulating factor 3 receptor (granulocyte)
X79676	0.0000117	PTPN13 | protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)
BC002415	0.0002872	GSTT2 | glutathione S-transferase theta 2
AI703322	0.0006439	PLIN | perilipin
NM_004370	0.0000819	COL12A1 | collagen, type XII, alpha 1
AW129056	0.0002021	KIAA0485 | KIAA0485 protein
AL512723	0.0000013	DKFZP547L112 | hypothetical protein DKFZp547L112
AW613521	0.0000207	CLST11240 | CLST 11240 protein

AI280246	0.0000795	ESTs
AA827649	0.0000004	ESTs
AL161983	0.0000075	Homo sapiens mRNA; cDNA DKFZp761K2024 (from clone DKFZp761K2024)
AW453001	0.0006444	CEBPD | CCAAT/enhancer binding protein (C/EBP), delta
AK025062	0.0000513	Homo sapiens cDNA: FLJ21409 fis, clone COL03924
H19223	0.0000011	ESTs, Weakly similar to JC5238 galactosylceramide-like protein, GCP [H.sapiens]
BC011628	0.0000027	EPHX2 | epoxide hydrolase 2, cytoplasmic
NM_007023	0.0000149	CAMP-GEFII | cAMP-regulated guanine nucleotide exchange factor II
AI888490	0.0002268	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
AL133606	0.0000006	FLJ11142 | hypothetical protein FLJ11142
AL096842	0.0000008	ATIP1 | AT2 receptor-interacting protein 1
AW301074	0.0000056	ESTs, Weakly similar to GTXH_HUMAN GLUTATHIONE-S-TRANSFERASE HOMOLO [H.sapiens]
AF131794	0.0004664	KIAA0878 | KIAA0878 protein
AI499501	0.0001437	ESTs, Weakly similar to FMOD_HUMAN FIBROMODULIN PRECURSOR [H.sapiens]
AF002672	0.0002138	LOH11CR2A | loss of heterozygosity, 11, chromosomal region 2, gene A
AK000785	0.0000103	FLJ20778 | epsin 3
AW183685	0.0000151	ESTs
BC017422	0.0000003	Homo sapiens, clone MGC:27375 IMAGE:4688423, mRNA, complete cds
BE501103	0.0000003	Homo sapiens cDNA FLJ32173 fis, clone PLACE6000953
BC005066	0.0000003	Homo sapiens, clone IMAGE:3347954, mRNA, partial cds
BC006534	0.0000028	SARCOSIN | sarcomeric muscle protein
AI800042	0.000004	ESTs
AB062787	0.0000042	TREM2 | triggering receptor expressed on myeloid cells 2
NM_001197	0.0000451	BIK | BCL2-interacting killer (apoptosis-inducing)
BC013151	0.0000006	Homo sapiens, Similar to RIKEN cDNA 4933433C09 gene, clone MGC:21628 IMAGE:4385421, mRNA, complete cds
BC001314	0.0000018	Homo sapiens, Similar to clone FLB3816, clone IMAGE:3454380, mRNA
BC000006	0.0000506	ATP1B1 | ATPase, Na+/K+ transporting, beta 1 polypeptide
R63503	0.0000015	ESTs
AI733491	0.0000215	ESTs
BC009753	0.0000598	Homo sapiens, clone IMAGE:3833472, mRNA
BC008857	0.0000022	NFATC4 | nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4
S77873	0.0000023	CYP2E | cytochrome P450, subfamily IIE (ethanol-inducible)
AF131833	0.0003466	LOC57795 | hypothetical protein from clone 24828

<table>
<tr><td>AF101477</td><td>0.0004668</td><td>GNMT | glycine N-methyltransferase</td></tr>
<tr><td>AA708035</td><td>0.0005873</td><td>ESTs</td></tr>
<tr><td>BC005997</td><td>0.0000003</td><td>MGC14801 | hypothetical protein MGC14801</td></tr>
<tr><td>BE501474</td><td>0.000001</td><td>Homo sapiens mRNA; cDNA DKFZp434P182 (from clone DKFZp434P182)</td></tr>
<tr><td>AI499593</td><td>0.0000015</td><td>IRX5 | iroquois homeobox protein 5</td></tr>
<tr><td>AW136984</td><td>0.0000906</td><td>FLJ11235 | hypothetical protein</td></tr>
<tr><td>BC007808</td><td>0.000002</td><td>MYH7B | myosin, heavy polypeptide 7B, cardiac muscle, beta</td></tr>
<tr><td>AI311127</td><td>0.0000065</td><td>ESTs</td></tr>
<tr><td>AF094754</td><td>0.0000257</td><td>GLRB | glycine receptor, beta</td></tr>
<tr><td>AW118445</td><td>0.0000387</td><td>CELSR2 | cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)</td></tr>
<tr><td>AL136678</td><td>0.0000276</td><td>FLJ12428 | hypothetical protein FLJ12428</td></tr>
<tr><td>AI733703</td><td>0.0004539</td><td>ESTs</td></tr>
<tr><td>AK025915</td><td>0.0000003</td><td>Homo sapiens cDNA FLJ10728 fis, clone NT2RP3001236</td></tr>
<tr><td>AW205835</td><td>0.0000026</td><td>ESTs</td></tr>
<tr><td>AI205008</td><td>0.0000041</td><td>SLC1A4 | solute carrier family 1 (glutamate/neutral amino acid transporter), member 4</td></tr>
<tr><td>AL161993</td><td>0.0000451</td><td>LOC57168 | similar to aspartate beta hydroxylase (ASPH)</td></tr>
<tr><td>NM_013267</td><td>0.00005</td><td>GA | breast cell glutaminase</td></tr>
<tr><td>AA758934</td><td>0.000002</td><td>Homo sapiens cDNA FLJ13362 fis, clone PLACE1000236</td></tr>
<tr><td>BC015947</td><td>0.0001039</td><td>KCNS3 | potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3</td></tr>
<tr><td>AF226730</td><td>0.0003918</td><td>Cyt19 | Cyt19 protein</td></tr>
<tr><td>AW139590</td><td>0.0002061</td><td>KIAA1443 | KIAA1443 protein</td></tr>
<tr><td>NM_005906</td><td>0.0003675</td><td>MAK | male germ cell-associated kinase</td></tr>
<tr><td>BC005124</td><td>0.0008792</td><td>HOXD3 | homeo box D3</td></tr>
<tr><td>AI922007</td><td>0.0000011</td><td>ESTs</td></tr>
<tr><td>AW082270</td><td>0.0000015</td><td>ESTs, Highly similar to AC004836 1 similar to cadherin and Drosophila Fat protein [H.sapiens]</td></tr>
<tr><td>AY014284</td><td>0.0000449</td><td>TSGA10 | testis specific, 10</td></tr>
<tr><td>AJ406933</td><td>0.0001677</td><td>KAP3.3 | keratin associated protein 3.3</td></tr>
<tr><td>AW470748</td><td>0.0000153</td><td>BCAR3 | breast cancer anti-estrogen resistance 3</td></tr>
<tr><td>U06641</td><td>0.0000758</td><td>UGT2B15 | UDP glycosyltransferase 2 family, polypeptide B15</td></tr>
<tr><td>AI658924</td><td>0.0006314</td><td>EST</td></tr>
<tr><td>BC002689</td><td>0.0000016</td><td>GLA | galactosidase, alpha</td></tr>
<tr><td>AF023676</td><td>0.000007</td><td>TM7SF2 | transmembrane 7 superfamily member 2</td></tr>
<tr><td>BC001109</td><td>0.0001481</td><td>CRABP2 | cellular retinoic acid binding protein 2</td></tr>
<tr><td>BC000897</td><td>0.0005356</td><td>IFITM1 | interferon induced transmembrane protein 1 (9-27)</td></tr>
</table>

BC017703	0.0002482	LRRFIP2 | leucine rich repeat (in FLII) interacting protein 2
BF436849	0.0000019	ESTs
AV661191	0.0000777	PDCD4 | programmed cell death 4 (neoplastic transformation inhibitor)
BC015657	0.0004846	OA1 | ocular albinism 1 (Nettleship-Falls)
N94443	0.0006496	KIAA0802 | KIAA0802 protein
AK025431	0.0000008	Homo sapiens cDNA: FLJ21778 fis, clone HEP00201
AF016267	0.0000016	TNFRSF10C | tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain
AF297872	0.000004	TReP-132 | transcriptional regulating protein 132
BC003180	0.0000047	SNRPN | small nuclear ribonucleoprotein polypeptide N
AI804733	0.0000051	Homo sapiens cDNA FLJ32322 fis, clone PROST2003577
AI026838	0.0000127	ESTs, Weakly similar to NUCL_HUMAN NUCLEOLIN [H.sapiens]
AI097422	0.0000658	LOC57100 | organic cation transporter
AA912183	0.0005194	ESTs
AI399698	0.0000126	EST
AI272951	0.0000286	SERPINC1 | serine (or cysteine) proteinase inhibitor, clade C (antithrombin), member 1
AW448954	0.0000899	FLJ14871 | hypothetical protein FLJ14871
AK027207	0.0007043	FLJ23554 | hypothetical protein FLJ23554
BC010691	0.0000064	MGC9564 | similar to RIKEN cDNA 1110002C08 gene
BC011973	0.0000109	FLJ20605 | hypothetical protein FLJ20605
AW341854	0.000012	SPAG8 | sperm associated antigen 8
BC014456	0.0006392	CHRNA6 | cholinergic receptor, nicotinic, alpha polypeptide 6
AF037070	0.0000154	KIAA0464 | ligand of neuronal nitric oxide synthase with carboxyl-terminal PDZ domain
BC007373	0.000041	MGC16179 | hypothetical protein MGC16179
BC010690	0.0003139	FLJ14529 | hypothetical protein FLJ14529
AI740671	0.0003413	Homo sapiens cDNA FLJ32430 fis, clone SKMUS2001129, weakly similar to NAD-DEPENDENT METHANOL DEHYDROGENASE (EC 1.1.1.244)
AI199647	0.0000028	SCNN1D | sodium channel, nonvoltage-gated 1, delta
AI659491	0.0000053	EST
AA854341	0.0000092	Homo sapiens cDNA FLJ12924 fis, clone NT2RP2004709
NM_005677	0.0000028	COLQ | collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase
AK057782	0.000412	Homo sapiens cDNA FLJ25053 fis, clone CBL04266
AL080078	0.0000036	Homo sapiens mRNA; cDNA DKFZp564D1462 (from clone DKFZp564D1462)
AI434326	0.0004414	ATP2A3 | ATPase, Ca++ transporting, ubiquitous
AF331643	0.000005	Homo sapiens chromosome 17 open reading frame 26 (C17orf26) mRNA, complete cds

BC007438	0.0000058	MGC4251 | hypothetical protein MGC4251
AA555036	0.0000147	SORD | sorbitol dehydrogenase
AK021467	0.0000544	Homo sapiens cDNA FLJ11405 fis, clone HEMBA1000769
BF001174	0.0000709	CAP2 | adenylyl cyclase-associated protein 2
AL136680	0.0004515	Homo sapiens mRNA; cDNA DKFZp564C2478 (from clone DKFZp564C2478); complete cds
AL110174	0.0005604	STMN2 | stathmin-like 2
AK026288	0.0004417	FLJ22635 | hypothetical protein FLJ22635
NM_003512	0.0005828	H2AFL | H2A histone family, member L
AW070686	0.000002	ESTs
BC000866	0.0000034	TIMP1 | tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)
AF070555	0.0000131	PRSS11 | protease, serine, 11 (IGF binding)
AI962213	0.0001497	KIAA0705 | atrophin-1 interacting protein 1; activin receptor interacting protein 1
AW419319	0.0008904	ODZ2 | odd Oz/ten-m homolog 2 (Drosophila, mouse)
N70848	0.0000023	ESTs, Moderately similar to I38022 hypothetical protein [H.sapiens]
NM_001773	0.0009366	CD34 | CD34 antigen
AK026301	0.0009911	Homo sapiens cDNA: FLJ22648 fis, clone HSI07329
F10094	0.0000158	ESTs
AK055747	0.0007753	FLJ13236 | hypothetical protein FLJ13236
AI797308	0.0000092	ESTs, Weakly similar to alternatively spliced product using exon 13A [H.sapiens]
AA746504	0.0000207	Homo sapiens cDNA FLJ30188 fis, clone BRACE2001267
AK025307	0.0000623	CPT1A | carnitine palmitoyltransferase I, liver
BC005357	0.0000049	MGC12458 | hypothetical protein MGC12458
U31214	0.0000475	FXYD3 | FXYD domain-containing ion transport regulator 3
AW243677	0.00001	FLJ22457 | hypothetical protein FLJ22457
AI868636	0.0001498	Homo sapiens cDNA FLJ30403 fis, clone BRACE2008480
AI659877	0.0008135	ESTs
AK025627	0.0000049	Homo sapiens, clone IMAGE:3937015, mRNA, partial cds
AI811067	0.0000149	Homo sapiens cDNA FLJ31422 fis, clone NT2NE2000384, weakly similar to MICRONUCLEAR LINKER HISTONE POLYPROTEIN
AW139902	0.0002142	ESTs
AB020711	0.0008427	KIAA0904 | KIAA0904 protein
AW339037	0.0000243	ESTs
AV647264	0.0000324	ESTs
AI002941	0.0000063	Human glucose transporter pseudogene

BC017073	0.0007021	Homo sapiens, Similar to RIKEN cDNA 1810054O13 gene, clone IMAGE:3845933, mRNA, partial cds
AW102641	0.0000112	ESTs
AK000341	0.0000133	ELOVL2 | elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2
NM_030878	0.0007446	CYP2C8 | cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 8
AF288399	0.0000055	C1orf25 | chromosome 1 open reading frame 25
BC005956	0.0000248	RLN1 | relaxin 1 (H1)
D50419	0.0000877	ZNF175 | zinc finger protein 175
AK025905	0.0002948	SOX17 | SRY-related HMG-box transcription factor SOX17
AK026760	0.0000265	C20orf119 | chromosome 20 open reading frame 119
AA999861	0.0001219	ESTs
AA883836	0.0003305	ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]
AJ420485	0.0000088	MRPL33 | mitochondrial ribosomal protein L33
BF511682	0.0004053	HSH2 | hematopoietic SH2 protein
M59303	0.0000685	PROZ | protein Z, vitamin K-dependent plasma glycoprotein
BM127823	0.0001431	KIAA1917 | KIAA1917 protein
U60975	0.0002497	SORL1 | sortilin-related receptor, L(DLR class) A repeats-containing
AA659779	0.0000288	ESTs
BC006289	0.0000416	FLJ11151 | hypothetical protein FLJ11151
AF059321	0.0000839	SIAT4A | sialyltransferase 4A (beta-galactosidase alpha-2,3-sialytransferase)
N59238	0.0000132	DKFZp761O0113 | hypothetical protein DKFZp761O0113
AB032417	0.0003999	FZD4 | frizzled homolog 4 (Drosophila)
L13220	0.0009771	CALB3 | calbindin 3, (vitamin D-dependent calcium binding protein)
AI085836	0.0000535	ESTs, Weakly similar to R5HU22 ribosomal protein L17, cytosolic [H.sapiens]
AI492117	0.0001096	Homo sapiens putative ion channel protein CATSPER2 (CATSPER2), mRNA
AI311775	0.0001113	ESTs
AW295401	0.0005407	FLJ10647 | hypothetical protein FLJ10647
BC013107	0.0000099	H326 | H326
BC000566	0.0000109	RAYL | putative GTP-binding protein similar to RAY/RAB1C
AA149305	0.0005606	ITGBL1 | integrin, beta-like 1 (with EGF-like repeat domains)
AK025757	0.0000282	FLJ22104 | hypothetical protein FLJ22104
AW070798	0.0000334	EST
BE549691	0.0000361	Homo sapiens cDNA FLJ30927 fis, clone FEBRA2006736
AI475953	0.0000816	ESTs
AK026438	0.0000114	Homo sapiens cDNA: FLJ22785 fis, clone KAIA2081

AL161961	0.0000246	KIAA1554 | KIAA1554 protein
AF242557	0.0001086	TSCOT | thymic stromal co-transporter
BC016628	0.0000127	DKFZP434D146 | DKFZP434D146 protein
AA761787	0.0000158	ESTs
BE670572	0.0009122	ESTs
BC006131	0.0000961	MGC13047 | hypothetical protein MGC13047
AF024690	0.0002962	GPR43 | G protein-coupled receptor 43
AI961887	0.0007391	COL3A1 | collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)
BC004471	0.0000513	APM2 | adipose specific 2
AK000542	0.0000616	FLJ20535 | hypothetical protein FLJ20535
BC010652	0.0000856	MGC9753 | hypothetical gene MGC9753
AI859284	0.0001958	ESTs, Weakly similar to T42709 hypothetical protein DKFZp586I0821.1 [H.sapiens]
BC005364	0.0000764	FLJ11218 | hypothetical protein FLJ11218
AI732388	0.0003354	MGAT4A | mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isoenzyme A
AI248610	0.0000466	ESTs
AK026720	0.0001708	Homo sapiens cDNA: FLJ23067 fis, clone LNG04993
NM_000609	0.0008601	SDF1 | stromal cell-derived factor 1
NM_006713	0.000127	PC4 | activated RNA polymerase II transcription cofactor 4
AK054839	0.0001666	Homo sapiens cDNA FLJ30277 fis, clone BRACE2002752
AI087975	0.0001916	ESTs
AF220030	0.0002753	TRIM6 | tripartite motif-containing 6
BC000632	0.0000354	S100A13 | S100 calcium binding protein A13
BC015613	0.0001785	GATA2 | GATA binding protein 2
AA603977	0.000372	KLK4 | kallikrein 4 (prostase, enamel matrix, prostate)
AW197863	0.0000468	ESTs
BM127867	0.0000528	MDM1 | nuclear protein double minute 1
AA830549	0.0003809	VAMP1 | vesicle-associated membrane protein 1 (synaptobrevin 1)
BF477905	0.0005735	ESTs
R45048	0.0001759	C22orf1 | chromosome 22 open reading frame 1
AB033110	0.0001596	KIAA1284 | KIAA1284 protein
AW293849	0.0001623	ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]
BC014117	0.0002492	TBXAS1 | thromboxane A synthase 1 (platelet, cytochrome P450, subfamily V)
AK022060	0.0005048	Homo sapiens cDNA FLJ11998 fis, clone HEMBB1001521
AA806859	0.0007266	FLJ14281 | hypothetical protein FLJ14281

AW291180	0.0000866	ADORA3 | adenosine A3 receptor
BF510778	0.0001368	ESTs
AA603743	0.0002352	EST
BC005305	0.0006323	COL4A6 | collagen, type IV, alpha 6
AF068180	0.0001499	BLNK | B-cell linker
R46824	0.0002785	SRGAP3 | KIAA0411 gene product
AI081593	0.0001534	ESTs
AF311325	0.0001578	GPD2 | glycerol-3-phosphate dehydrogenase 2 (mitochondrial)
AK055280	0.0001954	Homo sapiens cDNA FLJ30718 fis, clone FCBBF2001675
AB018316	0.0006996	KIAA0773 | KIAA0773 gene product
AK025168	0.0000869	OSBPL6 | oxysterol binding protein-like 6
AL117616	0.0001068	SRI | sorcin
AF332975	0.0005447	ZAN | zonadhesin
R43793	0.0001576	HSPA1L | heat shock 70kD protein 1-like
AI307801	0.000302	KIAA1072 | KIAA1072 protein
AK027036	0.0008803	RU2 | RU2S
BC006378	0.0001365	UBE1L | ubiquitin-activating enzyme E1-like
AL137559	0.0004641	PCANAP7 | prostate cancer associated protein 7
J03607	0.0001134	KRT19 | keratin 19
N93663	0.0003213	ESTs
AA767639	0.0006013	KIAA0227 | KIAA0227 protein
BF448987	0.0002835	ESTs
AL110131	0.0006287	KIAA1223 | KIAA1223 protein
NM_006455	0.0001119	SC65 | nucleolar autoantigen (55kD) similar to rat synaptonemal complex protein
R56793	0.0009148	AGXT2L1 | alanine-glyoxylate aminotransferase 2-like 1
AF059617	0.0006528	SNK | serum-inducible kinase
BC005055	0.0003206	FOXP1 | forkhead box P1
AF141332	0.0004598	APOB48R | apolipoprotein B48 receptor
AK025772	0.0001313	Homo sapiens cDNA: FLJ22119 fis, clone HEP18852
AI424409	0.0002138	ESTs, Highly similar to LB4D_HUMAN NADP-DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE [H.sapiens]
AK056154	0.0007347	Homo sapiens cDNA FLJ31592 fis, clone NT2RI2002447
BC014533	0.0001558	MEF-2 | myelin gene expression factor 2
AI089428	0.0007681	ESTs

BC017411	0.0001941	Homo sapiens, clone IMAGE:4618419, mRNA, partial cds
AF263462	0.0003563	CGN | cingulin
BC003608	0.0005011	RBPMS | RNA-binding protein gene with multiple splicing
AK027146	0.0004053	RPL5 | ribosomal protein L5
U90914	0.0009563	CPD | carboxypeptidase D
BF508058	0.0002228	DKFZP564D166 | putative ankyrin-repeat containing protein
AK026256	0.0007805	MGC4171 | hypothetical protein MGC4171
AB069698	0.0005545	ADAMTS13 | a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 13
BC005359	0.0002707	GMFB | glia maturation factor, beta
NM_021194	0.0002725	SLC30A1 | solute carrier family 30 (zinc transporter), member 1
AI311898	0.0003307	ESTs
NM_002538	0.0005858	OCLN | occludin
AF222340	0.0007234	ARTS-1 | type 1 tumor necrosis factor receptor shedding aminopeptidase regulator
W32171	0.0005402	Homo sapiens cDNA FLJ13613 fis, clone PLACE1010856
BC009869	0.0008215	SERF2 | small EDRK-rich factor 2
AK021674	0.0003543	Homo sapiens cDNA FLJ11612 fis, clone HEMBA1004011
AB039903	0.0007986	TRIM34 | tripartite motif-containing 34
AJ252236	0.0004879	CAMK2B | calcium/calmodulin-dependent protein kinase (CaM kinase) II beta
BC002745	0.0006025	ENO2 | enolase 2, (gamma, neuronal)
BE349538	0.000829	TM7SF1 | transmembrane 7 superfamily member 1 (upregulated in kidney)
NM_014583	0.0009047	LMCD1 | LIM and cysteine-rich domains 1
AL046192	0.0004687	PVT1 | Pvt1 oncogene homolog, MYC activator (mouse)
AK023312	0.0008557	Homo sapiens cDNA FLJ13250 fis, clone OVARC1000724
AF054181	0.0007103	NDUFB1 | NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1 (7kD, MNLL)
AI268717	0.000927	ESTs, Highly similar to AC004836 1 similar to cadherin and Drosophila Fat protein [H.sapiens]
AI733236	0.000961	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]

Table 4. Genes that are overexpressed in ER negative cells, and underexpressed in ER positive cells

GeneID	P-value	Description
NM_014211	$p < 1e-07$	GABRP | gamma-aminobutyric acid (GABA) A receptor, pi
BC017913	$p < 1e-07$	ART3 | ADP-ribosyltransferase 3
H29323	$p < 1e-07$	SFRP1 | secreted frizzled-related protein 1
AW192480	$p < 1e-07$	SLC6A14 | solute carrier family 6 (neurotransmitter transporter), member 14
AI332979	$p < 1e-07$	KCNG1 | potassium voltage-gated channel, subfamily G, member 1
AJ404611	$p < 1e-07$	BCL11A | B-cell CLL/lymphoma 11A (zinc finger protein)
AW139831	$p < 1e-07$	Homo sapiens cDNA FLJ11796 fis, clone HEMBA1006158, highly similar to Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene
BC008484	$p < 1e-07$	DKFZP564D206 | DKFZP564D206 protein
BC014152	$p < 1e-07$	KRT6A | keratin 6A
BC000045	$p < 1e-07$	TONDU | TONDU
AB028641	$p < 1e-07$	SOX11 | SRY (sex determining region Y)-box 11
AA452915	$p < 1e-07$	EN1 | engrailed homolog 1
AI367357	$p < 1e-07$	ESTs
U95089	$p < 1e-07$	EGFR | epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)
NM_001453	$p < 1e-07$	FOXC1 | forkhead box C1
AW136298	$p < 1e-07$	E48 | lymphocyte antigen 6 complex, locus D
AI358916	$p < 1e-07$	ZIC1 | Zic family member 1 (odd-paired homolog, Drosophila)
BC015525	$p < 1e-07$	KLK6 | kallikrein 6 (neurosin, zyme)
BC012089	$p < 1e-07$	PROML1 | prominin-like 1 (mouse)
AW004032	$p < 1e-07$	LOC56963 | hypothetical protein from EUROIMAGE 363668
AF084830	$p < 1e-07$	KCNK5 | potassium channel, subfamily K, member 5 (TASK-2)
AW450675	$p < 1e-07$	ESTs
AA452928	$p < 1e-07$	GPR51 | G protein-coupled receptor 51
AF308297	$p < 1e-07$	PPP1R14C | protein phosphatase 1, regulatory (inhibitor) subunit 14C
NM_003508	$p < 1e-07$	FZD9 | frizzled homolog 9 (Drosophila)
AW291189	$p < 1e-07$	ESTs
BC012299	$p < 1e-07$	FABP7 | fatty acid binding protein 7, brain
BC005910	$p < 1e-07$	MIA | melanoma inhibitory activity
AA609183	$p < 1e-07$	ESTs

Z73678	p < 1e-07	PKP1 | plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)
BC007008	p < 1e-07	CRYAB | crystallin, alpha B
NM_032047	p < 1e-07	B3GNT5 | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5
AY029179	p < 1e-07	JPO1 | c-Myc target JPO1
AF055982	p < 1e-07	KLK8 | kallikrein 8 (neuropsin/ovasin)
AI160174	p < 1e-07	ESTs
AF257472	p < 1e-07	C21orf68 | chromosome 21 open reading frame 68
R50991	p < 1e-07	FLJ11413 | hypothetical protein FLJ11413
AK025066	p < 1e-07	FLJ10901 | hypothetical protein FLJ10901
BC003628	p < 1e-07	HBP17 | heparin-binding growth factor binding protein
AI279525	p < 1e-07	ELF5 | E74-like factor 5 (ets domain transcription factor)
NM_024423	p < 1e-07	DSC3 | desmocollin 3
BC007394	p < 1e-07	MGC16291 | hypothetical protein MGC16291
AK026818	p < 1e-07	Homo sapiens cDNA: FLJ23165 fis, clone LNG09846
AA521195	p < 1e-07	LAMP3 | lysosomal-associated membrane protein 3
AA156097	p < 1e-07	ESTs, Weakly similar to LKHU proteoglycan link protein precursor [H.sapiens]
AW137881	p < 1e-07	RARRES1 | retinoic acid receptor responder (tazarotene induced) 1
BC014941	p < 1e-07	ID4 | inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
AA622986	p < 1e-07	ESTs
AA922144	p < 1e-07	AQP5 | aquaporin 5
AI800206	p < 1e-07	STAC | src homology three (SH3) and cysteine rich domain
NM_002964	p < 1e-07	S100A8 | S100 calcium binding protein A8 (calgranulin A)
BC007595	p < 1e-07	SOX10 | SRY (sex determining region Y)-box 10
AK000442	p < 1e-07	FLJ20435 | hypothetical protein FLJ20435
BC017352	p < 1e-07	TRIM29 | tripartite motif-containing 29
AJ000388	p < 1e-07	CAPN6 | calpain 6
AL137311	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp761G02121 (from clone DKFZp761G02121); partial cds
BC012914	p < 1e-07	Homo sapiens cDNA FLJ31360 fis, clone MESAN2000572
AA194943	p < 1e-07	DEFB1 | defensin, beta 1
AL110178	p < 1e-07	TRIM2 | tripartite motif-containing 2
AW204371	p < 1e-07	DSC2 | desmocollin 2
AI049783	p < 1e-07	ESTs
BC000183	p < 1e-07	TMSNB | thymosin, beta, identified in neuroblastoma cells
BI495988	p < 1e-07	MET | met proto-oncogene (hepatocyte growth factor receptor)

AL110126	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone DKFZp564H1916)
AW140023	p < 1e-07	FLJ13204 | hypothetical protein FLJ13204
BC003635	p < 1e-07	MMP7 | matrix metalloproteinase 7 (matrilysin, uterine)
BC016004	p < 1e-07	MARCO | macrophage receptor with collagenous structure
AW264415	p < 1e-07	Homo sapiens, clone MGC:24011 IMAGE:4091916, mRNA, complete cds
AI375448	p < 1e-07	GPM6B | glycoprotein M6B
N64339	p < 1e-07	GJB6 | gap junction protein, beta 6 (connexin 30)
AK026420	p < 1e-07	DMN | desmuslin
BF433019	p < 1e-07	ESTs, Weakly similar to TRHY_HUMAN TRICHOHYALI [H.sapiens]
AI885044	p < 1e-07	KIT | v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
AK021785	p < 1e-07	Homo sapiens cDNA FLJ11723 fis, clone HEMBA1005314
AF089854	p < 1e-07	TU3A | TU3A protein
AF033021	p < 1e-07	KCNN4 | potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4
AI948466	p < 1e-07	INDO | indoleamine-pyrrole 2,3 dioxygenase
AW291290	p < 1e-07	ESTs
AF052117	p < 1e-07	Homo sapiens clone 23809 mRNA sequence
NM_002965	p < 1e-07	S100A9 | S100 calcium binding protein A9 (calgranulin B)
NM_006522	p < 1e-07	WNT6 | wingless-type MMTV integration site family, member 6
U17077	p < 1e-07	BENE | BENE protein
AW449979	p < 1e-07	SLC15A1 | solute carrier family 15 (oligopeptide transporter), member 1
NM_001793	p < 1e-07	CDH3 | cadherin 3, type 1, P-cadherin (placental)
AY035400	p < 1e-07	PCOLCE2 | procollagen C-endopeptidase enhancer 2
AF047348	p < 1e-07	APBA2 | amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like)
AI732309	p < 1e-07	EPHB1 | EphB1
AA584033	p < 1e-07	KRT6B | keratin 6B
NM_002639	p < 1e-07	SERPINB5 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5
BC000332	p < 1e-07	UCHL1 | ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)
BF224381	p < 1e-07	ESTs
BC017583	p < 1e-07	SCRG1 | scrapie responsive protein 1
NM_004961	p < 1e-07	GABRE | gamma-aminobutyric acid (GABA) A receptor, epsilon
AI351524	p < 1e-07	DMD | dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272
BC001283	p < 1e-07	NFIB | nuclear factor I/B
BC004376	p < 1e-07	ANXA8 | annexin A8

AB037813	p < 1e-07	DKFZp762K222 | hypothetical protein DKFZp762K222
AK024990	p < 1e-07	PPARGC1 | peroxisome proliferative activated receptor, gamma, coactivator 1
AF241254	p < 1e-07	ACE2 | angiotensin I converting enzyme (peptidyl-dipeptidase A) 2
AI800677	p < 1e-07	SLPI | secretory leukocyte protease inhibitor (antileukoproteinase)
BC012908	p < 1e-07	NMU | neuromedin U
BC012097	p < 1e-07	OCA2 | oculocutaneous albinism II (pink-eye dilution homolog, mouse)
R44714	p < 1e-07	Homo sapiens cDNA FLJ13136 fis, clone NT2RP3003139
R15881	p < 1e-07	CHRM3 | cholinergic receptor, muscarinic 3
AK025909	p < 1e-07	Homo sapiens cDNA: FLJ22256 fis, clone HRC02860
AI754805	p < 1e-07	SMOC1 | secreted modular calcium-binding protein 1
BC009581	p < 1e-07	HSD17B2 | hydroxysteroid (17-beta) dehydrogenase 2
X59770	p < 1e-07	IL1R2 | interleukin 1 receptor, type II
M76482	p < 1e-07	DSG3 | desmoglein 3 (pemphigus vulgaris antigen)
AI368024	p < 1e-07	ESTs
BC015753	p < 1e-07	GRO2 | GRO2 oncogene
BC014950	p < 1e-07	CA9 | carbonic anhydrase IX
BC008366	p < 1e-07	DDC | dopa decarboxylase (aromatic L-amino acid decarboxylase)
AI970748	p < 1e-07	ESTs
BC001766	p < 1e-07	S100B | S100 calcium binding protein, beta (neural)
AW206460	p < 1e-07	KIAA0481 | KIAA0481 gene product
AF361486	p < 1e-07	MUC16 | mucin 16
BC000992	p < 1e-07	CSRP2 | cysteine and glycine-rich protein 2
AI202593	p < 1e-07	CYP7B1 | cytochrome P450, subfamily VIIB (oxysterol 7 alpha-hydroxylase), polypeptide 1
NM_006115	p < 1e-07	PRAME | preferentially expressed antigen in melanoma
BC011976	p < 1e-07	GRO1 | GRO1 oncogene (melanoma growth stimulating activity, alpha)
BC006226	p < 1e-07	DLX5 | distal-less homeo box 5
AL137289	p < 1e-07	ARHGEF4 | Rho guanine nucleotide exchange factor (GEF) 4
BC005083	p < 1e-07	MGC13057 | hypothetical protein MGC13057
AI261967	p < 1e-07	ADORA2B | adenosine A2b receptor
AI273928	p < 1e-07	ALDH1A3 | aldehyde dehydrogenase 1 family, member A3
BC005948	p < 1e-07	SMPX | small muscle protein, X-linked
NM_006769	p < 1e-07	LMO4 | LIM domain only 4
AL117452	p < 1e-07	DKFZP586G1517 | DKFZP586G1517 protein
AA587049	p < 1e-07	PLA2G4A | phospholipase A2, group IVA (cytosolic, calcium-dependent)

AI804716	p < 1e-07	ESTs
AI637899	p < 1e-07	GAL | galanin
AF269101	p < 1e-07	MID1 | midline 1 (Opitz/BBB syndrome)
NM_003034	p < 1e-07	SIAT8A | sialyltransferase 8A (alpha-N-acetylneuraminate: alpha-2,8-sialytransferase, GD3 synthase)
AF141339	p < 1e-07	DKFZP564D0764 | DKFZP564D0764 protein
AI095049	p < 1e-07	Homo sapiens cDNA FLJ31627 fis, clone NT2RI2003338
AI498405	p < 1e-07	ESTs, Weakly similar to B49647 GTP-binding protein rab8 [H.sapiens]
AF130728	p < 1e-07	DMRT1 | doublesex and mab-3 related transcription factor 1
AW206700	p < 1e-07	KLK7 | kallikrein 7 (chymotryptic, stratum corneum)
AB042405	p < 1e-07	MLZE | melanoma-derived leucine zipper, extra-nuclear factor
AF104032	p < 1e-07	SLC7A5 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
AA521486	p < 1e-07	CECR7 | cat eye syndrome chromosome region, candidate 7
AI024603	p < 1e-07	HAPIP | huntingtin-associated protein interacting protein (duo)
AI830532	p < 1e-07	ESTs
M57892	p < 1e-07	CA6 | carbonic anhydrase VI
NM_003914	p < 1e-07	CCNA1 | cyclin A1
S72493	p < 1e-07	KRT16 | keratin 16 (focal non-epidermolytic palmoplantar keratoderma)
NM_004938	p < 1e-07	DAPK1 | death-associated protein kinase 1
AW071804	p < 1e-07	ESTs
NM_002996	p < 1e-07	SCYD1 | small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)
NM_002299	p < 1e-07	LCT | lactase
R55787	p < 1e-07	KIAA1069 | KIAA1069 protein
AF271781	p < 1e-07	ITM3 | integral membrane protein 3
AA716090	p < 1e-07	BOC | brother of CDO
AJ420468	p < 1e-07	KIAA1209 | KIAA1209 protein
H09748	p < 1e-07	BCL11B | B-cell CLL/lymphoma 11B (zinc finger protein)
AA806280	p < 1e-07	Homo sapiens cDNA FLJ31951 fis, clone NT2RP7007177, weakly similar to Homo sapiens multiple membrane spanning receptor TRC8 mRNA
BI492630	p < 1e-07	SLC9A6 | solute carrier family 9 (sodium/hydrogen exchanger), isoform 6
BC004397	p < 1e-07	MGC10981 | hypothetical protein MGC10981
AF095719	p < 1e-07	CPA4 | carboxypeptidase A4
AF331525	p < 1e-07	SLC26A9 | solute carrier family 26, member 9
R38090	p < 1e-07	G2 | G2 protein
AF117108	p < 1e-07	KOC1 | IGF-II mRNA-binding protein 3

AF127563	p < 1e-07	DKK1 | dickkopf homolog 1 (Xenopus laevis)
AA633482	p < 1e-07	EST
BC008588	p < 1e-07	PLS3 | plastin 3 (T isoform)
NM_002852	p < 1e-07	PTX3 | pentaxin-related gene, rapidly induced by IL-1 beta
AF123074	p < 1e-07	DNCI1 | dynein, cytoplasmic, intermediate polypeptide 1
AK000123	p < 1e-07	C20orf42 | chromosome 20 open reading frame 42
AW444437	0.0000001	ESTs
AI557322	p < 1e-07	ESTs
AB053450	p < 1e-07	KIAA1776 | fibrillin3
X53578	p < 1e-07	FUT3 | fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group included)
AF043473	p < 1e-07	KCNS1 | potassium voltage-gated channel, delayed-rectifier, subfamily S, member 1
AF197137	p < 1e-07	FN5 | FN5 protein
BC017733	p < 1e-07	MRAS | muscle RAS oncogene homolog
AW265625	p < 1e-07	ESTs
AA527072	p < 1e-07	EST
BC016666	p < 1e-07	Homo sapiens, clone IMAGE:3917693, mRNA
AF220183	p < 1e-07	HT009 | uncharacterized hypothalamus protein HT009
AI356375	p < 1e-07	CDKN2A | cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)
AW780208	p < 1e-07	Homo sapiens, clone MGC:15887 IMAGE:3530481, mRNA, complete cds
BC006097	p < 1e-07	HLA-DOB | major histocompatibility complex, class II, DO beta
AI740531	p < 1e-07	MAPK4 | mitogen-activated protein kinase 4
L20433	p < 1e-07	POU4F1 | POU domain, class 4, transcription factor 1
NM_003806	p < 1e-07	HRK | harakiri, BCL2 interacting protein (contains only BH3 domain)
BC007541	p < 1e-07	MGC15437 | hypothetical protein MGC15437
AF091092	p < 1e-07	CL683 | weakly similar to glutathione peroxidase 2
AI609709	p < 1e-07	CXorf6 | chromosome X open reading frame 6
BG236645	0.0000003	ESTs
AF082868	p < 1e-07	BBOX1 | butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1
BE326342	p < 1e-07	ESTs, Highly similar to bK989H11.1 [H.sapiens]
AL080079	p < 1e-07	DKFZP564D0462 | hypothetical protein DKFZp564D0462
AF181862	p < 1e-07	GPRC5B | G protein-coupled receptor, family C, group 1, member B
BC012844	p < 1e-07	PRNP | prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)
AA977269	p < 1e-07	FOXD1 | forkhead box D1

AA999973	p < 1e-07	FLJ14054 | hypothetical protein FLJ14054
AW195038	p < 1e-07	KIP2 | DNA-dependent protein kinase catalytic subunit-interacting protein 2
AA433906	p < 1e-07	KSP37 | Ksp37 protein
AF070614	p < 1e-07	SCHIP1 | schwannomin interacting protein 1
BF511352	p < 1e-07	LYN | v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
BC011901	p < 1e-07	KRT17 | keratin 17
N31940	p < 1e-07	ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
BC002829	p < 1e-07	S100A2 | S100 calcium binding protein A2
AL137332	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp434K2172 (from clone DKFZp434K2172)
AB022918	p < 1e-07	ST3GALVI | alpha2,3-sialyltransferase
BC008709	p < 1e-07	ADD2 | adducin 2 (beta)
AK026733	p < 1e-07	Homo sapiens cDNA: FLJ23080 fis, clone LNG06052
H10667	p < 1e-07	ROR1 | receptor tyrosine kinase-like orphan receptor 1
X70340	p < 1e-07	TGFA | transforming growth factor, alpha
Y15723	p < 1e-07	GUCY1A3 | guanylate cyclase 1, soluble, alpha 3
NM_005044	p < 1e-07	PRKX | protein kinase, X-linked
AB018329	p < 1e-07	KIAA0786 | latrophilin
BF444945	p < 1e-07	HRASLS | HRAS-like suppressor
BF589790	p < 1e-07	ADM | adrenomedullin
AF132818	p < 1e-07	KLF5 | Kruppel-like factor 5 (intestinal)
D11613	p < 1e-07	VSNL1 | visinin-like 1
BC001275	p < 1e-07	ANXA1 | annexin A1
M99487	p < 1e-07	FOLH1 | folate hydrolase (prostate-specific membrane antigen) 1
AB052906	p < 1e-07	ULBP2 | UL16 binding protein 2
BC012107	p < 1e-07	SH2D2A | SH2 domain protein 2A
AA586749	0.0000001	KRT5 | keratin 5 (epidermolysis bullosa simplex, Dowling-Meara/Kobner/Weber-Cockayne types)
BC017918	p < 1e-07	LOC64148 | 17kD fetal brain protein
NM_005378	p < 1e-07	MYCN | v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)
AA767129	p < 1e-07	PRKY | protein kinase, Y-linked
AW139720	p < 1e-07	FLJ12649 | hypothetical protein FLJ12649
BC012432	p < 1e-07	FAT | FAT tumor suppressor homolog 1 (Drosophila)
BC010003	p < 1e-07	Homo sapiens, clone IMAGE:4134852, mRNA, partial cds
AF155651	p < 1e-07	PAK3 | p21 (CDKN1A)-activated kinase 3
BC018646	p < 1e-07	PLCG2 | phospholipase C, gamma 2 (phosphatidylinositol-specific)

BC011705	p < 1e-07	COL9A3 | collagen, type IX, alpha 3
AF242518	p < 1e-07	LOC57115 | hypothetical protein SBBI67
AL136755	p < 1e-07	DKFZP434A1315 | hypothetical protein DKFZp434A1315
NM_001238	p < 1e-07	CCNE1 | cyclin E1
AB023430	p < 1e-07	BIT | brain-immunoglobulin-like molecule with tyrosine-based activation motifs
AL050374	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp586C1619 (from clone DKFZp586C1619)
AK056040	p < 1e-07	RE2 | G-protein coupled receptor
BC007293	p < 1e-07	MGC15668 | hypothetical protein MGC15668
AY004253	p < 1e-07	PRDM13 | PR domain containing 13
BC012381	p < 1e-07	FLJ10430 | hypothetical protein FLJ10430
AW118456	p < 1e-07	CRABP1 | cellular retinoic acid binding protein 1
AF131789	p < 1e-07	DKFZP566A1524 | hypothetical protein DKFZp566A1524
BC007382	p < 1e-07	MGC16212 | hypothetical protein MGC16212
NM_014274	p < 1e-07	ABP/ZF | Alu-binding protein with zinc finger domain
AF239820	p < 1e-07	C4ST | chondroitin 4-sulfotransferase
AL389942	p < 1e-07	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2005635
AW574736	p < 1e-07	PRKCN | protein kinase C, nu
AL136566	p < 1e-07	FLJ12783 | hypothetical protein FLJ12783
BC012142	p < 1e-07	P5 | protein disulfide isomerase-related protein
AI560801	p < 1e-07	PRSS12 | protease, serine, 12 (neurotrypsin, motopsin)
BC000765	p < 1e-07	MGC2742 | hypothetical protein MGC2742
AK021728	p < 1e-07	Homo sapiens cDNA FLJ11666 fis, clone HEMBA1004672
AF051321	p < 1e-07	T-STAR | Sam68-like phosphotyrosine protein, T-STAR
BE965331	p < 1e-07	CTSL2 | cathepsin L2
R76294	p < 1e-07	ESTs
AL080235	p < 1e-07	RIS1 | Ras-induced senescence 1
NM_002988	0.0000575	SCYA18 | small inducible cytokine subfamily A (Cys-Cys), member 18, pulmonary and activation-regulated
BC009701	p < 1e-07	PDI2 | peptidyl arginine deiminase, type II
AF133059	p < 1e-07	NFE2L3 | nuclear factor (erythroid-derived 2)-like 3
AF356193	p < 1e-07	CARD6 | caspase recruitment domain family, member 6
BC009744	p < 1e-07	CSDA | cold shock domain protein A
BC015663	p < 1e-07	TNRC3 | trinucleotide repeat containing 3
BC010039	p < 1e-07	CLP | coactosin-like protein
N47717	p < 1e-07	FABP5 | fatty acid binding protein 5 (psoriasis-associated)

AF280086	p < 1e-07	CHST6 | carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6
AL117633	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp434E235 (from clone DKFZp434E235)
BC009010	p < 1e-07	Homo sapiens, clone MGC:18257 IMAGE:4158300, mRNA, complete cds
BC008568	p < 1e-07	CHI3L1 | chitinase 3-like 1 (cartilage glycoprotein-39)
BC005963	0.0000357	MAGEA3 | melanoma antigen, family A, 3
BC010920	p < 1e-07	CLDN10 | claudin 10
BC011460	p < 1e-07	CHI3L2 | chitinase 3-like 2
AF131235	p < 1e-07	CHST4 | carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4
BC004411	p < 1e-07	HCA127 | hepatocellular carcinoma-associated antigen 127
AK025347	p < 1e-07	KIAA1357 | KIAA1357 protein
BC000563	p < 1e-07	SLC6A2 | solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2
AF057352	p < 1e-07	IMP-2 | IGF-II mRNA-binding protein 2
X77197	p < 1e-07	CLCN4 | chloride channel 4
AF073515	p < 1e-07	CRLF1 | cytokine receptor-like factor 1
AW172994	0.0000008	MMP12 | matrix metalloproteinase 12 (macrophage elastase)
AI678454	p < 1e-07	MYO10 | myosin X
AK025251	p < 1e-07	CHST3 | carbohydrate (chondroitin 6) sulfotransferase 3
BC013300	p < 1e-07	STK12 | serine/threonine kinase 12
BC010379	0.0000002	CSTA | cystatin A (stefin A)
AI460151	0.0000025	ACTG2 | actin, gamma 2, smooth muscle, enteric
BC013153	p < 1e-07	LOXL4 | lysyl oxidase-like 4
BC007049	p < 1e-07	RGS2 | regulator of G-protein signalling 2, 24kD
AK056666	p < 1e-07	Homo sapiens cDNA FLJ32104 fis, clone OCBBF2001307
BC000871	p < 1e-07	ANXA3 | annexin A3
AI433792	p < 1e-07	ESTs
BC008952	p < 1e-07	LDHB | lactate dehydrogenase B
AF083066	p < 1e-07	CHST2 | carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
NM_003878	p < 1e-07	GGH | gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)
AA631303	p < 1e-07	Homo sapiens prostate-specific membrane antigen PSM mRNA, exon 18 alternative splice variant, partial cds
AF336127	p < 1e-07	SLC4A11 | solute carrier family 4, sodium bicarbonate transporter-like, member 11
AK026946	p < 1e-07	FLJ23293 | likely ortholog of mouse ADP-ribosylation-like factor 6 interacting protein 2
BC015359	p < 1e-07	Homo sapiens, Similar to RIKEN cDNA 1810037C20 gene, clone MGC:21481 IMAGE:3852062, mRNA, complete cds
AJ420564	p < 1e-07	Homo sapiens cDNA: FLJ22314 fis, clone HRC05250

AF052126	p < 1e-07	SRD5A1 | steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)
AK000708	p < 1e-07	FLJ20701 | hypothetical protein FLJ20701
NM_003504	p < 1e-07	CDC45L | CDC45 cell division cycle 45-like (S. cerevisiae)
BC000881	p < 1e-07	CENPA | centromere protein A (17kD)
AI142639	p < 1e-07	ESTs
AK026790	p < 1e-07	Homo sapiens cDNA: FLJ23137 fis, clone LNG08842
AA761512	p < 1e-07	LPIN1 | lipin 1
BC017293	p < 1e-07	MSN | moesin
AL049977	0.000019	CLDN8 | claudin 8
AL122077	p < 1e-07	DNAH17 | dynein, axonemal, heavy polypeptide 17
BC003554	p < 1e-07	UBE2E3 | ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)
AF245436	p < 1e-07	FLJ23518 | hypothetical protein FLJ23518
AF333769	p < 1e-07	CASPR3 | cell recognition molecule CASPR3
AB051513	p < 1e-07	KIAA1726 | KIAA1726 protein
AA766903	p < 1e-07	ESTs, Highly similar to A46297 beta-1,6-N-acetylglucosaminyltransferase [H.sapiens]
AI823561	p < 1e-07	LPL | lipoprotein lipase
NM_002284	p < 1e-07	KRTHB6 | keratin, hair, basic, 6 (monilethrix)
AA424146	p < 1e-07	LOC51312 | mitochondrial solute carrier
AI200443	0.0000155	MAGEA5 | melanoma antigen, family A, 5
H18932	p < 1e-07	XK | Kell blood group precursor (McLeod phenotype)
BF062000	p < 1e-07	ESTs, Highly similar to unnamed protein product [H.sapiens]
AF035594	p < 1e-07	Homo sapiens protein kinase C-alpha mRNA, partial 3' UTR
BC002895	p < 1e-07	GSTA2 | glutathione S-transferase A2
AA648922	p < 1e-07	CDC25A | cell division cycle 25A
BC004199	p < 1e-07	RLBP1 | retinaldehyde binding protein 1
BC002947	p < 1e-07	FOLR1 | folate receptor 1 (adult)
AA716439	p < 1e-07	BCE-1 | BCE-1 protein
AI275604	p < 1e-07	PRRG1 | proline-rich Gla (G-carboxyglutamic acid) polypeptide 1
BC017381	p < 1e-07	FLJ12929 | hypothetical protein FLJ12929
AI188827	p < 1e-07	PIM1 | pim-1 oncogene
AL080059	0.0000025	KIAA1750 | KIAA1750 protein
AY037298	p < 1e-07	ELOVL4 | elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4
AF245517	0.0000145	ATP6N1B | ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1B
BC017730	p < 1e-07	TNFRSF21 | tumor necrosis factor receptor superfamily, member 21

BC018652	p < 1e-07	FXYD6 | FXYD domain-containing ion transport regulator 6
AI741143	p < 1e-07	Homo sapiens cDNA FLJ32401 fis, clone SKMUS2000339
X64318	p < 1e-07	NFIL3 | nuclear factor, interleukin 3 regulated
AB047783	p < 1e-07	ANKRD3 | ankyrin repeat domain 3
AF038185	p < 1e-07	Homo sapiens clone 23700 mRNA sequence
BC016838	p < 1e-07	CPVL | carboxypeptidase, vitellogenic-like
AF193809	p < 1e-07	RHCG | Rh type C glycoprotein
AJ420473	p < 1e-07	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1502032
AF285109	p < 1e-07	3-Sep | septin 3
NM_001604	p < 1e-07	PAX6 | paired box gene 6 (aniridia, keratitis)
BC009945	p < 1e-07	KIAA0746 | KIAA0746 protein
AF026547	p < 1e-07	CSPG3 | chondroitin sulfate proteoglycan 3 (neurocan)
AF101051	p < 1e-07	CLDN1 | claudin 1
BC002710	p < 1e-07	KLK10 | kallikrein 10
AA873846	p < 1e-07	LOC91689 | hypothetical gene supported by AL449243
AI452634	p < 1e-07	GPR64 | G protein-coupled receptor 64
AK027126	p < 1e-07	ASS | argininosuccinate synthetase
AJ420542	p < 1e-07	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1090104
AK024818	0.000002	MMP1 | matrix metalloproteinase 1 (interstitial collagenase)
AW265278	p < 1e-07	IVL | involucrin
AW445220	0.0000115	HSJ001348 | cDNA for differentially expressed CO16 gene
AF108138	p < 1e-07	PIF1 | DNA helicase homolog PIF1
BC002660	p < 1e-07	TMOD | tropomodulin
AA909006	p < 1e-07	LBP-32 | LBP protein 32
AI097663	p < 1e-07	P450RAI-2 | cytochrome P450 retinoid metabolizing protein
BC009742	p < 1e-07	LAD1 | ladinin 1
AB028140	p < 1e-07	TMPRSS5 | transmembrane protease, serine 5 (spinesin)
AI569989	p < 1e-07	KIAA1755 | KIAA1755 protein
BF508352	p < 1e-07	DSG1 | desmoglein 1
R49390	p < 1e-07	KIAA1678 | KIAA1678
AI174254	p < 1e-07	Homo sapiens cDNA FLJ31586 fis, clone NT2RI2002211
BE046069	p < 1e-07	ESTs
AL109775	p < 1e-07	SH3GL3 | SH3-domain GRB2-like 3
AI522215	p < 1e-07	KIAA1804 | KIAA1804 protein

BC008682	p < 1e-07	ARP3BETA | actin-related protein 3-beta
L26584	p < 1e-07	RASGRF1 | Ras protein-specific guanine nucleotide-releasing factor 1
AL136856	p < 1e-07	NTT5 | NTT5 protein
AF038173	p < 1e-07	ATSV | axonal transport of synaptic vesicles
NM_003360	p < 1e-07	UGT8 | UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase)
BC015915	p < 1e-07	FZD7 | frizzled homolog 7 (Drosophila)
BG939593	p < 1e-07	ANGPT1 | angiopoietin 1
BF446789	p < 1e-07	CAV2 | caveolin 2
AI538937	p < 1e-07	GDF5 | growth differentiation factor 5 (cartilage-derived morphogenetic protein-1)
BC011672	p < 1e-07	KIAA0514 | KIAA0514 gene product
AI494546	p < 1e-07	ICB-1 | basement membrane-induced gene
BC008764	p < 1e-07	KNSL6 | kinesin-like 6 (mitotic centromere-associated kinesin)
BC010358	p < 1e-07	CYP39A1 | oxysterol 7alpha-hydroxylase
M14584	p < 1e-07	IL6 | interleukin 6 (interferon, beta 2)
R41459	p < 1e-07	KIAA1136 | KIAA1136 protein
AL157459	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp434B0425 (from clone DKFZp434B0425)
BC001068	p < 1e-07	C20orf129 | chromosome 20 open reading frame 129
AL133624	p < 1e-07	DKFZp434B1222 | AKAP-binding sperm protein ropporin
AJ243500	p < 1e-07	TRPV6 | transient receptor potential cation channel, subfamily V, member 6
AI950130	0.0000006	GZMB | granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)
AK023678	p < 1e-07	Homo sapiens cDNA FLJ13616 fis, clone PLACE1010916
BC002325	0.0000019	MGC4309 | hypothetical protein MGC4309
AB049586	p < 1e-07	B3GNT4 | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4
AL136840	p < 1e-07	MCM10 | MCM10 minichromosome maintenance deficient 10 (S. cerevisiae)
BC014039	p < 1e-07	KIAA0175 | likely ortholog of maternal embryonic leucine zipper kinase
AL122086	p < 1e-07	TIAM2 | T-cell lymphoma invasion and metastasis 2
AK055431	p < 1e-07	Homo sapiens cDNA FLJ30869 fis, clone FEBRA2004224
AW472810	p < 1e-07	IL12A | interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35)
BC010353	0.0000004	PTPLA | protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a
BI493178	p < 1e-07	KIAA0161 | KIAA0161 gene product
AA181334	p < 1e-07	TNNI2 | troponin I, skeletal, fast
AF067223	p < 1e-07	PDE9A | phosphodiesterase 9A
BC010954	0.0000008	SCYB10 | small inducible cytokine subfamily B (Cys-X-Cys), member 10
AI218529	p < 1e-07	KIAA1754 | KIAA1754 protein

AI380218	p < 1e-07	FLJ13385 | hypothetical protein FLJ13385
BC013134	p < 1e-07	Homo sapiens, clone IMAGE:4512785, mRNA
AJ245600	p < 1e-07	Homo sapiens mRNA for hypothetical protein (TR2/D15 gene)
BC007609	p < 1e-07	Homo sapiens, Similar to hypothetical protein PRO1722, clone MGC:15692 IMAGE:3351479, mRNA, complete cds
AW589741	p < 1e-07	FLJ10159 | hypothetical protein FLJ10159
BC016308	p < 1e-07	GRO3 | GRO3 oncogene
BC013362	p < 1e-07	RUNX3 | runt-related transcription factor 3
AI582813	p < 1e-07	CHRNA5 | cholinergic receptor, nicotinic, alpha polypeptide 5
AI436812	p < 1e-07	ESTs, Weakly similar to hyperpolarization-activated cyclic nucleotide-gated channel hHCN2 [H.sapiens]
AF039843	p < 1e-07	SPRY2 | sprouty homolog 2 (Drosophila)
AF097021	0.0003463	GW112 | differentially expressed in hematopoietic lineages
AF054839	p < 1e-07	TSPAN-2 | tetraspan 2
BC005029	p < 1e-07	FLJ10718 | hypothetical protein FLJ10718
AL137580	p < 1e-07	C20orf130 | chromosome 20 open reading frame 130
BF447279	0.0000004	ESTs
AI767898	0.0000015	GBP5 | guanylate binding protein 5
AI140061	p < 1e-07	E2F3 | E2F transcription factor 3
BI963794	p < 1e-07	PLA2G7 | phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)
AI632467	p < 1e-07	OKB1 | organic cation transporter OKB1
AI366784	p < 1e-07	TAF4B | TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105 kD
AW204385	p < 1e-07	PDE7A | phosphodiesterase 7A
AW451872	p < 1e-07	KIAA0173 | KIAA0173 gene product
AL162059	p < 1e-07	TLE4 | transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)
AA664218	p < 1e-07	ETV5 | ets variant gene 5 (ets-related molecule)
AL136836	p < 1e-07	LOC51678 | MAGUK protein p55T; Protein Associated with Lins 2
AL133590	p < 1e-07	WASF3 | WAS protein family, member 3
AK058009	0.0000022	Homo sapiens cDNA FLJ25280 fis, clone STM06543
AI207256	p < 1e-07	Homo sapiens mRNA for FLJ00074 protein, partial cds
AL137281	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp434C2016 (from clone DKFZp434C2016)
BF433296	p < 1e-07	GBP1 | guanylate binding protein 1, interferon-inducible, 67kD
AA714213	p < 1e-07	ESTs, Highly similar to T47163 hypothetical protein DKFZp762E1312.1 [H.sapiens]
BC013966	p < 1e-07	FLJ10156 | hypothetical protein
AI082049	p < 1e-07	ESTs

U74612	p < 1e-07	FOXM1 | forkhead box M1
W94858	p < 1e-07	GAS1 | growth arrest-specific 1
BI492329	p < 1e-07	KIAA1214 | KIAA1214 protein
AB041036	0.0001467	KLK11 | kallikrein 11
AA931563	p < 1e-07	OR7E27P | olfactory receptor, family 7, subfamily E, member 27 pseudogene
AF118070	p < 1e-07	DKFZp762A227 | hypothetical protein DKFZp762A227
AI567843	p < 1e-07	ESTs, Weakly similar to JC5314 CDC28/cdc2-like kinase associating arginine-serine cyclophilin [H.sapiens]
BC006443	p < 1e-07	LRP8 | low density lipoprotein receptor-related protein 8, apolipoprotein e receptor
AF178532	p < 1e-07	BACE2 | beta-site APP-cleaving enzyme 2
AA205947	p < 1e-07	HHGP | HHGP protein
U85267	p < 1e-07	DSCR1 | Down syndrome critical region gene 1
AW290960	p < 1e-07	ESTs, Highly similar to T00391 hypothetical protein KIAA0612 [H.sapiens]
AK025747	p < 1e-07	FIGN | fidgetin
AB027289	p < 1e-07	LOC51191 | cyclin-E binding protein 1
L20470	p < 1e-07	VLDLR | very low density lipoprotein receptor
BC015592	p < 1e-07	KIAA0937 | KIAA0937 protein
AF247820	p < 1e-07	CALD1 | caldesmon 1
AK000012	p < 1e-07	FLJ20005 | hypothetical protein FLJ20005
AL157483	p < 1e-07	FLJ11264 | hypothetical protein FLJ11264
AA810022	p < 1e-07	KIAA0846 | KIAA0846 protein
AB048286	p < 1e-07	DGAT2 | diacylglycerol O-acyltransferase homolog 2 (mouse)
BC017575	p < 1e-07	CHEK1 | CHK1 checkpoint homolog (S. pombe)
AA877761	p < 1e-07	ESTs, Weakly similar to SYN1 MOUSE SYNAPSIN I [M.musculus]
AJ010277	p < 1e-07	TBX19 | T-box 19
AF237763	0.0000112	GPR87 | G protein-coupled receptor 87
AW874308	p < 1e-07	OR7E38P | olfactory receptor, family 7, subfamily E, member 38 pseudogene
AF230904	p < 1e-07	SH3KBP1 | SH3-domain kinase binding protein 1
Y16645	0.0000455	SCYA8 | small inducible cytokine subfamily A (Cys-Cys), member 8 (monocyte chemotactic protein 2)
BC010466	p < 1e-07	B3GAT1 | beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)
AK024298	p < 1e-07	Homo sapiens cDNA FLJ14236 fis, clone NT2RP4000515
AK026095	p < 1e-07	SNTB1 | syntrophin, beta 1 (dystrophin-associated protein A1, 59kD, basic component 1)
AK022914	p < 1e-07	Homo sapiens cDNA FLJ12852 fis, clone NT2RP2003445
AJ276230	p < 1e-07	PLD1 | phospholipase D1, phophatidylcholine-specific
AK022089	p < 1e-07	PAMCI | peptidylglycine alpha-amidating monooxygenase COOH-terminal interactor

AI023133	p < 1e-07	ESTs
BC002536	p < 1e-07	PFKP | phosphofructokinase, platelet
NM_005401	p < 1e-07	PTPN14 | protein tyrosine phosphatase, non-receptor type 14
AI350087	0.0000002	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PRECURSOR [H.sapiens]
NM_005409	0.0000011	SCYB11 | small inducible cytokine subfamily B (Cys-X-Cys), member 11
AK024865	p < 1e-07	FLJ21212 | hypothetical protein FLJ21212
BC015484	p < 1e-07	CALB2 | calbindin 2, (29kD, calretinin)
AK025562	p < 1e-07	Homo sapiens cDNA: FLJ21909 fis, clone HEP03834
AI538226	0.0000006	GNG4 | guanine nucleotide binding protein 4
AW409700	0.0000002	ESTs, Weakly similar to similar to ankyrin of Chromatium vinosum [H.sapiens]
AI656548	p < 1e-07	ESTs
AJ223366	0.0000019	Homo sapiens mRNA for OCIM (Oncogene in Multiple Myeloma) protein
AI524385	p < 1e-07	ANLN | anillin, actin binding protein (scraps homolog, Drosophila)
AF241534	p < 1e-07	HYMAI | hydatidiform mole associated and imprinted
BC004379	0.0000005	GJB5 | gap junction protein, beta 5 (connexin 31.1)
BC012198	p < 1e-07	Homo sapiens, clone MGC:4408 IMAGE:2906200, mRNA, complete cds
AL136653	p < 1e-07	DEPP | decidual protein induced by progesterone
AK026139	p < 1e-07	GJB3 | gap junction protein, beta 3, 31kD (connexin 31)
BC012513	p < 1e-07	ARHE | ras homolog gene family, member E
BC010044	p < 1e-07	CDC20 | CDC20 cell division cycle 20 homolog (S. cerevisiae)
AL162079	p < 1e-07	SLC16A1 | solute carrier family 16 (monocarboxylic acid transporters), member 1
BC000218	p < 1e-07	DLL3 | delta-like 3 (Drosophila)
AK000770	p < 1e-07	Homo sapiens cDNA FLJ20763 fis, clone COL09911
BC001211	p < 1e-07	KIFC3 | kinesin family member C3
BC010612	p < 1e-07	Homo sapiens, clone IMAGE:4157546, mRNA, partial cds
BC003610	p < 1e-07	MFGE8 | milk fat globule-EGF factor 8 protein
AK025511	p < 1e-07	ATP11A | ATPase, Class VI, type 11A
AF102848	0.0001895	HAIK1 | type I intermediate filament cytokeratin
AL035878	0.0003777	DCX | doublecortex; lissencephaly, X-linked (doublecortin)
AI188749	0.0000001	ESTs
AI004681	p < 1e-07	ESTs, Weakly similar to T33068 hypothetical protein C35E7.9 - Caenorhabditis elegans [C.elegans]
AA988024	0.0000093	FLJ14503 | hypothetical protein FLJ14503
BC013106	p < 1e-07	RRAS2 | related RAS viral (r-ras) oncogene homolog 2
BC006537	0.0001025	HOXA9 | homeo box A9

BC007964	0.0000001	CD38 | CD38 antigen (p45)
AA903532	0.0000001	SV2B | synaptic vesicle protein 2B homolog
BC015839	p < 1e-07	Homo sapiens, clone IMAGE:4296901, mRNA
BC009232	0.0000005	Homo sapiens, Similar to G antigen 8, clone MGC:16513 IMAGE:3960352, mRNA, complete cds
AI015671	0.0000001	FLJ12604 | hypothetical protein FLJ12604
D25538	p < 1e-07	ADCY7 | adenylate cyclase 7
BC011000	p < 1e-07	MGC16386 | similar to RIKEN cDNA 2610036L13
BM052808	p < 1e-07	KIAA0237 | KIAA0237 gene product
AK026826	p < 1e-07	Homo sapiens cDNA: FLJ23173 fis, clone LNG10019
BC000078	0.0000001	MGC3279 | hypothetical protein MGC3279 similar to collectins
AL049933	p < 1e-07	GNAI1 | guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1
AF136631	p < 1e-07	LOC51299 | neuritin
AW205836	p < 1e-07	RAB6B | RAB6B, member RAS oncogene family
BC015640	0.0000005	CBR1 | carbonyl reductase 1
AI654872	p < 1e-07	RASSF2 | Ras association (RalGDS/AF-6) domain family 2
AF053305	p < 1e-07	BUB1 | BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)
AF331521	p < 1e-07	SLC26A7 | solute carrier family 26, member 7
AA993639	p < 1e-07	FLJ10748 | hypothetical protein FLJ10748
AL157443	p < 1e-07	FAT2 | FAT tumor suppressor homolog 2 (Drosophila)
BC007407	p < 1e-07	NMB | neuromedin B
AL080058	p < 1e-07	DKFZP564G202 | DKFZP564G202 protein
M59305	p < 1e-07	NPR3 | natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)
BC000703	p < 1e-07	FLJ10468 | hypothetical protein FLJ10468
S79869	p < 1e-07	HOXA1 | homeo box A1
BC008584	0.0000021	BMP7 | bone morphogenetic protein 7 (osteogenic protein 1)
BC008947	p < 1e-07	FLJ10540 | hypothetical protein FLJ10540
BC008036	0.0000079	KLK5 | kallikrein 5
BC012204	p < 1e-07	Homo sapiens, clone MGC:10002 IMAGE:3882800, mRNA, complete cds
BC001847	p < 1e-07	MGC4504 | hypothetical protein MGC4504
AA088779	p < 1e-07	MFHAS1 | malignant fibrous histiocytoma amplified sequence 1
AF177337	p < 1e-07	FLJ13391 | hypothetical protein FLJ13391
AF283670	0.0000011	KLK14 | kallikrein 14
BC015310	p < 1e-07	FLJ21069 | hypothetical protein FLJ21069
AF201933	p < 1e-07	DC11 | DC11 protein

AL136820	p < 1e-07	KIAA1411 | KIAA1411 protein
BC000260	p < 1e-07	AKR1B1 | aldo-keto reductase family 1, member B1 (aldose reductase)
AI081342	p < 1e-07	OR7E37P | olfactory receptor, family 7, subfamily E, member 37 pseudogene
BC007491	p < 1e-07	EXO1 | exonuclease 1
AK026061	p < 1e-07	FLJ22408 | hypothetical protein FLJ22408
W69074	p < 1e-07	S100A4 | S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog)
BC007707	0.0000112	HEY2 | hairy/enhancer-of-split related with YRPW motif 2
AK057943	0.0000001	Homo sapiens cDNA FLJ25214 fis, clone REC08615
AF222980	p < 1e-07	DISC1 | disrupted in schizophrenia 1
AF172852	p < 1e-07	CLSP | calmodulin-like skin protein
AI569288	p < 1e-07	ESTs
AF153609	p < 1e-07	SGK | serum/glucocorticoid regulated kinase
BF512938	p < 1e-07	RARB | retinoic acid receptor, beta
AI633770	p < 1e-07	ESTs
BC014645	p < 1e-07	PRX2 | paired related homeobox protein
BC007951	0.0000002	SOX9 | SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal)
AI299541	p < 1e-07	ESTs
BC001940	p < 1e-07	DKFZp762E1312 | hypothetical protein DKFZp762E1312
AA857853	0.0000006	LCN2 | lipocalin 2 (oncogene 24p3)
N22033	p < 1e-07	COL11A2 | collagen, type XI, alpha 2
AI200706	0.0000004	FLJ10134 | hypothetical protein FLJ10134
BC010100	p < 1e-07	TLE1 | transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)
BC010078	p < 1e-07	RISC | likely homolog of rat and mouse retinoid-inducible serine carboxypeptidase
AI936089	0.0000004	Homo sapiens cDNA FLJ14181 fis, clone NT2RP2004300
BC001207	0.0000153	MAGE-E1 | MAGE-E1 protein
AK056720	p < 1e-07	Homo sapiens cDNA FLJ32158 fis, clone PLACE6000231
M86609	0.0000002	AKR1C1 | aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)
AI688729	p < 1e-07	ATP11C | ATPase, Class VI, type 11C
J05428	0.0000025	UGT2B7 | UDP glycosyltransferase 2 family, polypeptide B7
AI298332	p < 1e-07	ESTs
AI097664	p < 1e-07	ESTs, Weakly similar to S23650 retrovirus-related hypothetical protein II [H.sapiens]
NM_002465	0.0000202	MYBPC1 | myosin binding protein C, slow type
BF939405	p < 1e-07	EST

AF166350	p < 1e-07	ST7 | potential tumor suppressor
BC009401	p < 1e-07	NK4 | natural killer cell transcript 4
BC009989	p < 1e-07	SMOH | smoothened homolog (Drosophila)
AV655170	p < 1e-07	C21orf35 | chromosome 21 open reading frame 35
BC005246	0.0001085	TM4SF3 | transmembrane 4 superfamily member 3
AK024732	p < 1e-07	FLJ21079 | hypothetical protein FLJ21079
NM_002281	p < 1e-07	KRTHB1 | keratin, hair, basic, 1
AW293632	0.0000467	ESTs, Weakly similar to YK33_YEAST HYPOTHETICAL 46.5 KD PROTEIN IN MRS4-DYN1 INTERGENIC REGION [S.cerevisiae]
X55362	p < 1e-07	ODC1 | ornithine decarboxylase 1
AF060877	p < 1e-07	RGS20 | regulator of G-protein signalling 20
BC007022	0.0000109	SAA1 | serum amyloid A1
BC007026	p < 1e-07	SAA4 | serum amyloid A4, constitutive
AA643687	0.000722	Homo sapiens cDNA FLJ11980 fis, clone HEMBB1001304
AI978664	p < 1e-07	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs
AW015394	0.0000083	OR2I6 | olfactory receptor, family 2, subfamily I, member 6
AW449368	p < 1e-07	PDL2 | programmed death ligand 2
AW139532	0.000027	Homo sapiens cDNA FLJ32375 fis, clone SALGL1000065, weakly similar to POLYHOMEOTIC-PROXIMAL CHROMATIN PROTEIN
AI278360	0.0000005	ESTs
BF939156	0.0000005	SCYA5 | small inducible cytokine A5 (RANTES)
AL137740	0.0001579	LBP-9 | LBP protein; likely ortholog of mouse CRTR-1
AI924205	0.000124	ADAMDEC1 | ADAM-like, decysin 1
BC002551	p < 1e-07	MGC2577 | hypothetical protein MGC2577
AF239668	p < 1e-07	CCKBR | cholecystokinin B receptor
BC013353	0.0000001	FLJ14166 | hypothetical protein FLJ14166
AW410306	0.0000021	NXPH4 | neurexophilin 4
BC008832	p < 1e-07	HMGIY | high-mobility group (nonhistone chromosomal) protein isoforms I and Y
AL080146	p < 1e-07	CCNB2 | cyclin B2
BE047139	p < 1e-07	ESTs
AL365412	0.0000115	LOC56932 | hypothetical protein from EUROIMAGE 1759349

BC008651	0.0002167	Homo sapiens, clone MGC:9913 IMAGE:3870821, mRNA, complete cds
AA398573	p < 1e-07	EIF5A2 | eukaryotic translation initiation factor 5A2
AI457921	p < 1e-07	Homo sapiens cDNA FLJ11436 fis, clone HEMBA1001213
AF280546	p < 1e-07	NRP2 | neuropilin 2
BF447302	p < 1e-07	ESTs
BC010091	p < 1e-07	BICD1 | Bicaudal D homolog 1 (Drosophila)
AK026015	p < 1e-07	FLJ22362 | hypothetical protein FLJ22362
BC014126	p < 1e-07	Homo sapiens, Similar to RIKEN cDNA 4932416D09 gene, clone IMAGE:4578228, mRNA, partial cds
U61374	p < 1e-07	SRPX | sushi-repeat-containing protein, X chromosome
AI280215	0.0000014	ESTs
NM_001559	p < 1e-07	IL12RB2 | interleukin 12 receptor, beta 2
BC011795	p < 1e-07	NDRG4 | NDRG family member 4
AA903387	p < 1e-07	SIL | TAL1 (SCL) interrupting locus
NM_021226	p < 1e-07	LOC58504 | hypothetical protein from clones 23549 and 23762
BC009942	p < 1e-07	FLJ10628 | hypothetical protein FLJ10628
AA772897	p < 1e-07	DNCH1 | dynein, cytoplasmic, heavy polypeptide 1
BC006322	0.0000001	ATF3 | activating transcription factor 3
AI765381	0.0000017	DJ434O14.3 | hypothetical protein dJ434O14.3
BC007631	p < 1e-07	MGC15827 | hypothetical protein MGC15827
AA937401	0.0006517	ESTs
BC001886	p < 1e-07	RRM2 | ribonucleotide reductase M2 polypeptide
AK057339	0.0000005	LOC81569 | actin like protein
BC007318	p < 1e-07	MAPRE2 | microtubule-associated protein, RP/EB family, member 2
AA573096	p < 1e-07	FLJ10829 | hypothetical protein FLJ10829
BC007656	p < 1e-07	UBE2C | ubiquitin-conjugating enzyme E2C
BM055132	0.0000057	CFTR | cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7)
AB011422	p < 1e-07	TRAD | serine/threonine kinase with Dbl- and pleckstrin homology domains
BC016040	p < 1e-07	STK17B | serine/threonine kinase 17b (apoptosis-inducing)
AK055323	p < 1e-07	Homo sapiens cDNA FLJ30761 fis, clone FEBRA2000538
BC005894	0.0000001	FMO2 | flavin containing monooxygenase 2
NM_001078	0.0000011	VCAM1 | vascular cell adhesion molecule 1
AL136819	p < 1e-07	DKFZP434G2226 | hypothetical protein DKFZp434G2226
AF054993	0.0000008	SNAP91 | synaptosomal-associated protein, 91 kD homolog (mouse)
AY044429	p < 1e-07	IL22RA2 | class II cytokine receptor

AB033109	0.0000196	KIAA1283 | KIAA1283 protein
AI871458	p < 1e-07	ESTs
AI569068	0.0000063	ESTs
AK056817	p < 1e-07	Homo sapiens cDNA FLJ32255 fis, clone PROST1000226
BC006267	0.0000711	FLJ22316 | hypothetical protein FLJ22316
AA810180	p < 1e-07	FLJ10517 | hypothetical protein FLJ10517
AF017790	p < 1e-07	HEC | highly expressed in cancer, rich in leucine heptad repeats
BC010935	0.0000241	CSN10 | casein, kappa
AI741771	p < 1e-07	RYR3 | ryanodine receptor 3
H06285	p < 1e-07	Homo sapiens cDNA FLJ30553 fis, clone BRAWH2003689, highly similar to Mus musculus clone mouse1-9 putative protein phosphatase type 2C mRNA
AA613572	p < 1e-07	ESTs
AL512731	0.0000001	Homo sapiens mRNA; cDNA DKFZp667B0711 (from clone DKFZp667B0711)
W57704	0.0000001	CNGA1 | cyclic nucleotide gated channel alpha 1
BF224101	p < 1e-07	DOCK3 | dedicator of cyto-kinesis 3
AJ420539	p < 1e-07	DEK | DEK oncogene (DNA binding)
D10522	p < 1e-07	MARCKS | myristoylated alanine-rich protein kinase C substrate
BC008691	p < 1e-07	RSU1 | Ras suppressor protein 1
AF207664	p < 1e-07	ADAMTS1 | a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1
AF070592	p < 1e-07	HSKM-B | HSKM-B protein
AK025290	p < 1e-07	ATP10B | ATPase, Class V, type 10B
BC001749	p < 1e-07	WNT5B | wingless-type MMTV integration site family, member 5B
AK025425	p < 1e-07	MGC21854 | hypothetical protein MGC21854
AA642589	p < 1e-07	SEMG2 | semenogelin II
BC010116	0.0000001	Homo sapiens, clone MGC:19762 IMAGE:3636045, mRNA, complete cds
NM_002510	0.0000001	GPNMB | glycoprotein (transmembrane) nmb
BC002744	p < 1e-07	MGC4090 | hypothetical protein MGC4090
AA574056	p < 1e-07	OR7E119P | olfactory receptor, family 7, subfamily A, member 119 pseudogene
AI500430	0.0000052	KIAA1909 | KIAA1909 protein
AI972591	0.0000062	ESTs
AA232651	p < 1e-07	SUV39H2 | suppressor of variegation 3-9 (Drosophila) homolog 2; hypothetical protein FLJ23414
BC009238	p < 1e-07	TUBA1 | tubulin, alpha 1 (testis specific)
NM_022977	p < 1e-07	FACL4 | fatty-acid-Coenzyme A ligase, long-chain 4
BC001844	0.000001	MEIS2 | Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse)

N51717	0.0000117	ESTs
BC010658	p < 1e-07	KIAA0008 | KIAA0008 gene product
BC013200	0.0000001	LCK | lymphocyte-specific protein tyrosine kinase
AF027866	p < 1e-07	SERPINB7 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 7
AK026964	p < 1e-07	FLJ23311 | hypothetical protein FLJ23311
BC010923	0.0000002	CART1 | cartilage paired-class homeoprotein 1
R38438	p < 1e-07	SLC15A2 | solute carrier family 15 (H+/peptide transporter), member 2
AL110202	p < 1e-07	PORIMIN | pro-oncosis receptor inducing membrane injury gene
AK025215	0.0000001	FLJ21562 | hypothetical protein FLJ21562
D90239	0.0005882	GLDC | glycine dehydrogenase (decarboxylating; glycine decarboxylase, glycine cleavage system protein P)
AI636660	p < 1e-07	C21orf91 | chromosome 21 open reading frame 91
BC000633	p < 1e-07	TTK | TTK protein kinase
BF511873	p < 1e-07	ESTs
AI816719	0.0000012	KIAA1870 | KIAA1870 protein
AF053306	p < 1e-07	BUB1B | BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)
NM_005257	0.0000001	GATA6 | GATA binding protein 6
BC011920	p < 1e-07	FLJ20896 | hypothetical protein FLJ20896
X12892	0.000001	PROS1 | protein S (alpha)
M62925	p < 1e-07	TGM1 | transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine-gamma-glutamyltransferase)
AF239821	0.0000003	GALNAC4ST-2 | GalNAc-4-sulfotransferase 2
BF437448	p < 1e-07	EST
AF098482	p < 1e-07	PSIP1 | PC4 and SFRS1 interacting protein 1
AI096342	p < 1e-07	RGC32 | RGC32 protein
BC015706	p < 1e-07	Homo sapiens, Similar to RIKEN cDNA 2810433K01 gene, clone MGC:10200 IMAGE:3909951, mRNA, complete cds
BC011561	0.0000001	HEPH | hephaestin
AA903183	0.0000011	IL2RA | interleukin 2 receptor, alpha
NM_001237	p < 1e-07	CCNA2 | cyclin A2
AL137502	p < 1e-07	RAGD | Rag D protein
BC006359	p < 1e-07	INA | internexin neuronal intermediate filament protein, alpha
BF592799	p < 1e-07	PRKCQ | protein kinase C, theta
AI697249	0.0000294	EBI2 | Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)
BC016719	0.000725	Homo sapiens, clone IMAGE:4070464, mRNA, partial cds
AF014398	p < 1e-07	IMPA2 | inositol(myo)-1(or 4)-monophosphatase 2

AL136828	0.0000001	DKFZP434K0427 | hypothetical protein DKFZp434K0427
AI972473	0.0000723	EST
AW104435	0.0000002	UBE2E2 | ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)
M74447	p < 1e-07	TAP2 | transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)
NM_005048	0.000801	PTHR2 | parathyroid hormone receptor 2
AK024854	p < 1e-07	DJ742C19.2 | phorbolin (similar to apolipoprotein B mRNA editing protein)
AK027274	p < 1e-07	Homo sapiens cDNA FLJ14368 fis, clone HEMBA1001122
AF147204	0.0000002	CXCR4 | chemokine (C-X-C motif), receptor 4 (fusin)
BC005232	p < 1e-07	RPP38 | ribonuclease P (38kD)
BC004897	0.0000011	CA3 | carbonic anhydrase III, muscle specific
NM_002963	0.0000573	S100A7 | S100 calcium binding protein A7 (psoriasin 1)
AF154845	0.0000003	MARK1 | MAP/microtubule affinity-regulating kinase 1
AK000659	p < 1e-07	MT-ACT48 | Mitochondrial Acyl-CoA Thioesterase
AJ420567	p < 1e-07	AMD1 | S-adenosylmethionine decarboxylase 1
AF030942	p < 1e-07	PPP1R14BP1 | protein phosphatase 1, regulatory (inhibitor) subunit 14B pseudogene 1
AL359561	p < 1e-07	DKFZP762N2316 | hypothetical protein DKFZp762N2316
NM_002417	p < 1e-07	MKI67 | antigen identified by monoclonal antibody Ki-67
NM_003503	p < 1e-07	CDC7L1 | CDC7 cell division cycle 7-like 1 (S. cerevisiae)
AA084672	0.0000034	MSI1 | musashi homolog 1 (Drosophila)
AL136919	p < 1e-07	DKFZp586J1119 | hypothetical protein DKFZp586J1119
BC001051	p < 1e-07	ARL7 | ADP-ribosylation factor-like 7
AF136715	0.0000176	TRAG3 | taxol resistance associated gene 3
X97868	0.0000001	ARSF | arylsulfatase F
AI568024	0.0000032	LAMB3 | laminin, beta 3 (nicein (125kD), kalinin (140kD), BM600 (125kD))
AW191026	0.0000001	PLSCR1 | phospholipid scramblase 1
BC017705	p < 1e-07	KNSL5 | kinesin-like 5 (mitotic kinesin-like protein 1)
AB032698	0.0000007	BIN2 | bridging integrator 2
BC001692	0.0000005	SLC2A5 | solute carrier family 2 (facilitated glucose/fructose transporter), member 5
AB043585	0.0000001	REPRIMO | candidate mediator of the p53-dependent G2 arrest
AA262504	p < 1e-07	EYA3 | eyes absent homolog 3 (Drosophila)
BC017656	p < 1e-07	MONDOA | Mlx interactor
AK055596	p < 1e-07	Homo sapiens cDNA FLJ31034 fis, clone HSYRA1000178
NM_000057	p < 1e-07	BLM | Bloom syndrome
BC012527	0.0000001	HIF1A | hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)

<table>
<tr><td>BF196234</td><td>0.0000026</td><td>ESTs</td></tr>
<tr><td>AA805970</td><td>0.0000034</td><td>KIAA0275 | KIAA0275 gene product</td></tr>
<tr><td>AL050066</td><td>p < 1e-07</td><td>NTT73 | homolog of rat orphan transporter v7-3</td></tr>
<tr><td>AF339763</td><td>p < 1e-07</td><td>ABCC4 | ATP-binding cassette, sub-family C (CFTR/MRP), member 4</td></tr>
<tr><td>AW189851</td><td>0.0000008</td><td>CUGBP2 | CUG triplet repeat, RNA binding protein 2</td></tr>
<tr><td>NM_003122</td><td>0.0000169</td><td>SPINK1 | serine protease inhibitor, Kazal type 1</td></tr>
<tr><td>AA826489</td><td>0.0000001</td><td>MY040 | hypothetical brain protein my040</td></tr>
<tr><td>AK000054</td><td>p < 1e-07</td><td>FLJ20047 | hypothetical protein FLJ20047</td></tr>
<tr><td>AI653207</td><td>p < 1e-07</td><td>ESTs</td></tr>
<tr><td>AL137735</td><td>p < 1e-07</td><td>ASB2 | ankyrin repeat and SOCS box-containing 2</td></tr>
<tr><td>AI273114</td><td>p < 1e-07</td><td>ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]</td></tr>
<tr><td>BI492625</td><td>p < 1e-07</td><td>Homo sapiens cDNA FLJ30075 fis, clone BGGI11000285</td></tr>
<tr><td>NM_006235</td><td>0.0002076</td><td>POU2AF1 | POU domain, class 2, associating factor 1</td></tr>
<tr><td>AK000208</td><td>p < 1e-07</td><td>Homo sapiens cDNA FLJ20201 fis, clone COLF1210</td></tr>
<tr><td>AI669751</td><td>0.0000664</td><td>ZIP2 | zinc transporter</td></tr>
<tr><td>BF513300</td><td>p < 1e-07</td><td>KIAA0074 | KIAA0074 protein</td></tr>
<tr><td>M15990</td><td>p < 1e-07</td><td>YES1 | v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1</td></tr>
<tr><td>BE671269</td><td>p < 1e-07</td><td>HAAO | 3-hydroxyanthranilate 3,4-dioxygenase</td></tr>
<tr><td>BC000404</td><td>p < 1e-07</td><td>TRIP13 | thyroid hormone receptor interactor 13</td></tr>
<tr><td>AL050388</td><td>0.0000001</td><td>Homo sapiens mRNA; cDNA DKFZp564M2422 (from clone DKFZp564M2422); partial cds</td></tr>
<tr><td>BC014526</td><td>0.0000024</td><td>ANKH | ankylosis, progressive homolog (mouse)</td></tr>
<tr><td>BC007585</td><td>p < 1e-07</td><td>MYBL2 | v-myb myeloblastosis viral oncogene homolog (avian)-like 2</td></tr>
<tr><td>AK025926</td><td>0.0000002</td><td>AK3 | adenylate kinase 3</td></tr>
<tr><td>BC005127</td><td>p < 1e-07</td><td>ADFP | adipose differentiation-related protein</td></tr>
<tr><td>AK054683</td><td>p < 1e-07</td><td>Homo sapiens cDNA FLJ30121 fis, clone BRACE1000084</td></tr>
<tr><td>BE206076</td><td>p < 1e-07</td><td>ALK | anaplastic lymphoma kinase (Ki-1)</td></tr>
<tr><td>R05446</td><td>p < 1e-07</td><td>KIAA1424 | KIAA1424 protein</td></tr>
<tr><td>BC003684</td><td>0.000076</td><td>CXADR | coxsackie virus and adenovirus receptor</td></tr>
<tr><td>BC016451</td><td>p < 1e-07</td><td>ADAMTS3 | a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3</td></tr>
<tr><td>AF070609</td><td>p < 1e-07</td><td>SLC1A3 | solute carrier family 1 (glial high affinity glutamate transporter), member 3</td></tr>
<tr><td>BF724533</td><td>p < 1e-07</td><td>MGC3169 | hypothetical protein MGC3169</td></tr>
<tr><td>AB053172</td><td>p < 1e-07</td><td>CDT1 | DNA replication factor</td></tr>
<tr><td>AF124735</td><td>0.0005833</td><td>LHX2 | LIM homeobox protein 2</td></tr>
<tr><td>AL157471</td><td>0.0000189</td><td>KIAA1500 | KIAA1500 protein</td></tr>
</table>

AF326731	p < 1e-07	NUF2R | hypothetical protein NUF2R
BC013767	p < 1e-07	Homo sapiens, Similar to RIKEN cDNA 2610528G05 gene, clone IMAGE:3875837, mRNA, partial cds
AA827777	p < 1e-07	ESTs
NM_006329	p < 1e-07	FBLN5 | fibulin 5
BC014018	p < 1e-07	FLJ11196 | hypothetical protein FLJ11196
BE047394	0.0000013	ESTs, Weakly similar to S71512 hypothetical protein T2 - mouse [M.musculus]
AW079735	0.0000016	SPRR2B | small proline-rich protein 2B
AK023080	p < 1e-07	HSNOV1 | novel protein
AL134596	0.0002539	ATP2B2 | ATPase, Ca++ transporting, plasma membrane 2
AF331796	p < 1e-07	HCAP-G | chromosome condensation protein G
AF329840	p < 1e-07	ZSIG37 | G protein coupled receptor interacting protein, complement-c1q tumor necrosis factor-related
R40565	p < 1e-07	FYN | FYN oncogene related to SRC, FGR, YES
BC002700	0.0000032	KRT7 | keratin 7
AA877996	0.0002536	ESTs, Weakly similar to JC5314 CDC28/cdc2-like kinase associating arginine-serine cyclophilin [H.sapiens]
R48461	0.0000037	ESTs
AA730123	0.0000001	PRDM1 | PR domain containing 1, with ZNF domain
AF230495	0.00002	DUOX1 | dual oxidase 1
AL039118	0.0000661	FOXG1B | forkhead box G1B
AF146761	0.0001401	BLAME | BCM-like membrane protein precursor
BC012885	0.0000035	TEM7R | tumor endothelial marker 7-related precursor
AK026949	0.0000964	ZNF300 | kruppel-like zinc finger protein
AF130988	p < 1e-07	EDAR | ectodysplasin 1, anhidrotic receptor
AA489383	p < 1e-07	BMP2 | bone morphogenetic protein 2
AF245356	p < 1e-07	TES | testis derived transcript (3 LIM domains)
AI184027	0.0000001	ESTs, Weakly similar to FATH_HUMAN CADHERIN-RELATED TUMOR SUPPRESSOR HOMOLOG PRECURSOR [H.sapiens]
AI687303	0.0000032	GPR49 | G protein-coupled receptor 49
BC000715	0.0000108	CLECSF9 | C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 9
H05918	0.0000019	KIAA1867 | KIAA1867 protein
BF437096	0.0000015	EST
AI193122	0.0000124	CYYR1 | cysteine and tyrosine-rich 1
AK027009	0.0002318	FLJ23356 | hypothetical protein FLJ23356
AI274576	p < 1e-07	CTSC | cathepsin C
M90366	0.000042	ZP2 | zona pellucida glycoprotein 2 (sperm receptor)

AY026763	$p < 1e-07$	GOA | gene overexpressed in astrocytoma
AI049877	$p < 1e-07$	KIAA0186 | KIAA0186 gene product
R85380	$p < 1e-07$	ESTs
AA812178	0.0000001	TLR1 | toll-like receptor 1
U18548	$p < 1e-07$	GPR12 | G protein-coupled receptor 12
AK000381	$p < 1e-07$	FLJ20374 | hypothetical protein FLJ20374
BC001346	0.0000005	LOC51700 | cytochrome b5 reductase b5R.2
U87460	0.0000026	GPR37 | G protein-coupled receptor 37 (endothelin receptor type B-like)
AW137459	0.0000029	TMOD2 | tropomodulin 2 (neuronal)
AA485276	0.0005783	CRTAC1 | cartilage acidic protein 1
AI283489	0.0000008	FACL2 | fatty-acid-Coenzyme A ligase, long-chain 2
AI433440	$p < 1e-07$	TNFAIP3 | tumor necrosis factor, alpha-induced protein 3
BC010940	$p < 1e-07$	AIM2 | absent in melanoma 2
AF202636	0.0000004	ANGPTL4 | angiopoietin-like 4
BC012126	0.0000002	CLDN14 | claudin 14
BC000748	0.0000003	TUBB4 | tubulin, beta, 4
AK025320	$p < 1e-07$	SCEL | sciellin
NM_003662	0.0000016	PIR | Pirin
AL133105	0.0000055	DKFZp434F2322 | hypothetical protein DKFZp434F2322
AK001643	0.000527	FLJ10781 | hypothetical protein FLJ10781
AW511572	0.0000029	FZD6 | frizzled homolog 6 (Drosophila)
AI796505	$p < 1e-07$	HOXA2 | homeo box A2
BF513683	$p < 1e-07$	GAJ | GAJ protein
BC008283	0.0000169	CCK | cholecystokinin
NM_001784	$p < 1e-07$	CD97 | CD97 antigen
BC007633	$p < 1e-07$	EIF2C2 | eukaryotic translation initiation factor 2C, 2
BC011403	$p < 1e-07$	GABRA5 | gamma-aminobutyric acid (GABA) A receptor, alpha 5
BC002812	$p < 1e-07$	CBR3 | carbonyl reductase 3
BC003630	0.0000048	KRT4 | keratin 4
AI362949	0.0000242	ESTs
AW138010	0.0001317	SAA2 | serum amyloid A2
NM_005985	$p < 1e-07$	SNAI1 | snail 1 homolog, zinc finger protein (Drosophila)
BC012609	$p < 1e-07$	SERPINB2 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2
BC010128	0.0000005	FLJ10970 | hypothetical protein FLJ10970

AK025309	0.0000032	C1S | complement component 1, s subcomponent
NM_025245	0.0000001	PBX4 | pre-B-cell leukemia transcription factor 4
BF507686	p < 1e-07	CERD4 | cer-d4 (mouse) homolog
AA731869	0.0002721	CD1A | CD1A antigen, a polypeptide
AK000193	p < 1e-07	FLJ20186 | hypothetical protein FLJ20186
BC015859	p < 1e-07	Homo sapiens, clone MGC:27381 IMAGE:4689539, mRNA, complete cds
AL136855	p < 1e-07	DKFZp434K2435 | hypothetical protein DKFZp434K2435
AF089868	p < 1e-07	MCAM | melanoma cell adhesion molecule
AL360258	0.0000009	FLJ11175 | hypothetical protein FLJ11175
AK026248	p < 1e-07	FLJ22595 | hypothetical protein FLJ22595
AI669793	p < 1e-07	ESTs
BC017840	0.0003003	Homo sapiens, clone IMAGE:4689305, mRNA, partial cds
BF112017	p < 1e-07	KCNE1L | potassium voltage-gated channel, Isk-related family, member 1-like
AI375142	0.0000095	LOC57822 | hypothetical protein LOC57822
BC002377	p < 1e-07	PTK7 | PTK7 protein tyrosine kinase 7
AB040057	0.0000006	MST4 | serine/threonine protein kinase MASK
AF027299	p < 1e-07	EPB41L2 | erythrocyte membrane protein band 4.1-like 2
AK026659	0.0000003	Homo sapiens cDNA: FLJ23006 fis, clone LNG00414
AF078749	0.0000014	SLC22A3 | solute carrier family 22 (extraneuronal monoamine transporter), member 3
AF277375	p < 1e-07	KIF4A | kinesin family member 4A
AA747541	0.000033	MYBL1 | v-myb myeloblastosis viral oncogene homolog (avian)-like 1
BC007921	0.0000042	SPIB | Spi-B transcription factor (Spi-1/PU.1 related)
AI823489	0.0005112	BARX2 | BarH-like homeobox 2
NM_004233	p < 1e-07	CD83 | CD83 antigen (activated B lymphocytes, immunoglobulin superfamily)
AI886575	p < 1e-07	ESTs
AI439152	0.0000001	KIAA1145 | KIAA1145 protein
NM_019035	0.0000022	PCDH18 | protocadherin 18
BF109847	0.0000025	ESTs
AL137558	0.0000353	VANGL2 | vang, van gogh-like 2 (Drosophila)
AI553863	p < 1e-07	KIAA1204 | KIAA1204 protein
AA866043	p < 1e-07	CBS | cystathionine-beta-synthase
AW341053	p < 1e-07	ESTs
AK025912	0.0000004	COL4A2 | collagen, type IV, alpha 2
AA634391	p < 1e-07	MAGEB4 | melanoma antigen, family B, 4

AI475447	0.0000043	FLJ12567 | hypothetical protein FLJ12567
NM_005430	p < 1e-07	WNT1 | wingless-type MMTV integration site family, member 1
NM_001998	p < 1e-07	FBLN2 | fibulin 2
AI803166	0.0000007	ESTs
AL040372	p < 1e-07	ESTs, Weakly similar to A54854 Ras GTPase activating protein-related protein [H.sapiens]
BC012385	p < 1e-07	FBG4 | F-box protein FBG4
AF045888	0.0000001	DNMT2 | DNA (cytosine-5-)-methyltransferase 2
AA588167	0.0000004	KIAA1729 | KIAA1729 protein
AF051152	0.0000006	TLR2 | toll-like receptor 2
AL136550	0.0000077	BCMP1 | brain cell membrane protein 1
AI969883	p < 1e-07	EST
AK026181	0.000001	Homo sapiens cDNA: FLJ22528 fis, clone HRC12825
AI469557	0.0000026	EPHB3 | EphB3
AB037670	0.0000007	SLC7A10 | solute carrier family 7, (cationic amino acid transporter, y+ system) member 10
AK027157	p < 1e-07	DKFZp547N157 | hypothetical protein DKFZp547N157
AB000520	p < 1e-07	APS | adaptor protein with pleckstrin homology and src homology 2 domains
AW204447	0.0000005	OATPRP4 | organic anion transporter polypeptide-related protein 4
AJ420520	0.0000813	MGC12335 | hypothetical protein MGC12335
AF146796	p < 1e-07	SLC34A2 | solute carrier family 34 (sodium phosphate), member 2
BC010659	0.0008625	FLJ12691 | hypothetical protein FLJ12691
AA732224	p < 1e-07	ESTs
AL136889	p < 1e-07	DKFZp434B227 | hypothetical protein DKFZp434B227
AW193227	p < 1e-07	ESTs
AK024680	0.0000032	PRO2714 | hypothetical protein PRO2714
AW069753	0.000012	CTGF | connective tissue growth factor
NM_004532	0.0000654	MUC4 | mucin 4, tracheobronchial
AF008203	0.0000116	ALX3 | aristaless-like homeobox 3
BF513361	p < 1e-07	MAP2 | microtubule-associated protein 2
BF507741	p < 1e-07	AF15Q14 | AF15q14 protein
BC011587	0.0000108	Homo sapiens, Similar to RIKEN cDNA 1700018O18 gene, clone IMAGE:4121436, mRNA, partial cds
NM_002514	0.0000778	NOV | nephroblastoma overexpressed gene
AA573170	0.0000001	EST
AK000520	0.0002189	FLJ20513 | hypothetical protein FLJ20513
AI459117	p < 1e-07	C6orf34 | chromosome 6 open reading frame 34

AF011468	p < 1e-07	STK15 | serine/threonine kinase 15
AI269345	0.0001152	FLJ10851 | hypothetical protein FLJ10851
AL050151	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp586J0720 (from clone DKFZp586J0720)
AI042183	0.0000001	TP53BP2 | tumor protein p53 binding protein, 2
AI307682	0.000746	IL18RAP | interleukin 18 receptor accessory protein
AL136712	0.0000795	KIAA0820 | KIAA0820 protein
BC000209	p < 1e-07	MGC2603 | hypothetical protein MGC2603
AK026777	0.0000001	KIAA1573 | KIAA1573 protein
AJ002367	p < 1e-07	SHOX2 | short stature homeobox 2
AK025624	0.0000144	MGC5350 | hypothetical protein MGC5350
BC016047	0.0000063	Homo sapiens, Similar to RIKEN cDNA 2310014B08 gene, clone IMAGE:4639904, mRNA, partial cds
BC010904	p < 1e-07	FLJ11252 | hypothetical protein FLJ11252
NM_004609	0.0000003	TCF15 | transcription factor 15 (basic helix-loop-helix)
BC002654	p < 1e-07	TUBB-5 | tubulin beta-5
NM_052813	0.0000001	CARD9 | caspase recruitment domain family, member 9
AA864938	0.0000005	LALBA | lactalbumin, alpha-
BC012136	0.0000022	FLJ10160 | hypothetical protein FLJ10160 similar to insulin related protein 2
BC001969	0.0000153	ROBO1 | roundabout, axon guidance receptor, homolog 1 (Drosophila)
AL137736	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp586P2321 (from clone DKFZp586P2321)
U64197	0.0000001	SCYA20 | small inducible cytokine subfamily A (Cys-Cys), member 20
BE465918	0.0000005	VNN1 | vanin 1
X78202	0.0001038	FOXG1A | forkhead box G1A
AF329454	0.0004222	TMPRSS2 | transmembrane protease, serine 2
BC011268	0.0000001	KIAA1796 | KIAA1796 protein
BC013919	0.0000001	TYMS | thymidylate synthetase
AB058769	0.0003505	KIAA1866 | KIAA1866 protein
BC005300	0.0004476	DTNA | dystrobrevin, alpha
AI199268	0.0000006	Homo sapiens, Similar to RIKEN cDNA 2010317E24 gene, clone IMAGE:3502019, mRNA, partial cds
X53587	0.000001	ITGB4 | integrin, beta 4
BF111883	0.0000093	bA430M15.1 | novel protein (ortholog of rat four repeat ion channel)
AF035279	0.0000001	IL15RA | interleukin 15 receptor, alpha
NM_004936	0.0000147	CDKN2B | cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)
AK000364	0.0000001	KIAA1416 | KIAA1416 protein
AF281255	0.0000014	BCLG | apoptosis regulator BCL-G

AK026265	0.0000121	FLJ22612 | hypothetical protein FLJ22612
AA515100	0.0001378	ESTs
AA461301	0.000014	Homo sapiens nanos mRNA, partial cds
AF007133	0.000076	SIAT1 | sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase)
AF186780	0.0000009	RGL | RalGDS-like gene
AK026054	0.0000025	Homo sapiens cDNA: FLJ22401 fis, clone HRC08032, highly similar to AB027466 Homo sapiens SPON2 mRNA for spondin 2
BC008191	p < 1e-07	PSCD3 | pleckstrin homology, Sec7 and coiled/coil domains 3
BC002707	0.0000011	SPON2 | spondin 2, extracellular matrix protein
BC001386	0.0000015	TM4SF4 | transmembrane 4 superfamily member 4
BC010120	p < 1e-07	RCN1 | reticulocalbin 1, EF-hand calcium binding domain
NM_001792	0.000069	CDH2 | cadherin 2, type 1, N-cadherin (neuronal)
AL133061	0.0000001	ATP11B | ATPase, Class VI, type 11B
AF290004	p < 1e-07	TSA1902 | eosinophil chemotactic cytokine
AF019386	0.0000011	HS3ST1 | heparan sulfate (glucosamine) 3-O-sulfotransferase 1
BC017409	0.0002052	Homo sapiens, clone IMAGE:4332938, mRNA
AA747738	0.0000004	STAG3 | stromal antigen 3
AK000337	0.0000003	FLJ20330 | hypothetical protein
AF081513	p < 1e-07	EBAF | endometrial bleeding associated factor (left-right determination, factor A; transforming growth factor beta superfamily)
AF131762	0.0000001	Homo sapiens clone 25218 mRNA sequence
U97105	0.0000002	DPYSL2 | dihydropyrimidinase-like 2
AL137308	0.000041	DKFZp761C07121 | hypothetical protein DKFZp761C07121
AW139156	0.0000001	CRMP5 | collapsin response mediator protein-5; CRMP3-associated molecule
M74297	p < 1e-07	HOXA4 | homeo box A4
AK055386	0.0000751	Homo sapiens cDNA FLJ30824 fis, clone FEBRA2001698
AL096737	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp434F152 (from clone DKFZp434F152)
AF267981	0.0000001	DUOX2 | dual oxidase 2
AF277289	0.0000005	FLJ21162 | hypothetical protein FLJ21162
BG655508	0.000001	SATB1 | special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's)
BC001400	p < 1e-07	LOC57228 | hypothetical protein from clone 643
BF195312	0.000023	ESTs
BC018127	0.0000141	PAM | peptidylglycine alpha-amidating monooxygenase
N56968	p < 1e-07	C21orf37 | chromosome 21 open reading frame 37

AI203899	0.0000001	EPIM | epimorphin
BC000117	p < 1e-07	GMDS | GDP-mannose 4,6-dehydratase
AJ276678	0.0000001	C20orf32 | chromosome 20 open reading frame 32
AK056230	0.0000105	Homo sapiens cDNA FLJ31668 fis, clone NT2RI2004916
AL137461	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp434K0621 (from clone DKFZp434K0621); partial cds
AF140242	0.0000048	OPN3 | opsin 3 (encephalopsin, panopsin)
AF161508	p < 1e-07	HSPC159 | HSPC159 protein
AJ251830	0.0000059	PIGPC1 | p53-induced protein PIGPC1
BC002641	0.0000064	KRT15 | keratin 15
AF161505	0.000013	HSPC156 | HSPC156 protein
AA923424	0.0001192	ESTs, Weakly similar to I54374 gene NF2 protein [H.sapiens]
AL157432	p < 1e-07	TERA | TERA protein
AK025494	0.0000003	FLJ21841 | hypothetical protein FLJ21841
AK022869	0.0000001	Homo sapiens cDNA FLJ12807 fis, clone NT2RP2002316
BC008765	p < 1e-07	SDC1 | syndecan 1
AI383975	0.0000034	SPRR2A | small proline-rich protein 2A
BE328136	0.0000034	DPYSL3 | dihydropyrimidinase-like 3
AF106912	0.0000003	WSX1 | class I cytokine receptor
BG054505	p < 1e-07	ESTs
BC008442	p < 1e-07	TM4SF1 | transmembrane 4 superfamily member 1
BE045473	p < 1e-07	EST
R41498	0.0000002	KIAA0231 | KIAA0231 protein
BC004277	p < 1e-07	FLJ10719 | hypothetical protein FLJ10719
BF509349	p < 1e-07	Homo sapiens cDNA: FLJ23020 fis, clone LNG00943
AA910884	0.0000202	ESTs
AA810953	0.0000001	BIC | Homo sapiens BIC noncoding mRNA, complete sequence
M84757	0.0000668	SPRR1B | small proline-rich protein 1B (cornifin)
AL359605	0.0000752	Homo sapiens mRNA; cDNA DKFZp547G036 (from clone DKFZp547G036)
L40377	0.0000001	SERPINB8 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8
AL136932	0.0000001	KIAA0922 | KIAA0922 protein
BE348529	0.0001864	ESTs, Weakly similar to SYN1 MOUSE SYNAPSIN I [M.musculus]
AI269387	0.0000001	BAG2 | BCL2-associated athanogene 2
BF434466	0.0000572	ITGA6 | integrin, alpha 6
AI251449	0.0000037	ESTs

AF063020	0.0000071	PSIP2 | PC4 and SFRS1 interacting protein 2
AF285592	p < 1e-07	FTHL17 | ferritin, heavy polypeptide-like 17
AL110124	0.0000017	DKFZP564A2416 | DKFZP564A2416 protein
AA521246	0.0000054	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
AA844695	0.0000014	ESTs
AI566899	0.0000195	NFIX | nuclear factor I/X (CCAAT-binding transcription factor)
BF512918	0.0001109	AGC1 | aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122)
L20971	0.0005197	PDE4B | phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)
AL136778	0.0000001	DKFZp434J0617 | hypothetical protein DKFZp434J0617
D84212	p < 1e-07	STK6 | serine/threonine kinase 6
S48196	0.0000007	KAI1 | kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))
AI743249	p < 1e-07	H_GS165L15.1 | cAMP response element-binding protein CRE-BPa
BC006376	0.0000001	NMT2 | N-myristoyltransferase 2
AK000140	0.0000629	LOC51316 | hypothetical protein
AL117410	0.0000003	SVIL | supervillin
BC005313	0.0000218	KLK1 | kallikrein 1, renal/pancreas/salivary
R42342	0.0000771	EFNB2 | ephrin-B2
BC017785	0.0000015	PTPN22 | protein tyrosine phosphatase, non-receptor type 22 (lymphoid)
AF068918	p < 1e-07	BIN1 | bridging integrator 1
BI792323	0.0000475	LOC51186 | pp21 homolog
NM_004038	0.0000731	AMY1A | amylase, alpha 1A; salivary
AL035295	0.0000001	H.sapiens gene from PAC 106H8, similar to Dynamin
NM_000935	0.0000159	PLOD2 | procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2
AB030000	0.0000805	IL23A | interleukin 23, alpha subunit p19
AL049332	p < 1e-07	BTG3 | BTG family, member 3
AI827546	0.0000001	ESTs, Highly similar to I39451 amyloid-beta protein [H.sapiens]
BC007836	0.0000005	MDFI | MyoD family inhibitor
AI591051	0.0000002	Homo sapiens, clone IMAGE:4100953, mRNA
NM_001262	0.0000005	CDKN2C | cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)
AA804433	0.0000182	MX2 | myxovirus (influenza virus) resistance 2 (mouse)
BC017901	0.0000307	Homo sapiens, Similar to phospholipid scramblase 1, clone MGC:23806 IMAGE:4253596, mRNA, complete cds
BC001459	0.0000001	RAD51 | RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)

AF191771	0.0000084	CED-6 | CED-6 protein
AW300933	0.0002531	AQP9 | aquaporin 9
AA731110	0.0000001	LOC51185 | protein x 0001
AA736984	0.0000004	ADARB1 | adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)
AI656385	0.000015	SETBP1 | SET binding protein 1
BC000612	0.0000021	MGC2599 | hypothetical protein MGC2599 similar to katanin p60 subunit A 1 2599
BC015940	0.0000202	NT5 | 5' nucleotidase (CD73)
AK026589	0.0000043	2-Sep | septin 6
AL117485	0.0000865	DKFZp434K191 | hypothetical protein DKFZp434K191
AF161398	0.0000012	PRO2013 | hypothetical protein PRO2013
BC017498	0.0000018	LOC65243 | hypothetical protein
BC008981	0.0000002	MGC9341 | similar to RIKEN cDNA 4930500C14 gene
AI970276	0.0000007	KIAA1676 | KIAA1676
AA732062	0.0000008	SIAT8D | sialyltransferase 8D (alpha-2, 8-polysialytransferase)
BC014564	0.0000347	MEST | mesoderm specific transcript homolog (mouse)
BC003536	0.0006849	MGC10796 | hypothetical protein MGC10796
AA861036	0.0000009	ESTs, Weakly similar to T33110 hypothetical protein C18H7.3 - Caenorhabditis elegans [C.elegans]
AF065857	0.0000272	OR7E2P | olfactory receptor, family 7, subfamily E, member 2 pseudogene
AF304051	0.0000001	NDRG2 | N-myc downstream-regulated gene 2
AL110298	0.0000045	SLC2A3 | solute carrier family 2 (facilitated glucose transporter), member 3
AI424406	0.0000004	FLJ14033 | hypothetical protein FLJ14033 similar to hypoxia inducible factor 3, alpha subunit
BC009791	0.0000042	HTN3 | histatin 3
AL137686	0.0003622	KIAA0855 | golgin-67
NM_002451	0.0000014	MTAP | methylthioadenosine phosphorylase
BE673992	0.0000187	ESTs
AL136612	0.0000417	NCALD | neurocalcin delta
BC001268	0.0000001	NMI | N-myc (and STAT) interactor
AF305083	0.0000048	FUT4 | fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
AJ420516	0.0000001	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 966164
AI805080	0.0000002	EST
AA669114	0.0000008	KIAA1842 | KIAA1842 protein
AI022925	0.0000167	EMP1 | epithelial membrane protein 1
NM_006271	0.0000516	S100A1 | S100 calcium binding protein A1
AK055576	0.0000001	MPN | marapsin

W46451	0.0000028	LIF | leukemia inhibitory factor (cholinergic differentiation factor)
AF217989	0.0000028	PP1665 | hypothetical protein PP1665
U66065	0.000005	GRB10 | growth factor receptor-bound protein 10
AI245337	0.0001557	HSPB2 | heat shock 27kD protein 2
AI969251	0.0000054	RAB7L1 | RAB7, member RAS oncogene family-like 1
AW016075	0.0000125	ESTs, Weakly similar to ALUA_HUMAN !!!! ALU CLASS A WARNING ENTRY !!! [H.sapiens]
W60891	0.000027	LGALS7 | lectin, galactoside-binding, soluble, 7 (galectin 7)
AF153820	0.0001128	KCNJ2 | potassium inwardly-rectifying channel, subfamily J, member 2
NM_006089	0.0001405	SCML2 | sex comb on midleg-like 2 (Drosophila)
AI492884	0.0000558	IRF4 | interferon regulatory factor 4
NM_006308	0.0000187	HSPB3 | heat shock 27kD protein 3
AI632869	0.00004	UPK1B | uroplakin 1B
AI821911	0.0000007	ESTs
H06481	0.0000921	KCNK9 | potassium channel, subfamily K, member 9 (TASK-3)
NM_001254	0.0000022	CDC6 | CDC6 cell division cycle 6 homolog (S. cerevisiae)
BF446419	0.0000022	LOC85414 | prostein protein
AL136570	0.000012	LHX6 | LIM homeobox protein 6
M62626	0.0000301	HOX11 | homeo box 11 (T-cell lymphoma 3-associated breakpoint)
AK025796	0.0002692	LOC55862 | uncharacterized hypothalamus protein HCDASE
BF513331	0.0001054	ESTs, Weakly similar to S26689 hypothetical protein hc1 - mouse [M.musculus]
AL117592	0.0000001	EMILIN-2 | extracellular glycoprotein EMILIN-2 precursor
BC007348	0.0000024	UP | uridine phosphorylase
AA761284	0.0000027	FMR2 | fragile X mental retardation 2
X70297	0.0000226	CHRNA7 | cholinergic receptor, nicotinic, alpha polypeptide 7
D87119	0.0000128	GS3955 | GS3955 protein
AI128198	0.0000516	ESTs
BC016330	0.0000018	PIR51 | RAD51-interacting protein
BF510979	0.0000355	DHDH | dihydrodiol dehydrogenase (dimeric)
AI758745	0.0000001	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
AI467849	0.0000008	TBC1D1 | TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1
BC008729	0.0005722	KIAA1309 | KIAA1309 protein
BC012328	0.0000048	RPL39L | ribosomal protein L39-like
AA588742	0.0000561	XDH | xanthene dehydrogenase
M99061	0.0001016	KRT2A | keratin 2A (epidermal ichthyosis bullosa of Siemens)

AK024822	0.0000003	ELAC1 | elaC homolog 1 (E. coli)
BC011393	0.0000597	CHN1 | chimerin (chimaerin) 1
AI950844	0.0000171	AIM1L | absent in melanoma 1-like
BC007636	0.0000194	C20orf100 | chromosome 20 open reading frame 100
BC017401	0.0000342	SERPINB4 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4
AF414120	0.0001959	CTLA4 | cytotoxic T-lymphocyte-associated protein 4
BC002776	0.000003	SEMA5B | sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B
AW014507	0.0000143	KIAA1858 | KIAA1858 protein
AI740744	0.0001645	ESTs
X97859	0.0000085	S100A12 | S100 calcium binding protein A12 (calgranulin C)
BC013982	0.0000365	KIAA1921 | KIAA1921 protein
AK024896	0.0000017	Homo sapiens cDNA: FLJ21243 fis, clone COL01164
BC007079	0.0000158	AF1Q | ALL1-fused gene from chromosome 1q
BC007556	0.0000321	Homo sapiens, Similar to TEA domain family member 2, clone MGC:15481 IMAGE:2967735, mRNA, complete cds
AF011333	0.0000364	LY75 | lymphocyte antigen 75
M26683	0.0003079	SCYA2 | small inducible cytokine A2 (monocyte chemotactic protein 1)
AW151360	0.0000384	TNFSF13B | tumor necrosis factor (ligand) superfamily, member 13b
AW131780	0.0005158	NCAM1 | neural cell adhesion molecule 1
BM126079	0.000573	ESTs
AF316113	0.0000034	GAL3ST-4 | beta-galactose-3-O-sulfotransferase, 4
AF064254	0.0000111	VLCS-H1 | VLCS-H1 protein
BC001492	0.0001032	CNTFR | ciliary neurotrophic factor receptor
AI200660	0.0000004	ESTs, Weakly similar to T26845 hypothetical protein Y43F4B.7 - Caenorhabditis elegans [C.elegans]
NM_004137	0.0000019	KCNMB1 | potassium large conductance calcium-activated channel, subfamily M, beta member 1
AL110257	0.0000839	Homo sapiens mRNA; cDNA DKFZp566P2346 (from clone DKFZp566P2346)
AI096369	0.0004741	ESTs
AL133035	0.0000002	DKFZp434G171 | hypothetical protein DKFZp434G171
BM129291	0.0001921	LMO1 | LIM domain only 1 (rhombotin 1)
AA731866	0.00026	ESTs, Weakly similar to A45841 T-complex-associated-testes-expressed-1 protein - mouse [M.musculus]
AL039716	0.0000003	CDC2L2 | cell division cycle 2-like 2
AW137630	0.000012	ESTs
AI283926	0.0000099	CSPG4 | chondroitin sulfate proteoglycan 4 (melanoma-associated)

AI445650	0.000064	PRF1 | perforin 1 (pore forming protein)
BC005861	0.0000175	ITGB2 | integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)
AI927378	0.0000334	H. sapiens cDNA FLJ31267 fis, clone KIDNE2006053, moderately similar to M. musculus mRNA for acetylglucosaminyltransferase-like protein
AI144219	0.0005353	Human l-myc gene exon 3 and 3'-flanking region
AI268609	0.0000005	ESPL1 | extra spindle poles like 1 (S. cerevisiae)
AF257182	0.0007686	GPR48 | G protein-coupled receptor 48
H17636	0.0000004	GNAL | guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type
BC015050	0.0000026	OIP5 | Opa-interacting protein 5
AF208043	0.0000872	IFI16 | interferon, gamma-inducible protein 16
AB042624	0.0001852	SIRPB2 | signal-regulatory protein beta 2
AW014836	0.0000065	ESTs
BC013011	0.000118	MGC2555 | hypothetical protein MGC2555
R42108	0.0003179	KIAA0378 | KIAA0378 protein
AI371090	0.0000082	KIF3C | kinesin family member 3C
BC004295	0.0000105	PTRF | polymerase I and transcript release factor
AB017800	0.0004322	NOL4 | nucleolar protein 4
BC006458	0.000002	CKS2 | CDC28 protein kinase 2
AA883715	0.0000007	ESTs
AF118088	0.0000086	PRO2000 | PRO2000 protein
NM_005864	0.0000268	EFS2 | signal transduction protein (SH3 containing)
BC009055	0.0001277	FLJ13942 | hypothetical protein FLJ13942
AF257238	0.0007241	KIAA1634 | KIAA1634 protein
AW451039	0.0000006	FLJ11808 | hypothetical protein FLJ11808
AI910678	0.0000136	WASF1 | WAS protein family, member 1
AF286095	0.0004553	IL22R | interleukin 22 receptor
NM_002497	0.0000048	NEK2 | NIMA (never in mitosis gene a)-related kinase 2
NM_006142	0.000009	SFN | stratifin
AL136842	0.0002278	CEP3 | Cdc42 effector protein 3
AL049443	0.0000451	Homo sapiens mRNA; cDNA DKFZp586N2020 (from clone DKFZp586N2020)
BC006000	0.0000675	MGC12536 | hypothetical protein MGC12536
AL133706	0.0001957	ESTs
BF433809	0.0000769	SCYC1 | small inducible cytokine subfamily C, member 1 (lymphotactin)

AK025953	0.0001653	Homo sapiens cDNA: FLJ22300 fis, clone HRC04759
AK025428	0.0000283	KIAA0172 | KIAA0172 protein
BE858970	0.000055	EST
AA827154	0.0003051	PAG | phosphoprotein associated with glycosphingolipid-enriched microdomains
AW512550	0.0004485	ESTs
AA946776	0.0000011	FGF9 | fibroblast growth factor 9 (glia-activating factor)
AF018253	0.0000509	TNFRSF11A | tumor necrosis factor receptor superfamily, member 11a, activator of NFKB
N32241	0.0003411	Homo sapiens cDNA FLJ32214 fis, clone PLACE6003705
AW293306	0.0001228	K6HF | cytokeratin type II
BC000141	0.0001528	MYC | v-myc myelocytomatosis viral oncogene homolog (avian)
AF009227	0.0007033	NRG1 | neuregulin 1
AI597863	0.0007186	ESTs
AI659900	0.0003695	EST
AW194680	0.0004206	HOXD11 | homeo box D11
AA868889	0.0000187	RFPL3S | ret finger protein-like 3 antisense
BC009352	0.0001185	DKFZp762L0311 | hypothetical protein DKFZp762L0311
AW291447	0.0001196	CCR1 | chemokine (C-C motif) receptor 1
AK002052	0.0005596	C20orf46 | chromosome 20 open reading frame 46
AI446519	0.0000451	ESTs
NM_000734	0.0000771	CD3Z | CD3Z antigen, zeta polypeptide (TiT3 complex)
NM_032968	0.0000017	PCDH11 | protocadherin 11
BF509016	0.0000177	Homo sapiens cDNA FLJ30899 fis, clone FEBRA2005726
M93426	0.0000025	PTPRZ1 | protein tyrosine phosphatase, receptor-type, Z polypeptide 1
AK026663	0.0000204	FLJ21034 | hypothetical protein FLJ21034
BF433635	0.0000216	ESTs
AF104313	0.0002268	ESDN | endothelial and smooth muscle cell-derived neuropilin-like protein
BC000356	0.0000032	MAD2L1 | MAD2 mitotic arrest deficient-like 1 (yeast)
AI625086	0.0000526	FLJ11585 | hypothetical protein FLJ11585
AI560377	0.0003146	ESTs
BF112041	0.0000027	KIAA0401 | KIAA0401 protein
AI831078	0.0003873	ESTs, Weakly similar to CA18 MOUSE COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR [M.musculus]
AF007194	0.0000116	MUC3A | mucin 3A, intestinal
NM_000436	0.0000291	OXCT | 3-oxoacid CoA transferase
BC007828	0.0000485	MGC14128 | hypothetical protein MGC14128

AF396928	0.000446	EPSTI1 | epithelial stromal interaction 1 (breast)
U43203	0.0004703	TITF1 | thyroid transcription factor 1
BC000012	0.0002624	GFPT2 | glutamine-fructose-6-phosphate transaminase 2
AF047711	0.0000029	RASAL2 | RAS protein activator like 2
AF053453	0.0001192	TM4SF6 | transmembrane 4 superfamily member 6
BC017054	0.0000027	MTHFD2 | methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase
AI769930	0.0000068	Homo sapiens (clone B3B3E13) Huntington's disease candidate region mRNA fragment
BC002914	0.0000453	WASPIP | Wiskott-Aldrich syndrome protein interacting protein
BE671403	0.0004777	ESTs
AI249782	0.0001099	PPP4R2 | protein phosphatase 4 regulatory subunit 2
AJ420537	0.0000104	dJ55C23.6 | dJ55C23.6 gene
AI239743	0.0001411	LTA | lymphotoxin alpha (TNF superfamily, member 1)
NM_001890	0.0003456	CSN1 | casein, alpha
AF303058	0.0000457	NP25 | neuronal protein
BC004336	0.0000035	MGC10946 | hypothetical protein MGC10946
AI590055	0.0000213	ESTs
AW301017	0.0001513	ESTs
BC015497	0.0000283	TEAD4 | TEA domain family member 4
BC008483	0.0000566	SERPINB3 | serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 3
BC007072	0.0000858	MGC12538 | hypothetical protein MGC12538
AI384087	0.0001257	KIAA0603 | KIAA0603 gene product
AB023135	0.000755	ICOS | inducible T-cell co-stimulator
AB023967	0.0000858	ROD1 | ROD1 regulator of differentiation 1 (S. pombe)
AI560576	0.0006927	PTPRK | protein tyrosine phosphatase, receptor type, K
AK024951	0.0000497	C1R | complement component 1, r subcomponent
AW452231	0.0004972	CD244 | natural killer cell receptor 2B4
AK027515	0.0000623	Homo sapiens cDNA FLJ14609 fis, clone NT2RP1000944
AL043170	0.0001136	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
AK025636	0.0001079	Homo sapiens cDNA: FLJ21983 fis, clone HEP06219
NM_006278	0.0000121	SIAT4C | sialyltransferase 4C (beta-galactosidase alpha-2,3-sialytransferase)
BC003388	0.0001059	TANK | TRAF family member-associated NFKB activator
AA777592	0.0005802	ESTs, Weakly similar to ubiquitous TPR motif, Y isoform [H.sapiens]
BC016623	0.0000111	ETV4 | ets variant gene 4 (E1A enhancer binding protein, E1AF)

BC005408	0.0000236	FLJ23119 | hypothetical protein FLJ23119
AF233588	0.0001101	LOC51285 | Ris
BC018644	0.0001366	NUDT8 | nudix (nucleoside diphosphate linked moiety X)-type motif 8
AW057670	0.0000078	ESTs, Weakly similar to S65824 reverse transcriptase homolog [H.sapiens]
AF414088	0.000153	COL21A1 | collagen, type XXI, alpha 1
X96757	0.0001749	MAP2K6 | mitogen-activated protein kinase kinase 6
NM_005965	0.0002044	MYLK | myosin, light polypeptide kinase
R40207	0.00041	PIP5K1B | phosphatidylinositol-4-phosphate 5-kinase, type I, beta
AK026315	0.0005265	FLJ22662 | hypothetical protein FLJ22662
AK025130	0.0000064	FLJ21477 | hypothetical protein FLJ21477
BC014444	0.0000298	ASML3B | acid sphingomyelinase-like phosphodiesterase
AJ012214	0.0000751	11-Oct | POU transcription factor
AL137343	0.0000089	Homo sapiens mRNA for putative NSE1 protein
AK024855	0.0000346	CTSS | cathepsin S
BC002727	0.0001627	SDCBP2 | syndecan binding protein (syntenin) 2
AK026337	0.0000268	FLJ22684 | hypothetical protein FLJ22684
AK025346	0.0009842	Homo sapiens cDNA: FLJ21693 fis, clone COL09609
AI536895	0.0001916	LOX | lysyl oxidase
AF339783	0.0004293	FLJ20159 | hypothetical protein FLJ20159
AB038781	0.0000178	MUC3B | mucin 3B
BC011969	0.0001809	Homo sapiens, clone IMAGE:3880654, mRNA
AF326964	0.0001063	BCL2L10 | BCL2-like 10 (apoptosis facilitator)
AF033347	0.0004868	KCNQ3 | potassium voltage-gated channel, KQT-like subfamily, member 3
AF070631	0.0000349	TMPO | thymopoietin
BC015507	0.000679	CST7 | cystatin F (leukocystatin)
AI811072	0.000041	VGF | VGF nerve growth factor inducible
BC006346	0.000113	APEG1 | nuclear protein, marker for differentiated aortic smooth muscle and down-regulated with vascular injury
AF247167	0.0001179	AD031 | AD031 protein
L27711	0.0001896	CDKN3 | cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)
AA810577	0.0000119	ARSB | arylsulfatase B
AF328296	0.0000516	FLJ14437 | myopalladin
AI147926	0.0001123	CSF2RB | colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)
AF017988	0.00017	SFRP5 | secreted frizzled-related protein 5
AI151185	0.0000495	LHPP | phospholysine phosphohistidine inorganic pyrophosphate phosphatase

AW271272	0.0000564	FOXC2 | forkhead box C2 (MFH-1, mesenchyme forkhead 1)
BI324932	0.0000637	PTGER4 | prostaglandin E receptor 4 (subtype EP4)
AF105378	0.00025	HS3ST4 | heparan sulfate (glucosamine) 3-O-sulfotransferase 4
BC009642	0.0000406	FXYD5 | FXYD domain-containing ion transport regulator 5
BF002341	0.0000493	ESTs, Moderately similar to AF174605 1 F-box protein Fbx25 [H.sapiens]
H06160	0.0001828	C1orf17 | chromosome 1 open reading frame 17
NM_001839	0.0000549	CNN3 | calponin 3, acidic
BC015397	0.0001164	Homo sapiens, Similar to RIKEN cDNA 4921507P07 gene, clone MGC:21710 IMAGE:4448480, mRNA, complete cds
AK026144	0.0006923	TEL2 | transcription factor ets
BC008749	0.0000146	MBP | myelin basic protein
BC007678	0.0000353	ADA | adenosine deaminase
AA814043	0.0004392	ESTs
AW291196	0.0001248	ESTs
AI090561	0.0005695	M160 | scavenger receptor cysteine-rich type 1 protein M160 precursor
AF098066	0.0000203	SART-2 | squamous cell carcinoma antigen recognized by T cell
AK025615	0.0001353	Homo sapiens cDNA: FLJ21962 fis, clone HEP05564
AU152414	0.0004928	DNAH11 | dynein, axonemal, heavy polypeptide 11
U49395	0.0006226	P2RX5 | purinergic receptor P2X, ligand-gated ion channel, 5
AI611312	0.0002789	KIAA0942 | KIAA0942 protein
AI689069	0.0001012	CORO1A | coronin, actin binding protein, 1A
AF117386	0.0000326	USP1 | ubiquitin specific protease 1
NM_001452	0.0001101	FOXF2 | forkhead box F2
AI025919	0.0000271	ESTs
AF225416	0.0000275	AD024 | AD024 protein
AA910331	0.0006572	COL4A1 | collagen, type IV, alpha 1
AA743321	0.0000364	ESTs
AI290556	0.0000413	ESTs
BE676183	0.0002021	KIAA1798 | KIAA1798 protein
AA831508	0.0008458	ESTs
BC012945	0.0000572	MGC11271 | hypothetical protein MGC11271
BC004278	0.0000617	FLJ23239 | hypothetical protein FLJ23239
BC004267	0.0001122	MGC10818 | hypothetical protein MGC10818
AW449550	0.0001866	GAP1IP4BP | RAS p21 protein activator (GTPase activating protein) 3 (Ins(1,3,4,5)P4-binding protein)

BC000049	0.0002093	FLJ10493 | hypothetical protein FLJ10493
R56080	0.0003624	RELN | reelin
AF039655	0.0000292	BFSP1 | beaded filament structural protein 1, filensin
AI656630	0.0002032	TMEM7 | transmembrane protein 7
AW411170	0.0003073	EAF1 | EAF1 protein
AI280476	0.0004985	APG-1 | heat shock protein (hsp110 family)
BF510271	0.0000551	LOC51063 | hypothetical protein
BC007533	0.0001578	NRP1 | neuropilin 1
AI671448	0.00021	ESTs
U62824	0.0009236	H.sapiens mRNA for HLA-C alpha chain (Cw*1701)
AF025887	0.0000808	GSTA4 | glutathione S-transferase A4
BF513346	0.0004176	ESTs
AW452418	0.0006057	RYR2 | ryanodine receptor 2 (cardiac)
AL117401	0.0006587	DKFZP434P211 | DKFZp434P211 protein
AF324830	0.0007875	ILT11 | leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 7
BC004291	0.0000444	KIAA0080 | KIAA0080 protein
AF223943	0.0000452	GLS | glutaminase
AK000626	0.000305	FLJ20619 | hypothetical protein FLJ20619
AI766890	0.0008599	ESTs, Weakly similar to NAH6_HUMAN SODIUM/HYDROGEN EXCHANGER 6 [H.sapiens]
BM141806	0.0002858	Homo sapiens cDNA FLJ30365 fis, clone FEBRA2004099
Y13786	0.0001617	ADAM19 | a disintegrin and metalloproteinase domain 19 (meltrin beta)
BF508503	0.0000643	Homo sapiens cDNA FLJ32102 fis, clone OCBBF2001196
AW073971	0.0000986	ESTs, Weakly similar to T00705 N-chimerin homolog F25965_3 [H.sapiens]
M87507	0.0002201	CASP1 | caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)
AJ315514	0.000686	NR3C2 | nuclear receptor subfamily 3, group C, member 2
AI240521	0.0002527	CHML | choroideremia-like (Rab escort protein 2)
NM_057749	0.0003057	CCNE2 | cyclin E2
BC012113	0.000344	HOMER-3 | Homer, neuronal immediate early gene, 3
BE551149	0.0005021	ESTs
AW081673	0.0000873	SAH | SA hypertension-associated homolog (rat)
AB016901	0.0001215	HGC6.2 | HGC6.2 protein
BC006093	0.0001312	MMP9 | matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase)
NM_000795	0.000318	DRD2 | dopamine receptor D2
AA630788	0.000387	TOP2A | topoisomerase (DNA) II alpha (170kD)

AL137274	0.000862	MIG-6 | Gene 33/Mig-6
U89995	0.0001892	FOXE1 | forkhead box E1 (thyroid transcription factor 2)
M85294	0.0002409	PRKR | protein kinase, interferon-inducible double stranded RNA dependent
BC003097	0.0000678	ICAM2 | intercellular adhesion molecule 2
AL137346	0.0000816	Homo sapiens mRNA; cDNA DKFZp761M0111 (from clone DKFZp761M0111)
AK027138	0.0000856	KIAA0914 | KIAA0914 gene product
BC009628	0.0000828	Homo sapiens, clone IMAGE:3898148, mRNA, partial cds
AB037715	0.0002083	FLJ10210 | hypothetical protein FLJ10210
AW084130	0.0008664	NOS3 | nitric oxide synthase 3 (endothelial cell)
AA807955	0.0002328	EST
AK024697	0.0007384	FLJ21044 | hypothetical protein FLJ21044 similar to Rbig1
AL137662	0.0002524	Homo sapiens mRNA; cDNA DKFZp434P086 (from clone DKFZp434P086); partial cds
AI732321	0.0001257	ESTs
AL137506	0.0007917	FLJ23563 | hypothetical protein FLJ23563
R43523	0.0005701	FLJ22202 | hypothetical protein FLJ22202
AI869243	0.0003403	ESTs
AW291368	0.0002584	ESTs, Weakly similar to KIAA0738 protein [H.sapiens]
BC001350	0.0009786	ARG2 | arginase, type II
AK022735	0.0001058	FLJ12673 | hypothetical protein FLJ12673
BF510331	0.0001294	MCM3AP | MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) associated protein
AL136703	0.0004855	DKFZP566J091 | hypothetical protein DKFZp566J091
AI953054	0.0001233	TKT | transketolase (Wernicke-Korsakoff syndrome)
BC014317	0.0002587	NX-17 | kidney-specific membrane protein
BC014890	0.0004285	SLUG | slug homolog, zinc finger protein (chicken)
BC001645	0.000697	SYK | spleen tyrosine kinase
AI188578	0.0002173	FLJ11036 | hypothetical protein FLJ11036
AI733497	0.0005164	ESTs
AW293496	0.00068	ESTs
AF269223	0.0005681	TCP11 | t-complex 11 (mouse)
AB012643	0.0006384	ALPL | alkaline phosphatase, liver/bone/kidney
U75309	0.0006677	TAF5 | TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100 kD
NM_015901	0.0001783	LOC51055 | unknown
AK021801	0.0002326	Homo sapiens cDNA FLJ11739 fis, clone HEMBA1005497
AW295061	0.0002448	WSX1 | class I cytokine receptor

AI559983	0.0004987	CDC2 | cell division cycle 2, G1 to S and G2 to M
BC015496	0.000254	INPP1 | inositol polyphosphate-1-phosphatase
X93595	0.0002125	KIR3DL2 | killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2
AI765908	0.0005868	Homo sapiens cDNA FLJ30999 fis, clone HLUNG1000110, weakly similar to PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR
NM_005923	0.00086	MAP3K5 | mitogen-activated protein kinase kinase kinase 5
BC016757	0.0002739	SAP30 | sin3-associated polypeptide, 30kD
AK027121	0.0002624	FLJ23468 | hypothetical protein FLJ23468
BE644686	0.0005227	KIAA0509 | KIAA0509 protein
AI418207	0.0007707	ESTs
BC009198	0.0004215	Homo sapiens, Similar to RNA polymerase I transcription factor RRN3, clone MGC:15321 IMAGE:3678732, mRNA, complete cds
AA761502	0.0005644	KIAA0009 | KIAA0009 gene product
BC018112	0.0005867	PROL2 | proline rich 2
BC002718	0.000673	FN14 | type I transmembrane protein Fn14
AL353948	0.0009563	Homo sapiens mRNA; cDNA DKFZp761P0114 (from clone DKFZp761P0114)
AK023806	0.0009698	FLJ13744 | hypothetical protein FLJ13744
AI264615	0.0007686	SIRT4 | sirtuin silent mating type information regulation 2 homolog 4 (S. cerevisiae)
BC002715	0.0007069	PPARD | peroxisome proliferative activated receptor, delta
M96843	0.0007716	ID2B | striated muscle contraction regulatory protein
BC007289	0.0008457	ARPM1 | actin related protein M1
AI338498	0.0008464	ZNF295 | zinc finger protein 295
W46976	0.0009251	EST

Table 5

GenBank accession	CloneID	UnigeneID
AW473119	725321	Hs.1657
AW015443	841621	Hs.100686
NM_001218	594633	Hs.5338
AF131785	2284924	Hs.90419
AJ009985	239568	Hs.279928
AF088867	2321113	Hs.91011
AF007153	726703	Hs.7888
BC014948	1558642	Hs.321130
AA542898	782688	Hs.33846
AA569340	1631209	Hs.330780
AW137092	1554430	Hs.94694
NM_005080	725968	Hs.149923
BC006793	214068	Hs.169946
NM_004496	1610546	Hs.299867
U95089	137017	Hs.77432
U95089	183468	Hs.77432
AJ404611	1584563	Hs.130881
AI128582	1691237	Hs.190642
NM_020974	242778	Hs.222399
AI332979	2321529	Hs.118695
AA688021	111389	Hs.179808
AI820662	1607198	Hs.129598
AI125908	51185	Hs.125019
AK026818	69378	Hs.279898
BC014962	1700429	Hs.105445
AW024203	530197	Hs.349344
AL137566	504959	Hs.32405
AI874215	299332	Hs.193914
BC013732	66599	Hs.155956
R41823	1558233	Hs.7413
AK000442	1562618	Hs.11408
AK025256	1632235	Hs.129691
NM_006763	213136	Hs.75462
NM_006763	71428	Hs.75462
NM_001238	68950	Hs.9700
BC011348	785795	Hs.15929
N31940	866488	Hs.14434
BC014601	839382	Hs.88417
AF356492	431003	Hs.63931
BC012375	179212	Hs.279937
BC012375	767289	Hs.279937
GenBank accession	CloneID	UnigeneID
AI200852	1836699	Hs.127780
AA130089	490965	Hs.23136
AA255953	243100	Hs.81934
NM_012244	415670	Hs.22891
NM_003508	2149968	Hs.158335
BC017859	298417	Hs.82961
NM_000352	1558108	Hs.54470
AA804407	325515	Hs.29716
AF176012	120138	Hs.260720
AF052504	26294	Hs.241471
AI263695	502173	Hs.72050
AW139831	258167	Hs.284186
AA156097	969843	Hs.29283
BC006428	139354	Hs.15093
AK024872	487932	Hs.92254
AK024872	826194	Hs.92254
BC016861	590310	Hs.351461
AI272823	83358	Hs.76704
AI674226	279720	Hs.125201
AI373462	155072	Hs.29190
AK000978	505575	Hs.79741
AA807457	243549	Hs.1334
AL133622	1571106	Hs.301011
R49089	179212	Hs.24811
AJ420423	593431	Hs.23703
BC017352	377275	Hs.82237
U62325	1470333	Hs.324125
AI804588	1733262	Hs.167380
AI733682	1637829	Hs.130239
BC012372	868652	Hs.278625
AF007170	1492468	Hs.125783
BC007008	839736	Hs.1940
BC013438	1640821	Hs.42792
BC017733	1909775	Hs.349227
BC017733	877772	Hs.349227
AY029179	753198	Hs.333893
AF271781	471196	Hs.111577
BC007681	1911343	Hs.3797
H29323	270917	Hs.7306
AY043361	813281	Hs.324275
AF070632	669359	Hs.23729
NM_004310	302591	Hs.109918
BE967259	342181	Hs.79241
NM_000044	2250839	Hs.99915
AI823785	782497	Hs.6349
BC012914	592832	Hs.180059
AF084830	1901562	Hs.127007
AI637899	2237353	Hs.1907
AL110126	813265	Hs.326416
AF033021	756708	Hs.10082
AA749341	814054	Hs.158282
BC000558	647397	Hs.101174
AI364725	809779	Hs.9729
X70340	1553998	Hs.170009

AI471793	415550	Hs.60257	NM_004938	2043415	Hs.153924
BC017701	823655	Hs.21941	AW206460	454632	Hs.6360
NM_014599	730288	Hs.55058	BC018035	1557994	Hs.127043
AA659816	795851	Hs.23830	BC014189	854763	Hs.10260
AA622986	731047	Hs.104830	BF433570	1557637	Hs.144479
AI871614	344959	Hs.58241	BC008915	1323591	Hs.76353
AK026946	220395	Hs.27099	AA806280	772913	Hs.349306
AA761512	783698	Hs.81412	AI140061	304908	Hs.1189
AL136579	219929	Hs.109315	AI828071	1616253	Hs.129057
AW574736	261541	Hs.143460	AF269101	796539	Hs.27695
AI337740	41569	Hs.4243	AW294316	1847093	Hs.125608
AI382972	773170	Hs.82128	AF104032	1702742	Hs.184601
AJ249248	685516	Hs.97101	AF104032	755578	Hs.184601
BC013300	531319	Hs.180655	BC013430	139835	Hs.28309
AA587049	2494805	Hs.211587	BC008317	52933	Hs.79136
NM_005044	1869486	Hs.147996	BC007541	1570910	Hs.55067
NM_005044	310034	Hs.147996	BC014941	788234	Hs.34853
NM_001502	1412344	Hs.53985	AA069179	1661732	Hs.153687
AW204371	293689	Hs.239727	BC009211	125788	Hs.8739
AB023430	2019426	Hs.156114	AI351524	796197	Hs.169470
AW136298	2449841	Hs.3185	AF153605	1554009	Hs.107528
AL117452	767068	Hs.44155	BC017758	724888	Hs.687
NM_014211	563598	Hs.70725	NM_007210	470964	Hs.151678
AA845338	197525	Hs.14286	AF131789	32489	Hs.4863
AI741657	683569	Hs.198443	BI492630	20115	Hs.62185
AW195038	2017930	Hs.129867	BC017918	868396	Hs.302766
AK000012	1517212	Hs.184634	AL080192	2312454	Hs.101282
BF434467	82869	Hs.11805	AF091092	768007	Hs.43728
BC005395	1854648	Hs.346935	AW207201	1507713	Hs.97220
BC005395	85488	Hs.346935	BC001283	416959	Hs.33287
AA767129	310034	Hs.56336	NM_005401	2390593	Hs.159238
AB022918	272706	Hs.34578	NM_007050	41647	Hs.225952
AA648922	127510	Hs.1634	BC003610	785744	Hs.3745
AF026477	1536215	Hs.6079	AI631667	344073	Hs.351344
AJ420468	1901310	Hs.51965	S72493	1486533	Hs.115947
AA775255	2299609	Hs.284163	AF193809	1456468	Hs.279682
BC018646	204897	Hs.75648	BC012107	391949	Hs.103527
BC010626	214205	Hs.28149	X83301	470261	Hs.324728
AL161952	1609836	Hs.170171	BC002738	1323448	Hs.17409
AI095049	1686314	Hs.6786	BE464993	2062533	Hs.112158
AK055698	1860909	Hs.349189	BG272534	289505	Hs.44829
AI261967	377252	Hs.45743	R50991	1586124	Hs.12247
H10667	80727	Hs.274243	AF117108	429494	Hs.79440
AK025347	415766	Hs.170162	AL157505	32050	Hs.21380
BC000088	137940	Hs.2006	N22687	266500	Hs.8236
BC003628	1486082	Hs.1690	AJ278018	1637767	Hs.12079
BE965331	2309234	Hs.87417	AW294857	25274	Hs.21050
AI432615	785745	Hs.264	AI804716	544639	Hs.95612
AF100759	416374	Hs.284243	NM_004923	1518890	Hs.121378
R15881	2118505	Hs.7138	AA177001	809674	Hs.112184

BC009722	1637893	Hs.105887	BC006168	840333	Hs.82432
BC000703	292936	Hs.48855	BC005910	346688	Hs.279651
Z73678	1662279	Hs.198382	BC008682	726582	Hs.12887
BC007595	1558675	Hs.44317	BF446789	1946448	Hs.139851
BC009203	212456	Hs.25925	BF446789	840984	Hs.139851
AF132818	132711	Hs.84728	AB050468	1533710	Hs.4193
AF132818	2062507	Hs.84728	AB050468	592594	Hs.4193
BF110928	1556859	Hs.126932	AI126271	488202	Hs.49433
BM126815	1753085	Hs.316433	NM_003806	1671299	Hs.87247
AY048757	23819	Hs.10237	BC001211	753038	Hs.23131
AK026420	1161564	Hs.10587	AW194426	1518845	Hs.20726
AI567843	51078	Hs.349090	BC001940	66406	Hs.104859
AK025562	418049	Hs.18612	R42732	214996	Hs.283705
AL080079	786695	Hs.44197	AA716439	1898758	Hs.99824
BC002660	723986	Hs.170453	AI202593	2119039	Hs.144877
BC008764	742798	Hs.69360	BF511352	193913	Hs.80887
AL137311	281392	Hs.234074	BC009373	1635059	Hs.326391
BI493178	415191	Hs.78894	NM_006769	1706027	Hs.3844
AF181862	2016775	Hs.242407	X55362	796646	Hs.75212
BC010039	144849	Hs.289092	AI636974	811774	Hs.238126
BE326342	155532	Hs.129043	AI494546	307255	Hs.10649
NM_004419	342378	Hs.2128	AJ420562	26883	Hs.106106
BC000881	2017415	Hs.1594	BC015338	2063284	Hs.180884
AI498405	754346	Hs.34145	AL050227	784178	Hs.27860
AL137332	754157	Hs.23869	BF433019	950355	Hs.110080
AI367357	255285	Hs.112083	AK025296	204790	Hs.95549
AB048286	161484	Hs.334305	AA088779	1635970	Hs.24724
AL110139	1844765	Hs.27373	AA846278	51700	Hs.5740
BC014913	786663	Hs.247525	BI495988	626841	Hs.285754
AB018329	897731	Hs.24212	BI495988	754509	Hs.285754
AF038191	51097	Hs.134846	AI150439	208387	Hs.15370
AF043473	249687	Hs.117780	AI732309	153760	Hs.78436
AK057601	752903	Hs.54985	BC006526	810873	Hs.2794
AK057601	768031	Hs.54985	AF035282	293569	Hs.12532
BC012844	812048	Hs.74621	AF089854	1947911	Hs.8022
AL512749	752625	Hs.93961	AA714213	66406	Hs.352002
BC011721	757489	Hs.349695	AY007114	296679	Hs.44898
NM_001793	773301	Hs.2877	N89991	772962	Hs.44070
AI273928	814798	Hs.75746	BC000576	23776	Hs.75438
Y17978	1968246	Hs.118722	BE672557	282980	Hs.42640
BC004143	741977	Hs.69771	BC015525	809784	Hs.79361
AI694966	490178	Hs.49597	AL136539	768068	Hs.169333
AI694966	501868	Hs.49597	BC009742	121551	Hs.18141
U74612	564803	Hs.239	BC017338	308437	Hs.576
BC007609	2112387	Hs.231444	D50840	812196	Hs.152601
AL117633	190325	Hs.348724	BC017575	246524	Hs.20295
AF222980	767471	Hs.26985	BC012089	27544	Hs.112360
AI678454	2052032	Hs.61638	AJ420473	797038	Hs.7869
BC000809	786607	Hs.95243	M57892	823718	Hs.100322
BC014213	746373	Hs.159505	AI436812	1553560	Hs.143640

M57609	767447	Hs.72916	BC008832	782811	Hs.139800
M57609	767495	Hs.72916	AK000708	191882	Hs.169764
AI797041	382787	Hs.182231	AI631708	1048592	Hs.121554
AI741143	767164	Hs.235857	NM_002852	1691868	Hs.2050
BC001766	759948	Hs.83384	BC016004	840466	Hs.67726
BC009945	813697	Hs.49500	AL137281	24958	Hs.17110
BC014851	40887	Hs.159142	BC015663	199367	Hs.21858
AF039843	813698	Hs.18676	AI524385	128711	Hs.62180
AK025000	782787	Hs.103147	BC002551	743810	Hs.30114
AL133033	785710	Hs.4084	BG939593	415769	Hs.2463
AF053305	781047	Hs.98658	AI557322	186965	Hs.27342
AI207256	752837	Hs.13766	AK000532	1457205	Hs.98491
AW780208	825343	Hs.38516	BC011976	323238	Hs.789
D25538	2115545	Hs.172199	AA648777	79576	Hs.11090
AL136653	135811	Hs.93675	BC004199	1618987	Hs.1933
AI866286	740788	Hs.71962	AW450693	782199	Hs.104258
BF476123	1583198	Hs.321176	BC002668	951125	Hs.15250
X64318	858153	Hs.79334	AI740531	741429	Hs.269222
BC008185	526945	Hs.288354	AA181334	611532	Hs.83760
AA903387	154999	Hs.323032	BC010607	428184	Hs.104679
BC003098	840606	Hs.75441	NM_001604	230882	Hs.89506
BC012142	123627	Hs.182429	BC017730	1534888	Hs.159651
R41429	266312	Hs.84999	AW070918	358936	Hs.323445
AL049933	753215	Hs.203862	BC004161	591157	Hs.95583
BC000232	263727	Hs.178112	AF141339	796767	Hs.26799
U85267	884462	Hs.184222	BC007318	133518	Hs.78335
BC010658	686172	Hs.77695	AW083384	79726	Hs.11067
BE676675	1609372	Hs.268551	BC010078	1519143	Hs.106747
AI039854	112525	Hs.348415	BC012432	1603358	Hs.166994
BC005153	1086070	Hs.198551	BC016615	1492587	Hs.147066
AF280086	2405856	Hs.157439	N47717	2012523	Hs.153179
NM_004961	209137	Hs.22785	BC008962	788832	Hs.296638
BC000332	878833	Hs.76118	AL136939	839081	Hs.250175
M76558	49630	Hs.23838	BF446757	470348	Hs.31841
BC001278	1909457	Hs.25338	AI885044	265060	Hs.81665
BC001278	782547	Hs.25338	AF230904	1604005	Hs.153260
AI147370	1839935	Hs.143653	NM_002639	2499237	Hs.55279
AI288717	505334	Hs.100007	M59305	1762111	Hs.123655
R42185	41826	Hs.102720	AJ010277	2273365	Hs.50403
BC000183	306771	Hs.56145	AJ276230	745007	Hs.82587
BC015182	196189	Hs.83834	AL080222	782306	Hs.7358
BC012727	1035359	Hs.101265	AA262504	685912	Hs.46925
S61953	855563	Hs.199067	BC008947	504308	Hs.14559
NM_002996	140574	Hs.80420	BC014039	1517595	Hs.184339
BC013362	291478	Hs.170019	BC001068	200402	Hs.70704
AI200759	767322	Hs.44737	BC011705	361204	Hs.53563
BC008588	1568391	Hs.4114	BC011705	897646	Hs.53563
AK025732	855487	Hs.75811	AF131784	155227	Hs.25318
AK024892	1603583	Hs.14368	AF131784	25194	Hs.25318
BC008832	771224	Hs.139800	AF136631	140197	Hs.103291

NM_001237	814270	Hs.85137	NM_022977	858167	Hs.81452
NM_001237	950690	Hs.85137	BC016308	1556433	Hs.89690
AW070746	181877	Hs.177691	AK055431	768246	Hs.349611
R74353	202577	Hs.81182	AW007851	2009779	Hs.326056
AK025511	1910785	Hs.29189	BC007407	2306697	Hs.83321
NM_002145	1526826	Hs.2733	BC013591	143661	Hs.102541
AA573096	768393	Hs.57655	AL122077	2291557	Hs.144672
AA664218	796542	Hs.43697	AF123074	43865	Hs.65248
AA424146	70201	Hs.300496	AI031941	136954	Hs.25119
AI262988	897593	Hs.6728	BC016040	1897302	Hs.120996
AL122086	366591	Hs.12598	X59770	233583	Hs.25333
BC001051	712139	Hs.111554	BC008703	1898619	Hs.39122
BC009744	810057	Hs.198726	BC009581	1576468	Hs.155109
AA706017	550141	Hs.119944	AI275604	268188	Hs.40637
AI399653	33817	Hs.22917	R05446	241308	Hs.11611
BF513300	244767	Hs.1192	AA258057	703383	Hs.175511
AL136911	841415	Hs.10706	AF055982	2243051	Hs.104570
AW472810	1912458	Hs.673	AA993573	486208	Hs.2025
AF051321	844703	Hs.13565	AF248053	758347	Hs.305971
AF247820	758088	Hs.325474	AA873846	788617	Hs.306083
AK026139	1858230	Hs.98485	BF589790	774446	Hs.394
BC015839	155768	Hs.350038	U38276	809526	Hs.32981
BC012625	502198	Hs.303090	AW290960	289760	Hs.6382
AI279525	1864302	Hs.11713	BC003554	795809	Hs.4890
AI961444	2010012	Hs.155545	AI004681	1035796	Hs.339665
AF239668	844601	Hs.203	AI142639	155857	Hs.146662
NM_006113	415229	Hs.267659	BI494440	306924	Hs.48450
AI800677	378813	Hs.251754	NM_001559	1587390	Hs.73165
AK027126	882461	Hs.160786	AF280546	271215	Hs.17778
AI000682	1610158	Hs.144312	AI128331	132381	Hs.83790
BC017656	713238	Hs.52081	NM_003489	809627	Hs.155017
AF133059	345069	Hs.22900	BC001886	1422338	Hs.75319
NM_002965	1459376	Hs.112405	BC001886	624627	Hs.75319
BC015753	153340	Hs.75765	W94858	725365	Hs.65029
AA846684	321945	Hs.25545	AI356375	1161155	Hs.1174
BC008366	2028959	Hs.150403	Z11162	210687	Hs.89472
AB047783	344854	Hs.55565	AA633845	1637647	Hs.269760
AA922144	755881	Hs.298023	BC004376	666879	Hs.87268
AI366784	838408	Hs.48820	AF027866	1509935	Hs.138202
AW270334	1877697	Hs.50831	AW206445	35147	Hs.118338
BF475464	33852	Hs.22883	AK027024	2017917	Hs.94952
AV656862	1877206	Hs.25252	BC016838	39833	Hs.95594
BC001275	208718	Hs.78225	AI457921	768271	Hs.29692
X77197	2063419	Hs.199250	R36615	137344	Hs.268779
AI217517	130781	Hs.101414	AL133636	1493383	Hs.119475
BC000633	2062329	Hs.169840	AL133636	69124	Hs.119475
AW296675	815794	Hs.3164	AW247958	144740	Hs.84700
AI028773	85450	Hs.9795	L20470	358527	Hs.73729
NM_033380	1592039	Hs.169825	BC013106	773674	Hs.206097
AI538937	1708335	Hs.1573	BC012900	143169	Hs.346735

AF004222	44287	Hs.3803	BC012513	415851	Hs.6838
AF004222	685185	Hs.3803	BF508352	1837155	Hs.2633
NM_057158	756596	Hs.2359	AA831831	381166	Hs.27590
AI668602	160532	Hs.176588	AA877761	1257131	Hs.184727
AI468574	147826	Hs.171965	BC015571	742862	Hs.50868
AA205947	1588924	Hs.22835	AK024865	502625	Hs.47099
AA627358	1683411	Hs.142156	AI332972	726699	Hs.23650
BC013083	949938	Hs.135084	AA766903	1550894	Hs.116346
AF153609	2013515	Hs.296323	NM_053056	526757	Hs.82932
BC012381	815556	Hs.6823	NM_053056	841641	Hs.82932
BF591743	2709505	Hs.204096	AI569288	787860	Hs.45057
AJ000388	838676	Hs.169172	NM_005985	810119	Hs.48029
BC002536	950682	Hs.99910	AW074266	280602	Hs.23071
L13773	302190	Hs.114765	NM_001784	2309141	Hs.3107
L13773	381021	Hs.114765	AL133590	884355	Hs.82318
AI560801	1553054	Hs.22404	NM_004694	266389	Hs.114924
AF053306	842968	Hs.36708	BC017583	796148	Hs.7122
AF038185	31818	Hs.66187	NM_004525	143846	Hs.153595
AA865325	838278	Hs.155106	NM_004525	1899878	Hs.153595
BC007656	769921	Hs.93002	NM_002964	562729	Hs.100000
AW076080	669379	Hs.18987	AF101051	664975	Hs.7327
AW076080	73659	Hs.18987	AK024715	364865	Hs.151258
BC015706	564981	Hs.134726	NM_003878	809588	Hs.78619
BC000404	856427	Hs.6566	BC003635	470393	Hs.2256
AI948466	740925	Hs.840	NM_002281	1903066	Hs.32952
NM_003914	2091001	Hs.79378	AI655104	1850224	Hs.22047
AF070592	1925681	Hs.66170	AK026790	357396	Hs.24139
AF178532	810454	Hs.271411	AI553863	773329	Hs.300670
BC000465	85195	Hs.9701	AI553863	813396	Hs.300670
BC015915	298122	Hs.173859	AF089868	897531	Hs.211579
AK026698	52103	Hs.101774	AA642589	2313898	Hs.180016
NM_003503	287749	Hs.28853	BC000218	1469966	Hs.127792
AA399226	741919	Hs.25527	BC011806	150003	Hs.29724
AA962285	795379	Hs.23860	BF433296	841008	Hs.62661
AF140240	70500	Hs.267182	AI198522	2054122	Hs.5944
AL157483	1759290	Hs.11260	AI198522	767706	Hs.5944
AJ420567	1542749	Hs.262476	NM_014274	417424	Hs.289104
U78168	795382	Hs.8578	BC012613	80221	Hs.646
AI732534	1609005	Hs.46452	AI304875	705274	Hs.115907
AF117708	2063982	Hs.240395	AI963850	1609538	Hs.104696
AW015327	148379	Hs.239176	NM_002417	769513	Hs.80976
BC002829	810813	Hs.38991	AK027311	1693189	Hs.182585
BC018636	25154	Hs.274404	AK027311	417637	Hs.182585
BC018636	813841	Hs.274404	BC001526	687289	Hs.173179
AF161423	431286	Hs.41767	AA574174	85561	Hs.250615
AW139414	138788	Hs.1906	AB000509	563621	Hs.29736
AI656548	1569658	Hs.110168	AA489383	843398	Hs.73853
AA933076	1553996	Hs.252938	AW265625	325247	Hs.56105
NM_000792	296702	Hs.251415	AF183421	784150	Hs.223025
AB038518	284100	Hs.29423	AF183421	785701	Hs.223025

AF146192	1573946	Hs.28555	AF027299	785967	Hs.7857
AJ420539	1571910	Hs.110713	AL157432	815015	Hs.180780
AJ420539	46213	Hs.110713	AL050151	121898	Hs.324504
BC002710	809616	Hs.69423	AK026275	79960	Hs.324841
BC001749	490023	Hs.306051	AF014398	32299	Hs.5753
NM_005378	41565	Hs.25960	AW207060	785571	Hs.13015
U80811	1703455	Hs.75794	NM_005518	757222	Hs.59889
BC007633	2115155	Hs.193053	BE464662	140635	Hs.95893
BF511644	42389	Hs.271920	AJ243500	417424	Hs.302740
BC002377	813742	Hs.90572	AI097387	503602	Hs.197922
AK024298	357264	Hs.183114	AI421708	2012854	Hs.288905
AK000381	138059	Hs.8562	AW080831	2019750	Hs.277728
AI459117	83156	Hs.111029	R39691	971399	Hs.154679
AK026015	233679	Hs.27836	NM_007069	785293	Hs.37189
BC015484	2430219	Hs.106857	BC002709	277426	Hs.274329
AY044429	1570670	Hs.126891	T23696	767171	Hs.80618
AW589741	376844	Hs.22505	AF011468	209066	Hs.250822
BC006359	784876	Hs.76888	BC010522	40100	Hs.343666
AF017790	345787	Hs.58169	R15800	53203	Hs.94834
AA993639	726830	Hs.10414	AK000691	38213	Hs.7734
AW016396	415962	Hs.170414	AL049223	2284803	Hs.31218
BE856073	2018084	Hs.199263	BC010466	47460	Hs.3353
BC002947	131639	Hs.73769	AI299541	1897953	Hs.150124
BC010100	79898	Hs.28935	AW205836	731360	Hs.350251
NM_003979	595037	Hs.194691	AW206700	1710172	Hs.151254
N22033	255182	Hs.121509	AK025532	1572710	Hs.128003
AF245356	1466237	Hs.165986	BF444945	950667	Hs.36761
AB011422	40011	Hs.162189	AF094758	1870550	Hs.158450
AK024898	823615	Hs.99785	M15990	133178	Hs.194148
AF026547	2163910	Hs.169047	AB025904	251938	Hs.235168
AI350518	36491	Hs.129692	U61374	785933	Hs.15154
AI433440	141806	Hs.211600	AW104057	757489	Hs.19193
AF038173	221828	Hs.259873	AF035408	2114193	Hs.151407
NM_001771	1847497	Hs.171763	AK000770	1690262	Hs.299329
BC010003	767982	Hs.20953	AI378647	266323	Hs.42502
AA866043	769857	Hs.84152	AW118456	739193	Hs.346950
L07738	344091	Hs.147989	X53578	2509539	Hs.169238
AL117393	278430	Hs.6641	AA613572	271356	Hs.40369
D10522	840865	Hs.75607	BC004277	122821	Hs.334828
BF511873	1648516	Hs.170278	BC004277	626206	Hs.334828
AA398573	1642846	Hs.104660	AI565489	1593849	Hs.89901
BC011690	1580874	Hs.44396	H06285	44096	Hs.28068
AL109775	179283	Hs.80315	AI912080	1882481	Hs.128443
AI810347	366039	Hs.349764	AI338252	470092	Hs.25220
M14584	310406	Hs.93913	AA810022	754702	Hs.24024
AW195539	1870049	Hs.174441	AF070609	1669248	Hs.75379
BC005029	1472797	Hs.42824	AI214383	418159	Hs.6139
BC009401	810859	Hs.943	BC011795	795499	Hs.322430
BC003559	109316	Hs.234726	AF098277	2054945	Hs.136529
AK000193	624867	Hs.65021	NM_006115	897956	Hs.30743

BC008765	525926	Hs.82109	BC009989	530958	Hs.197366
AK026095	731373	Hs.95011	AL137502	1686766	Hs.238679
AF127563	669375	Hs.40499	AL162079	486175	Hs.75231
AI471839	205185	Hs.2030	NM_017458	591281	Hs.80680
BC007049	2321596	Hs.78944	AA854788	50182	Hs.89591
AA745593	1558151	Hs.41691	AW205080	179548	Hs.172700
AI744756	1947144	Hs.157117	BC008442	840567	Hs.351316
AA827777	156270	Hs.153084	AI123176	1910895	Hs.98838
AL096737	625623	Hs.5167	AI939560	2017773	Hs.345183
AW148827	2244016	Hs.194766	BF512938	46180	Hs.171495
AK024964	813154	Hs.173933	BC010940	814410	Hs.105115
AK024964	898228	Hs.173933	NM_002847	812968	Hs.74624
AL136693	159380	Hs.31297	AI218954	1521361	Hs.62113
BF509349	66694	Hs.6127	BC010120	613056	Hs.167791
AF290004	1588326	Hs.128814	AI274576	845355	Hs.10029
AI193043	854831	Hs.128685	AL050143	306005	Hs.7949
BC000117	2062415	Hs.105435	AK027274	503671	Hs.330716
AK026216	415610	Hs.314314	BC011460	47043	Hs.154138
BC014000	415564	Hs.58461	BC011460	815214	Hs.154138
BC007026	1917449	Hs.1955	BC007617	839980	Hs.132760
AA054983	377081	Hs.63158	AL110202	2159983	Hs.172089
AF146796	810911	Hs.105039	BC013134	1883756	Hs.127039
BF436282	82322	Hs.11916	BC004488	469306	Hs.1473
AW341053	366848	Hs.173638	AI753700	754474	Hs.98073
NM_001998	789012	Hs.198862	AF261655	770785	Hs.8910
AW291846	1473914	Hs.351321	AW451965	155197	Hs.131831
AB027289	2009491	Hs.26663	BC001400	509458	Hs.206501
AA584033	2610539	Hs.335952	NM_002284	1509761	Hs.278658
AA584033	366481	Hs.335952	BC000691	487327	Hs.279772
AI097664	897509	Hs.173030	BC002812	1948085	Hs.154510
AI668861	277463	Hs.153498	AL049949	489509	Hs.28264
BC001356	1422723	Hs.50842	BC004504	39929	Hs.90207
AW265278	2114195	Hs.157091	AI823561	868169	Hs.180878
AF264784	1709786	Hs.26102	AF207664	62263	Hs.8230
R49390	1881774	Hs.254129	NM_006329	50483	Hs.11494
BC012609	70692	Hs.75716	AF435925	1493596	Hs.153692
AB026707	1056172	Hs.112242	BC014018	503335	Hs.6166
AW148329	1584889	Hs.175208	AF132197	46896	Hs.301824
AK026813	244796	Hs.118258	BC002895	82710	Hs.89552
R40565	271683	Hs.169370	AI076506	1675273	Hs.133314
AI561078	2320932	Hs.38972	NM_005257	234736	Hs.50924
AW292522	812954	Hs.88253	AF304051	75859	Hs.243960
AI973194	1456937	Hs.1154	AK026642	898276	Hs.179666
BC009238	612274	Hs.75318	AI015671	588960	Hs.126485
Y10183	26617	Hs.10247	AI269387	768008	Hs.55220
BC008568	770212	Hs.75184	BC000314	28364	Hs.99947
AL049332	246304	Hs.77311	L40377	341978	Hs.41726
NM_004029	1159963	Hs.166120	AI567961	127970	Hs.14480
AJ002367	773322	Hs.55967	AI221721	712600	Hs.110099
AA601573	430623	Hs.272056	BI492432	133273	Hs.103724

AI439152	156962	Hs.173392	AI922204	301740	Hs.351546
BC005894	811061	Hs.132821	AI866858	840687	Hs.89603
AJ420516	41987	Hs.21177	AI866867	486591	Hs.171921
AF000546	303109	Hs.189999	AW664923	282958	Hs.89582
AK024986	366966	Hs.27865	AI984359	39178	Hs.16341
NM_000909	143332	Hs.169266	BC000187	278531	Hs.351875
AI393709	841357	Hs.105658	M86609	196992	Hs.306098
NM_002510	773330	Hs.82226	AW069800	796152	Hs.250705
AF159570	853809	Hs.24950	AW004703	1574914	Hs.9547
BC013919	278483	Hs.82962	AI350087	1859319	Hs.214410
BC013919	853368	Hs.82962	AW104435	795197	Hs.108323
BC000078	812187	Hs.32603	BC017586	1950691	Hs.55150
BC006322	51448	Hs.460	AA401311	1894931	Hs.188790
AA586749	592540	Hs.195850	AK025494	1470278	Hs.29076
AK027056	743146	Hs.293907	X08020	180561	Hs.301961
AW139156	41720	Hs.299315	AL080213	49385	Hs.52792
AF035279	488019	Hs.12503	BG236645	2032251	Hs.102793
AA731110	731236	Hs.18925	AW057705	2542486	Hs.385
AA730123	2507971	Hs.158303	AI969835	176606	Hs.79389
AW082090	1708791	Hs.170673	AA906471	310832	Hs.100748
AI208471	23454	Hs.120869	AF038633	2271343	Hs.134932
AW191026	489320	Hs.198282	AL117410	754018	Hs.154567
AF285836	2017597	Hs.105547	BC018043	564621	Hs.78589
AI273078	1468220	Hs.173334	BC003667	590338	Hs.108957
AI188749	1723400	Hs.271594	BC003513	345034	Hs.24395
AA903532	40893	Hs.8071	AK024822	244654	Hs.47572
U64197	1874367	Hs.75498	AF106912	1634832	Hs.132781
R52665	240505	Hs.7911	AI936089	1632248	Hs.130874
BC010116	810002	Hs.343214	BC018001	611443	Hs.118836
AA810953	713158	Hs.89104	AI200391	1585713	Hs.98641
AW150018	811162	Hs.230	BC002842	1500000	Hs.180779
BC001268	704532	Hs.54483	BC004925	1635601	Hs.330425
AI042183	212198	Hs.44585	AA747738	788355	Hs.20132
BC013200	730410	Hs.1765	AI424406	43764	Hs.284256
AL512731	239724	Hs.235709	AF202636	69002	Hs.9613
BC012527	897806	Hs.197540	AK025912	769959	Hs.75617
AI244129	345663	Hs.25691	AA765256	1915080	Hs.135191
BC001459	1476053	Hs.343807	H17636	50492	Hs.288642
AW149773	2016022	Hs.29353	AA736984	842939	Hs.85302
BC006376	855657	Hs.122647	BC001692	704085	Hs.33084
BC010379	345957	Hs.2621	BC015640	711552	Hs.88778
AW450142	257135	Hs.77239	BF939156	840753	Hs.241392
BC010923	767475	Hs.41683	BC001346	49794	Hs.22142
AF147204	79629	Hs.89414	BE465918	1553696	Hs.12114
BC007951	753184	Hs.2316	BC014105	86035	Hs.11085
BC010963	1409509	Hs.73980	AI268609	1416055	Hs.153479
AI247211	1517749	Hs.24133	NM_001262	291057	Hs.4854
AF073770	487697	Hs.12743	AJ420521	1572196	Hs.22209
NM_006006	2499829	Hs.37096	AI278360	1655480	Hs.31409
U97105	841620	Hs.173381	AB040057	254029	Hs.23643

AI538226	1911864	Hs.32976	AW082270	1895781	Hs.12496
AW340797	773152	Hs.98434	AW082270	52071	Hs.12496
AW006452	366526	Hs.58006	AI499593	152453	Hs.25351
AF116660	50562	Hs.283683	AA053400	127063	Hs.203213
AI199268	511096	Hs.19322	AF016267	110226	Hs.119684
AF051152	80633	Hs.63668	AL119854	361587	Hs.296317
AA857853	302127	Hs.204238	BC014277	489519	Hs.245188
R38689	35812	Hs.12376	AL110124	502446	Hs.5297
AA883715	1461550	Hs.125494	BF447150	1556897	Hs.119383
AL043469	785975	Hs.80424	AF218006	2297394	Hs.24391
AL360254	46843	Hs.30965	AW450080	241043	Hs.322149
AF191017	205049	Hs.111676	BC001314	130835	Hs.96125
S48196	1474284	Hs.323949	AJ223366	1915759	Hs.116051
S48196	1536168	Hs.323949	BC002325	1570427	Hs.32417
AB032698	1722980	Hs.14770	BF436849	1499900	Hs.8917
AW172994	196612	Hs.1695	AK024818	589115	Hs.83169
AA732062	1896556	Hs.170180	BC006458	725454	Hs.83758
AW189851	488956	Hs.211610	BC008584	344430	Hs.170195
AL096842	744395	Hs.7946	BF509554	1842331	Hs.144921
BC010954	1493160	Hs.2248	NM_001254	204214	Hs.69563
AK027191	510273	Hs.240443	BC008857	725649	Hs.77810
AI283489	2014138	Hs.154890	U96136	51083	Hs.80220
L11672	2455403	Hs.8597	NM_000139	1591736	Hs.30
AF186780	505864	Hs.79219	S77873	179403	Hs.75183
AA086248	1910516	Hs.114889	BC014526	25763	Hs.168640
BG655508	345764	Hs.74592	BC014526	429065	Hs.168640
N95437	1663716	Hs.134479	BC007348	489677	Hs.77573
X53587	811096	Hs.85266	AW732240	22500	Hs.16365
AK026181	2012257	Hs.288850	M93426	785148	Hs.78867
AK026181	753071	Hs.288850	AI460151	81289	Hs.78045
BC001844	41358	Hs.104105	AL080059	745011	Hs.173094
AI921122	1504268	Hs.148218	BF196234	1884217	Hs.147491
AA946776	1589786	Hs.111	NM_004430	26568	Hs.74088
H08145	48033	Hs.23606	U87460	41658	Hs.27747
NM_001078	44477	Hs.109225	AI469557	813520	Hs.2913
AY029191	78921	Hs.10760	AW205835	1867357	Hs.110418
AA903183	1517171	Hs.1724	AF130068	207735	Hs.297681
AF019386	220372	Hs.40968	BC011628	156473	Hs.113
NM_005409	1030351	Hs.103982	L10386	301735	Hs.2022
AF161398	701115	Hs.238205	BC017054	2014034	Hs.154672
AI587351	509823	Hs.73848	BC006534	767284	Hs.50550
AI027237	284160	Hs.127436	W46451	153025	Hs.2250
AL133102	251870	Hs.127842	AI199647	2021882	Hs.112842
BE047394	753236	Hs.8208	AF217989	782501	Hs.6748
NM_002451	2436784	Hs.152817	AF047711	486304	Hs.227806
AW575162	127821	Hs.1211	AA843666	490946	Hs.172510
AW134884	2273445	Hs.37023	BC002700	843321	Hs.23881
AI335013	417884	Hs.237642	AB028967	770427	Hs.202687
BC017785	1638481	Hs.87860	BC000356	814701	Hs.79078
AI767898	841492	Hs.237809	NM_033014	629906	Hs.109439

AA883246	782537	Hs.131740	X97859	342458	Hs.19413
AK025309	85634	Hs.169756	AF118088	280375	Hs.46677
U63008	1649374	Hs.15113	NM_006103	786675	Hs.2719
BC002757	1475803	Hs.114346	AJ420485	325520	Hs.14454
AA084672	182750	Hs.158311	AL137343	1688965	Hs.260855
AA805970	726678	Hs.74583	AL137343	177665	Hs.260855
AI383975	811955	Hs.11261	AK025583	767069	Hs.82845
AI383975	868168	Hs.11261	NM_006142	2027515	Hs.184510
AA668884	124128	Hs.19155	BC007659	813387	Hs.80706
NM_006186	898221	Hs.82120	AA854341	186301	Hs.38034
AL080078	322511	Hs.85335	AI797308	194638	Hs.193651
AI251449	323322	Hs.171939	AA988024	34720	Hs.127951
AL157455	31299	Hs.22543	NM_014279	52076	Hs.74376
AI205008	1709233	Hs.323878	BC013107	327304	Hs.110707
NM_003155	565075	Hs.25590	AI283926	40056	Hs.9004
BC007921	295093	Hs.192861	AI373939	839101	Hs.74471
AK026589	143966	Hs.90998	AW207140	363590	Hs.6111
AL110298	202201	Hs.7594	BC004295	767993	Hs.29759
BC009522	2171573	Hs.184841	AK056230	343695	Hs.349319
BC003180	74119	Hs.48375	NM_012168	179269	Hs.132753
AF140242	504461	Hs.279926	BC000566	431632	Hs.50267
NM_002497	462926	Hs.153704	BC007022	161456	Hs.332053
BC003630	1035889	Hs.3235	BC016623	414999	Hs.77711
AF305083	133213	Hs.2173	AW138839	1537001	Hs.24210
AF305083	366778	Hs.2173	AL365412	144880	Hs.107203
AA905217	2450261	Hs.121269	AW445220	782575	Hs.69517
AF331643	1900362	Hs.3402	N51717	156962	Hs.29410
U66065	565379	Hs.81875	X79676	866702	Hs.211595
NM_001094	2122306	Hs.6517	AI263595	344091	Hs.333199
AL512743	49883	Hs.12365	AW069753	898092	Hs.75511
AI969251	1942497	Hs.115325	NM_006278	813751	Hs.75268
AA521246	1715608	Hs.210792	AW140108	347726	Hs.301963
AW301074	591422	Hs.293533	AI193122	162308	Hs.132275
BM055132	2498575	Hs.663	AW016075	160609	Hs.284192
BC007438	753252	Hs.74266	BC016628	1668067	Hs.240845
AW050970	666128	Hs.155597	BC016628	361659	Hs.240845
AI569068	812294	Hs.22247	AI026838	280763	Hs.30120
AI002941	1698784	Hs.347970	D87119	360155	Hs.155418
BC002641	1474900	Hs.80342	NM_000142	752631	Hs.1420
BC010691	321455	Hs.343553	AF161505	788524	Hs.99291
AI311127	246194	Hs.125522	AK000341	44387	Hs.246107
AW014836	415326	Hs.18844	AI910678	284734	Hs.75850
BC014651	773296	Hs.98428	AF085233	261609	Hs.279696
AF023676	2020772	Hs.31130	AF085233	3316104	Hs.279696
AF063020	745118	Hs.82110	BC018127	140806	Hs.83920
AI866828	2421971	Hs.179729	AW014507	703541	Hs.54925
AL161983	502096	Hs.21415	AK025624	1637791	Hs.71331
AI125473	2029503	Hs.157281	AK025624	587992	Hs.71331
BC008036	344588	Hs.50915	AF119815	788698	Hs.99231
AI371090	784257	Hs.21611	AW139237	796480	Hs.30875

AI656385	1562231	Hs.151717	AK024750	726860	Hs.32017
AA613425	2062432	Hs.1584	M62626	429368	Hs.89583
BC001969	595162	Hs.301198	BC017901	489320	Hs.292358
BC001207	841057	Hs.7457	AF117386	1581685	Hs.35086
AL110252	49204	Hs.168950	AA747541	1526789	Hs.300592
AA761787	49482	Hs.315482	AK024855	687875	Hs.181301
BC007079	812105	Hs.75823	BC014564	898219	Hs.79284
F10094	22428	Hs.333319	AF070631	1500821	Hs.11355
NM_000935	263013	Hs.41270	AF070631	454083	Hs.11355
AA910336	1520559	Hs.135186	AF070631	79761	Hs.11355
U67784	246786	Hs.23016	BC007678	505881	Hs.1217
AI022925	1589468	Hs.79368	BC000632	530035	Hs.14331
BC008283	258790	Hs.80247	BC005963	1631546	Hs.36978
NM_003122	1412481	Hs.181286	AA233494	2284619	Hs.159468
AA804433	701481	Hs.926	BE549691	1860836	Hs.244391
BC017772	289057	Hs.47166	L02785	1873533	Hs.1650
NM_006308	2088978	Hs.41707	AW151360	593690	Hs.270737
BE673992	1584638	Hs.128211	AW118445	175103	Hs.57652
AA868889	1638827	Hs.274285	BC009799	1410444	Hs.270833
AL157471	33837	Hs.15420	R40176	27769	Hs.167406
X59766	1456160	Hs.71	AL136612	768520	Hs.90063
BC007636	41332	Hs.26608	AL136612	838478	Hs.90063
AI566899	753034	Hs.35841	AA600175	230560	Hs.39720
AA910884	1520895	Hs.130217	BC004291	780937	Hs.74554
BC015940	42070	Hs.153952	NM_001197	1916575	Hs.155419
NM_030761	1909317	Hs.302428	AW207696	2250736	Hs.97644
AI590055	1523411	Hs.124110	BC002914	700299	Hs.24143
NM_004425	301122	Hs.81071	R61469	53122	Hs.281587
AI733491	1608923	Hs.129230	Y16645	1911099	Hs.271387
BF433635	1911471	Hs.145711	AF303058	325160	Hs.169330
BC005313	1705861	Hs.123107	AI248610	110578	Hs.15060
AL133591	2016924	Hs.141480	U31214	588460	Hs.301350
AI362949	2019009	Hs.75169	AK024951	83549	Hs.1279
AF334710	78946	Hs.8364	NM_013267	1911706	Hs.325443
AL161961	1500766	Hs.17767	BC000006	897950	Hs.78629
AF094754	155038	Hs.32973	BC004471	740941	Hs.74120
AF094754	1685363	Hs.32973	AK025062	564801	Hs.172129
AK026760	75059	Hs.251946	NM_006271	179046	Hs.292707
AF052224	2432360	Hs.194684	NM_001839	486787	Hs.194662
NM_005864	795730	Hs.24587	BF510271	2049813	Hs.241545
AW205768	2300372	Hs.91877	AB067468	85660	Hs.11006
AW139532	814154	Hs.105069	AI492884	1358229	Hs.82132
AI025919	1757930	Hs.131674	AA588742	127709	Hs.250
AF065857	2809853	Hs.248185	AW271272	2769084	Hs.239571
AL136678	1455603	Hs.87729	BC008483	727147	Hs.227948
AK025428	812975	Hs.77546	BF434466	32493	Hs.227730
BC015497	346696	Hs.94865	NM_002963	1088345	Hs.112408
AI272951	85643	Hs.75599	NM_002988	768497	Hs.16530
NM_000436	28469	Hs.177584	BC011393	898258	Hs.169965
AI697249	1566793	Hs.784	BC009753	1635307	Hs.234898

BC004278	1417886	Hs.34516	J03607	810131	Hs.182265
AK025307	1554646	Hs.259785	AL043170	758284	Hs.160881
AK000140	491644	Hs.107139	NM_005410	530814	Hs.3314
BI324932	363569	Hs.199248	BC015397	1908705	Hs.122055
AI445650	1670188	Hs.2200	BC009352	842896	Hs.351623
AL039118	33051	Hs.2714	AF053453	252382	Hs.121068
M84757	813614	Hs.1076	AA923424	289025	Hs.135567
BC003097	130201	Hs.347326	AW291447	472008	Hs.301921
NM_001792	325182	Hs.161	AA999861	1636369	Hs.126892
R92436	196305	Hs.131837	AI953054	530875	Hs.89643
BF001174	487297	Hs.296341	BC002591	1384851	Hs.2258
BC006267	1524001	Hs.7331	AI384087	753162	Hs.173802
BC005257	2251833	Hs.183752	AI732321	154795	Hs.348819
NM_004038	809998	Hs.274376	BF510331	203896	Hs.168481
AK055386	365991	Hs.285050	BC006093	22040	Hs.151738
AJ012214	2191807	Hs.227115	BC006378	250883	Hs.16695
U06641	78294	Hs.150207	BF510778	898058	Hs.53997
BF433809	1896981	Hs.3195	AF146761	288807	Hs.20450
NM_000734	1572298	Hs.97087	AI239743	345232	Hs.36
R42342	796198	Hs.30942	BM127823	1584449	Hs.294151
NM_002514	1505534	Hs.235935	BM127823	786525	Hs.294151
AI280246	1893765	Hs.149504	AB041036	740780	Hs.57771
AF025887	504791	Hs.169907	AI962213	1467799	Hs.22599
AL137346	22917	Hs.13299	AF068180	1565079	Hs.167746
NM_004370	786609	Hs.101302	AW301017	1712825	Hs.146492
BC009628	1569815	Hs.127771	AI241077	461727	Hs.1870
AF059321	1610146	Hs.301698	BC000141	812965	Hs.79070
BC010652	415589	Hs.91668	AI245337	1870305	Hs.78846
AW291180	1455566	Hs.258	BC014533	1908758	Hs.44268
AF208043	824602	Hs.155530	R43793	50615	Hs.80288
AW081673	296529	Hs.181345	BC007533	489535	Hs.69285
D50419	1404841	Hs.119014	AA973836	1586043	Hs.128739
AF034996	44164	Hs.173034	Y13786	1557714	Hs.278679
AW448954	490784	Hs.143046	BC002727	1555478	Hs.64179
AI741469	1732247	Hs.57787	AI740744	22773	Hs.10475
NM_003248	758266	Hs.75774	AK025953	126341	Hs.288965
AW073971	345234	Hs.238954	BC005989	1874603	Hs.143113
AI689069	487988	Hs.109606	X96757	45578	Hs.118825
BC015947	2138030	Hs.47584	R45048	29954	Hs.159538
BC003388	502486	Hs.146847	BC015613	135688	Hs.334695
AL117616	280950	Hs.300741	BC011969	771004	Hs.347534
BC005246	509731	Hs.84072	H06160	1519985	Hs.106794
AI492117	1641837	Hs.131905	AI204186	1754094	Hs.146076
AF233588	1614140	Hs.27018	AF102848	454970	Hs.9029
NM_001452	310138	Hs.44481	L27711	700792	Hs.84113
BF512918	2363954	Hs.2159	AF030186	358217	Hs.58367
AI311775	2046679	Hs.192819	AI536895	248829	Hs.102267
NM_006455	347434	Hs.207251	BM129291	2017950	Hs.1149
BC004267	950451	Hs.135200	AL133706	283748	Hs.4257
AI147926	141115	Hs.285401	BE676183	1670836	Hs.103483

NM_005965	841308	Hs.211582	AL035878	896968	Hs.34780
BC017409	1696831	Hs.88594	AA830549	859192	Hs.20021
BC017409	486626	Hs.88594	AA630788	825470	Hs.156346
AW139590	1571882	Hs.156051	AI831078	1620905	Hs.14587
NM_006235	1541958	Hs.2407	NM_001337	283023	Hs.78913
AB037715	32122	Hs.183639	AB032417	1891563	Hs.19545
AI424409	1493107	Hs.348909	AK027146	469235	Hs.180946
AF002672	2502722	Hs.152944	AW293219	785694	Hs.288467
BC008651	50892	Hs.23133	BF513346	841480	Hs.88780
M87507	120106	Hs.2490	BC009198	746373	Hs.348989
BF508058	744374	Hs.4996	BC014890	293339	Hs.93005
AI888490	666707	Hs.55902	AF339783	72811	Hs.288809
AF104313	782460	Hs.173374	AB017800	781091	Hs.6414
BF056618	2019526	Hs.233634	AI434326	1435103	Hs.5541
AL136842	683059	Hs.260024	BC001638	774082	Hs.1619
M85294	323185	Hs.274382	AI733703	1742850	Hs.143735
BC017703	884789	Hs.57672	AF141332	3117993	Hs.200333
BC014117	143443	Hs.2001	NM_003221	363144	Hs.33102
U60975	2413337	Hs.278571	AL137559	767475	Hs.27495
AF105378	1569187	Hs.8040	AF131794	843250	Hs.10432
AL137662	85193	Hs.274401	AF131794	950450	Hs.10432
AL134596	2098508	Hs.89512	AF101477	2345693	Hs.144914
BC015496	180803	Hs.32309	AL046192	2165360	Hs.8854
AW291368	196435	Hs.34455	AL046192	295410	Hs.8854
AK027121	795746	Hs.38178	AL046192	563985	Hs.8854
AF062595	39600	Hs.18268	U43203	81427	Hs.197764
AK025796	595420	Hs.239218	AI096369	668007	Hs.348862
BC005359	2016194	Hs.151413	AL136703	854678	Hs.57209
AA731869	1847618	Hs.1309	AF033347	45636	Hs.40866
BC016757	502142	Hs.20985	AI280476	786605	Hs.71992
BM141806	772373	Hs.47094	AI559983	712505	Hs.334562
BC002415	823928	Hs.1581	BE551149	1620366	Hs.129319
NM_057749	773345	Hs.30464	AI373912	611407	Hs.241363
M26683	768561	Hs.303649	AI823489	1609665	Hs.167218
BC010690	1554167	Hs.334703	AW131780	1883065	Hs.167988
NM_000795	2017689	Hs.73893	AW131780	2164744	Hs.167988
BC005055	1049346	Hs.274344	AA912183	284383	Hs.47447
N93663	307019	Hs.118240	L20971	788136	Hs.188
AI311898	2047361	Hs.140197	AK026315	79565	Hs.178470
AI732388	159362	Hs.177576	AK001643	1585650	Hs.8395
AI869243	898249	Hs.17882	AI144219	138917	Hs.92137
AI740671	299274	Hs.351568	BC000897	755599	Hs.146360
BC012113	1592715	Hs.166146	AL110174	2306752	Hs.90005
AF097021	2312470	Hs.273321	R43523	32777	Hs.217754
AB058769	754126	Hs.334838	BM126079	1894405	Hs.124130
AF263462	296444	Hs.18376	BF477905	366209	Hs.58104
AL137686	712166	Hs.182982	AA777592	71116	Hs.288582
R56080	34888	Hs.12246	NM_003512	283919	Hs.28777
NM_005906	1841007	Hs.148496	NM_002538	1881469	Hs.171952
AA603977	2321042	Hs.218366	BC018112	857002	Hs.75969

AI765908	1883327	Hs.129166
AI216751	1884505	Hs.143977
AA767639	34149	Hs.79170
BC002745	789147	Hs.146580
U49395	486678	Hs.77807
AL110131	726599	Hs.28783
BC005305	2322038	Hs.408
AI571426	841282	Hs.105700
AA398015	726645	Hs.287364
AB012643	1475595	Hs.250769
M93119	22895	Hs.89584
AI703322	108330	Hs.103253
AW453001	487820	Hs.76722
AA937401	1569876	Hs.13234
AF059617	795877	Hs.3838
AA910331	491692	Hs.119129
BC002718	1759582	Hs.10086
AJ315514	784296	Hs.1790
AI560576	146123	Hs.79005
BC001645	897822	Hs.74101
BC017073	128695	Hs.22015
AF009227	155716	Hs.172816
AF054181	809455	Hs.183435
AF222340	725126	Hs.247043
BC016719	626348	Hs.17558
AA806859	147651	Hs.266957
AK024697	300632	Hs.25477
AI961887	418262	Hs.119571
AI089428	278404	Hs.21964
AF257182	430717	Hs.160271
AK026256	796079	Hs.289015
BE349538	826256	Hs.15791
AA831508	366830	Hs.32553
AI766890	428163	Hs.30022
NM_005923	1880757	Hs.151988
NM_000609	2239290	Hs.237356
AL137274	742642	Hs.11169
AW084130	1468820	Hs.166373
AK027036	490329	Hs.61345
NM_014583	786550	Hs.279943
BE670572	430237	Hs.181297
W46976	325070	Hs.94667
AI268717	1910959	Hs.128401
NM_001773	213635	Hs.85289
AL353948	343079	Hs.6272
U90914	1896838	Hs.5057
AI733236	1909535	Hs.128312
BC001350	50480	Hs.172851
AK025346	812256	Hs.48965
NM_001873	40558	Hs.75360

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

EXAMPLES

Example I:

Clinical specimen collection and clinicopathological parameters. 86 patients were expression profiled, 57 of these had clinical follow-up, specifically overall survival. Biomarker status is shown below in Table 3 for all 86 patients

Table 3: Age and biomarker status for the 86 patients subsequently gene expression profiled

		No. of Cases	Percentage
Age			
	<45	12	14%
	45-55	24	28%
	>55	50	58%
Estrogen-receptor status			
	positive	41	48%
	negative	45	52%
Progesterone-receptor status			
	positive	32	37%
	negative	54	63%
Her2/Neu status			
	positive	16	19%
	intermediate	23	27%
	negative	45	54%

The estrogen receptor (ER) status profile was discovered by the following steps

(i) patient biopsy set was divided up into two groups based on prior knowledge of their respective ER status (ER-positive and ER-negative);

(ii) a standard t-test was completed on each gene to identify genes whose expression was different between ER-/+; and

(iii) the P values were adjusted via the Benjamini-Hochberg false discovery rate method procedure for the inclusion of all genes which had $p < 0.05$.

This example was used for a hierarchical clustering of 86 patients with an overall total of 3,105 genes that correspond to an ER signature. The results are shown in Tables 1 and 2.

Example II:

Frozen biological breast cancer samples from 247 patients were used for expression profiling to identify genes that correlate with ER+ and ER- states in a manner analogous to the previous example. The analysis identified 2608 genes that correlated with one of two ER states. The results are shown in Tables 3 and 4.

All references cited herein, including patents, patent applications, and publications, are hereby incorporated by reference in their entireties, whether previously specifically incorporated or not.

Having now fully described this invention, it will be appreciated by those skilled in the art that the same can be performed within a wide range of equivalent parameters, concentrations, and conditions without departing from the spirit and scope of the invention and without undue experimentation.

While this invention has been described in connection with specific embodiments thereof, it will be understood that it is capable of further modifications. This application is intended to cover any variations, uses, or adaptations of the invention following, in general, the principles of the invention and including such departures from the present disclosure as come within known or customary practice within the art to which the invention pertains and as may be applied to the essential features hereinbefore set forth.

We claim:

1. An array comprising polynucleotide probes capable of hybridizing to nucleic acid molecules of one or more of the genes listed in Table 1, 2, 3, or 4 and comprising sequences within 350 nucleotides of the polyadenylation site of said genes, said probes hybridized to nucleic acids derived from a cell of a subject afflicted with, or suspected of having, breast cancer .

2. The array of claim 1 comprising 11 or more of the genes in Table 1, 2, 3, or 4.

3. The array of claim 2 comprising all the genes in Table 1, 2, 3, or 4.

4. The array of any one of claims 1-3 wherein said cell is from a human subject or such a subject afflicted with breast cancer.

5. The array of any one of claims 1-4 wherein said nucleic acids derived from one or more breast cancer cells are prepared by mRNA amplification.

6. The array of any one of claims 1-4 wherein said nucleic acids derived from one or more breast cancer cells are cDNA.

7. The array of any one of the preceding claims wherein said cell is in a section of tissue from a subject or is microdissected from said section.

8. A method to determine the ER status of breast cancer cells in a sample from a subject comprising assaying said sample for expression of one or more genes in Table 1 or 3 and/or one or more genes in Table 2 or 4.

9. The method of claim 8 wherein said assaying comprises preparing RNA, optionally labeled, from said sample and optionally converting said RNA into cDNA, optionally labeled.

10. The method of claim 9 wherein said RNA is not labeled and used for quantitative PCR.

11. The method of claim 8 wherein said assaying comprises using an array.

12. The method of any one of claims 8-11wherein said sample is a ductal lavage or fine needle aspiration or FFPE breast tissue sample.

13. The method of claim 12 wherein said sample is microdissected to isolate one or more cells that are breast cancer cells or suspected of being breast cancer cells.

14. The method of any one of claims 8-13 further comprising determination of the ratio of the expression of a gene in Table 1 or 3 to the expression of a gene in Table 2 or 4 as an indicator of ER status.

15. A method to determine therapeutic treatment for a patient having breast cancer comprising

identifying said patient as being ER positive or ER negative after assaying breast cancer cells of said patient for expression of one or more genes listed in Table 1, 2, 3, and/or 4 and

selecting the appropriate treatment for a patient having cells of such ER status.

16. The method of claim 15 wherein said assaying comprises preparing RNA, optionally labeled, from said sample and optionally converting said RNA into cDNA, optionally labeled.

17. The method of claim 16 wherein said RNA is not labeled and used for quantitative PCR.

18. The method of claim 16 wherein said assaying comprises using an array.

19. The method of any one of claims 15-18 wherein said sample is a ductal lavage or fine needle aspiration or FFPE breast tissue sample.

20. The method of claim 19 wherein said sample is microdissected to isolate one or more cells that are breast cancer cells or suspected of being breast cancer cells.

21. The method of any one of claims 15-20 wherein said assaying comprises determination of the ratio of the expression of a gene in Table 1 or 3 to the expression of a gene in Table 2 or 4 as an indicator of ER status.