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(54) Title: COMPOSITIONS AND METHODS FOR TREATING OSTEOARTHRITIS

(57) Abstract: The present invention provides compositions and methods for treatment of abnormal conditions in a subject, wherein the abnormal condition affects the musculoskeletal joints of the subject.

COMPOSITIONS AND METHODS FOR TREATING OSTEOARTHRITIS

FIELD OF THE INVENTION

[0001] The invention relates to compositions and methods for treating abnormal joint conditions in an animal, wherein the abnormal joint condition involves the musculoskeletal joints of the animal. In particular, this invention relates to treatment of abnormal musculoskeletal joint conditions including osteoarthritis, rheumatoid arthritis and local joint inflammation and the relief of symptoms associated with such abnormal musculoskeletal joint conditions. The application also encompasses modulating genes differentially expressed in animals, for example, genes differentially expressed in arthritic animals compared to non-arthritic animals, by administering a composition of the invention. The present invention also related to the identification of novel biomarkers in companion animals, including dogs and cats, diagnostic methods, compositions and kits related thereto.

BACKGROUND OF THE INVENTION

[0002] It is generally accepted in the scientific community that genes play a role in animal development and that the regulation of gene expression plays a key role in the development of some diseases or conditions that affect an animal's health and well being. Similarly, the differential expression of genes is one factor in the development of such diseases and conditions and the evaluation of gene expression patterns has become widely recognized as crucial to understanding the development and control of such diseases and conditions at the molecular level. To advance the understanding of genes and their relationship to disease, a number of methods have been developed for studying differential gene expression, e.g., DNA microarrays, expressed tag sequencing (EST), serial analysis of gene expression (SAGE), subtractive hybridization, subtractive cloning and differential display (DD) for mRNA, RNA-arbitrarily primed PCR (RAP-PCR), Representational Difference Analysis (RDA), two-dimensional gel electrophoresis, mass spectrometry, and protein microarray based antibody-binding for proteins.

[0003] Virtually all joints in the body of a mammal have cartilage. Cartilage is the supporting structure of the body and consists of thick bundles of fibrous protein (collagen) which are woven to form an articular surface. Proteoglycans fill extracellular spaces not occupied by collagen. Such proteoglycans are comprised of a combination of a protein and a sugar. Each proteoglycan subunit contains a protein core consisting of long chains of modified sugars known as glycosaminoglycans (GAGs). Glucosamine is the single most important component and precursor for GAGs. Synthesis of collagen by the body is dependent upon GAG synthesis. Chondrocytes in the cartilage utilize glucosamine to produce N-acetylglucosamine (NAG) and glucuronic acid, which are utilized by the body to form hyaluron. Hyaluron confers a lubricating property to the joint of the animal's body.

[0004] Cartilage is important in the body of animals for providing flexibility, compressibility under pressure, cushion, tensile strength, range of motion and smoothness of movement within joints. Examples of joints having cartilage include fingers and toes, neck, knee, hip, shoulder and the like. Animals can suffer from a number of conditions where cartilage is degraded thereby bringing about a reduction in the joint's flexibility, compressibility and often times resulting in a generalized inflammation of the joint and/or tissue surrounding the joint and in some cases the development of conditions such as osteoarthritis and rheumatoid arthritis. Such animals then have significant loss of joint function and experience pain.

[0005] Arthritis is a musculoskeletal disorder. Osteoarthritis is the most common type of arthritis in animals and humans. Osteoarthritis is a degenerative joint disease commonly occurring in humans and companion animals and the disease is characterized by degenerative changes in the articular cartilage, with loss of proteoglycan and collagen and proliferation of new bone formation at articular margins. These changes are accompanied by a variable inflammatory response within the synovial membrane. A principal defect in hyaline cartilage at the articular surface of a joint is the alteration in the ratio of glycosaminoglycans to the collagen fiber content of the matrix. Bones directly underlying cartilage in the joints are called subchondral bones. These subchondral bones nourish the overlying cartilage which itself is devoid of blood vessels, nerves or lymphatic tissue.

[0006] A natural erosion of cartilage occurs with age, but may also result from excessive loads placed on joints, obesity, heredity, trauma, decreased circulation, poor bone alignment and repetitive stress may exacerbate the condition of the joint. It is postulated that free radical damage may contribute to the development of osteoarthritis.

[0007] Cells of hyaline cartilage known as chondrocytes produce and maintain the surrounding extracellular matrix. Maintenance of homeostatis of the cartilage matrix depends upon catabolism of matrix proteins such as type II collagen and aggrecan. These proteins are digested and replaced by new proteins synthesized by chondrocytes. Catabolism is in part carried out by proteolytic enzymes such as matrix metalloproteinase (MMP) and aggrecanase proteins. In a normal animal, a balance is achieved between synthesis and degradation, thereby maintaining healthy cartilage. When the balance shifts to degradation, pathogenesis ensues and may result in joint inflammation and osteoarthritis.

[0008] A homeostatic condition in cartilage is dependent upon regulation through intercellular signaling between chondrocytes. Chondrocytes thus produce and respond to signaling molecules. Such signaling molecules may comprise cytokines and growth factors which may directly influence cellular metabolism. Intercellular signaling is complex and has not been fully characterized. Growth factor molecules such as TGF-beta are involved and believed to promote type II collagen production and to, inhibit collagen cleavage. Cytokines, such as TNF-alpha and IL-1-beta, also play a role. These cytokines are believed to promote production of proteases that may degrade cartilage. Numerous other complex interactions are believed to be occurring as a result of intercellular signaling.

[0009] Due to the complexity of the intercellular signaling process, it is highly desirable to understand at a genetic level the interactions that are taking place. Detection of dysregulated genes in a pre-arthritic or an arthritic condition is helpful in understanding the biology of abnormal musculoskeletal joint disorders, especially on a genome-wide basis. A more detailed understanding of the biological pathways involved through gene expression profiling will aid in the development of salutary pharmaceutical, nutraceutical and nutritional (dietary) interventions in the disease pathways. These approaches may enable prevention, early detection and treatment of the underlying abnormal musculoskeletal joint conditions as well as in monitoring the prognosis of such abnormal musculoskeletal joint disorders, especially in osteoarthritis. Dysregulated genes involved in the pathology of such disorders may serve as important biomarkers to optimize selection of appropriate pharmaceutical, nutraceutical and nutritional (dietary) interventions.

[0010] There is yet to be identified a drug that reverses the course of osteoarthritis. Currently available therapeutic agents are employed to reduce inflammation and/or to relieve pain. Current therapy employs a class of drugs known as non-steroidal anti-inflammatory drugs (NSAIDs) to treat musculoskeletal joint disorders such as osteoarthritis, but these therapies have a variety of drawbacks, including, in particular, gastrointestinal disorders and they may also inhibit cartilage formation.

[0011] Large dogs may develop arthritis as they age. Large dog breeds are more susceptible to arthritis due to their increased mass and/or genetic disposition. Large dogs are not the only animals at risk of arthritis and other cartilage conditions. Arthritis and other degenerative joint diseases have been commonly recognized in dogs and such conditions have been shown to be prevalent in cats. Feline osteoarthritis is a disease primarily affecting aged felines ten years of age or older. Animals at risk of developing cartilage-affecting abnormal musculoskeletal joint disorders include, but are not limited to, mammals such as canine, feline, equine, hircine, ovine, porcine, bovine, human and non-human primate species, and birds including turkeys and chickens.

[0012] Diet plays an important role in disease causation and progression because it is fundamentally involved in metabolism. Disease regulated genes are at some level regulated by nutritional factors. Thus, dietary components present in foods as nutrients may regulate gene expression at the transcriptional and translational level, as well as in certain post-translational modifications. They may similarly be involved in degradation and enzymatic activities. Nutrient levels may influence the equilibrium of metabolic pathways. Metabolic pathways are frequently complex and may involve many redundancies and interrelationships among different metabolic pathways. Altering the concentration of a single enzyme, growth factor, cytokine or metabolite may impact a number of metabolic pathways involved in disease-related physiology. Hormones and other cell signaling molecules are well-understood to be regulated by diet and are also known to be implicated in the development and progression of disease.

[0013] The same disease phenotype may result from disturbances in different metabolic pathways, and the genetic make-up of each animal differs, thereby causing variation in responses to the same factors, including nutritional and environmental factors. The interplay of genetic, nutritional and environmental factors is important in understanding the etiology, prevention, treatment and progression of diseases in animals. Finding gene expression responses to nutrients associated with various diseases and disorders permits formulation of diets for animals susceptible to disease such as abnormal musculoskeletal joint disorders, and further permits diagnosis, treatment and monitoring the prognosis of the underlying disease.

[0014] Nutritional components influence gene expression, including mRNA production (transcription), mRNA processing, protein production (translation) and post-translational modifications, thereby influencing the overall metabolic status of an animal. As a result, the use of biomarkers for early detection and monitoring of disease progression and/or genotype-based diets may enable prevention or treatment of diseases as well as new therapies to be developed for animals, particularly for companion animals. Diet is arguably the most important environmental factor affecting the phenotype of an animal, including susceptibility to disease.

[0015] Gene expression may be regulated through unstable processes that are controlled by activators and repressors of gene function. Nutritional status may cause significant changes in gene transcription rates. Macronutrients such as glucose, fatty acids and amino acids and micronutrients such as iron, zinc and vitamins can regulate gene expression. Various bioactive food components such as carotenoids, flavonoids, monoterpenes and phenolic acids may act as transcription factors affecting gene expression. These substances tend to have direct effects on gene expression. In other situations, substances like dietary fiber, which is fermented in the gut by bacteria, may lead to the production of nutrients such as short chain fatty acids. Such substances may act as indirect activators or repressors of gene expression.

[0016] Identification of nutrient-related changes upon transcription and translation may be detected in experiments of the type described in this specification. In view of the extensive array of genes profiled in the examples of this specification, alterations in gene expression and quantification are readily detected by the methods taught in this specification. Thus, dietary and metabolic gene expression signatures may be readily ascertained using the techniques taught in the Examples of this specification. Biomarkers of the invention are proteins and/or nucleic acids that are differentially expressed in animals. Biomarker expression can be assessed at the protein or nucleic acid level using various methods known to the skilled artisan.

[0017] Only very limited work has been done to date in screening the canine and feline genomes for gene expression profiles in response to nutritional components in the diet of these companion animals. Work has been done in the area of cancer employing a canine gene microarray for CG analysis of tumors. Thomas R. et al. A canine cancer gene microarray for CGH analysis tumors, Cyrogenet. Genome Res., 2003; 102:254-260. Further works has been done in the area of dilated cardiomyopathy. Oyayma, M.A. et al., Genomic expression patterns of cardiac tissue from dogs with dilated cardiomyopathy, Am. J. Vet. Res. 2005; 66:1140-1155. To date the study of the canine genome with respect to osteoarthritis has been very limited. In one study, the MIG-6 gene was found to be elevated in dogs in the high risk osteoarthritis group and it has been hypothesized that this gene may be implicated in cartilage degradation and in the production of cartilage in dogs. Mateescu, R.G. et al., Increased MIG-6 mRNA transcipts in osteoarthritic cartilage. Biochem. Biophy. Res. Commun. 2005; 332:482-486.

[0018] Studies in healthy populations of animals versus populations having a disease such as the abnormal musculoskeletal joint disorders described in this specification have not been extensively conducted. Little data is available with respect to the canine genome and far less with respect to the feline genome. Gene expression data contained in this specification identifies genes associated with cartilage degradation in dogs and cats. Such gene expression data enables identification of nutritional compositions capable of modulating expression of such genes in a favorable manner. This is also the case with respect to genes generally associated with inflammation. Analogous data in felines is additionally set forth in the specification, figures and examples of this specification.

[0019] Gene expression data contained in the specification and examples enables a variety of desirable inventions based on the gene expression profiles described herein. The data permits identification and quantification of gene expression products as biomarkers of nutrition as well as disease prevention, identification and treatment of the underlying abnormal musculoskeletal joint disorder. Gene expression data elicited as a result of the practice of the methods of the invention also permits monitoring the progression of such abnormal musculoskeletal joint disorders. These inventions further include genetic testing to identify susceptible subpopulations of animals likely to be afflicted with such abnormal musculoskeletal joint disorders, to identify optimal diets for the prevention or treatment of such disorders, to identify pharmaceutical, nutraceutical and nutritional (dietary) interventions based on the findings set forth in this specification in order to treat the underlying diseases and inflammation. The inventions also include biomarkers for early disease detection, targeted therapeutics, diagnostic reagents and kits for the analysis of tissue and blood samples from animals susceptible to or having such abnormal musculoskeletal joint disorders.

[0020] In designing foods for animals, for example, companion animals such as cats and dogs, optimal animal health or wellness through good nutrition is an important goal. However, even the most nutritious animal food is of little value if the animal rejects or refuses to eat the food, or if the animal's intake of the food is restricted because the animal finds the food unpalatable. Thus, the inventions set forth in this specification further comprise nutritional compositions capable of promoting the health and wellness of animals susceptible to or having such abnormal musculoskeletal joint disorders. The invention thus encompasses edible food compositions for companion animals, which have therapeutic and prophylactic efficacy and possess increased palatability over currently marketed companion animal food products.

SUMMARY OF THE INVENTION

[0021] The invention relates to compositions comprising at least one omega-3 fatty acid, at least one glycosaminoglycan, at least one amino sugar, at least one antioxidant, and carnitine or acetylcarnitine. The invention includes, but is not limited to, nutritional compositions, dietary supplements, nutraceuticals and treats for administration to animals, especially companion animals.

[0022] The invention also relates to methods of treating animals having an abnormal musculoskeletal joint condition, the methods comprising administering to the subject at least one of the compositions of the invention.

[0023] The invention still further relates to methods of delaying the onset in an animal or reducing the pain of an animal having an abnormal musculoskeletal joint condition, the methods comprising administering to the subject at least one of the compositions of the present invention.

[0024] In one embodiment, the invention encompasses a canine pet food composition comprising at least one omega-3 fatty acid, at least one glycosaminoglycan, at least one amino sugar, at least one antioxidant, and carnitine or acetylcarnitine.

[0025] In another embodiment, the invention encompasses a feline pet food composition comprising at least one omega-3 fatty acid, at least one glycosaminoglycan, at least one amino sugar, at least one antioxidant, and carnitine or acetylcarnitine.

[0026] Another embodiment encompasses a method of treating or preventing an abnormal musculoskeletal joint disorder in an animal in need thereof with a composition of the invention.

[0027] Yet another embodiment encompasses a method of treating or preventing an abnormal musculoskeletal joint disorder, selected from the group consisting of osteoarthritis, rheumatoid arthritis and local joint inflammation, in an animal in need thereof with a composition of the invention.

[0028] A still further embodiment of the invention encompasses a method of treating or preventing a musculoskeletal joint disorder selected from the group consisting of osteoarthritis, rheumatoid arthritis and local joint inflammation in a companion animal in need thereof with a composition of the invention.

[0029] Another embodiment of the invention encompasses a method of treating or preventing a musculoskeletal joint disorder, selected from the group consisting of osteoarthritis, rheumatoid arthritis and local joint inflammation, in a canine in need thereof with a composition of the invention.

[0030] Another embodiment of the invention encompasses a method of treating or preventing a musculoskeletal joint disorder, selected from the group consisting of osteoarthritis, rheumatoid arthritis and local joint inflammation, in a feline in need thereof with a composition of the invention.

[0031] Another embodiment of the invention encompasses a method of treating or preventing osteoarthritis in a canine in need thereof with a composition of the invention.

[0032] Another embodiment of the invention encompasses a method of treating or preventing osteoarthritis in a feline in need thereof with a composition of the invention.

[0033] Another embodiment of the invention encompasses a method of treating or preventing rheumatoid arthritis in a canine in need thereof with a composition of the invention.

[0034] Another embodiment of the invention encompasses a method of treating or preventing rheumatoid arthritis in a feline in need thereof with a composition of the invention.

[0035] Another embodiment of the invention encompasses a method of treating or preventing joint inflammation in a canine in need thereof with a composition of the invention.

[0036] Another embodiment of the invention encompasses a method of treating or preventing joint inflammation in a feline in need thereof with a composition of the invention.

[0037] Another embodiment of the invention encompasses one or more genes or gene segments that are differentially expressed in animals having an abnormal musculoskeletal joint disorder, which may include by way of example osteoarthritis, rheumatoid arthritis or local joint inflammation, compared with animals not having such an abnormal musculoskeletal joint disorder.

[0038] Another embodiment of the invention encompasses combinations of two or more polynucleotides or polypeptides that are differentially expressed in animals having an abnormal musculoskeletal joint disorder, which may include by way of example osteoarthritis, rheumatoid arthritis or local joint inflammation, compared with animals not having such an abnormal musculoskeletal joint disorder.

[0039] Another embodiment of the invention encompasses compositions of two or more polynucleotide or polypeptide probes suitable for detecting the expression of genes differentially expressed in animals having an abnormal musculoskeletal joint disorder, which may include by way of example osteoarthritis, rheumatoid arthritis or local joint inflammation, compared with animals not having such an abnormal musculoskeletal joint disorder.

[0040] Another embodiment of the invention encompasses methods and compositions for detecting the differential expression of one or more genes differentially expressed in animals having an abnormal musculoskeletal joint disorder, which may include by way of example osteoarthritis, rheumatoid arthritis or local joint inflammation, compared with animals not having such a musculoskeletal disorder.

[0041] Another embodiment of the invention encompasses methods for measuring the effect of a test substance on the expression profile of one or more genes differentially expressed in animals having an abnormal musculoskeletal joint disorder, which may include by way of example osteoarthritis, rheumatoid arthritis or local joint inflammation, compared with animals not having such an abnormal musculoskeletal disorder as a method for screening a test substance to determine if it is likely to be useful for modulating such disorder in such animal.

[0042] Another embodiment of the invention encompasses methods for formulating a prognosis that an animal is likely to develop an abnormal musculoskeletal joint disorder, which may include by way of example osteoarthritis, rheumatoid arthritis or local joint inflammation or in developing a diagnosis that an animal has such a musculoskeletal joint disorder.

[0043] A further aspect of the invention is that it relates to the identification of novel biomarkers of abnormal musculoskeletal joint disorders, particularly osteoarthritis, in animals, particularly companion animals, as well as methods of detection of abnormal musculoskeletal joint disorders in such animals based on a characteristic pattern of gene expression of such biomarkers in vivo. Specifically, the methods of the invention comprise detecting differential expression, compared to a control expression level, of at least one biomarker, in a body sample, preferably a blood sample, wherein the detection of differential expression of such biomarker specifically identifies animals that have an abnormal musculoskeletal joint disorder, especially osteoarthritis. Thus, such methods rely upon the detection of at least one biomarker that is differentially expressed in an abnormal musculoskeletal joint disorder in comparison to cells from normal or control animals.

[0044] It is also an embodiment of the invention to modulate various canine biomarkers related to an abnormal musculoskeletal joint disorder, in particular osteoarthritis, rheumatoid arthritis, or a local joint inflammatory condition by administering a composition of the invention to an animal in need thereof in an amount effective to modulate the biomarker. Examples of biomarkers related to an abnormal musculoskeletal joint disorder that can be modulated include, but are not limited to, Annexin A1, Cathepsin D, Cathepsin F, Cathepsin S, RELA, HMGB1, IL-1β, TNFα, TNFβ, TLR-2, TLR-4, p38 MAPK, TIMP-1, TIMP-2, MMP-1, MMP-2, MMP-13, IL-15 and IL-17 receptor, COL2A1, COL1A2, COL3A1, COL4A1, MMP-13, TIMP-2, MMP-2, C2C, C1,2C, FLAP, PLA2, MAPK1, MAPK2 and Aggrecan.

[0045] The biomarkers of the invention are proteins and/or nucleic acids that are differentially expressed in an animal having or likely to develop an abnormal musculoskeletal joint disorder, in particular osteoarthritis, rheumatoid arthritis or a local joint inflammatory condition.

[0046] It is further contemplated herein that the methods of the present invention may be used in combination with traditional diagnostic techniques that are able to detect the physical and morphological characteristics of degenerative musculoskeletal joint disease. Thus, for example, the characterization of differential expression in genes for osteoarthritis biomarkers in cells obtained from a blood sample of an animal may be combined with conventional diagnostic (e.g., radiological) techniques in order to corroborate a diagnosis of osteoarthritis.

[0047] In a further aspect, the invention relates to compositions comprising one or more nucleic acid probes that specifically hybridize to a nucleic acid, or fragment thereof, encoding a biomarker of the present invention.

[0048] In an additional aspect, the invention relates to compositions comprising antibodies that specifically bind to a polypeptide encoded by a gene expressing a biomarker of the present invention.

[0049] The invention also relates to kits to diagnose an abnormal musculoskeletal join disorder in an animal comprising component that can be used to detect expression of the biomarkers of the present invention, including, but not limited to, the compositions and microarrays described herein.

[0050] In another aspect, it is also contemplated herein that the invention relates to methods for identifying bioactive dietary components or other natural compounds (referred to hereafter as "dietary components" or "components") that may be tested for their ability to treat or ameliorate an abnormal musculoskeletal joint condition in an animal comprising: (a) contacting a cell capable of expressing an RNA or protein product of one or more biomarkers disclosed in Table 2 and/or Table 3 with a test component; (b) determining the amount of said RNA and/or product produced in the cells contacted with the test component; and (c) comparing the amount of said RNA and/or protein product in the cells contacted with the test component to the amount of the same said RNA or protein product present in a corresponding control cell that has not been contacted with the test component; wherein if the amount of the RNA or protein product is altered relative to the amount in the control, the component is identified as one to be tested for its ability to treat or ameliorate an abnormal musculoskeletal joint disorder, especially osteoarthritis, rheumatoid arthritis or a local joint inflammatory condition.

[0051] A further aspect of the invention is a method for diagnosis and/or prognosis of osteoarthritis in an animal, wherein the method comprises the steps of: obtaining at least one tissue sample or bodily fluid specimen from the animal; determining the amount of one or more biomarkers selected from Table 2 and/or Table 3 in said at least one sample or specimen obtained from the animal, wherein said biomarker is a polypeptide, protein, RNA, DNA, polynucleotide or metabolite thereof. A still further embodiment is such method where such one or more biomarkers is selected from the group consisting of Annexin A1, Cathepsin D, Cathepsin F, Cathepsin S, RELA, HMGB1, IL-1β, TNFα, TNFβ, TLR-2, TLR-4, p38 MAPK, TIMP-1, TIMP-2, MMP-1, MMP-2, MMP-13, IL-15 and IL-17 receptor.

[0052] Yet another embodiment of the invention is a kit for diagnosis and/or prognosis of osteoarthritis in an animal, particularly for carrying out the method for diagnosis and/or prognosis of osteoarthritis in an animal, wherein the method comprises the steps of: obtaining at least one tissue sample or bodily fluid specimen from the animal; determining the amount of one or more biomarkers selected from Table 2 and/or Table 3 in said at least one sample or specimen obtained from the animal, wherein said biomarker is a polypeptide, protein, RNA, DNA, polynucleotide or metabolite thereof, and optionally, further comprising a detectable agent linked to said biomarker.

[0053] A still further embodiment of the invention is a reagent for diagnosis and/or prognosis of osteoarthritis in an animal, particularly for carrying out the method for diagnosis and/or prognosis of osteoarthritis in an animal, wherein the method comprises the steps of: obtaining at least one tissue sample or bodily fluid specimen from the animal; determining the amount of one or more biomarkers selected from Table 2 and/or Table 3 in said at least one sample or specimen obtained from the animal, wherein said biomarker is a polypeptide, protein, RNA, DNA, polynucleotide or metabolite thereof, and optionally further comprising a detectable agent linked to said biomarker.

[0054] Another embodiment of the invention is the use of one or more polypeptides, proteins, RNAs, DNAs, polynucleotide or metabolites thereof, as identified on Table 2 and/or Table 3, as a biomarker for diagnosis and/or prognosis of an abnormal musculoskeletal joint disorder, particularly for forming a kit for diagnosis or prognosis of an abnormal musculoskeletal joint disorder. A still further embodiment is such kit where such one or more biomarkers is selected from the group consisting of Annexin A1, Cathepsin D, Cathepsin F, Cathepsin S, RELA, HMGB1, IL-1β, TNFα, TNFβ, TLR-2, TLR-4, p38 MAPK, TIMP-1, TIMP-2, MMP-1, MMP-2, MMP-13, IL-15 and IL-17 receptor. Yet another embodiment is such kit, wherein the reagents and equipment comprise DNA microarray analysis materials including oligonucleotide microarray, c-DNA microarray, and focused gene chip, or a combination thereof.

[0055] Another embodiment of the invention is a method of detecting osteoarthritis in an animal, comprising providing a sample from the animal comprising a tissue sample or specimen of a bodily fluid; detecting levels of a biomarker, as identified on Table 2 and/or Table 3, which is a polypeptide, protein, RNA, DNA, polynucleotide or metabolite thereof in the sample or specimen; and comparing the levels of said biomarker in the sample or specimen to levels of said biomarker in a control sample; wherein expression of the biomarker has at least a 1-fold or greater difference in gene expression compared with expression in a cell of a control animal.

[0056] A still further embodiment of the invention is a method of detecting osteoarthritis in an animal, comprising contacting the sample or specimen of the aforesaid method with a first primer that comprises a polynucleotide sequence that hybridizes selectively to said biomarker and a second primer comprising a polynucleotide sequence that hybridizes to said biomarker polynucleotide, performing an amplification reaction, and quantifying an amplification product of the biomarker polynucleotide in the sample or the specimen.

[0057] Another embodiment of the invention is a method of assessing the effectiveness of a course of treatment or nutritional management for an animal suffering from osteoarthritis, the method comprising (a) measuring a first level of a biomarker polypeptide, protein, RNA, DNA, polynucleotide or metabolite thereof, as identified on Table 2 and/or Table 3, in a tissue sample or a specimen of bodily fluid from said animal at a first time point in time during the course of treatment, (b) measuring a second level of said biomarker in said sample or specimen from said animal at a second point in time during the course of treatment, and (c) comparing the measurements of the biomarker at said first point and said second point; wherein expression of the biomarker has at least an 1-fold or greater difference in gene expression compared with expression in a cell of a control animal.

[0058] Another embodiment of the invention is a method of assessing the progression of a course of treatment or nutritional management for an animal suffering from osteoarthritis, the method comprising (a) measuring a first level of a biomarker polypeptide, protein, RNA, DNA, polynucleotide or metabolite thereof, as identified on Table 2 and/or Table 3, in a tissue sample or a specimen of bodily fluid from said animal at a first point in time during the course of treatment, (b) measuring a second level of said biomarker in said sample or specimen from said animal at a second point in time during the course of treatment, and (c) comparing the measurements of the biomarker at said first point and said second point; wherein expression of the biomarker has at least an 1-fold or greater difference in gene expression compared with expression in a cell of a control animal.

[0059] A further embodiment of the invention is a method for identifying a molecule for diagnosing osteoarthritis in an animal, the method comprising: (1) providing a sample of a tissue sample or a specimen of bodily fluid from said animal comprising a biomarker, as identified on Table 2 and/or Table 3, which is a polypeptide, protein, RNA, DNA, polynucleotide or metabolite thereof; (2) contacting the sample or specimen with a test molecule; (3) determining whether the test molecule binds to, or is bound by, said biomarker; wherein expression of the biomarker has at least an 1-fold or greater difference in expression compared with expression of said biomarker of a control animal.

[0060] A still further embodiment of the invention is a method for screening for osteoarthritis in an animal comprising the steps of: i) obtaining a tissue sample or a specimen of bodily fluid from said animal and determining a gene expression profile of one or more biomarker polypeptides, proteins, RNAs, DNAs, polynucleotides or metabolites in the sample; and ii) comparing the gene expression profile of said one or more biomarkers in the sample to a positive control comprising an average gene expression level of said one or more biomarkers in a plurality of reference samples that are derived from animals displaying symptoms of osteoarthritis to determine differential gene expression between the sample and the positive control, wherein presence of osteoarthritis is indicated if there is no statistically significant differential gene expression between the gene expression profile of one or more biomarkers in the sample and the positive control, wherein the biomarkers comprise one or more genes of Table 2 and/or Table 3.

[0061] Yet another embodiment of the invention is a method for screening for osteoarthritis in an animal comprising the steps of: i) obtaining a tissue sample a specimen of bodily fluid from said animal and determining a gene expression profile of one or more biomarker polypeptides, proteins, RNAs, DNAs, polynucleotides or metabolites in the sample; and ii) comparing the gene expression profile of said one or more biomarkers in the sample to a positive control comprising an average gene expression level of said one or more biomarkers in a plurality of reference samples that are derived from control animals displaying no symptoms of osteoarthritis to determine differential gene expression between the sample and a reference sample of said control animals, wherein presence of osteoarthritis is indicated if there is a 1-fold differential gene expression between the gene expression profile of one or more biomarkers in the sample and the positive control, wherein the biomarkers comprise one or more genes of Table 2 and/or Table 3.

[0062] Another embodiment of the invention is an assay for screening an agent for its ability to treat or prevent one or more symptoms of osteoarthritis comprising the steps of: i) isolating a nucleic acid control sample from a tissue sample from said animal that produces a differential gene expression profile representative of osteoarthritis and determining the level of gene expression in the control sample; ii) subjecting the tissue sample to said agent; iii) isolating a nucleic acid test sample from said tissue sample after subjecting said tissue sample to the agent of step (ii) and determining the level of gene expression in the test sample; iv) comparing production, stability, degradation and/or activation of gene expression between the control sample and the test sample to find the differential gene expression profile between the test sample and the control sample; wherein a differential gene expression profile between the test sample as compared with the control sample is indicative of the ability of the agent to prevent or treat one or more symptoms of osteoarthritis.

[0063] Still another embodiment of the invention is a method for identifying a plurality of genes that are differentially expressed between tissue samples for use in an informative array, comprising: providing a first set of heterogeneous nucleic acid probes derived from a first tissue sample; providing a second set of heterogeneous nucleic acid probes derived from a second tissue sample; hybridizing a nucleic acid array comprising a plurality of sequences derived from genes of a biological process with the first set of probes and determining a first level of expression for sequences of the array; hybridizing the array with said second set of probes and determining a second level of expression for sequences of the array; identifying a plurality of genes that are differentially expressed in said biological process by comparing the first level of expression with said second level of expression for hybridized sequences; and establishing a ranking of the identified genes by a step selected from the group of steps consisting of: determining an absolute value of the difference between the first level of expression and the second level of expression, and ranking genes having a higher difference over genes having a lower difference; and determining a standard deviation of the difference between the first level of expression and the second level of expression, and ranking genes having a higher standard deviation over genes having a lower standard deviation, wherein the genes comprise one or more genes on Table 2 and/or Table 3.

[0064] Another embodiment of the invention is a method for converting a nucleic acid array into an informative array comprising: providing a first set of heterogeneous nucleic acid probes derived from a first tissue sample; providing a different, second set of heterogeneous nucleic acid probes derived from a second tissue sample; hybridizing a nucleic acid array comprising a plurality of sequences with the first set of probes and determining a first level of expression for sequences of the array; hybridizing the array with said second set of probes and determining a second level of expression for sequences of the array; identifying a plurality of genes that are differentially expressed in said biological process based on a difference between the first level of expression and the second level of expression for identified genes, by a step selected from the group of steps consisting of: determining an absolute value for the difference between the first level of expression and the second level of expression, and ranking genes having a higher difference over genes having a lower difference; and determining a standard deviation of the difference between the first level of expression and the second level of expression, and ranking genes having a higher standard deviation over genes having a lower standard deviation; and selecting genes from the plurality of identified differentially expressed genes for inclusion on the informative array, wherein said genes are selected from the genes listed in Table 2 and/or Table 3.

[0065] Yet another embodiment of the invention is a computer-implemented method for analyzing gene expression to screen for osteoarthritis comprising the steps of: i) compiling data comprising a plurality of measured gene expression signals derived from nucleic acid microarray analysis, selected from the group consisting of oligonucleotide microarray, c-DNA microarray, and focused gene chip analysis, or a combination thereof, of tissue samples into a form suitable for computer-based analysis: and ii) analyzing the compiled data, wherein the analyzing comprises identifying gene networks from a number of upregulated biomarker genes and down-regulated biomarker genes, wherein the biomarker genes are genes that have been identified as associating with presence or severity of osteoarthritis, said genes comprising genes listed in Table 2 and/or Table 3.

[0066] Another embodiment of the invention is a method of in vitro screening a drug candidate, the method comprising determining the capacity of the candidate to modulate expression of a selected gene or activity of the selected gene expression product wherein the selected gene or gene expression product is an osteoarthritis biomarker or gene expression product selected from the group consisting of the genes or gene products listed on Table 2 and/or Table 3.

[0067] Another embodiment of the invention is a method of in vitro screening a nutritional foodstuff, dietary supplement, nutraceutical or treat, the method comprising determining the capacity of the candidate to modulate expression of a selected gene or activity of the selected gene expression product wherein the selected gene or gene expression product is an osteoarthritis biomarker or gene expression product selected from the group consisting of the genes or gene products listed on Table 2 and/or Table 3.

[0068] Another embodiment of the invention is a method of in vitro screening a drug candidate, the method comprising a) collecting at least two biological samples; wherein a first sample mimics osteoarthritis and a second sample mimics a healthy condition; b) contacting at least one sample or a mixture of samples with one or more drug candidates to be tested; c) measuring gene expression or gene expression product level or activity of genes listed on Table 2 and/or Table 3 or activity in the biological samples or mixture obtained in b); and d) selecting drug candidates which are capable of modulating gene expression or gene expression product level or activity measured in the samples or mixture obtained in b) and comparing the levels with a sample not mixed with the drug candidate.

[0069] Another embodiment of the invention is a method of in vitro screening a nutritional foodstuff, dietary supplement, nutraceutical or treat, the method comprising a) collecting at least two biological samples; wherein a first sample mimics osteoarthritis and a second sample mimics a healthy condition; b) contacting at least one sample or a mixture of samples with one or more nutritional foodstuff, dietary supplement, nutraceutical or treat to be tested; c) measuring gene expression or gene expression product level or activity of genes listed on Table 2 and/or Table 3 or activity in the biological samples or mixture obtained in b); and d) selecting a nutritional foodstuff, dietary supplement, nutraceutical or treat which is capable of modulating gene expression or gene expression product level or activity measured in the samples or mixture obtained in b) and comparing the levels with a sample not mixed with the nutritional foodstuff, dietary supplement, nutraceutical or treat.

[0070] Another embodiment of the invention is a method of in vitro determination of an animal's sensitivity to osteoarthritis, the method comprising comparing gene expression or gene expression product levels or activity of biomarkers selected from the group consisting of the genes and gene products listed on Table 2 and/or Table 3.

[0071] Another embodiment of the invention is a method of preparing a composition for treating osteoarthritis, the method comprising preparing a composition comprising a modulator of osteoarthritis biomarkers selected from the group consisting of genes and gene products listed on Table 2 and/or Table 3.

[0072] Another embodiment of the invention is a method of determining the efficacy of a treatment for osteoarthritis, comprising the steps of: (a) providing a biological sample from an animal affected by osteoarthritis, who has been subjected to said treatment, (b) determining the level in said sample of one or more biomarkers for osteoarthritis, to create an expression profile for said animal, and (c) comparing said expression profile with: i) a comparable expression profile obtained from said test animal before initiation of said treatment, and/or ii) a comparable expression profile obtained from said test animal at an earlier stage of said treatment, and/or iii) a comparable expression profile characteristic of a subject who is unaffected by osteoarthritis, wherein the one or more biomarkers for osteoarthritis, comprise expression products of one or more genes shown in Table 2 and/or Table 3.

[**0073**] Another embodiment of the invention is a method of selecting a food composition for an animal for its ability to treat or prevent one or more symptoms of osteoarthritis, comprising the steps of: i) accessing at least one database that comprises a first data set relating a gene expression profile of a tissue sample or a biological fluid specimen of a tissue sample from an animal having osteoarthritis; ii) accessing a least one database that comprises a second data set relating to effects of bioactive dietary components on said gene expression profile; and iii) by use of a first algorithm using said first and said second data sets, processing said first data set and said second data set to derive a nutritional formula useful for selecting and preparing a food composition for said animal; and iv) storing or using said nutritional formula in a user readable format.

[**0074**] Other and further objects, features, and advantages of the present invention will be readily apparent to those skilled in the art.

[0074A] Throughout this specification the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element, integer or step, or group of elements, integers or steps, but not the exclusion of any other element, integer or step, or group of elements, integers or steps.

[74B] Any discussion of documents, acts, materials, devices, articles or the like which has been included in the present specification is not to be taken as an admission that any or all of these matters form part of the prior art base or were common general knowledge in the field relevant to the present disclosure as it existed before the priority date of each claim of this application.

BRIEF DESCRIPTION OF THE DRAWINGS

[0075] FIGURE 1 depicts a decrease in gene expression of various genes associated with cartilage degradation in dogs after being fed at least one composition of the invention identified as canine composition j/d.

[0076] FIGURE 2 depicts a decrease in gene expression of various genes associated with cartilage degradation in dogs after being fed at least one composition of the invention identified as canine composition j/d. [0077] FIGURE 3 depicts an increase in gene expression of various genes associated with inflammation in arthritic cats compared to non-arthritic cats.

[0077] FIGURE 3 depicts an increase in gene expression of various genes associated with inflammation in arthritic cats compared to non-arthritic cats.

[0078] FIGURE 4 depicts one embodiment of the compositions of the present invention identified as composition j/d.

[0079] FIGURE 5 depicts upregulation of gene C2C in arthritic dogs compared to normal dogs.

[0080] FIGURE 6 depicts upregulation of gene C1,2C in arthritic dogs compared to non-arthritic dogs.

[0081] FIGURE 7 depicts certain genes expressing proteins associated with arthritis in arthritic versus non-arthritic cartilage in dogs.

[0082] FIGURE 8 depicts certain genes expressing proteins associated with arthritis in arthritic versus non-arthritic cartilage in dogs.

[0083] FIGURE 9 depicts serum levels of EPA and DHA after feeding canine food composition j/d to dogs for 14 and 18 days, respectively.

[0084] FIGURE 10 depicts modulating expression of gene C2C after feeding dogs with canine composition j/d for a period of 14 days.

[0085] FIGURE 11 depicts modulating expression of gene C1,2C after feeding dogs with canine composition j/d for a period of 14 days.

[0086] FIGURE 12 depicts modulating expression of gene CTX-II after feeding dogs with composition j/d for a period of 14 days.

[0087] FIGURE 13 depicts upregulation of gene C2C in arthritic versus non-arthritic cats.

[0088] FIGURE 14 depicts upregulation of gene CTX-II in arthritic cats versus non-arthritic cats.

[0089] FIGURE 15 depicts upregulation of various genes associated with cartilage repair in arthritic versus non-arthritic cats.

[0090] FIGURE 16 depicts an increase in mobility of cats after receiving feline composition j/d.

[0091] FIGURE 17 depicts a reduction in nighttime activity of dogs indicating improved comfort in dogs administered canine food composition j/d

DETAILED DESCRIPTION OF THE INVENTION

[0092] The invention relates to compositions and methods of treating abnormal conditions in an animal, wherein the abnormal condition affects the musculoskeletal joints of the animal. The compositions can be formulated for oral administration, including but not limited to animal feeds. The animal feeds can be given to any type of animal for which the compositions have been formulated. For example, the feeds can be formulated for companion animals, including but not limited to, dogs or cats.

[0093] As used herein an abnormal animal is an animal that has been diagnosed with or is apparently suffering from a condition that affects the musculoskeletal joints in the animal or for which the gene expression data contained herein suggests a predisposition for such condition. For example, a dog or cat diagnosed with or apparently suffering from osteoarthritis would be considered an abnormal animal.

[0094] The compositions of the present invention comprise at least one omega-3 fatty acid. Omega-3 fatty acids are well known in the art. Omega-3 fatty acids are essential nutrients for the health of animals and such fatty acids either cannot be made or cannot be made in sufficient quantities by animals. Such fatty acids are employed as a dietary component or components in the compositions and methods taught by the inventions herein. The formulation of the nutritional compositions contained herein is based in part upon the impact of such nutritional compositions on gene expression in animals suffering from musculoskeletal joint disorders of the types described herein. Examples of omega-3 fatty acids include, but are not limited to, alpha-linoleic acid (ALA), docosahexanoic acid (DHA) and eicosapentaenoic acid (EPA). In one embodiment of the present invention, the composition comprises one of ALA, DHA or EPA. In another embodiment, the composition comprises at least two of ALA, DHA or EPA. In yet another embodiment of the present invention, the composition comprises all three of ALA, DHA and EPA.

[0095] The compositions also comprise at least one glycosaminoglycan (GAG). GAGs are well know in the art and are considered to be unbranched polysaccharides comprised of repeating disaccharide units. Provided that the polysaccharide is unbranched and comprised of repeating disaccharide units, the molecule or polymer is considered to be a GAG. Examples of GAGs include, but are not limited to, chondroitin sulfate, dermatan sulfate, keratan sulfate, heparin, heparan sulfate and hyaluronan. In one embodiment of the present invention, the composition comprises at least one of chondroitin sulfate, dermatan sulfate, keratan sulfate, heparin, heparan sulfate or hyaluronan. In another embodiment of the present invention, the composition comprises at least two of chondroitin sulfate, dermatan sulfate, keratan sulfate, heparin, heparan sulfate or hyaluronan. In yet another embodiment of the present invention, the composition comprises at least three of chondroitin sulfate, dermatan sulfate, keratan sulfate, heparin, heparan sulfate or hyaluronan. In still another embodiment of the present invention, the composition comprises at least four, five or all of chondroitin sulfate, dermatan sulfate, keratan sulfate, heparin, heparan sulfate and/or hyaluronan.

[0096] The compositions also comprise at least one amino sugar. An amino sugar is well understood in the art and simply means a sugar moiety wherein an amine group replaces or occurs in addition to a hydroxyl group. Examples of amino sugars include, but are not limited to, galactosamine, glucosamine, sialic acid and N-acetylglucosamine. In one embodiment of the present invention, the compositions comprise at least one of galactosamine, glucosamine, sialic acid or N-acetylglucosamine. In another embodiment of the present invention, the compositions comprise at least two of galactosamine, glucosamine, sialic acid or N-acetylglucosamine. In yet another embodiment of the present invention, the compositions comprise at least three of galactosamine, glucosamine, sialic acid or N-acetylglucosamine. In still another embodiment of the present invention, the compositions comprise all four of galactosamine, glucosamine, sialic acid or N-acetylglucosamine.

[0097] The compositions also comprise at least one antioxidant. Antioxidants are well known in the art. Examples of antioxidants include but are not limited to vitamin C, vitamin E (tocopherols and/or tocotrienols), glutathione, lipoic acid, melatonin, carnitine and beta-carotene. In one embodiment of the present invention, the compositions comprise at least one of vitamin C, vitamin E (tocopherols and/or tocotrienols), glutathione, lipoic acid, melatonin, or beta-carotene. In another embodiment of the present invention, the compositions comprise at least two of vitamin C, vitamin E (tocopherols and/or tocotrienols), glutathione, lipoic acid, melatonin, or beta-carotene. In yet another embodiment of the present invention, the compositions comprise at least three of vitamin C, vitamin E (tocopherols and/or tocotrienols), glutathione, lipoic acid, melatonin, or beta-carotene. In still another embodiment of the present invention, the compositions comprise at least four of vitamin C, vitamin E (tocopherols and/or tocotrienols), glutathione, lipoic acid, melatonin, or beta-carotene. In still another embodiment of the present invention, the compositions comprise at least five or more of vitamin C, vitamin E (tocopherols and/or tocotrienols), glutathione, lipoic acid, melatonin, and/or beta-carotene.

[0098] The compositions of the present invention also comprise carnitine or acetylcarnitine, which are quaternary ammonium compounds with antioxidant effects.

[0099] In select embodiments, the compositions further comprise at least one dietary mineral and/or at least one natural amino acid. Examples of dietary minerals and natural amino acids are well known. Examples of dietary minerals include, but are not limited to, calcium, chloride, magnesium, phosphorus, potassium, sodium, cobalt, copper, fluorine, iodine, iron, manganese, molybdenum, nickel, selenium, sulfur, zinc and vanadium. In one embodiment, the composition comprises at least one of calcium, chloride, magnesium, phosphorus, potassium, sodium, cobalt, copper, fluorine, iodine, iron, manganese, molybdenum, nickel, selenium, sulfur, zinc or vanadium. In another embodiment, the composition comprises at least two of calcium, chloride, magnesium, phosphorus, potassium, sodium, cobalt, copper, fluorine, iodine, iron, manganese, molybdenum, nickel, selenium, sulfur, zinc or vanadium. In yet another embodiment, the composition comprises at least three of calcium, chloride, magnesium, phosphorus, potassium, sodium, cobalt, copper, fluorine, iodine, iron, manganese, molybdenum, nickel, selenium, sulfur, zinc or vanadium. In still another embodiment, the composition comprises at least four of calcium, chloride, magnesium, phosphorus, potassium, sodium, cobalt, copper, fluorine, iodine, iron, manganese, molybdenum, nickel, selenium, sulfur, zinc or vanadium. In still another embodiment, the composition comprises at least five or more of calcium, chloride, magnesium, phosphorus, potassium, sodium, cobalt, copper, fluorine, iodine, iron, manganese, molybdenum, nickel, selenium, sulfur, zinc or vanadium.

[00100] The natural amino acids are well known in the art and are the amino acids found in proteins. In one specific embodiment, the composition comprises an essential amino acid, wherein the term essential amino acid is relative to the species of the subject. For example, essential amino acids for dogs and cats include Arginine, Methionine, Histidine, Phenylalanine, Isoleucine, Threonine, Leucine, Tryptophan, Lysine and Valine. Taurine may also be considered to be an essential amino acid in cats.

[00101] In one embodiment canine food composition j/d comprises a composition as generally set forth in Figure 4, and includes a glycosaminoglycan in the form of chondroitin sulfate, and an amino sugar in the form of glucosamine hydrochloride as well as carnitine and at least one antioxidant. The composition may also contain additional sources of nutrients, for example: Ground Whole Grain Corn, Chicken By-Product Meal, Flaxseed, Soybean Mill Run, Brewers Rice, Soybean Meal, Pork Fat (preserved with mixed tocopherols and citric acid), Chicken Liver Flavor, Powdered Cellulose, Fish Oil, Potassium Chloride, L-Lysine, Calcium Carbonate, Choline Chloride, Iodized Salt, DL-Methionine, Vitamin E Supplement, vitamins (L-Ascorbyl-2-Polyphosphate (source of vitamin C), Vitamin E Supplement, Niacin, Thiamine Mononitrate, Vitamin A Supplement, Calcium Pantothenate, Biotin, Vitamin B12 Supplement, Pyridoxine Hydrochloride, Riboflavin, Folic Acid, Vitamin D3 Supplement), L-Threonine, Taurine, Soy Lecithin, Glucosamine Hydrochloride, minerals (Ferrous Sulfate, Zinc Oxide, Copper Sulfate, Manganous Oxide, Calcium Iodate, Sodium Selenite), L-Tryptophan, L-Carnitine, preserved with Mixed Tocopherols and Citric Acid, Chondroitin Sulfate, Beta-Carotene, Rosemary Extract.

[00102] The feline j/k food composition of the invention utilized in the Examples contained omega-3 fatty acids, omega-6 fatty acids and also contained alpha-linolenic acid. The composition contained a glycosaminoglycan in the form of chondroitin sulfate, and an amino sugar in the form of glucosamine hydrochloride. In addition, the composition contained carnitine and at least one antioxidant, for example, vitamin C and beta-carotene.

[00103] The term "animal" means a human or non-human animal, including avian, bovine, canine, equine, feline, hicrine, murine, ovine, primate, and porcine animals.

[00104] The term "antibody" means any immunoglobulin that binds to a specific antigen, including IgG, IgM, IgA, IgD, and IgE antibodies. The term includes polyclonal, monoclonal, monovalent, humanized, heteroconjugate, antibody compositions with polyepitopic specificity, chimeric, bispecific antibodies, diabodies, single-chain antibodies, and antibody fragments such as Fab, Fab', $F(ab')_2$, and Fv, or other antigen-binding fragments.

[00105] The term "array" means an ordered arrangement of at least two probes on a substrate. At least one of the probes is a control or standard and at least one of the probes is a diagnostic probe. The arrangement of from about two to about 40,000 probes on a substrate assures that the size and signal intensity of each labeled complex formed between a probe and a sample polynucleotide or polypeptide is individually distinguishable.

[00106] The term "differential expression" or "differentially expressed" means increased or unregulated gene expression or means decreased or downregulated gene expression as detected by the absence, presence, or at least two-fold, or at least a 1.5, 1.4, 1.3, 1.2, 1.1 or 1- fold change in the amount of transcribed messenger RNA or translated protein in a sample.

[00107] The term "fold" when used as a measure of differential gene expression means an amount of gene expression in an animal that is a multiple or a fraction of gene expression compared to the amount of gene expression in a comparison animal, e.g., an arthritic animal compared to a non-arthritic animal. For example, a gene that is expressed three times as much in the animal as in the comparison animal has a 3-fold differential gene expression and a gene that is expressed one-third as much in the animal as in the comparison animal also has a 3 fold differential gene expression.

[00108] The term "fragment" means (1) an oligonucleotide or polynucleotide sequence that is a portion of a complete sequence and that has the same or similar activity for a particular use as the complete polynucleotide sequence or (2) a peptide or polypeptide sequence that is a portion of a complete sequence and that has the same or similar activity for a particular use as the complete polypeptide sequence. Such fragments can comprise any number of nucleotides or amino acids deemed suitable for a particular use. Generally, oligonucleotide or polynucleotide fragments contain at least about 10, 50, 100, or 1000 nucleotides and polypeptide fragments contain at least about 4, 10, 20, or 50 consecutive amino acids from the complete sequence. The term encompasses polynucleotides and polypeptides variants of the fragments.

[00109] The term “gene” or “genes” means a complete or partial segment of DNA involved in producing a polypeptide, including regions preceding and following the coding region (leader and trailer) and intervening sequences (introns) between individual coding segments (exons). The term encompasses any DNA sequence that hybridizes to the complement of gene coding sequences.

[00110] The term “homolog” means (1) a polynucleotide, including polynucleotides from the same or different animal species, having greater than 30%, 50%, 70%, or 90% sequence similarity to a polynucleotide and having the same or substantially the same properties and performing the same or substantially the same function as the complete polynucleotide, or having the capability of specifically hybridizing to a polynucleotide under stringent conditions or (2) a polypeptide, including polypeptides from the same or different animal species, having greater than 30%, 50%, 70%, or 90% sequence similarity to a polypeptide identified by the expression of polynucleotides and having the same or substantially the same properties and performing the same or substantially the same function as the complete polypeptide, or having the capability of specifically binding to a polypeptide identified by the expression of polynucleotides. Sequence similarity of two polypeptide sequences or of two polynucleotide sequences is determined using methods known to skilled artisans, e.g., the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 87:2264-2268 (1990)). Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al. (J. Mol. Biol. 215:403-410 (1990)). To obtain gapped alignments for comparison purposes, Gapped Blast can be utilized as described in Altschul et al. (Nucl. Acids Res. 25: 3389-3402 (1997)). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) are used. See http://ww.ncbi.nlm.nih.gov.

[00111] The term “hybridization complex” means a complex that is formed between sample polynucleotides when the purines of one polynucleotide hydrogen bond with the pyrimidines of the complementary polynucleotide, e.g., 5’-A-G-T-C-3’ base pairs with 3’-T-C-A-G-5’. The degree of complementarily and the use of nucleotide analogs affect the efficiency and stringency of hybridization reactions.

[00112] The term "in conjunction" means that a drug, food, or other substance is administered to an animal (1) together in a composition, particularly food composition, or (2) separately at the same or different frequency using the same or different administration routes at about the same time or periodically. "Periodically" means that the substance is administered on a dosage schedule acceptable for a specific substance. "About the same time" generally means that the substance (food or drug) is administered at the same time or within about 72 hours of each other. "In conjunction" specifically includes administration schemes wherein substances such as drugs are administered for a prescribed period and compositions of the present invention are administered indefinitely.

[00113] The term "polynucleotide" or "oligonucleotide" means a polymer of nucleotides. The term encompasses DNA and RNA (including cDNA and mRNA) molecules, either single or double stranded and, if single stranded, its complementary sequence in either linear or circular form. The term also encompasses fragments, variants, homologs, and alleles, as appropriate for the sequences that have the same or substantially the same properties and perform the same or substantially the same function as the original sequence. The sequences may be fully complementary (no mismatches) when aligned or may have up to about a 30% sequence mismatch. Preferably, for polynucleotides, the chain contains from about 50 to 10,000 nucleotides, more preferably from about 150 to 3,500 nucleotides. Preferably, for oligonucleotides, the chain contains from about 2 to 100 nucleotides, more preferably from about 6 to 30 nucleotides. The exact size of a polynucleotide or oligonucleotide will depend on various factors and on the particular application and use of the polynucleotide or oligonucleotide. The term includes nucleotide polymers that are synthesized and that are isolated and purified from natural sources. The term "polynucleotide" is inclusive of "oligonucleotide."

[00114] The term "polypeptide," "peptide," or "protein" means a polymer of amino acids. The term encompasses naturally occurring and non-naturally occurring (synthetic) polymers and polymers in which artificial chemical mimetics are substituted for one or more amino acids. The term also encompasses fragments, variants, and homologs that have the same or substantially the same properties and perform the same or substantially the same function as the original sequence. The term encompass polymers of any length, preferably polymers containing from about 2 to 1000 amino acids, more preferably from about 5 to 500 amino acids. The term

includes amino acid polymers that are synthesized and that are isolated and purified from natural sources.

[00115] The term "probe" means (1) an oligonucleotide or polynucleotide, either RNA or DNA, whether occurring naturally as in a purified restriction enzyme digest or produced synthetically, that is capable of annealing with or specifically hybridizing to a polynucleotide with sequences complementary to the probe or (2) a peptide or polypeptide capable of specifically binding a particular protein or protein fragment to the substantial exclusion of other proteins or protein fragments. An oligonucleotide or polynucleotide probe may be either single or double stranded. The exact length of the probe will depend upon many factors, including temperature, source, and use. For example, for diagnostic applications, depending on the complexity of the target sequence, an oligonucleotide probe typically contains about 10 to 100, 15 to 50, or 15 to 25 nucleotides. In certain diagnostic applications, a polynucleotide probe contains about 100-1000, 300-600, nucleotides, preferably about 300 nucleotides. The probes herein are selected to be "substantially" complementary to different strands of a particular target sequence. This means that the probes must be sufficiently complementary to specifically hybridize or anneal with their respective target sequences under a set of predetermined conditions. Therefore, the probe sequence need not reflect the exact complementary sequence of the target. For example, a noncomplementary nucleotide fragment may be attached to the 5' or 3' end of the probe, with the remainder of the probe sequence being complementary to the target sequence. Alternatively, noncomplementary bases or longer sequences can be interspersed into the probe provided that the probe sequence has sufficient complementarity with the sequence of the target polynucleotide to specifically anneal to the target polynucleotide. A peptide or polypeptide probe may be any molecule to which the protein or peptide specifically binds, including DNA (for DNA binding proteins), antibodies, cell membrane receptors, peptides, cofactors, lectins, sugars, polysaccharides, cells, cell membranes, organelles and organellar membranes.

[00116] The term "sample" means any animal tissue or fluid containing, e.g., polynucleotides, polypeptides, antibodies, metabolites, and the like, including cells and other tissue containing DNA and RNA. Examples include, blood, cartilage, connective, epithelial, lymphoid, muscle, nervous, sputum, and the like. A sample may be solid or liquid and may be DNA, RNA, cDNA, bodily fluids such as blood or urine, cells, cell preparations or soluble fractions or media aliquots thereof, chromosomes, organelles, and the like.

[00117] The term "single package" means that the components of a kit are physically associated in or with one or more containers and considered a unit for manufacture, distribution, sale, or use. Containers include, but are not limited to, bags, boxes, bottles, shrink wrap packages, stapled or otherwise affixed components, or combinations thereof. A single package may be containers of individual food compositions physically associated such that they are considered a unit for manufacture, distribution, sale, or use.

[00118] The term "useful variations" means (1) for a polynucleotide, the complements of the polynucleotide; the homologs of the polynucleotide and its complements; the variants of the polynucleotide, its complements, and its homologs; and the fragments of the polynucleotide, its complements, its homologs, and its variants and (2) for a polypeptide, the homologs of the polypeptide; the variants of the polypeptide and its homologs; and the fragments of the polynucleotide, its homologs, and its variants.

[00119] The term "virtual package" means that the components of a kit are associated by directions on one or more physical or virtual kit components instructing the user how to obtain the other components, e.g., in a bag containing one component and directions instructing the user to go to a website, contact a recorded message, view a visual message, or contact a caregiver or instructor to obtain instructions on how to use the kit.

[00120] The term "standard" means (1) a control sample that contains tissue from a normal animal if, for example, an arthritic animal is being tested or tissue from, for example, an arthritic animal if a normal animal is being tested or (2) a control sample that contains tissue from a normal or, for example, arthritic animal that has not been exposed to a test substance being examined in the corresponding normal or, for example arthritic animal to determine if the test substance causes differential gene expression, as appropriate for the context of its use.

[00121] The term "stringent conditions" means (1) hybridization in 50% (vol/vol) formamide with 0.1% bovine serum albumin, 0.1% Ficoll, 0.1% polyvinylpyrrolidone, 50 mM sodium phosphate buffer at pH 6.5 with 750 mM NaCl, 75 mM sodium citrate at 42°C, (2) hybridization

in 50% formamide, 5x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5x Denhardt's solution, sonicated salmon sperm DNA (50 μg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C; with washes at 42°C in 0.2x SSC and 0.1% SDS or washes with 0.015 M NaCl, 0.0015 M sodium citrate, 0.1% Na_2SO_4 at 50°C or similar procedures employing similar low ionic strength and high temperature washing agents and similar denaturing agents.

[00122] The term "substance" means an element, compound, molecule, or a mixture thereof or any other material that could potentially be useful for diagnosing, prognosing, or modulating the onset or severity of an abnormal joint condition in an animal, including any drug, chemical entity, or biologic entity.

[00123] The term "siRNA" means a polynucleotide that forms a double stranded RNA that reduces or inhibits expression of a gene when the siRNA is expressed in the same cell as the gene. The term encompasses double stranded RNA formed by complementary strands. The siRNA complementary portions that hybridize to form the double stranded molecule typically have substantial or complete identity. Typically, siRNA contains at least about 15-50 nucleotides and the double stranded siRNA contains about 15-50 base pairs, preferably about 20-30 nucleotides and base pairs.

[00124] The term "specifically bind" means a special and precise interaction between two molecules which is dependent upon their structure, particularly their molecular side groups. For example, the intercalation of a regulatory protein into the major groove of a DNA molecule, the hydrogen bonding along the backbone between two single stranded nucleic acids, or the binding between an epitope of a protein and an agonist, antagonist, or antibody.

[00125] The term "specifically hybridize" means an association between two single stranded polynucleotides of sufficiently complementary sequence to permit such hybridization under predetermined conditions generally used in the art (sometimes termed "substantially complementary"). For example, the term may refer to hybridization of a polynucleotide probe with a substantially complementary sequence contained within a single stranded DNA or RNA molecule according to an aspect of the invention, to the substantial exclusion of hybridization of the polynucleotide probe with single stranded polynucleotides of non-complementary sequence.

[00126] The term "variant" means (1) a polynucleotide sequence containing any substitution, variation, modification, replacement, deletion, or addition of one or more nucleotides from or to a polynucleotide sequence and that has the same or substantially the same properties and performs the same or substantially the same function as the original sequence and (2) a polypeptide sequence containing any substitution, variation, modification, replacement, deletion, or addition of one or more amino acids from or to a polypeptide sequence and that has the same or substantially the same properties and performs the same or substantially the same function as the original sequence. The term therefore includes single nucleotide polymorphisms (SNPs) and allelic variants and includes conservative and non-conservative amino acid substitutions in polypeptides. The term also encompasses chemical derivatization of a polynucleotide or polypeptide and substitution of nucleotides or amino acids with nucleotides or amino acids that do not occur naturally, as appropriate.

[00127] The invention is not limited to the particular methodology, protocols, and reagents described herein because they may vary. Further, the terminology used herein is for the purpose of describing particular embodiments only and is not intended to limit the scope of the present invention. As used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise, e.g., reference to "a variant" includes a plurality of variants. Further, defined terms include variations of the terms used in the proper grammatical context, e.g., the term "specifically binds" includes "specific binding" and other forms of the term. Similarly, the words "comprise", "comprises", and "comprising" are to be interpreted inclusively rather than exclusively.

[00128] Unless defined otherwise, all technical and scientific terms and any acronyms used herein have the same meanings as commonly understood by one of ordinary skill in the art in the field of the invention. Although any compositions, methods, articles of manufacture, or other means or materials similar or equivalent to those described herein can be used in the practice of the present invention, the preferred compositions, methods, articles of manufacture, or other means or materials are described herein.

[00129] All patents, patent applications, publications, and other references cited or referred to herein are incorporated herein by reference to the extent allowed by law. The discussion of those

references is intended merely to summarize the assertions made therein. No admission is made that any such patents, patent applications, publications or references, or any portion thereof, is relevant prior art for the present invention and the right to challenge the accuracy and pertinence of such patents, patent applications, publications, and other references is specifically reserved.

[00130] In one embodiment, the present invention encompasses one or more genes or gene segments ("genes" as defined herein) that are differentially expressed in abnormal animals compared to normal animals. The invention is based upon the discovery of polynucleotides that are differentially expressed in abnormal animals compared to normal animals. The genes were identified by comparing the expression of genes in lymphocytes from animals diagnosed as abnormal with genes in lymphocytes from animals diagnosed as normal using Affymetrix GeneChip® technology.

[00131] The polynucleotides and genes are identified by measuring differences in gene expression from lymphocytes from canines diagnosed as abnormal with gene expression in lymphocytes from canines diagnosed as normal. Changes in gene expression can be determined by any method known to skilled artisans. Generally, changes in gene expression are determined by measuring transcription (determining the amount of mRNA produced by a gene) or measuring translation (determining the amount of protein produced by a gene). The amount of RNA or protein produced by a gene can be determined using any method known to skilled artisans for quantifying polynucleotides and proteins. Generally, RNA expression is determined using polymerase chain reaction (PCR) (including, without limitation, reverse transcription-PCR (RT-PCR) and quantitative real-time PCR (qPCR)), RNase protection, Northern blotting, and other hybridization methods. The RNA measured is typically in the form of mRNA or reverse transcribed mRNA. Protein or polypeptide expression is determined using various colormetric and spectroscopic assays and methods such as the lowry assay, the biuret assay, fluorescence assays, turbidimetric methods, the bicinchoninic assay, protein chip technology, infrared absorbance, ninhydrin, the bradford assay, and ultraviolet absorbance. In a preferred method, changes in gene expression are determined using Affymetrix Canine-1 and Canine-2 gene chips available for purchase from Affymetrix, Inc. and the instructions for using such chips to determine gene expression.

[00132] Generally, differential gene expression in abnormal animals compared to normal animals is determined by measuring the expression of at least one gene. Preferably, the expression of two or more differentially expressed genes is measured to provide a gene expression pattern or gene expression profile. More preferably, the expression of a plurality of differentially expressed genes is measured to provide additional information for a more significant gene expression pattern or profile.

[00133] In another aspect, the invention provides a device suitable for detecting the expression of a plurality of genes differentially expressed in abnormal animals compared to normal animals. The device comprises a substrate having a plurality of the oligonucleotide or polynucleotide probes of the present invention affixed to the substrate at known locations. The device is essentially an immobilized version of the oligonucleotide or polynucleotide probes described herein. The device is useful for rapid and specific detection of genes and polynucleotides and their expression patterns and profiles. Typically, such probes are linked to a substrate or similar solid support and a sample containing one or more polynucleotides (e.g., a gene, a PCR product, a ligase chain reaction (LCR) product, a DNA sequence that has been synthesized using amplification techniques, or a mixture thereof) is exposed to the probes such that the sample polynucleotide(s) can hybridize to the probes. Either the probes, the sample polynucleotide(s), or both, are labeled, typically with a fluorophore or other tag such as streptavidin, and detected using methods known to skilled artisans. If the sample polynucleotide(s) is labeled, hybridization may be detected by detecting bound fluorescence. If the probes are labeled, hybridization is typically detected by label quenching. If both the probe and the sample polynucleotide(s) are labeled, hybridization is typically detected by monitoring a color shift resulting from proximity of the two bound labels. A variety of labeling strategies and labels are known to skilled artisans, particularly for fluorescent labels. Preferably, the probes are immobilized on substrates suitable for forming an array (known by several names including DNA microarray, gene chip, biochip, DNA chip, and gene array) comparable to those known in the art.

[00134] The polypeptide probes may be made according to conventional methods, e.g., using the nucleotide sequence data provided for polynucleotides of the present invention and methods known in the art. Such methods include, but are not limited to, isolating polypeptide directly from cells, isolating or synthesizing DNA or RNA encoding the polypeptides and using the DNA

or RNA to produce recombinant products, synthesizing the polypeptides chemically from individual amino acids, and producing polypeptide fragments by chemical cleavage of existing polypeptides.

[00135] In another aspect, the invention provides a device suitable for detecting the expression of a plurality of genes differentially expressed in abnormal animals compared to normal animals. The device comprises a substrate having a plurality of the peptide or polypeptide probes of the present invention affixed to the substrate at known locations. The device is essentially an immobilized version of the peptide or polypeptide probes described herein. The device is useful for the rapid and specific detection of proteins and their expression patterns. Typically, such probes are linked to a substrate and a sample containing one or more proteins is exposed to the probes such that the sample proteins can hybridize to the probes. In certain embodiments, the probes, the sample proteins, or both, are labeled and detected, typically with a fluorophore or other agent known to skilled artisans. Generally, the same methods and instrumentation used for reading polynucleotide microarrays is applicable to protein arrays. Preferably, the probes are immobilized on a substrate suitable for forming an array.

[00136] Methods for determining the amount or concentration of protein in a sample are known to skilled artisans. Such methods include radioimmunoassays, competitive-binding assays, Western blot analysis, and ELISA assays. For methods that use antibodies, polyclonal and monoclonal antibodies are suitable. Such antibodies may be immunologically specific for a protein, protein epitope, or protein fragment.

[00137] Some embodiments of the invention utilize antibodies for the detection and quantification of proteins produced by expression of the polynucleotides of the present invention. Although proteins may be detected by immunoprecipitation, affinity separation, Western blot analysis, protein arrays, and the like, a preferred method utilizes ELISA technology wherein the antibody is immobilized on a solid support and a target protein or peptide is exposed to the immobilized antibody. Either the probe, or the target, or both, can be labeled using known methods.

[00138] In some embodiments, expression patterns or profiles of a plurality of genes differentially expressed in abnormal animals compared to normal animals are observed utilizing

an array of probes for detecting polynucleotides or polypeptides. In one embodiment, arrays of oligonucleotide or polynucleotide probes may be utilized, whereas another embodiment may utilize arrays of antibodies or other proteins that specifically bind to the differentially expressed gene products of the present invention. Such arrays may be commercially available or they may be custom made using methods known to skilled artisans, e.g., in-situ synthesis on a solid support or attachment of pre-synthesized probes to a solid support via micro-printing techniques. In various embodiments, arrays of polynucleotides or polypeptides probes are custom made to specifically detect transcripts or proteins produced by the differentially expressed genes of the present invention.

[00139] In one embodiment, arrays of polynucleotide or polypeptide probes are custom made to specifically detect transcripts or proteins produced by two or more polynucleotides or genes identified in Table 2 and/or Table 3. These probes are designed to detect genes associated with lipid and glucose metabolism pathways in animals. In another embodiment, arrays of polynucleotide or polypeptide probes are custom made to specifically detect transcripts or proteins produced by two or more polynucleotides or genes identified in Table 3. These probes are designed to detect genes that are particularly relevant to abnormal animals compared to normal animals.

[00140] In a further aspect, the invention provides a method for detecting the differential expression of one or more genes differentially expressed in abnormal animals compared to normal animals in a sample. The method comprises (a) hybridizing a combination comprising a plurality of polynucleotide probes that are differentially expressed in abnormal animals compared to normal animals with polynucleotides in the sample to form one or more hybridization complexes; (b) optionally, hybridizing a combination comprising a plurality of polynucleotide probes that are differentially expressed in abnormal animals compared to normal animals with polynucleotides in a standard to form one or more hybridization complexes; (c) detecting the hybridization complexes from the sample and, optionally, the standard from step (b); and (d) comparing the hybridization complexes from the sample with the hybridization complexes from a standard, wherein a difference in the amount of hybridization complexes between the standard and sample indicate differential expression of genes differentially expressed in abnormal animals compared to normal animals in the sample.

[00141] Step (b) and part of step (c) are optional and are used if a relatively contemporaneous comparison of two or more test systems is to be conducted. However, in a preferred embodiment, the standard used for comparison is based upon data previously obtained using the method.

[00142] These probes are exposed to a sample to form hybridization complexes that are detected and compared with those of a standard. The differences between the hybridization complexes from the sample and standard indicate differential expression of polynucleotides and therefore genes differentially expressed in abnormal animals compared to normal animals in the sample. In a preferred embodiment, probes are made to specifically detect polynucleotides or fragments thereof produced by one or more of the genes or gene fragments identified by the present invention. Methods for detecting hybridization complexes are known to skilled artisans.

[00143] In one embodiment, the method further comprises exposing the animal or sample to a test substance before hybridization. Then, the comparison is indicative of whether the test substance altered the expression of genes differentially expressed in abnormal animals compared to normal animals, particularly abnormal-associated genes, in the sample.

[00144] In another aspect, the invention provides a method for detecting the differential expression of genes differentially expressed in abnormal animals compared to normal animals in a sample. The method comprises (a) reacting a combination comprising a plurality of polypeptide probes with proteins in the sample under conditions that allow specific binding between the probes and the proteins to occur, wherein the proteins bound by the probes are differentially expressed in a abnormal animal compared to a normal animal; (b) optionally, reacting a combination comprising a plurality of polypeptide probes with proteins in a standard under conditions that allow specific binding between the probes and the proteins to occur, wherein the proteins bound by the probes are differentially expressed in a abnormal animal compared to a normal animal; (c) detecting specific binding in the sample and, optionally, the standard from step (b); and (d) comparing the specific binding in the sample with that of a standard, wherein differences between the specific binding in the standard and the sample indicate differential expression of genes differentially expressed in abnormal animals compared to normal animals in the sample.

[00145] These probes are exposed to a sample to form specific binding that is detected and compared with those of a standard. The differences between the specific binding from the sample and standard indicate differential expression of proteins and therefore genes differentially expressed in abnormal animals compared to normal animals, particularly abnormal-associated genes, in the sample. In a preferred embodiment, probes are made to specifically detect proteins or fragments thereof produced by one or more of the genes or gene fragments identified by the present invention.

[00146] In one embodiment, the method further comprises exposing the animal or sample to a test substance before reacting the polypeptides with the proteins. Then, the comparison is indicative of whether the test substance altered the expression of genes differentially expressed in abnormal animals compared to normal animals, particularly abnormal-associated genes, in the sample.

[00147] In another aspect, the method for detecting the expression of genes differentially expressed in abnormal animals compared to normal animals in a sample is used to monitor an animal's progress when attempting to modulate the amount of, for example, arthritis, tissue on the animal in response to a cartilage tissue modulation program. The method is performed at intervals, preferably set intervals, during the modulation program and the animal's progress monitored by comparing the results of the method at two or more points during the modulation program. A change in expression of one or more of the genes differentially expressed in abnormal animals compared to normal animals, particularly abnormal-associated genes, or in the pattern of gene expression, or the lack of any change, resulting from the comparison indicates the effectiveness of the modulation program.

[00148] Test substances can be any substance that may have an effect on polynucleotides or genes differentially expressed in abnormal animals compared to normal animals, particularly abnormal-associated genes. Test substances include, but are not limited to, amino acids; proteins, peptides, polypeptides, nucleic acids, oligonucleotides, polynucleotides, small molecules, macromolecules, vitamins, minerals, simple sugars; complex sugars; polysaccharides; carbohydrates; medium-chain triglycerides (MCTs); triacylglycerides (TAGs); n-3 (omega-3) fatty acids including DHA, EPA, ALA; n-6 (omega-6) fatty acids including LA, γ-linolenic acid

(GLA) and ARA; SA, conjugated linoleic acid (CLA); choline sources such as lecithin; fat-soluble vitamins including vitamin A and precursors thereof such as carotenoids (e.g., β-carotene), vitamin D sources such as vitamin D2 (ergocalciferol) and vitamin D3 (cholecalciferol), vitamin E sources such as tocopherols (e.g., α-tocopherol) and tocotrienols, and vitamin K sources such as vitamin K1 (phylloquinone) and vitamin K2 (menadione); water-soluble vitamins including B vitamins such as riboflavin, niacin (including nicotinamide and nicotinic acid), pyridoxine, pantothenic acid, folic acid, biotin and cobalamin; and vitamin C (ascorbic acid); antioxidants, including some of the vitamins listed above, especially vitamins E and C; also bioflavonoids such as catechin, quercetin and theaflavin; quinones such as ubiquinone; carotenoids such as lycopene and lycoxanthin; resveratrol; and α-lipoic acid; L-carnitine; D-limonene; glucosamine; S-adenosylmethionine; and chitosan. In a preferred embodiment, test substances are nutrients that may be added to food or consumed as a supplement. Examples include, but are not limited to, fatty acids such as omega-3 fatty acids (e.g., DHA and EPA) and omega-6 fatty acids (e.g., ARA), carnitine, methionine, vitamin C, vitamin E, and vitamin D.

[00149] I n a preferred embodiment, the substances useful for affecting the expression of genes differentially expressed in abnormal animals compared to normal animals, particularly abnormal-associated genes, may be identified using methods discloses in co-pending US Provisional Patent Application No. 60/657980, filed March 2, 2005, and any subsequent US or foreign patent application that claims priority thereto.

[00150] The expression profile for normal animals used in the comparison can be obtained from one or more normal animals contemporaneously with the expression profile for the animal being tested of from a database of normal animal expression profiles. Preferably, a database of expression profiles for normal animals accumulated over time is available for use as a reference.

[00151] Determining if the polynucleotides or polypeptides are differentially expressed can be accomplished by detecting the polynucleotides or polypeptides using methods known to skilled artisans, some of which are described herein.

[00152] In another aspect, the invention provides a composition suitable for manipulating the genome of an animal. The composition comprises one or more substances that interfere with the expression of one or more genes differentially expressed in abnormal animals compared to normal animals, particularly abnormal-associated genes.

[00153] In another embodiment, the invention encompasses a method for modulating the expression of one or more genes differentially expressed in animals having abnormal musculoskeletal joint disorders compared to normal animals, particularly abnormal musculoskeletal joint disorder-associated genes. In preferred embodiments the composition comprises, in milligrams per kilogram of body weight per day (mg/kg/day), DHA in amounts of from about 1 to about 30, preferably from about 3 to about 15; EPA in amounts of from about 1 to about 30, preferably from about 3 to about 15; EPA/DHA Combo (1.5:1 ratio) in amounts of from about 4/2 to about 30/45, preferably from about 9/6 to about 18/12; ALA in amounts of from about 10 to about 100, preferably from about 30 to about 60; LA in amounts of from about 30 to about 600, preferably from about 60 to about 300; ARA in amounts of from about 5 to about 50, preferably from about 15 to about 30; SA in amounts of from about 3 to about 60, preferably from about 6 to about 30; and CLA (as a control) in amounts of from about 6 to about 120, preferably from about 12 to about 60. The composition can be administered to the animal in any manner or form suitable for the composition. Preferably, the composition is administered to the animal orally in the form of a food composition or a supplement. The food composition may be of any form, e.g., a nutritionally balanced food composition known in the art such as dry foods, semi-moist foods, and wet foods for animals, particularly companion animals such as feline and canine animals. Supplements include dosage forms such as tablets, capsules, and similar forms. In a further aspect, the composition is administered in combination with one or more drugs or other substances that modulate the amount of cartilage tissue in an animal.

[00154] In another aspect, the invention provides a composition suitable for modulating the expression of one or more genes differentially expressed in animals having abnormal musculoskeletal joint disorders compared to normal animals, particularly abnormal musculoskeletal joint disorder-associated genes, or modulating the amount of cartilage tissue in an animal. The composition comprises a gene expression or tissue modulating amount of one or more of DHA, EPA, EPA and DHA, ALA, LA, ARA, and SA. In various embodiments, the composition comprises, in mg/kg/day, DHA in amounts sufficient to administer to an animal from about 1 to about 30; EPA in amounts sufficient to administer to an animal from about 1 to

about 30; EPA/DHA Combo (1.5:1 ratio) in amounts sufficient to administer to an animal from about 4/2 to about 30/45; ALA in amounts sufficient to administer to an animal from about 10 to about 100; LA in amounts sufficient to administer to an animal from about 30 to about 600; ARA in amounts sufficient to administer to an animal from about 5 to about 50; SA in amounts sufficient to administer to an animal from about 3 to about 60; and CLA (as a control) in amounts sufficient to administer to an animal from about 6 to about 120. Such substances may be useful for modulating the amount of cartilage tissue in an animal. Preferably, the substances affect the expression of a plurality of such genes. In one embodiment, the composition further comprises one or more drugs or other substances that modulate the amount of cartilage tissue in an animal.

[00155] In a further aspect, the present invention provides kits suitable for determining the differential expression of one or more genes differentially expressed in animals having abnormal musculoskeletal joint disorders compared to normal animals, particularly abnormal musculoskeletal joint disorder-associated genes, in a test system.

[00156] Example 1: Determining the Effect of Various Substances or Ingredients on Gene Expression in Canine Cell Lines

[00157] Affymetrix canine gene chips Canine Genome-1 and Canine Genome-2 are used to determine the effect of various test substances or ingredients such as MCTs; TAGs; ALA; EPA; DHA; linoleic acid; stearic acid (SA), conjugated linoleic acid (CLA), GLA; arachidonic acid; lecithin; vitamin A, vitamin D, vitamin E, vitamin K, riboflavin, niacin, pyridoxine, pantothenic acid, folic acid, biotin vitamin C, catechin, quercetin, theaflavin; ubiquinone; lycopene, lycoxanthin; resveratrol; α-lipoic acid; L-carnitine; D-limonene; glucosamine; S-adenosylmethionine; chitosan, various materials containing one or more of these compounds, and various combination thereof on gene expression in four canine cell lines and appropriate controls. Each ingredient is tested in two concentrations as illustrated for selected sample ingredients shown in Table 1. The solvent at the higher of the two concentrations is used as a control. Four canine cell lines are used: CCL34 (kidney), CRL1430 (thymus), CCL183 (bone) (obtained from The American Tissue Culture Collection) and CTAC (thyroid) (See, Measurement of NK Activity in Effector Cells Purified from Canine Peripheral Lymphocytes,

Veterinary Immunology and Immunopathology, 35 (1993) 239-251). A cell line treated with an ingredient at a specific concentration is referred to as "treatment" and an untreated sample is referred to as "control." The words "genes" and "probes" are used synonymously in this method. Gene expression is measured for the treatment cell lines and controls using the instructions provided with the Affymetrix chips. Detailed sequence information for each unique probe identification number is available from the manufacturer.

[00158] The gene expression data is determined to be either "up" or "down" -regulated for any given treatment. The decision on whether a gene is "up" or "down" is based on the fold change, which is calculated as treatment intensity/control intensity for each individual probe. The fold change is considered down-regulated if its value is < 1/1.5 (for across all 4 cell lines analysis) or < 1/2 (for within cell lines analysis) and is up-regulated if it is > 1.5 (for across all 4 cell lines analysis) or > 2 (for within cell lines analysis). Also, a probe is considered significant for further scrutiny if it is called as present in only one of the conditions being compared (treatment or control) and is "absent" or "marginal" in the other and the fold change is significant according to the software used. Probes that appear to be regulated in opposite directions in the two treatments are excluded from further analysis.

[00159] The raw data is analyzed using GeneSpring version 7.0 (GS) software (Agilent Corporation) and validated using the R-Bioconductor (RB) freeware. Both software packages are used to compute probe intensities from the CEL files generated by the Affymetrix Instrument. The Present/Absent/Marginal calls per probe and P-values are computed using the R-Bioconductor and GeneSpring software separately.

[00160] Two schemes are used for data analysis. First; "across cell lines" and "within individual cell lines." In the first scheme, genes are selected for scoring provided they are found to be significant and common across all cell-lines. The "across cell lines" yields the highest confidence data with minimum noise and may provide the best possible clues as to which genes are affected by individual ingredients. In the second scheme, only those genes that show a significant fold change in the two treatments according to both software packages within an individual cell lines are scored. A sample of the data obtained from these experiments is shown in Table 2. Table 2 shows the correlation between treatment substance (Column 1), Probe (data link) (Column 2), Direction (Column 3), Best BLAST Annotation (determined statistically) (Column 4), and Human Accession Number (Column 5). The information for all ingredients tested is stored in a database for reference.

[00161] Based upon the physiological condition of the canines (a diagnosis as abnormal) and a comparison of the information from the Tables 1-2, i.e, noting genes that are influenced by a test substance or ingredient and are also differentially expressed in abnormal canines compared to normal canines, a nutritional formula useful for selecting and preparing a food composition for abnormal canines would be believed to contain one or more of the following ingredients in the following amounts (in vivo amounts in milligrams per kilogram of body weight per day (mg/kg/day) are based upon extrapolation from amounts used in vitro, for example: DHA - from about 1 to about 30; EPA - from about 1 to about 30; EPA/DHA Combo (1.5:1 ratio) - from about 4/2 to about 30/45; ALA - from about 10 to about 100; LA - from about 30 to about 600; ARA - from about 5 to about 50; and SA - from about 3 to about 60. Based upon these data, a food composition and related diet containing one or more of these ingredients can be prepared and used to regulate the genes that are differentially expressed in abnormal animals compared to normal animals. Such regulation will cause the modulation of abnormal musculoskeletal joint disorders in the animal and, therefore, in one embodiment, promote a shift to a desirable or normal status and promote better health and wellness of the animal.

[00162] Example 2: RNA Isolation Procedures

[00163] Materials and Methods. The following general procedures may be used to isolate RNA from tissue samples of dogs and cats for gene expression profiling utilizing gene chips as further described in the Examples of this specification. It will be apparent to a person of ordinary skill in the art that these procedures or modifications thereof as recognized within the art can be applied to isolate RNA from tissue or body fluid samples for further gene expression analysis using a variety of analytical procedures available to a person of ordinary skill in the art, in particular microarray technologies.

Isolation of Ribonucleic Acid (RNA) from Tissue

[00164] Tissue samples may be collected, frozen in liquid nitrogen, thawed and then homogenized and processed using a TRIzol® RNA extraction method to produce good quality RNA which is then subjected to further genomic analysis.

[00165] Materials: ice, liquid nitrogen, frozen canine or feline tissue, TRIzol® lysis reagent, chloroform minimum 99%, isopropyl alcohol, 70% ethanol (prepared with ethanol, absolute and deionized, RNase-free water), RNase Zap®, deionized water, RNA Storage Solution®, from Ambion.

[00166] Equipment: Ultra-Turrax T25 Power Homogenizer, Beckman Coulter Allegra 25R Centrifuge, Eppendorf Centrifuge, forceps, scalpel, hard cutting surface, i.e. cutting board, 1.5mL DNase and RNase free/sterile microcentrifuge tubes, 50mL DNase and RNase free/sterile disposable polypropylene tubes, P1000, P200, P20, P10 and P2 Rainin Pipetman pipettes, filter pipette tips for P1000, P200, P20, P10 and P2 pipettes, DNase and RNase free/sterile, and lint free wipes.

[00167] Preparations: Prepare 50mL polypropylene tubes with 4mL TRIzol® (one tube for each tissue selected for RNA isolation).

[00168] Tissue Homogenization: Fill a container capable of holding liquid nitrogen with 3-4 scoops of liquid nitrogen. Place a piece of frozen tissue immediately into the aforementioned container (the tissue should be about the size of a pea) and place the tissue into the appropriate labeled 50mL polypropylene tube (that already contains 4mL TRIzol®). Immediately begin homogenization using the Ultra-Turrax T25 Power Homogenizer. Homogenize on the highest setting (6) for 10-15 seconds. Cool the sample on ice for another 10-15 seconds and then repeat. Continue until the tissue is fully homogenized and the solution is cloudy. Upon complete homogenization, cap the 50mL tube and return to the ice. Incubate the homogenized tissues at room temperature for 5 minutes before proceeding with the isolation procedure.

[00169] **Example 3: RNA Preparation Procedures**

[00170] RNA Isolation: The procedures given in the Invitrogen instructions provided with the TRIzol® reagent are generally followed. Separate the homogenized sample into four 1mL aliquots in four 1.5mL microcentrifuge tubes. Add 200uL of chloroform to each 1mL aliquot.

Cap the tubes, vortex for 15 seconds and then shake up and down. The result should be a pink milky liquid. Incubate the tubes at room temperature for 2-3 minutes. Centrifuge the tubes for 15 minutes at 14,000 rpm and 4°C. Transfer the aqueous phase (top layer) to a sterile 1.5mL microcentrifuge tube. The typical volume of the aqueous phase which should be transferred to the new tube is about 500uL. Be sure not to transfer any of the intermediate or lower phase. Precipitate the RNA from solution by adding 500uL of Isopropyl Alcohol to each microcentrifuge tube containing the aqueous layer. Shake the tubes up and down for at least 20 seconds. Incubate the samples at room temperature for 10 minutes. Centrifuge the samples for 10 minutes, 14,000 rpm at 4°C. Remove the supernatant carefully by aspirating off the liquid being sure not to lose the pellet. Add 1mL of 70% ethanol to wash the pellet. Dislodge the pellet by flicking the tube (or tapping the tube on the bench top) and shake to mix. Centrifuge for 5 minutes, 8,200 rpm at 4°C. Remove the supernatant carefully by aspirating off the liquid being sure not to lose the pellet. Using a lint free wipe to carefully soak up excess ethanol to make sure the pellet is dry. Resuspend each pellet into 30uL of RNA Storage Solution. Mix gently by pipetting until the RNA goes back into solution and then store at -80°C. It may be necessary to vortex the sample for a few seconds at a low speed to facilitate the resuspension of the RNA. If this is necessary, spin down the samples, using the microcentrifuge, prior to freezing.

[00171] RNA Cleaning: The procedures given in the RNeasy® Mini Handbook are followed.

RNA Isolation from Cells Cultured in OptiCell Chambers Using the RNeasy Mini Kit.

[00172] Cells cultured from mammalian cell lines are used to isolate good quality RNA which is then used for future downstream genomic analysis. All work related to the culturing of the cells is to be done under strict aseptic conditions.

[00173] Reagents: 10X PBS, deionized H_2O, absolute ethanol, RNA Storage Solution, β-Mercaptoethanol, RNase Zap®, Buffer RLT, and Buffer RW1 and Buffer RPE (provided in the RNeasy Mini Kit)

[00174] Equipment/Materials: RNeasy Mini Kit, QIAshredder spin columns, OptiCell knife, 20mL sterile syringe, OptiCell tips, Cell scraper, P1000 Pipetman pipette, Rainin, P200 Pipetman pipette, Rainin, 100-100uL filtered pipette tips, 1-200uL filtered pipette tips, sterile

transfer pipettes, 55mL sterile solution basin, 1.5mL sterile microcentrifuge tubes, and Eppendorf Microcentrifuge.

[00175] Solutions: Buffer RLT (stock provided in RNeasy Mini Kit); -Add 100uL of β-Mercaptoethanol per 10mL of Buffer RLT prior to beginning protocol. 70% Ethanol: Make 50mL of 70% ethanol by adding 35mL absolute ethanol to 15mL deionized, RNase-free water. 1X PBS: RNase-free water. Filter the solution using a .22um filter.

[00176] Procedure: Removing Cells from the OptiCell Chamber (proceed one OptiCell at a time). Check the cells under a microscope to ensure that the cells are alive before isolating RNA. Remove and discard the cell culture medium. Using the OptiCell knife, cut away the top membrane exposing the cells on the lower membrane. Wash the membrane to which the cells are attached three times with 1X PBS. Pipette 600uL of the Buffer RLT solution (containing β-Mercaptoethanol) onto the center of the membrane to which the cells are attached. Using the cell scraper, gently spread the Buffer RLT over the entire surface of the membrane, and then collect the liquid in one corner. Pipette off the entire volume of Buffer RLT and place into a QIAshredder spin column.

[00177] RNA Isolation: Centrifuge the QIAshredder spin columns at 14,000 rpm for 2 minutes. Discard the spin column but keep the collection tube and its contents. Add 600uL of 70% ethanol to the collection tube and mix well by pipetting (the total volume now = 1.2mL). Transfer 600uL of the cell lysate to an RNeasy mini column and centrifuge for 15 seconds at 14,000 rpm. Discard the flow through but keep the collection tube and the spin column. Transfer the remaining volume of cell lysate (~600uL) to the spin column and repeat the centrifugation. Discard the flow through but keep the collection tube and the spin column. Add 700uL Buffer RW1 to the spin column. Centrifuge for 15 seconds at 14,000 rpm to wash the column. Discard the flow through and the collection tube. Transfer the spin column to a new 2mL collection tube and add 500uL Buffer RPE to the column. Centrifuge for 15 seconds at 14,000 rpm. Discard the flow through, keep the collection tube/column. Add another 500uL Buffer RPE to the column. Centrifuge for 2 minutes at 14,000 rpm. Transfer the spin column to a 1.5mL collection tube. Add 30uL of RNA Storage Solution directly to the silica gel membrane and centrifuge for 1 minute at 14,000 rpm to elute the RNA. Store the final RNA at -70°C.

RNA 6000 Nano Assay

[00178] Using the Agilent 2100 Bioanalyzer and the RNA 6000 Nano Assay, analyze RNA isolated from cultured mammalian cells, lymphocytes or tissues for quality.

[00179] Reagents: RNA 6000 Nano gel matrix, RNA 6000 Nano dye concentrate, RNA 6000 Nano Marker, (all of the above reagents are contained in the RNA 6000 Nano Assay kit, Agilent), RNA 6000 ladder, RNase Zap , and RNase-free water, from Ambion.

[00180] Equipment/Other Materials: Agilent Chip Priming Station, Agilent, RNA 6000 chip, Agilent, electrode cleaners, P2, P10, P200, and P1000 Rainin Pipetman pipettes, sterile, DNase/RNase free filtered pipette tips, 1.5mL microcentrifuge tubes, sterile, vortex, IKA vortex mixer, microcentrifuge, and heating block.

[00181] Procedure: The procedure is given in the Reagent Kit Guide, RNA 6000 Nano Assay, Edition November 2003, by Agilent Technologies. The procedures are followed as given in the Guide, with the following modifications: Preparing the Gel, pg. 17- rather than separating the filtered gel into aliquots of 65uL each, keep the stock filtered gel in the original microcentrifuge tube and aliquot the 65uL as needed. Loading the RNA 6000 Nano Marker, pg. 22- add 1uL of RNase-free water (instead of RNA 6000 Nano Marker) to each sample well that will not contain sample. Not only will this conserve the amount of Marker used but also serves as a negative control to see that none of the reagents are contaminated, including the RNase-free water. Loading the Ladder and Samples, pg. 23- heat denature the samples and RNA 6000 Ladder for an additional 30 seconds (total of 2.5 minutes) at 71°C. Starting the Chip Run, pg. 26- choose the "Eukaryote Total RNA Nano" option from the assay menu.

Example 4: Affymetrix GeneChip Expression Analysis

[00182] Gene expression is analyzed using Affymetrix Canine 1 and Canine 2 GeneChip®. Arrays which are commercially available from Affymetrix, Inc., Santa Clara, CA 95051. Total RNA is reverse transcribed into cDNA. The cDNA is used to generate cRNA which is fragmented and used as probes for GeneChip hybridization. The gene chip is washed and the hybridization signal is measured with an Affymetrix laser scanner. The hybridization data is then validated and normalized for further analysis.

[00183] Materials: Affymetrix provides most of the reagents and kit. Other reagents listed in the Affymetrix Manual but not supplied in the kit may be obtained separately (refer to GeneChip Expression Analysis Technical Manual (701021 Rev.4) for details), RNase Zap® and deionized water.

[00184] Equipment: Eppendorf microcentrifuge, 1.5mL DNase and RNase free/sterile microcentrifuge tubes, 50mL DNase and RNase free/sterile disposable polypropylene tubes, P1000, P200, P20, P10 and P2 Rainin Pipetman pipettes, Filter pipette tips for P1000, P200, P20, P10 and P2 pipettes, DNase and RNase free/sterile, and Peltier Thermal Cycler PTC-200.

[00185] Procedure: follow all procedures exactly as described in GeneChip Expression Analysis Technical Manual (Affymetrix Copyright 1999-2003). Use 5 microgram of total RNA for the first strand cDNA synthesis. Use either Peltier Thermal Cycler PTC-200 or heat block for temperature control on reactions and probe denaturing. The quality control is performed using RNA NanoDrop chips with BioAnalyer 2100. Use 100 Format (Midi Array) for the canine genechip..

[00186] Example 5: Assay Procedures in Cats

[00187] Whole blood is obtained from the cats in the studies provided herein using PAXgene™ RNA tubes and total RNA is isolated from whole blood samples using PAXgene™ RNA isolation kit according to the methods detailed below.

[00188] PAXgene™ Blood RNA Isolation: PAXgene™ Blood RNA tubes and the PAXgene™ Blood RNA Kit (Qiagen) are used together to isolate and purify intracellular RNA from whole blood obtained from felines as provided below (see also PAXgene™ Blood RNA Kit Handbook, PreAnalytix, June 2005). Briefly, blood is collected using a Vacutainer® needle, directly into the PAXgene™ Blood RNA tube and then subjected to several rounds of centrifugation, wash and purification steps which ultimately result in high-quality RNA. The RNA then undergoes a quality control step and is then used in future quantitative real-time PCR and/or microarray analyses using a custom manufactured proprietary feline gene chip produced on the Affymetrix platform.

[00189] Assay Preparations: Incubate PAXgene™ tubes (containing blood) for at minimum of 2 hours at room temperature before beginning the assay. If the tubes are frozen, and are not allowed to incubate for 2 hours prior to freezing, they will need to sit at room temperature to thaw an additional 2 hours. Invert each PAXgene™ tube 8-10 times before the first centrifugation. If using Buffer BR4 (buffers are included with the PAXgene™ Blood RNA Kit) for the first time, add 4 volumes of 96-100% ethanol to the concentrated buffer to obtain a working solution. Preheat two heating blocks prior to beginning the assay—65°C and 55°C. Prepare the DNase I stock solution (the RNase-Free DNase Set is included with the PAXgene™ Blood RNA Kit). Dissolve the solid DNase I enzyme in 550μL of RNase-free water provided with the kit. Be sure not to lose any DNase I when removing the lid. Mix gently by inverting the tube. Do not vortex or centrifuge. Make a mixture of DNase I enzyme and Buffer RDD (kit component) (enough volume for the number of samples being processed per batch). Each sample needs 70μL of Buffer RDD and 10μL of DNase I (i.e. 20 samples would require a cocktail of 1.4mL Buffer RDD and 200μL DNase I). The cocktail should be stored at 2-8°C until needed. The reconstituted enzyme is good for up to 6 weeks at 2-8°C.

[00190] **Sample storage:** PAXgene™ tubes (which contain blood) can be stored at room temperature for up to 3 days before processing. According to the product insert provided with the PAXgene™ Blood RNA tubes, the cellular RNA profile is stable under these conditions for up to 3 days. This, however, may vary between species. PAXgene™ tubes can also be stored at 4°C for up to 5 days. If long term storage is required, PAXgene™ tubes can be stored at -20°C or -70°C for up to 6 months. Tubes should be frozen in a loose wire rack in an upright position. It is recommended to freeze first at -20°C and then transfer to -70°C if tubes will be stored at -70°C. Upon removing the tubes from the freezer they should be thawed at room temperature (temperature not to exceed 22°C). Each tube is to be inverted 10 times before proceeding with the assay.

[00191] **RNA Isolation from Whole Blood:** Centrifuge the PAXgene™ Blood RNA tubes at 4000 x g for 10 minutes. Remove the supernatant by decanting and discard. Blot excess supernatant remaining on rim of PAXgene™ tube. Add 4mL of RNase-free water to the pellet and cap with a new Hemogard closure. Resuspend the pellet by vortexing and then centrifuge at 4000 x g for 10 minutes. Remove the supernatant by decanting and discard. Blot excess supernatant remaining on rim of PAXgene™. Add 360μL of Buffer BR1 (kit component) to the pellet and gently pipette until pellet is completely resuspended. Transfer the sample to a sterile 1.5mL microcentifuge tube and add 300μL Buffer BR2 (kit component) and 40μL Proteinase K (do not mix Buffer BR2 and Proteinase K prior to adding to the sample). Mix each tube thoroughly by vortexing and place into a thermomixer preheated to 55°C. Incubate/shake the tubes for 10 minutes at 1400 rpm. Pipet the lysate into a QIAshredder spin column placed into a 2mL collection tube. Centrifuge at 14,000 rpm for 3 minutes. Transfer the supernatant of the flow-through fraction to a sterile 1.5mL microcentrifuge tube. Add 350μL of 96-100% ethanol and gently mix by pipetting. Add 700μL of the sample to the PAXgene™spin column placed in a 2mL collection tube and centrifuge at 14,000 rpm for 1 minute. Transfer the PAXgene™ spin column into a new 2mL collection tube and discard the flow-through and old collection tube. Add the remaining volume of the sample to the PAXgene™ spin column. Centrifuge at 14,000 rpm for 1 minute.

[00192] Discard the old collection tube and the flow-through from the centrifugation of the spin column described immediately above. Place the PAXgene™ spin column into a new 2mL collection tube. Add 350μL of Buffer BR3 (kit component) to the PAXgene™ spin column and centrifuge at 14,000 rpm for 1 minute. Discard the flow-through and collection tube. Place the column into a new 2mL collection tube and add 80μL of the DNase I/Buffer RDD cocktail (see "Assay Preparations") directly to the column membrane and incubate for 15 minutes at room temperature. Add another 350μL Buffer BR3 to the PAXgene™ spin column. Centrifuge at 14,000 rpm for 1 minute. Transfer the PAXgene™ spin column to a new 2mL collection tube and discard the old collection tube and flow-through.

[00193] Add 500μL of Buffer BR4 (kit component) to the PAXgene™ spin column. Centrifuge at 14,000 rpm for 1 minute. Place the PAXgene™ spin column into a new 2mL collection tube and discard the old collection tube and flow-through. Add another 500μL Buffer BR4 to the PAXgene™ spin column. Centrifuge at 14,000 rpm for 3 minutes to dry the spin column membrane. Discard the collection tube and flow-through and place the columns in another 2mL collection tube. Spin the samples again at 14,000 rpm for an additional minute to further dry the column membrane. Discard the flow-through and the collection tube. Transfer the PAXgene™ spin column to a 1.5mL elution tube. Add 40μL Buffer BR5 (kit component) directly to the PAXgene™ spin column membrane. Centrifuge at 14,000 rpm for 1 minute. Remove the PAXgene™ spin column and pipette the eluate in the 1.5mL tube onto the same PAXgene™ spin column. Return the PAXgene™ spin column to the same 1.5mL elution tube and centrifuge at 14,000 rpm for 1 minute. Incubate the final eluate at 65°C for 5 minutes and immediately chill on ice. Store final RNA sample at -80°C for future use.

Example 6: Gene Expression in Cats with Osteoarthritis Compared to Control Cats

[00194] Studies are conducted in accordance with Example 5 using non-arthritic cats and cats with osteoarthritis to determine the underlying gene expression differences between non-arthritic cats and cats with osteoarthritis. In a first study, a baseline comparison is performed between the two groups of cats to determine the underlying gene expression differences between non-arthritic cats and cats with osteoarthritis. Procedures as generally described in the Examples of this specification may be used to prepare tissue and bodily fluid samples.

[00195] With regard to the studies provided herein, cats with osteoarthritis are graded according to a previously published method, i.e., all non-arthritic cats are "grade 0" indicating that the joint appears to be normal, cats with osteoarthritis have grades that are either 1 (small enthesophytes or small osteophytes present) or 2 (more prominent enthesophytes and osteophytes). Cats with severe osteoarthritis (grade 3) are not included in this study.

[00196] A proprietary, custom made feline gene chip (Affymetrix) is used to evaluate base line gene expression in cats with and without osteoarthritis (10 normals, 10 arthritic animals). As provided above, gene chip analyses are performed using conventional methods and according to the manufacturer's instructions in order to obtain a baseline comparison between the two groups to determine the underlying gene expression differences between non-arthritic cats and cats with osteoarthritis.

[00197] The raw gene chip data is normalized using the Robust Multiarray Average (RMA) normalization algorithm (Irizarry, et al., Biostatistics 2003 Vol 4, Page 249-264) and is then subjected to statistical analysis using Support Vector Machine (SVM) algorithm (Partek Genomic Suite, Version 6) to determine the gene expression differences that can differentiate between arthritic and non-arthritic animals. Genes identifying OA biomarkers are selected based on p value cut off and fold change (FC).

[00198] Gene expression profiling was determined in arthritic and non-arthritic cats and the results are reported in Figures 3 and 15. The genes found to be upregulated by greater than 1-fold in arthritic cats were the following: IL-1beta, TNF, HMGB1, p38, TLR2 and TLR4. These genes and their gene products are associated with inflammatory processes and would be considered as markers of abnormal musculoskeletal disorders, particularly osteoarthritis. In addition, the following genes were found to be up-regulated by greater than 1-fold in arthritic cats: COL2A1, COL1A1, COL3A1, COL4A1 and Aggrecan. These genes and their gene products are associated with cartilage degradation and would serve as markers of abnormal musculoskeletal disorders, particularly osteoarthritis.

[00199] The results from a study conducted in accordance with Example 6 indicates that gene expression can be used to differentiate between normal cats and cats with osteoarthritis. Differentially expressed genes associated with inflammation in arthritic cats appear on Figures 3

and 15. Thus, the identified genes may serve as biomarkers in cats for the inventions described herein and include the following genes: IL-1 beta, TNF, HMGB1, p38, TLR2, TLR4, COL2A1, COL1A1, COL3A1, COL4A1 and Aggrecan.

[00200] Example 7: Average activity of arthritic cats following administration of feline food composition j/d.

[00201] Clinical data obtained from nutritional studies involving the arthritic and non-arthritic cats as described in Example 6 indicate that dietary intervention can affect and enhance the mobility of arthritic cats. Cats fed a diet of feline food composition j/d of the invention evidenced a statistically significant increase in activity over cats fed a control diet. The results of a clinical investigation are reported on Figure 16. Based on observational data, cats feed the food composition j/d of the present invention showed greater than a 30% increase in movement signifying an improvement in the underlying symptomatology of osteoarthritis was achieved through administration of the test diet of the invention. A skilled worker can infer from the data presented in Figure 16 that the cats had greater motility, less pain and inflammation as a result of the administration of the test diet food composition j/d.

[00202] Example 8: Nighttime activity in dogs following administration of composition j/d.

[00203] A clinical trial involving administration of canine food composition j/d of the present invention was conducted in dogs. Observations of nighttime activity of arthritic dogs fed food composition j/d were performed and recorded versus dogs fed a control food and in dogs receiving no medications. Measurements were made with ACTIWATCH® devices. These devices are actigraphy-based data loggers that record a digitally integrated measure of gross motor activity. Each device uses actigraphy principles to provide sleep schedule variability, sleep quantity and quality statistics and daytime activity patterns. The devices collect objective data relating to the animal's ambulatory environment. The results of this clinical trial demonstrated a significant reduction in nighttime activity of the arthritic dogs, thereby demonstrating that the dogs fed food composition j/d enjoyed greater relief and comfort from the underlying arthritic symptomatology including joint stiffness and pain. Data from this clinical trial is reported in Figure 17.

[00204] Example 9: Protein marker levels in dogs after receiving canine food composition j/d.

[00205] Baseline levels of two protein markers associated with cartilage degradation in dogs, C2C and C1,C2 were obtained in arthritic and non-arthritic dogs. Blood samples of the animals were drawn and tested by conventional means described in this specification. The results of the testing demonstrated that the gene products of these markers were elevated in arthritic dogs and could be used as markers to determine the effectiveness of dietary components upon gene expression. The baseline data is presented in Figures 5 and 6.

[00206] Clinical data obtained from nutritional studies involving arthritic and non-arthritic dogs. Test dogs as described in this Example were fed a diet of the present invention, which is identified as food composition j/d on Figure 4. Evaluations of the C2C and C1,C2 arthritic marker levels and the level of another protein marker known to be relevant to abnormal musculoskeletal joint disorders, namely Collagen CTX-II, were made. Data depicted on Figures 10, 11 and 12 present protein marker levels as determined in the blood of test and control animals. Dogs fed a diet of canine food composition j/d as set forth on Figure 4 evidenced a statistically significant decrease in plasma C2C, C1,C2 and CTX-II levels as depicted on Figures 10, 11 and 12. A skilled worker will recognize that this biomarker data supports the clinical observation that dogs fed the dietary compositions of the invention, in particular, food composition j/d as demonstrated in this Example, exhibit an improvement in clinical symptomatology of the underlying disease process, in this case osteoarthritis, which correlates with the down-regulation of certain genes and the reduced expression of certain gene products which have been associated with cartilage degradation and local joint inflammatory conditions, including osteoarthritis.

[00207] Example 10: Gene Chip Analyses of Up- and Down-Regulated Canine Genes in Arthritic and Non-Arthritic Canines

[00208] A commercially-available canine gene chip (Affymetrix GeneChip2) was used to evaluate baseline gene expression in two groups of dogs with and without arthritis, as determined in accordance with standard clinical diagnostic criteria known in the art. Gene chip analyses were performed using conventional methods and according to the manufacturer's instructions.

Using the general expression profiling procedures of Example 1 and the analytical techniques outlined in other Examples set forth in this specification, gene expression profiling was performed to obtain a baseline comparison between the two groups to determine the underlying gene expression differences between non-arthritic dogs and dogs.

[00209] Following standard animal nutrition testing procedures familiar to one of ordinary skill in the art, arthritic and normal dogs were fed test diets comprising the food composition designated j/d and then changes in gene expression in the animals were analyzed using qRT-PCR.

[00210] The raw gene chip data is normalized using the Robust Multiarray Average (RMA) normalization algorithm (Irizarry, et al., Biostatistics 2003 Vol 4, Page 249-264) and is then subjected to statistical analysis using Support Vector Machine (SVM) algorithm (Partek Genomic Suite, Version 6) to determine the gene expression differences that can differentiate between arthritic and non-arthritic animals. Genes identifying arthritis biomarkers are selected based on p value cut off and fold change (FC).

[00211] The raw gene chip data is normalized using the Robust Multiarray Average (RMA) normalization algorithm (Irizarry, et al., Biostatistics 2003 Vol 4, Page 249-264) and is then subjected to statistical analysis using Support Vector Machine (SVM) algorithm (Partek Genomic Suite, Version 6) to determine the gene expression differences that can differentiate between arthritic and non-arthritic animals. Genes identifying OA biomarkers are selected based on p value cut off and fold change (FC).

[00212] The results from these studies indicate that gene expression can be used to differentiate between normal dogs and dogs with arthritis. Differentially expressed genes associated with inflammation in arthritic dogs appear on Figures 1, 2, 7 and 8. Without limiting the generality of the disclosures set forth in this application, the genes presented in Figures 1, 2, 7 and 8 may serve as biomarkers for the inventions described herein and include Annexin A1, Cathepsin D, Cathepsin F, Cathepsin S, RELA, HMGB1,IL-15, IL-17 receptor, TLR4, COL2A1, COL1A1, COL4A1, MMP-13, TIMP-2, MMP-2, FLAP, PLA2, MAPK1, MAPK2.

[00213] **Example 11: Gene Chip Analyses of Up- and Down-Regulated Canine Genes in Arthritic and Non-Arthritic Canines Fed a Diet of Food Composition j/d**

[00214] A commercially-available canine gene chip (Affymetrix GeneChip2) was used to evaluate gene expression in two groups of dogs with and without osteoarthritis. A total of 30 arthritic dogs and 31 non-arthritic dogs were studied. Gene chip analyses were performed using conventional methods and according to the manufacturer's instructions. Using the general expression profiling procedures of Example 1 and the analytical techniques outlined in other Examples set forth in this specification, gene expression profiling was performed. The first group of 30 test animals was determined to be arthritic in accordance with clinical diagnostic procedures that are well known in the art. The second group of canines was considered to be non-arthritic in accordance with the same clinical diagnostic criteria. Following standard animal nutrition testing procedures familiar to one of ordinary skill in the art, arthritic and normal dogs were fed test diets comprising the food composition designated j/d and then changes in gene expression in the animals were analyzed using qRT-PCR.

[00215] Following standard animal nutrition testing procedures familiar to one of skill in the art, arthritic and normal dogs were fed the test diet designated j/d and then changes in gene expression in the animals were analyzed using qRT-PCR.

[00216] With regard to q RT-PCR, Taqman probe technology is used and all analyses are carried out using an Applied Biosystems 7500 real-time PCR machine. The data is analyzed using the sequence detection software package version 1.2.2. provided by the manufacturer.

[00217] Using tissue samples prepared as described in the Examples, a commercially-available canine gene chip (Affymetrix GeneChip2) was used to evaluate gene expression in dogs with and without arthritis. The raw gene chip data is normalized using the Robust Multiarray Average (RMA) normalization algorithm (Irizarry, et al., Biostatistics 2003 Vol 4, Page 249-264) and is then subjected to statistical analysis using Support Vector Machine (SVM) algorithm (Partek Genomic Suite, Version 6) to determine the gene expression differences that can differentiate between arthritic and non-arthritic animals. Genes identifying arthritis and inflammation biomarkers are selected based on p value cut off and fold change (FC).

[00218] The data from this Example is set forth in Table 3. The data comprises 2383 records when a fold change cut-off of 1.1 is employed, a p-value cut-off of 0.05 and a Q-value cut-off of 0.3. Using these analytical criteria, a fold change of greater than 1 implies that the probes are UP regulated in samples taken from the arthritic dog group. The data presented in Table 3 identifies in the first column the unique Affymetrix probe identification number, and respectively thereafter the p-values, q-values, fold change, 1/fold change values, Top BLAST annotation, match percentage, human accession number, top hit accession number, gene symbol and gene description. A skilled worker will deduce from this data the following information using only ordinary experimental analysis: fold change cut-off criteria, the genes of interest that have been up or down regulated and the identification of such genes by BLAST annotation, related human accession numbers and the sequence for each such identified gene as well as the corresponding gene products and sequences of such gene products based on the information available from the manufacturer as well as from gene sequence databases that are readily available to the skilled artisan. In addition, sequences for the unique probes utilized in the Affymetrix arrays are publicly available by reference to published sources of the manufacturer. Similarly, published sequence information and identification of the respective probes utilized on versions 1 and 2 of the Affymetrix chips are readily and publicly available from the manufacturer as well as comparison of the probe sets to each other. From this data a skilled worked can identify and utilize such gene expression data, the identified genes that have been dysregulated and their corresponding gene products in the practice of manufacturing and using compositions and article of manufacture of the present invention as well as in practicing methods of manufacturing and using inventions taught in this specification. Without intending to limit the extent of the inventions disclosed and claimed in this application, certain genes and gene products of interest may be identified as highly pertinent to arthritic conditions in dogs and cats. These and other genes and gene products taught in the data set forth in Table 3 may be inferred as having a beneficial effect upon the underlying abnormal musculoskeletal joint disorder, in particular arthritic conditions, experienced by dogs and cats when the animals are fed the compositions of the invention, in particular the food compositions designated j/d, which modulates the genes of interest set forth in Table 3.

[00219]

Table 1: Ingredients Tested in Canine Cell Lines

Substance	**Concentration 1**	**Concentration 2**	**Solvent**
DHA	0.005 mg/ml (5 micro g/ml)	0.025 mg/ml (25 micro g/ml)	ETOH
EPA	0.005 mg/ml (5 micro g/ml)	0.025 mg/ml (25 micro g/ml)	ETOH
EPA/DHA Combo 1.5:1 ratio (like in fish oil)	0.015 mg/ml EPA & 0.010 mg/ml DHA (total is 0.025 mg/ml)	0.030 mg/ml EPA & 0.02 mg/ml DHA (total is 0.050 mg/ml)	ETOH
Alpha linolenic acid	0.05 mg/ml (50 micro g/ml)	0.1 mg/ml (100 micro g/ml)	ETOH
Linoleic acid	0.1 mg/ml (100 micro g/ml)	0.5 mg/ml (500 micro g/ml)	ETOH
Arachidonic acid	0.025 mg/ml (25 micro g/ml)	0.05 mg/ml (50 micro g/ml)	ETOH
Stearic acid	0.01mg/ml (10 micro g/ml)	0.05 mg/ml (50 micro g/ml)	ETOH
Conjugated Linoleic acid	0.02 mg/ml (20 micro g/ml)	0.1 mg/ml (100 micro g/ml)	MEOH

Table 2: Expression Profiling Results From Canine Cell Lines in the Presence of Listed Ingredients

Column 1	**Column 2**	**Column 3**	**Column 4**	**Column 5**
DHA	1582387_at	DOWN	Canis familiaris type I iodothyronine deiodinase (dio 1) mRNA, complete cds	AC027016
DHA	1582824_at	UP	PREDICTED: Canis familiaris carnitine palmitoyl transferase I isoform (CPT1), mRNA	BC000185

Column 1	Column 2	Column 3	Column 4	Column 5
DHA	1584133_at	UP	PREDICTED: Canis familiaris similar to dynein, cytoplasmic, heavy polypeptide 2 (LOC479461), mRNA	BC038344
DHA	1584742_at	UP	Human DNA sequence from clone RP11-151J10 on chromosome 9 Contains the 5' end of a novel gene (FLJ20060) (contains FLJ12902, KIAA1574), the ADFP gene for adipose differentiation-related protein (ADRP)	AL591206
DHA	1584951_at	UP	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP) (LOC474720), mRNA	CR605429
DHA	1585355_at	UP	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP) (LOC474720), mRNA	CR597463
DHA	1586474_at	DOWN	Mus musculus RIKEN cDNA 1500031L02 gene (1500031L02Rik), mRNA	AC078834
DHA	1587029_at	UP	Homo sapiens 12 BAC RP11-545P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence	AC089999
DHA	1587141_at	UP	PREDICTED: Canis familiaris similar to SEC14-like protein 2 (Alpha-tocopherol associated protein) (TAP) (hTAP) (Supernatant protein factor) (SPF) (Squalene transfer protein) (LOC477539), mRNA	CR456571
DHA	1587268_at	UP	Canis familiaris urate oxidase (UOX) mRNA, complete cds	NA
DHA	1587328_at	UP	Homo sapiens mRNA; cDNA DKFZp686O1232 (from clone DKFZp686O1232)	AP001324

Column 1	Column 2	Column 3	Column 4	Column 5
DHA	1587418_at	DOWN	PREDICTED: Canis familiaris similar to RPGR-interacting protein 1 isoform b (LOC475400), mRNA	AJ417060
DHA	1587734_at	UP	PREDICTED: Canis familiaris similar to Na/Pi cotransporter 4 (LOC478741), mRNA	BC017952
DHA	1588058_at	DOWN	Homo sapiens toll-interleukin 1 receptor (TIR) domain containing adaptor protein, mRNA (cDNA clone MGC:40573 IMAGE:5216171), complete cds	BC032474
DHA	1588088_at	UP	Homo sapiens hypoxia-inducible protein 2, mRNA (cDNA clone MGC:17005 IMAGE:4182067), complete cds	BC008573
DHA	1589548_at	DOWN	Mus musculus chromosome 14 clone RP24-304G19, complete sequence	AC115282
DHA	1590835_at	DOWN	Homo sapiens interleukin 8 receptor, beta pseudogene, mRNA (cDNA clone IMAGE:5450999), with apparent retained intron	AC055863
DHA	1591083_at	UP	Homo sapiens clone DNA22780 NL2 (UNQ171) mRNA, complete cds	AC010323
DHA	1591971_at	UP	PREDICTED: Canis familiaris similar to complement C1s (LOC486714), mRNA	AK055183
DHA	1592507_at	DOWN	Homo sapiens prodynorphin (PDYN), mRNA	BC026334
DHA	1593226_at	UP	Human DNA sequence from clone RP11-423C15 on chromosome 9 Contains the 5' end of the MAPKAP1 gene for mitogen-activated protein kinase associated protein 1, a novel gene, the 5' end of the PBX3 gene f	AL358074

Column 1	Column 2	Column 3	Column 4	Column 5
DHA	1593388_at	DOWN	PREDICTED: Canis familiaris similar to SDA1 domain containing 1 (LOC478431), mRNA	BC063797
DHA	1593590_at	DOWN	Homo sapiens lymphocyte adaptor protein, mRNA (cDNA clone IMAGE:4861744), complete cds	AB208911
DHA	1593831_at	DOWN	PREDICTED: Canis familiaris similar to Clathrin heavy chain 1 (CLH-17) (LOC480578), mRNA	BC015854
DHA	1594976_at	UP	PREDICTED: Bos taurus similar to glutamate receptor, metabotropic 1 (LOC540485), mRNA	AL035698
DHA	1596448_at	UP	PREDICTED: Canis familiaris similar to sperm associated antigen 16 (LOC478899), mRNA	AK095036
DHA	1596711_at	DOWN	Homo sapiens cDNA: FLJ21199 fis, clone COL00235	AK024852
DHA	1597677_at	UP	Homo sapiens, clone IMAGE:5271096, mRNA	AC012516
DHA	1597789_at	UP	Homo sapiens 12 BAC RP11-337L12 (Roswell Park Cancer Institute Human BAC Library) complete sequence	AC130404
DHA	1597832_at	DOWN	Homo sapiens hypothetical protein LOC92558 (LOC92558), mRNA	NM_207311
DHA	1598607_at	DOWN	PREDICTED: Canis familiaris similar to Thioredoxin domain containing protein 6 (Thioredoxin-like protein 2) (Txl-2) (LOC485685), mRNA	AC099518
DHA	1598932_at	DOWN	PREDICTED: Canis familiaris similar to SAP90/PSD-95 associated protein 2 (LOC488556), mRNA	AL354836
DHA	1599339_at	DOWN	Canis familiaris clone RP81-117B1,	NA

Column 1	Column 2	Column 3	Column 4	Column 5
			complete sequence	
DHA	1599453_at	DOWN	PREDICTED: Canis familiaris LOC475099 (LOC475099), mRNA	NA
DHA	1600090_at	UP	PREDICTED: Canis familiaris similar to SEC22 vesicle trafficking protein-like 2 (LOC478590), mRNA	AY405366
DHA	1601347_at	DOWN	Debaryomyces hansenii CBS767, DEHA0D14146g predicted mRNA	NA
DHA	1602156_at	UP	Mus musculus mRNA for mKIAA4184 protein	AL590139
DHA	1602790_at	UP	Homo sapiens aryl hydrocarbon receptor nuclear translocator (ARNT) gene, complete cds	AC115282
DHA	1602966_at	DOWN	Zebrafish DNA sequence from clone DKEYP-75A7 in linkage group 21, complete sequence	AL590621
DHA	1603771_at	DOWN	Canis familiaris clone RP81-117B1, complete sequence	NA
DHA	1604372_at	UP	PREDICTED: Canis familiaris LOC475665 (LOC475665), mRNA	AY411810
DHA	1605486_at	UP	Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence	AK096428
EPA	1583329_at	DOWN	Homo sapiens, Similar to secreted frizzled-related protein 4, clone IMAGE:4828181, mRNA	AC018634
EPA	1583403_at	UP	Sus scrofa carnitine palmitoyltransferase I mRNA, nuclear gene encoding mitochondrial protein, complete cds	AK172798
EPA	1584742_at	UP	Human DNA sequence from clone RP11-151J10 on chromosome 9 Contains the 5' end of a novel gene (FLJ20060) (contains FLJ12902,	AL591206

Column 1	Column 2	Column 3	Column 4	Column 5
			KIAA1574), the ADFP gene for adipose differentiation-related protein (ADRP)	
EPA	1584951_at	UP	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP) (LOC474720), mRNA	CR605429
EPA	1585292_at	UP	Homo sapiens methyl CpG binding protein 2 (Rett syndrome) (MECP2), mRNA	AF030876
EPA	1585355_at	UP	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP) (LOC474720), mRNA	CR597463
EPA	1586420_at	DOWN	Homo sapiens RAB37, member RAS oncogene family (RAB37), mRNA	BC016615
EPA	1587196_at	UP	PREDICTED: Canis familiaris LOC475684 (LOC475684), mRNA	NM_147223
EPA	1587428_at	DOWN	Human DNA sequence from clone RP11-436D23 on chromosome 6 Contains part of a novel gene, complete sequence	AL589740
EPA	1588088_at	UP	Homo sapiens hypoxia-inducible protein 2, mRNA (cDNA clone MGC:17005 IMAGE:4182067), complete cds	BC008573
EPA	1589797_at	DOWN	Homo sapiens chromosome 15 clone RP11-344A16 map 15q21.3, complete sequence	AC090651
EPA	1589829_s_at	DOWN	PREDICTED: Bos taurus similar to ATP-dependent DNA helicase Q4 (RecQ protein-like 4) (RecQ4) (LOC515289), partial mRNA	AC004486
EPA	1590407_s_at	UP	Homo sapiens integrin-linked kinase 1 (ILK) gene, complete cds	AJ404847

Column 1	Column 2	Column 3	Column 4	Column 5
EPA	1591083_at	UP	Homo sapiens clone DNA22780 NL2 (UNQ171) mRNA, complete cds	AC010323
EPA	1592920_at	DOWN	Homo sapiens 12 BAC RP11-407P2 (Roswell Park Cancer Institute Human BAC Library) complete sequence	AC090013
EPA	1593146_s_at	UP	Homo sapiens Kruppel-like factor 11 (KLF11), mRNA	BC063286
EPA	1593677_at	DOWN	PREDICTED: Canis familiaris similar to hypothetical protein (LOC475308), mRNA	AB070003
EPA	1594091_at	DOWN	PREDICTED: Canis familiaris similar to FLJ23129 protein isoform 1 (LOC479538), mRNA	NM_024763
EPA	1594227_at	UP	Homo sapiens RNA binding motif protein, X-linked (RBMX), mRNA	AK096015
EPA	1594231_at	UP	Sus scrofa peptidyl-prolyl cis-trans isomerase A (PPIA), mRNA	NA
EPA	1594415_at	DOWN	PREDICTED: Bos taurus similar to GTPase, IMAP family member 4 (Immunity-associated protein 4) (Immunity-associated nucleotide 1 protein) (hIAN1) (MSTP062) (LOC510751), mRNA	AP001675
EPA	1594824_at	DOWN	Homo sapiens chromosome 16 clone CTA-233A7, complete sequence	AC130449
EPA	1594939_at	UP	Homo sapiens chromosome 8, clone RP11-813L8, complete sequence	AC090133
EPA	1595021_at	DOWN	Bos taurus mRNA for sodium chloride cotransporter, partial	NM_000339
EPA	1595265_at	UP	Yarrowia lipolytica CLIB99, YALI0C20339g predicted mRNA	NG_001333
EPA	1595301_at	UP	H.sapiens mRNA for skeletal muscle	AC113382

Column 1	Column 2	Column 3	Column 4	Column 5
			abundant protein	
EPA	1596553_s_at	DOWN	Homo sapiens chromosome 16 open reading frame 55 (C16orf55), mRNA	AK056168
EPA	1597390_at	DOWN	PREDICTED: Canis familiaris similar to Ataxin-10 (Spinocerebellar ataxia type 10 protein) (Brain protein E46 homolog) (LOC474467), mRNA	AY400068
EPA	1597801_at	DOWN	Homo sapiens, clone IMAGE:4822875, mRNA	AL442128
EPA	1597802_at	DOWN	Mus musculus BAC clone RP23-451I11 from 12, complete sequence	AL078583
EPA	1598585_at	DOWN	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds	AC011306
EPA	1599557_at	DOWN	PREDICTED: Canis familiaris similar to hypothetical protein MGC12103 (LOC481489), mRNA	AY414168
EPA	1599565_at	DOWN	Human DNA sequence from clone RP4-615P17 on chromosome 1p13-14.3, complete sequence	AL139175
EPA	1599601_s_at	DOWN	PREDICTED: Canis familiaris similar to male-enhanced antigen - bovine (LOC474906), mRNA	AY403773
EPA	1600959_at	UP	PREDICTED: Canis familiaris similar to IgA heavy chain constant region (LOC480452), mRNA	NA
EPA	1601005_at	DOWN	PREDICTED: Canis familiaris LOC479025 (LOC479025), mRNA	XM_372592
EPA	1602471_at	DOWN	Homo sapiens cDNA clone IMAGE:4797645, partial cds	AC073120
EPA	1603225_at	UP	Haemonchus contortus microsatellite Hcms51 sequence	AC008429

Column 1	Column 2	Column 3	Column 4	Column 5
EPA	1603875_at	DOWN	Homo sapiens cDNA FLJ33460 fis, clone BRAMY2000653, highly similar to Homo sapiens tousled-like kinase 1 (TLK1) mRNA	AC010092
EPA	1604439_at	DOWN	Homo sapiens mRNA; cDNA DKFZp761M0111 (from clone DKFZp761M0111)	AL137346
EPA	1604600_at	DOWN	Homo sapiens mRNA; cDNA DKFZp686K122 (from clone DKFZp686K122)	AC010733
EPA	1605028_at	DOWN	Canis familiaris secreted B7-1 protein (CD80) gene, alternatively spliced exon 4 and complete cds	NA
EPA	1605486_at	UP	Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence	AK096428
EPA	1605654_at	UP	Mus musculus mbt domain containing 1, mRNA (cDNA clone MGC:29000 IMAGE:2646754), complete cds	AK028503
EPA	1605669_s_at	UP	Homo sapiens cDNA FLJ38323 fis, clone FCBBF3024623, weakly similar to Homo sapiens C2H2 (Kruppel-type) zinc finger protein mRNA	AK095642
DHA/EPA	1582781_at	UP	Canis familiaris L-type Ca channel alpha 1 subunit mRNA, partial cds	AF465484
DHA/EPA	1583031_at	UP	Canis familiaris fibroblast growth factor-8 (FGF-8) mRNA, partial cds	NM_006119
DHA/EPA	1583254_x_at	DOWN	Bos taurus clone IMAGE:7961516 thymosin beta-4-like mRNA, complete cds	X02493
DHA/EPA	1583403_at	UP	Sus scrofa carnitine palmitoyltransferase I mRNA, nuclear gene encoding mitochondrial	AK172798

Column 1	Column 2	Column 3	Column 4	Column 5
			protein, complete cds	
DHA/EPA	1584742_at	UP	Human DNA sequence from clone RP11-151J10 on chromosome 9 Contains the 5' end of a novel gene (FLJ20060) (contains FLJ12902, KIAA1574), the ADFP gene for adipose differentiation-related protein (ADRP)	AL591206
DHA/EPA	1584951_at	UP	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP) (LOC474720), mRNA	CR605429
DHA/EPA	1585033_at	DOWN	PREDICTED: Canis familiaris similar to KIAA2025 protein (LOC480065), mRNA	AL121983
DHA/EPA	1585339_at	DOWN	Homo sapiens mRNA for UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 2 variant protein	AL672237
DHA/EPA	1585355_at	UP	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP) (LOC474720), mRNA	CR597463
DHA/EPA	1586172_at	DOWN	Homo sapiens chromosome 11, clone RP11-348A11, complete sequence	AC131263
DHA/EPA	1586287_at	DOWN	Bos taurus mRNA for transcription factor COUP-TFI (COUP-TFI gene)	AC106818
DHA/EPA	1586614_at	DOWN	PREDICTED: Canis familiaris similar to F-box protein SEL10 (LOC475465), mRNA	BC037320
DHA/EPA	1586695_at	DOWN	Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, mRNA	BX161515
DHA/EPA	1587254_at	DOWN	PREDICTED: Canis familiaris janus kinase 1 (JAK1), mRNA	AC008785

Column 1	Column 2	Column 3	Column 4	Column 5
DHA/EPA	1587413_at	UP	Hirudo medicinalis intermediate filament gliarin mRNA, complete cds	AC005996
DHA/EPA	1587813_s_at	UP	PREDICTED: Pan troglodytes similar to dJ109F14.3 (novel putative ring finger protein) (LOC472236), mRNA	AL160175
DHA/EPA	1589293_at	DOWN	Homo sapiens mRNA for KIAA1804 protein, partial cds	AB058707
DHA/EPA	1589678_s_at	UP	Homo sapiens clone alpha1 mRNA sequence	BK001411
DHA/EPA	1589929_at	DOWN	Homo sapiens solute carrier family 34 (sodium phosphate), member 1, mRNA (cDNA clone IMAGE:5182821), with apparent retained intron	AC145098
DHA/EPA	1590942_at	DOWN	Human netrin-2 like protein (NTN2L) gene, complete cds	AC106820
DHA/EPA	1591029_at	UP	PREDICTED: Homo sapiens KIAA0146 protein (KIAA0146), mRNA	AC023991
DHA/EPA	1591083_at	UP	Homo sapiens clone DNA22780 NL2 (UNQ171) mRNA, complete cds	AC010323
DHA/EPA	1591601_at	DOWN	Human DNA sequence from clone RP11-787B4 on chromosome 9 Contains the 5' end of the PAPPA gene for pregnancy-associated plasma protein A, a novel gene and a CpG island, complete sequence	AL691426
DHA/EPA	1591782_at	UP	PREDICTED: Bos taurus similar to hypothetical protein (LOC514986), partial mRNA	AC069335
DHA/EPA	1592123_at	DOWN	PREDICTED: Canis familiaris similar to vimentin (LOC477991), mRNA	AY891766

Column 1	Column 2	Column 3	Column 4	Column 5
DHA/EPA	1592160_at	DOWN	PREDICTED: Canis familiaris similar to Fibrinogen alpha/alpha-E chain precursor (LOC475473), mRNA	BC070246
DHA/EPA	1592915_s_at	UP	PREDICTED: Canis familiaris similar to hypothetical protein MGC33867 (LOC478228), mRNA	BC004501
DHA/EPA	1593146_s_at	UP	Homo sapiens Kruppel-like factor 11 (KLF11), mRNA	BC063286
DHA/EPA	1593855_at	DOWN	Felis catus clone RP86-117J4, complete sequence	AL353710
DHA/EPA	1593993_at	DOWN	Pan troglodytes BAC clone RP43-7512 from 7, complete sequence	AC004949
DHA/EPA	1594205_at	UP	PREDICTED: Pan troglodytes similar to putative transcription factor ZNF131 (LOC461893), mRNA	DQ048939
DHA/EPA	1594291_s_at	DOWN	PREDICTED: Canis familiaris similar to methylcrotonoyl-Coenzyme A carboxylase 2 (beta) (LOC478091), mRNA	BC014897
DHA/EPA	1594379_x_at	UP	Felis catus growth arrest and DNA damage-inducible protein 45 (GADD45), mRNA	AL136120
DHA/EPA	1594413_at	UP	Homo sapiens cytochrome P450, family 26, subfamily B, polypeptide 1 (CYP26B1), mRNA	AC007002
DHA/EPA	1594564_at	UP	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes	AF111168
DHA/EPA	1594848_at	UP	PREDICTED: Pan troglodytes hypothetical protein XP_513164 (LOC456583), mRNA	AC073263
DHA/EPA	1594939_at	UP	Homo sapiens chromosome 8, clone	AC090133

Column 1	Column 2	Column 3	Column 4	Column 5
			RP11-813L8, complete sequence	
DHA/EPA	1595083_at	DOWN	PREDICTED: Canis familiaris similar to hypothetical protein MGC18257 (LOC474943), mRNA	AK055530
DHA/EPA	1595280_at	DOWN	Homo sapiens mRNA; cDNA DKFZp686N1929 (from clone DKFZp686N1929)	AL355298
DHA/EPA	1595481_at	DOWN	PREDICTED: Canis familiaris LOC478639 (LOC478639), mRNA	NM_002492
DHA/EPA	1595587_at	DOWN	PREDICTED: Canis familiaris similar to copine VIII (LOC477646), mRNA	BC048260
DHA/EPA	1595673_at	DOWN	PREDICTED: Canis familiaris similar to SDA1 domain containing 1 (LOC478431), mRNA	BC048351
DHA/EPA	1596041_at	DOWN	Homo sapiens mRNA; cDNA DKFZp686I15205 (from clone DKFZp686I15205)	AL354707
DHA/EPA	1596238_at	UP	PREDICTED: Canis familiaris similar to palmitoyl-protein thioesterase 2 isoform a precursor (LOC474856), mRNA	AL110128
DHA/EPA	1596301_at	DOWN	Mouse DNA sequence from clone RP23-440D4 on chromosome 4, complete sequence	AC000007
DHA/EPA	1597387_at	UP	PREDICTED: Canis familiaris similar to Alpha-N-acetylglucosaminidase precursor (N-acetyl-alpha-glucosaminidase) (NAG) (LOC490965), mRNA	BC032398
DHA/EPA	1597847_at	UP	PREDICTED: Gallus gallus similar to ubiquitin specific protease 37 (LOC424217), mRNA	AC098935
DHA/EPA	1599572_at	DOWN	PREDICTED: Canis familiaris similar to ORF2 (LOC475183),	NA

Column 1	Column 2	Column 3	Column 4	Column 5
			mRNA	
DHA/EPA	1599950_at	DOWN	PREDICTED: Canis familiaris similar to male-enhanced antigen - bovine (LOC474906), mRNA	AL136304
DHA/EPA	1600310_at	DOWN	PREDICTED: Canis familiaris similar to piggyBac transposable element derived 1 (LOC488322), mRNA	AK223446
DHA/EPA	1600683_at	DOWN	Canis familiaris clone RP81-391L22, complete sequence	NA
DHA/EPA	1601351_at	UP	Canis Familiaris, clone XX-25A1, complete sequence	NA
DHA/EPA	1601383_at	UP	PREDICTED: Canis familiaris similar to Putative GTP-binding protein RAY-like (Rab-like protein 4) (LOC474517), mRNA	BT007509
DHA/EPA	1601782_at	DOWN	Homo sapiens lactamase, beta 2, mRNA (cDNA clone IMAGE:3452575)	AC022731
DHA/EPA	1602033_at	DOWN	PREDICTED: Bos taurus similar to G protein-coupled receptor 23 (LOC539738), mRNA	AL445467
DHA/EPA	1602162_at	DOWN	Homo sapiens BAC clone RP11-489P15 from 2, complete sequence	AC093850
DHA/EPA	1603521_at	DOWN	Homo sapiens cDNA FLJ33134 fis, clone UMVEN2000453, weakly similar to Mus musculus fetal globin inducing factor mRNA	BC017798
DHA/EPA	1603534_at	DOWN	PREDICTED: Canis familiaris similar to protein tyrosine phosphatase, receptor type, Q isoform 1 precursor (LOC482581), mRNA	AL592064
DHA/EPA	1603559_s_at	DOWN	PREDICTED: Canis familiaris similar to neural activity-related ring	AY413985

Column 1	Column 2	Column 3	Column 4	Column 5
			finger protein (LOC475470), mRNA	
DHA/EPA	1603658_s_at	UP	Homo sapiens mRNA; cDNA DKFZp451E012 (from clone DKFZp451E012); complete cds	AL834247
DHA/EPA	1603674_at	DOWN	Homo sapiens cDNA FLJ13648 fis, clone PLACE1011340, weakly similar to Homo sapiens IDN3-B mRNA	AK023710
DHA/EPA	1605317_at	DOWN	Homo sapiens chromosome 16 clone CTD-2337L2, complete sequence	AC093509
DHA/EPA	1605486_at	UP	Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence	AK096428
DHA/EPA	1605832_at	DOWN	Homo sapiens mRNA; cDNA DKFZp451J152 (from clone DKFZp451J152); complete cds	AK097112
DHA/EPA	1605935_at	DOWN	Mus musculus mRNA for NFI-B protein, complete cds	AK024964
ALA	1582455_at	DOWN	Canis familiaris type I collagen pre-pro-alpha1(I) chain (COL1A1) mRNA, complete cds	AB209597
ALA	1584508_at	DOWN	PREDICTED: Pan troglodytes LOC464838 (LOC464838), mRNA	AK122763
ALA	1584742_at	UP	Human DNA sequence from clone RP11-151J10 on chromosome 9 Contains the 5' end of a novel gene (FLJ20060) (contains FLJ12902, KIAA1574), the ADFP gene for adipose differentiation-related protein (ADRP)	AL591206
ALA	1584951_at	UP	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP) (LOC474720), mRNA	CR605429

Column 1	Column 2	Column 3	Column 4	Column 5
ALA	1585266_at	DOWN	PREDICTED: Canis familiaris similar to FLJ20859 protein (LOC475396), mRNA	BC005053
ALA	1585355_at	UP	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP) (LOC474720), mRNA	CR597463
ALA	1585515_at	UP	PREDICTED: Canis familiaris LOC476210 (LOC476210), mRNA	AF303134
ALA	1585553_at	DOWN	PREDICTED: Canis familiaris similar to tenascin-N (LOC490335), mRNA	BC032361
ALA	1586185_at	UP	PREDICTED: Canis familiaris similar to hypothetical protein LOC90637 (LOC480809), mRNA	AC093611
ALA	1587312_at	UP	PREDICTED: Canis familiaris LOC491404 (LOC491404), mRNA	AC124862
ALA	1587413_at	UP	Hirudo medicinalis intermediate filament gliarin mRNA, complete cds	AC005996
ALA	1587838_at	DOWN	Homo sapiens fibroblast growth factor 13 (FGF13), transcript variant 1B, mRNA	AL031386
ALA	1588093_at	DOWN	Homo sapiens hypothetical protein FLJ20507, mRNA (cDNA clone MGC:47628 IMAGE:5725347), complete cds	BC039892
ALA	1588502_at	DOWN	Homo sapiens mRNA for cAMP responsive element binding protein 5 isoform beta variant protein	AB209262
ALA	1589017_at	UP	Homo sapiens mRNA for microtubule-associated protein 2 isoform 2 variant protein	AB209330
ALA	1590554_at	UP	PREDICTED: Canis familiaris similar to ATP/GTP binding protein	AC025842

Column 1	Column 2	Column 3	Column 4	Column 5
			1 (LOC479034), mRNA	
ALA	1591083_at	UP	Homo sapiens clone DNA22780 NL2 (UNQ171) mRNA, complete cds	AC010323
ALA	1591749_at	UP	Canis familiaris natural resistance associated macrophage protein (NRAMP1), mRNA	AY400098
ALA	1592201_at	UP	HIV-2 strain A|G1612 from Ghana gag protein (gag) gene, partial cds	AL929410
ALA	1593146_s_at	UP	Homo sapiens Kruppel-like factor 11 (KLF11), mRNA	BC063286
ALA	1593222_at	UP	Human DNA sequence from clone RP11-439D8 on chromosome 10 Contains a novel gene, the HPS1 gene for Hermansky-Pudlak syndrome 1, the 3' end of the HPSE2 gene for heparanase 2 and a CpG island, complete	AL139243
ALA	1593224_at	UP	PREDICTED: Canis familiaris similar to hemojuvelin isoform a (LOC475830), mRNA	AL138842
ALA	1593710_at	UP	PREDICTED: Bos taurus similar to glutathione reductase (LOC506406), partial mRNA	AY338490
ALA	1593836_at	UP	Canis familiaris clone RP81-142A6, complete sequence	NA
ALA	1595172_s_at	UP	PREDICTED: Canis familiaris similar to glyceraldehyde-3-phosphate dehydrogenase (LOC479078), mRNA	NA
ALA	1595533_at	UP	Human DNA sequence from clone RP11-548K23 on chromosome 10 Contains the ANKRD2 gene for ankyrin repeat domain 2 (stretch responsive muscle), six novel genes, the gene for phosphatidylinositol 4-	AL355315

Column 1	Column 2	Column 3	Column 4	Column 5
			kinase	
ALA	1595722_at	UP	Homo sapiens chromosome 17, clone CTD-3022L24, complete sequence	AC015920
ALA	1595801_at	UP	Homo sapiens cDNA FLJ34120 fis, clone FCBBF3009541	AK091439
ALA	1596406_at	UP	Pongo pygmaeus mRNA; cDNA DKFZp459C032 (from clone DKFZp459C032)	AC023795
ALA	1599614_at	UP	PREDICTED: Canis familiaris LOC477772 (LOC477772), mRNA	AL365364
ALA	1600037_at	DOWN	Homo sapiens, clone IMAGE:5294477, mRNA	AC007163
ALA	1600155_at	UP	PREDICTED: Canis familiaris LOC479296 (LOC479296), mRNA	AC011389
ALA	1600793_at	UP	Drosophila melanogaster CG18408-PA, isoform A (CAP) mRNA, complete cds	AL157781
ALA	1601394_x_at	UP	PREDICTED: Canis familiaris similar to ubiquitin-specific protease 7 isoform (LOC479854), mRNA	AC022167
ALA	1602423_at	DOWN	PREDICTED: Canis familiaris similar to interferon regulatory factor 2 binding protein 1 (LOC484433), mRNA	AC078880
ALA	1602589_at	UP	Mustela vison tyrosine aminotransferase gene, complete cds	NA
ALA	1603636_at	DOWN	Human DNA sequence from clone RP4-715N11 on chromosome 20q13.1-13.2 Contains two putative novel genes, ESTs, STSs and GSSs, complete sequence	AL031674
ALA	1604861_at	DOWN	Homo sapiens chromosome 5 clone CTB-53I9, complete sequence	AC008680

Column 1	Column 2	Column 3	Column 4	Column 5
ALA	1605047_at	DOWN	Human DNA sequence from clone RP11-10C13 on chromosome 10 Contains the 5' end of the TRIP8 gene for thyroid hormone receptor interactor 8 (KIAA1380, DKFZp761F0118) and the 3' end of a novel gene (FLJ	AL713895
ALA	1605187_at	UP	Human DNA sequence from clone RP11-8N6 on chromosome 9 Contains the 3' end of the MELK gene for maternal embryonic leucine zipper kinase (KIAA0175), complete sequence	AL442063
ALA	1605429_at	DOWN	Human DNA sequence from clone RP11-458I7 on chromosome 1 Contains the 5' end of the ZA20D1 gene for zinc finger, A20 domain containing 1, a ribosomal protein L6 (RPL6) pseudogene, the VPS45A gene for	AL358073
ALA	1605486_at	UP	Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence	AK096428
LA	1582385_at	DOWN	Canis familiaris Na+-dependent glutamate transporter (GLAST), mRNA	D26443
LA	1582824_at	UP	PREDICTED: Canis familiaris carnitine palmitoyl transferase I isoform (CPT1), mRNA	BC000185
LA	1583273_s_at	DOWN	Homo sapiens mRNA; cDNA DKFZp761G179 (from clone DKFZp761G179)	BC008990
LA	1584258_at	UP	Homo sapiens calsyntenin 2, mRNA (cDNA clone IMAGE:4130487), partial cds	BC007943
LA	1584677_at	DOWN	PREDICTED: Pan troglodytes similar to cystatin T (LOC469901),	BC024006

Column 1	Column 2	Column 3	Column 4	Column 5
			mRNA	
LA	1584742_at	UP	Human DNA sequence from clone RP11-151J10 on chromosome 9 Contains the 5' end of a novel gene (FLJ20060) (contains FLJ12902, KIAA1574), the ADFP gene for adipose differentiation-related protein (ADRP)	AL591206
LA	1584951_at	UP	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP) (LOC474720), mRNA	CR605429
LA	1585355_at	UP	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP) (LOC474720), mRNA	CR597463
LA	1585417_at	UP	Mus musculus microtubule associated monoxygenase, calponin and LIM domain containing 3, mRNA (cDNA clone IMAGE:30637988), partial cds	AC105754
LA	1585604_at	DOWN	Human DNA sequence from clone RP11-175J10 on chromosome 10 Contains a transforming, acidic coiled-coil containing protein 1 (TACC1) pseudogene and a mitochondrial NADH dehydrogenase 1 (MTND1) pseudoge	AL121927
LA	1585686_at	UP	PREDICTED: Bos taurus similar to Cold-inducible RNA-binding protein (Glycine-rich RNA-binding protein CIRP) (A18 hnRNP) (LOC507120), mRNA	CR625198
LA	1586295_at	DOWN	Homo sapiens downregulated in ovarian cancer 1, mRNA (cDNA clone MGC:34368 IMAGE:5228947), complete cds	BC027860

Column 1	Column 2	Column 3	Column 4	Column 5
LA	1588088_at	UP	Homo sapiens hypoxia-inducible protein 2, mRNA (cDNA clone MGC:17005 IMAGE:4182067), complete cds	BC008573
LA	1589569_at	DOWN	PREDICTED: Canis familiaris similar to male germ cell-associated kinase (LOC478721), mRNA	BC039825
LA	1591083_at	UP	Homo sapiens clone DNA22780 NL2 (UNQ171) mRNA, complete cds	AC010323
LA	1592172_at	UP	Homo sapiens BAC clone CTB-17C20 from 7, complete sequence	AC004543
LA	1594511_s_at	UP	Homo sapiens RGM domain family, member B, mRNA (cDNA clone IMAGE:3852164)	AK054622
LA	1594801_at	DOWN	Homo sapiens HMGIC fusion partner-like 2 (LHFPL2) mRNA, complete cds	AY309920
LA	1594973_at	UP	PREDICTED: Canis familiaris LOC478197 (LOC478197), mRNA	AL031387
LA	1595021_at	DOWN	Bos taurus mRNA for sodium chloride cotransporter, partial	NM_000339
LA	1595753_at	DOWN	Homo sapiens CrkRS mRNA, complete cds	CR954985
LA	1596117_at	DOWN	Mus musculus piccolo (presynaptic cytomatrix protein) (Pclo), mRNA	AP001266
LA	1600646_at	DOWN	Homo sapiens mRNA; cDNA DKFZp547F213 (from clone DKFZp547F213)	AC103736
LA	1600703_at	UP	PREDICTED: Canis familiaris similar to budding uninhibited by benzimidazoles 3 homolog (LOC477857), mRNA	AC012391
LA	1601942_at	DOWN	PREDICTED: Canis familiaris similar to family with sequence	AC026358

Column 1	Column 2	Column 3	Column 4	Column 5
			similarity 20, member A (LOC480458), mRNA	
LA	1603578_at	DOWN	PREDICTED: Canis familiaris similar to CD63 antigen (LOC474391), mRNA	CR609892
LA	1605486_at	UP	Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence	AK096428
LA	1605822_at	DOWN	Human dipeptidyl aminopeptidase like protein mRNA, complete cds	M96859
ARA	1582824_at	UP	PREDICTED: Canis familiaris carnitine palmitoyl transferase I isoform (CPT1), mRNA	BC000185
ARA	1582851_at	UP	Rattus norvegicus nuclear receptor subfamily 1, group D, member 1, mRNA (cDNA clone MGC:72288 IMAGE:5598020), complete cds	BC047875
ARA	1582999_at	DOWN	Canis familiaris cyclin-dependent kinase inhibitor (WAF1) mRNA, partial cds	AY399342
ARA	1583403_at	UP	Sus scrofa carnitine palmitoyltransferase I mRNA, nuclear gene encoding mitochondrial protein, complete cds	AK172798
ARA	1584742_at	UP	Human DNA sequence from clone RP11-151J10 on chromosome 9 Contains the 5' end of a novel gene (FLJ20060) (contains FLJ12902, KIAA1574), the ADFP gene for adipose differentiation-related protein (ADRP)	AL591206
ARA	1584951_at	UP	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP) (LOC474720), mRNA	CR605429

Column 1	Column 2	Column 3	Column 4	Column 5
ARA	1585355_at	UP	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP) (LOC474720), mRNA	CR597463
ARA	1586047_s_at	DOWN	Mouse DNA sequence from clone RP23-348N2 on chromosome 11 Contains the 5' end of the Ppp3r1 gene for protein phospatase 3 regulatory subunit B alpha isoform (calcineurin B, type I), a ribosomal protein	AL512655
ARA	1586172_at	DOWN	Homo sapiens chromosome 11, clone RP11-348A11, complete sequence	AC131263
ARA	1586185_at	UP	PREDICTED: Canis familiaris similar to hypothetical protein LOC90637 (LOC480809), mRNA	AC093611
ARA	1586281_at	UP	PREDICTED: Pan troglodytes similar to DEP domain containing protein 5 (LOC458777), mRNA	BX640828
ARA	1587792_at	UP	PREDICTED: Bos taurus similar to phosphoglycerate kinase 1 (LOC533730), partial mRNA	AL049589
ARA	1588088_at	UP	Homo sapiens hypoxia-inducible protein 2, mRNA (cDNA clone MGC:17005 IMAGE:4182067), complete cds	BC008573
ARA	1588903_at	UP	Homo sapiens mRNA; cDNA DKFZp686I2148 (from clone DKFZp686I2148)	U32996
ARA	1590656_at	UP	PREDICTED: Canis familiaris similar to SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c1 (LOC476640), mRNA	AY404349
ARA	1590755_at	DOWN	Homo sapiens BAC clone RP11-1246C19 from 7, complete sequence	AC102953

Column 1	Column 2	Column 3	Column 4	Column 5
ARA	1591083_at	UP	Homo sapiens clone DNA22780 NL2 (UNQ171) mRNA, complete cds	AC010323
ARA	1592286_s_at	DOWN	Homo sapiens clone DNA77624 SHATr/JAM3 (UNQ859) mRNA, complete cds	BC057284
ARA	1592610_at	DOWN	Homo sapiens cDNA clone IMAGE:4611512, partial cds	BC071790
ARA	1592947_at	UP	Homo sapiens hypothetical protein FLJ11795 (FLJ11795), mRNA	AC016585
ARA	1593146_s_at	UP	Homo sapiens Kruppel-like factor 11 (KLF11), mRNA	BC063286
ARA	1593254_at	DOWN	PREDICTED: Canis familiaris similar to 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1 (6PF-2-K/Fru-2,6-P2ASE liver isozyme) (LOC491903), mRNA	AL020991
ARA	1593907_s_at	DOWN	PREDICTED: Bos taurus similar to 26S proteasome non-ATPase regulatory subunit 10 (26S proteasome regulatory subunit p28) (Gankyrin) (LOC535414), mRNA	AL034553
ARA	1594108_at	UP	Gallus gallus mRNA for hypothetical protein, clone 15k1	AC100847
ARA	1594939_at	UP	Homo sapiens chromosome 8, clone RP11-813L8, complete sequence	AC090133
ARA	1595334_at	DOWN	Homo sapiens mRNA; cDNA DKFZp779M1134 (from clone DKFZp779M1134)	AL031290
ARA	1595495_s_at	UP	Mustela vison NADH dehydrogenase subunit 5 (ND5) gene, complete cds; mitochondrial gene for mitochondrial product	NA
ARA	1595956_at	UP	PREDICTED: Gallus gallus similar to KIAA1389 protein (LOC421523),	AC025467

Column 1	Column 2	Column 3	Column 4	Column 5
			mRNA	
ARA	1596476_at	DOWN	Oryza sativa (japonica cultivar-group) chromosome 11 clone OSJNBb0071K13, complete sequence	Z84490
ARA	1596787_at	DOWN	Homo sapiens CASK interacting protein 2 (CASKIN2), mRNA	AC100787
ARA	1597116_at	UP	PREDICTED: Canis familiaris similar to cytoplasmic polyadenylation element binding protein 4 (LOC479287), mRNA	BX538213
ARA	1598013_at	UP	PREDICTED: Canis familiaris similar to InaD-like protein isoform 1 (LOC479550), mRNA	BC021135
ARA	1598063_at	UP	PREDICTED: Rattus norvegicus similar to proacrosin-binding protein (LOC500316), mRNA	AC112198
ARA	1598902_at	UP	Homo sapiens cDNA clone IMAGE:3878708, partial cds	BC009735
ARA	1599787_at	UP	Homo sapiens, clone IMAGE:4821877, mRNA, partial cds	AL035703
ARA	1599851_at	UP	PREDICTED: Gallus gallus frizzled-3 (FZ-3), mRNA	AC092040
ARA	1601092_at	UP	Homo sapiens TRIAD1 type I mRNA, complete cds	AF099149
ARA	1601561_at	DOWN	PREDICTED: Canis familiaris similar to RIKEN cDNA 2010100O12 (LOC477215), mRNA	AL357374
ARA	1601912_at	DOWN	Mus musculus expressed sequence AW538196 (AW538196), mRNA	AL359494
ARA	1602749_at	UP	Homo sapiens BAC clone RP11-44D21 from 4, complete sequence	AC108866

Column 1	Column 2	Column 3	Column 4	Column 5
ARA	1603093_at	UP	Homo sapiens genomic DNA, chromosome 11q clone:RP11-179B7, complete sequence	AP003083
ARA	1603151_at	UP	Rattus norvegicus chromosome 20, major histocompatibility complex, assembled from 40 BACs, strain Brown Norway (BN/ssNHsd), RT1n haplotype; segment 7/11	AL033380
ARA	1603452_s_at	DOWN	Homo sapiens cDNA clone IMAGE:4611044, partial cds	AC006211
ARA	1603454_at	UP	Bos taurus mRNA for similar to cytochrome c oxidase subunit VIb, partial cds, clone: ORCS10538	AL158068
ARA	1603839_at	DOWN	PREDICTED: Rattus norvegicus transcription factor EB (predicted) (Tcfeb_predicted), mRNA	BX284687
ARA	1604372_at	UP	PREDICTED: Canis familiaris LOC475665 (LOC475665), mRNA	AY411810
ARA	1604969_at	DOWN	Homo sapiens chromosome 17, clone hRPK.147_L_13, complete sequence	AC005332
ARA	1605486_at	UP	Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence	AK096428
SA	Cfa.10737.1.A1_at	DOWN	PREDICTED: Canis familiaris similar to HP1-BP74, transcript variant 4 (LOC478203), mRNA	AL663074
SA	Cfa.10872.1.A1_at	UP	Homo sapiens Kruppel-like factor 11, mRNA (cDNA clone MGC:71570 IMAGE:30343877), complete cds	CR591795
SA	Cfa.12323.1.A1_at	UP	PREDICTED: Canis familiaris similar to angiopoietin-like 4 protein (LOC476724), mRNA	AC010323
SA	Cfa.12533.1.	UP	PREDICTED: Bos taurus similar to insulin induced gene 1 isoform 1	AC144438

Column 1	Column 2	Column 3	Column 4	Column 5
	A1_at		(LOC511899), mRNA	
SA	Cfa.12594.1.A1_at	UP	Homo sapiens G protein-coupled receptor 17, mRNA (cDNA clone MGC:35264 IMAGE:5174146), complete cds	AC096920
SA	Cfa.12839.1.A1_at	DOWN	PREDICTED: Canis familiaris similar to nexilin isoform s (LOC490202), mRNA	AC103591
SA	Cfa.17.1.S1_s_at	UP	Canis familiaris organic anion transporting polypeptide A (OATPA) mRNA, partial cds	NM_134431
SA	Cfa.17302.1.S1_s_at	DOWN	PREDICTED: Canis familiaris similar to pleckstrin homology domain containing, family G, member 3 (LOC611460), mRNA	NM_015549
SA	Cfa.17415.1.S1_s_at	DOWN	PREDICTED: Canis familiaris similar to regucalcin gene promotor region related protein (LOC607434), mRNA	XM_088459
SA	Cfa.17931.1.S1_s_at	DOWN	PREDICTED: Canis familiaris similar to von Willebrand factor A domain-related protein isoform 1 (LOC607112), mRNA	NM_022834
SA	Cfa.1854.1.A1_at	UP	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA	AP002380
SA	Cfa.18958.1.S1_at	DOWN	PREDICTED: Canis familiaris similar to OCIA domain containing 1, transcript variant 3 (LOC475140), mRNA	BC003409
SA	Cfa.19447.1.S1_at	DOWN	Homo sapiens lamin B1 (LMNB1), mRNA	NM_005573
SA	Cfa.19635.1.S1_at	DOWN	Lotus corniculatus var. japonicus gene for hypothetical proteins, complete and partial cds, clone:BAC259.12D-1	AF165140

Column 1	Column 2	Column 3	Column 4	Column 5
SA	Cfa.19704.1.S1_at	DOWN	PREDICTED: Bos taurus similar to immunity-related GTPase family, Q1 (LOC616834), mRNA	AC006276
SA	Cfa.20892.1.S1_s_at	UP	PREDICTED: Canis familiaris similar to Ectonucleoside triphosphate diphosphohydrolase 6 (NTPDase6) (CD39 antigen-like 2) (LOC485564), mRNA	CR936765
SA	Cfa.21023.1.S1_at	UP	PREDICTED: Canis familiaris similar to non-POU domain containing, octamer-binding, transcript variant 11 (LOC612773), mRNA	AL590762
SA	Cfa.2282.1.S1_at	UP	PREDICTED: Canis familiaris similar to [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4, mitochondrial precursor (Pyruvate dehydrogenase kinase isoform 4) (LOC482310), mRNA	AK096428
SA	Cfa.394.1.A1_x_at	UP	PREDICTED: Canis familiaris similar to 60S ribosomal protein L23a (LOC478212), mRNA	NM_000984
SA	Cfa.431.1.A1_at	UP	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP), transcript variant 4 (LOC474720), mRNA	AL591206
SA	Cfa.431.2.A1_s_at	UP	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP), transcript variant 1 (LOC474720), mRNA	NM_001122
SA	Cfa.5582.1.A1_at	DOWN	Homo sapiens mRNA for dual oxidase 2 precursor variant protein	AB209010
SA	Cfa.6339.1.A1_at	UP	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP), transcript variant 3	NM_001122

Column 1	Column 2	Column 3	Column 4	Column 5
			(LOC474720), mRNA	
SA	Cfa.6361.1.A1_at	DOWN	PREDICTED: Canis familiaris similar to 60S ribosomal protein L17 (L23), transcript variant 4 (LOC480221), mRNA	BX679664
SA	Cfa.6482.1.A1_at	DOWN	PREDICTED: Canis familiaris hypothetical protein LOC612422 (LOC612422), mRNA	AL162191
SA	Cfa.6915.1.A1_at	DOWN	Homo sapiens 12 BAC RP11-1105G2 (Roswell Park Cancer Institute Human BAC Library) complete sequence	AC073655
SA	Cfa.7119.1.A1_s_at	DOWN	PREDICTED: Canis familiaris similar to coilin (LOC480564), mRNA	AC109357
SA	Cfa.743.2.S1_a_at	UP	PREDICTED: Bos taurus hypothetical protein LOC614918 (LOC614918), mRNA	BC001282
SA	Cfa.7531.1.A1_at	UP	Mouse DNA sequence from clone RP23-287B22 on chromosome 11 Contains a CpG island, complete sequence	AC008732
SA	Cfa.7705.2.A1_s_at	DOWN	PREDICTED: Canis familiaris similar to chromatin-specific transcription elongation factor large subunit, transcript variant 2 (LOC612874), mRNA	NM_007192
SA	Cfa.791.4.A1_at	UP	PREDICTED: Canis familiaris similar to ribosomal protein L24, transcript variant 2 (LOC478547), mRNA	NM_000986
SA	Cfa.9014.1.A1_at	DOWN	Mus musculus SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae), mRNA (cDNA clone IMAGE:5372918)	AC091133

Column 1	Column 2	Column 3	Column 4	Column 5
SA	Cfa.9506.1.A1_at	UP	Homo sapiens hypoxia-inducible protein 2 (HIG2) mRNA, complete cds	AF144755
SA	Cfa.9531.1.A1_at	DOWN	Homo sapiens cyclophilin-related protein mRNA, complete cds	AC092041
SA	Cfa.9685.2.S1_a_at	UP	PREDICTED: Canis familiaris short tandem repeat locus PEZ20 variant 19 (LOC476927), mRNA	AL138960
SA	Cfa.9694.1.A1_at	DOWN	Plasmodium yoelii yoelii str. 17XNL hypothetical protein (PY00634) mRNA, partial cds	AL359317
SA	CfaAffx.1102.1.S1_at	DOWN	PREDICTED: Canis familiaris similar to RAB5B, member RAS oncogene family, transcript variant 3 (LOC474394), mRNA	BC065298
SA	CfaAffx.12967.1.S1_at	DOWN	Canis familiaris isolate cOR5D23 olfactory receptor family 5 subfamily D gene, partial cds	AF399364
SA	CfaAffx.13599.1.S1_at	DOWN	Nicotiana benthamiana clone 6-272 unknown mRNA	NA
SA	CfaAffx.14479.1.S1_at	DOWN	PREDICTED: Canis familiaris similar to Protein KIAA0652 (LOC483632), mRNA	AK223603
SA	CfaAffx.14595.1.S1_s_at	DOWN	PREDICTED: Canis familiaris similar to diacylglycerol kinase zeta (LOC611321), mRNA	NM_201532
SA	CfaAffx.15202.1.S1_s_at	DOWN	PREDICTED: Canis familiaris similar to Syndecan-4 precursor (Amphiglycan) (SYND4) (Ryudocan core protein) (LOC485893), mRNA	AK222695
SA	CfaAffx.16302.1.S1_x_at	DOWN	PREDICTED: Canis familiaris similar to zinc finger protein 25 (LOC611218), mRNA	AB169501
SA	CfaAffx.1649	DOWN	PREDICTED: Bos taurus similar to Phosphatidylinositol 4-kinase beta	AL079340

Column 1	Column 2	Column 3	Column 4	Column 5
	3.1.S1_at		(PtdIns 4-kinase) (PI4Kbeta) (PI4K-beta) (NPIK) (PI4K92) (LOC613348), mRNA	
SA	CfaAffx.19197.1.S1_at	UP	Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) (ALS2), mRNA	NM_020919
SA	CfaAffx.19206.1.S1_at	DOWN	Ipomoea nil Magenta gene for flavonoid 3'-hydroxylase, complete cds	BX647478
SA	CfaAffx.197.1.S1_s_at	DOWN	PREDICTED: Canis familiaris bZIP protein, transcript variant 1 (LCR-F1), mRNA	NM_003204
SA	CfaAffx.20515.1.S1_s_at	UP	PREDICTED: Canis familiaris similar to protein tyrosine phosphatase, non-receptor type 23 (LOC609220), mRNA	AL110210
SA	CfaAffx.21182.1.S1_s_at	DOWN	PREDICTED: Canis familiaris similar to CG4699-PA, isoform A, transcript variant 4 (LOC480489), mRNA	BC098376
SA	CfaAffx.21280.1.S1_at	DOWN	PREDICTED: Canis familiaris similar to Mitogen-activated protein kinase kinase 14 (NF-kappa beta-inducing kinase) (Serine/threonine-protein kinase NIK) (HsNIK) (LOC490926), mRNA	BC035576
SA	CfaAffx.22082.1.S1_s_at	DOWN	PREDICTED: Canis familiaris similar to zinc finger CCCH type containing 12A (LOC489416), mRNA	XM_370654
SA	CfaAffx.22560.1.S1_at	DOWN	PREDICTED: Canis familiaris similar to Cullin-5 (CUL-5) (Vasopressin-activated calcium-mobilizing receptor) (VACM-1) (LOC489422), mRNA	BC063306
SA	CfaAffx.23320.1.S1_at	DOWN	PREDICTED: Canis familiaris similar to RAD52B (LOC480794),	BC032114

Column 1	Column 2	Column 3	Column 4	Column 5
			mRNA	
SA	CfaAffx.23784.1.S1_s_at	DOWN	PREDICTED: Canis familiaris similar to aldehyde dehydrogenase 4A1 precursor (LOC612452), mRNA	BC023600
SA	CfaAffx.23872.1.S1_s_at	UP	PREDICTED: Canis familiaris similar to cleavage stimulation factor, 3 pre-RNA subunit 2, tau (LOC486459), mRNA	AL136747
SA	CfaAffx.24040.1.S1_at	UP	PREDICTED: Canis familiaris similar to serine/threonine kinase 11 interacting protein (LOC488541), mRNA	NA
SA	CfaAffx.25844.1.S1_at	UP	PREDICTED: Canis familiaris hypothetical LOC22889, transcript variant 1 (LOC612936), mRNA	AK170490
SA	CfaAffx.28301.1.S1_s_at	UP	PREDICTED: Canis familiaris similar to angiopoietin-like 4 protein (LOC476724), mRNA	AK222489
SA	CfaAffx.2896.1.S1_at	DOWN	PREDICTED: Canis familiaris similar to Mitogen-activated protein kinase kinase kinase 7 interacting protein 1 (TAK1-binding protein 1), transcript variant 1 (LOC481245), mRNA	NM_006116
SA	CfaAffx.29858.1.S1_s_at	UP	PREDICTED: Canis familiaris similar to melanoma ubiquitous mutated protein (LOC612320), mRNA	BC110874
SA	CfaAffx.3314.1.S1_at	UP	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP), transcript variant 4 (LOC474720), mRNA	NM_001122
SA	CfaAffx.4425.1.S1_at	UP	PREDICTED: Canis familiaris similar to zinc finger protein 329 (LOC484234), mRNA	NM_024620

Column 1	Column 2	Column 3	Column 4	Column 5
SA	CfaAffx.4438.1.S1_at	UP	PREDICTED: Canis familiaris similar to FERM and PDZ domain containing 1 (LOC481614), mRNA	AB023184
SA	CfaAffx.5367.1.S1_at	DOWN	PREDICTED: Canis familiaris similar to claudin 6 (LOC490048), mRNA	CR614114
SA	CfaAffx.654.1.S1_at	UP	PREDICTED: Homo sapiens similar to ribosomal protein S27 (LOC442598), mRNA	XM_499342
SA	CfaAffx.668.1.S1_at	DOWN	Homo sapiens Kazal type serine protease inhibitor 5-like 2 (SPINK5L2), mRNA	NM_001001325
SA	CfaAffx.6703.1.S1_at	DOWN	PREDICTED: Canis familiaris similar to pumilio homolog 2, transcript variant 6 (LOC607618), mRNA	AK093847
SA	CfaAffx.7822.1.S1_s_at	DOWN	PREDICTED: Canis familiaris similar to FYVE-finger-containing Rab5 effector protein rabenosyn-5 (LOC484642), mRNA	BC106940
SA	CfaAffx.7845.1.S1_s_at	UP	Homo sapiens mRNA for TSC-22 protein	AJ222700
SA	CfaAffx.8861.1.S1_at	UP	Homo sapiens hypothetical LOC387790 (LOC387790), mRNA	AK095089
SA	CfaAffx.9083.1.S1_at	UP	PREDICTED: Canis familiaris similar to FLJ20859 protein isoform 2 (LOC475396), mRNA	AK155096
SA	CfaAffx.9353.1.S1_s_at	DOWN	PREDICTED: Canis familiaris similar to chromatin-specific transcription elongation factor large subunit, transcript variant 1 (LOC612874), mRNA	NM_007192
SA	CfaAffx.9845.1.S1_s_at	UP	PREDICTED: Canis familiaris similar to leucine rich repeat containing 45 (LOC483375), mRNA	NM_144999

Column 1	Column 2	Column 3	Column 4	Column 5
CLA	Cfa.10478.1.A1_at	UP	PREDICTED: Bos taurus similar to Type II inositol-1,4,5-trisphosphate 5-phosphatase precursor (Phosphoinositide 5-phosphatase) (5PTase) (75 kDa inositol polyphosphate-5-phosphatase) (LOC538291), partial mRNA	AC005691
CLA	Cfa.11267.1.A1_at	DOWN	Homo sapiens cDNA clone IMAGE:4456146, partial cds	BC024645
CLA	Cfa.11358.1.A1_at	UP	Homo sapiens solute carrier family 20 (phosphate transporter), member 2 (SLC20A2), mRNA	AF170802
CLA	Cfa.11413.1.A1_at	DOWN	Homo sapiens BAC clone RP11-17N4 from 2, complete sequence	AC016673
CLA	Cfa.11483.1.A1_at	DOWN	Danio rerio POU domain, class 4, transcription factor 1, mRNA (cDNA clone MGC:77341 IMAGE:6967996), complete cds	AL138810
CLA	Cfa.11868.1.A1_at	DOWN	PREDICTED: Canis familiaris similar to pleckstrin homology domain containing, family H (with MyTH4 domain) member 1 (LOC480363), mRNA	AL132640
CLA	Cfa.12323.1.A1_at	UP	PREDICTED: Canis familiaris similar to angiopoietin-like 4 protein (LOC476724), mRNA	AC010323
CLA	Cfa.1284.1.S1_at	UP	Homo sapiens mRNA; cDNA DKFZp434C136 (from clone DKFZp434C136)	AL133026
CLA	Cfa.13221.1.A1_at	UP	Human DNA sequence from clone RP11-241O12 on chromosome Xq26.3-27.3 Contains a novel gene, complete sequence	AL137840
CLA	Cfa.13649.1.A1_s_at	DOWN	PREDICTED: Canis familiaris similar to Sodium- and chloride-dependent transporter XTRP2 (Solute carrier family 6 member 18)	AK074468

Column 1	Column 2	Column 3	Column 4	Column 5
			(LOC478631), mRNA	
CLA	Cfa.13707.1.A1_at	DOWN	PREDICTED: Bos taurus similar to Ssu72 RNA polymerase II CTD phosphatase homolog, transcript variant 2 (LOC614837), mRNA	BC008070
CLA	Cfa.13930.1.A1_at	DOWN	Aspergillus nidulans FGSC A4 hypothetical protein (AN0430.2), mRNA	AL031779
CLA	Cfa.14103.1.A1_at	DOWN	Arabidopsis thaliana clone RAFL15-15-K01 (R20657) putative cytochrome P450 (At1g13150) mRNA, complete cds	AC099053
CLA	Cfa.15679.1.A1_at	UP	PREDICTED: Canis familiaris similar to C10C5.4 (LOC607282), mRNA	BC039170
CLA	Cfa.19017.1.S1_at	UP	PREDICTED: Canis familiaris similar to CG5537-PA, transcript variant 2 (LOC480960), mRNA	AL137013
CLA	Cfa.1935.1.A1_at	DOWN	PREDICTED: Canis familiaris hypothetical LOC481916 (LOC481916), mRNA	AL590440
CLA	Cfa.20000.1.S1_s_at	UP	PREDICTED: Canis familiaris similar to sperm-associated cation channel 2 isoform 1 (LOC609008), mRNA	AC021754
CLA	Cfa.20451.1.S1_at	UP	Mus musculus ubiquitin-like 4, mRNA (cDNA clone MGC:19132 IMAGE:4215699), complete cds	AC012153
CLA	Cfa.21599.1.S1_s_at	UP	PREDICTED: Canis familiaris similar to smooth muscle myosin heavy chain 11 isoform SM1-like, transcript variant 3 (LOC474586), mRNA	BC040721
CLA	Cfa.2308.1.A1_at	UP	Mus musculus piwi-like 4 (Drosophila) (Piwil4), mRNA	AC108065

Column 1	Column 2	Column 3	Column 4	Column 5
CLA	Cfa.2586.1.S1_at	UP	Homo sapiens CDC14 cell division cycle 14 homolog B (S. cerevisiae) (CDC14B) gene, complete cds	AY675321
CLA	Cfa.3584.1.S1_s_at	UP	Canis familiaris gonadotropin-releasing hormone receptor (GNRHR), mRNA	NM_000406
CLA	Cfa.4761.1.S1_at	UP	PREDICTED: Bos taurus similar to GATA zinc finger domain containing 2A, transcript variant 6 (LOC508384), mRNA	AK125974
CLA	Cfa.4817.1.A1_at	DOWN	Mus musculus nephrin NPHS1 (Nphs1) gene, partial cds	AC024166
CLA	Cfa.5394.1.A1_at	DOWN	Xenopus laevis MGC80410 protein, mRNA (cDNA clone MGC:80410 IMAGE:5155047), complete cds	AC012618
CLA	Cfa.5400.1.A1_at	DOWN	Homo sapiens glutathione peroxidase 6 (olfactory) (GPX6), mRNA	AY324826
CLA	Cfa.5759.1.A1_at	UP	Homo sapiens fibroblast growth factor 5 (FGF5) gene, complete cds	AC006441
CLA	Cfa.5949.1.A1_x_at	UP	Mus musculus RIKEN cDNA 2500001K11 gene (2500001K11Rik), mRNA	AC009230
CLA	Cfa.6989.1.A1_at	DOWN	Human mRNA for KIAA0297 gene, partial cds	AL589763
CLA	Cfa.7584.1.A1_at	DOWN	Canis familiaris forssman synthetase mRNA, complete cds	AC091826
CLA	Cfa.7855.1.A1_at	UP	PREDICTED: Canis familiaris similar to FKBP12-rapamycin complex-associated protein (FK506-binding protein 12-rapamycin complex-associated protein 1) (Rapamycin target protein) (RAPT1) (Mammalian target of rapamycin) (MTOR), transcript variant 2 (LOC478232), mRNA	AL162595

Column 1	Column 2	Column 3	Column 4	Column 5
CLA	Cfa.8008.2.A1_at	UP	PREDICTED: Canis familiaris similar to GTPase activating Rap/RanGAP domain-like 1 isoform 1 (LOC490653), mRNA	AL137818
CLA	Cfa.8798.1.A1_at	UP	Arabidopsis thaliana At1g50920 mRNA sequence	AC007269
CLA	CfaAffx.10853.1.S1_at	UP	PREDICTED: Canis familiaris cOR2AG1 olfactory receptor family 2 subfamily AG-like (cOR2AG1), mRNA	AC090440
CLA	CfaAffx.1228.1.S1_at	DOWN	Homo sapiens gene for LIM-homeodomain protein Lhx8, partial cds	AP002762
CLA	CfaAffx.13210.1.S1_s_at	UP	Homo sapiens olfactory receptor, family 6, subfamily C, member 6 (OR6C6), mRNA	NM_001005493
CLA	CfaAffx.13599.1.S1_at	DOWN	Nicotiana benthamiana clone 6-272 unknown mRNA	NA
CLA	CfaAffx.13793.1.S1_at	DOWN	PREDICTED: Strongylocentrotus purpuratus similar to apurinic/apyrimidinic endonuclease (44.7 kD) (apn-1) (LOC592745), mRNA	AL391114
CLA	CfaAffx.17003.1.S1_s_at	UP	PREDICTED: Canis familiaris similar to actinin, alpha 2, transcript variant 11 (LOC479191), mRNA	CR593118
CLA	CfaAffx.18214.1.S1_s_at	UP	PREDICTED: Canis familiaris complement component receptor 2 (CR2), mRNA	AK223627
CLA	CfaAffx.18414.1.S1_at	DOWN	PREDICTED: Canis familiaris similar to Cytochrome P450 24A1, mitochondrial precursor (P450-CC24) (Vitamin D(3) 24-hydroxylase) (1,25-dihydroxyvitamin D(3) 24-hydroxylase) (24-OHase) (LOC485935), mRNA	S67623

Column 1	Column 2	Column 3	Column 4	Column 5
CLA	CfaAffx.18922.1.S1_at	DOWN	PREDICTED: Canis familiaris similar to dystonia 2, torsion (autosomal recessive) (LOC488341), mRNA	U18799
CLA	CfaAffx.24169.1.S1_at	UP	Mus musculus solute carrier family 6 (neurotransmitter transporter, GABA), member 13, mRNA (cDNA clone MGC:19082 IMAGE:4195373), complete cds	U76343
CLA	CfaAffx.24675.1.S1_x_at	UP	PREDICTED: Canis familiaris similar to expressed in non-metastatic cells 1, protein (NM23A) (nucleoside diphosphate kinase) (LOC611984), mRNA	BC000293
CLA	CfaAffx.2488.1.S1_at	UP	PREDICTED: Canis familiaris hypothetical protein LOC612694 (LOC612694), mRNA	AL583806
CLA	CfaAffx.29768.1.S1_s_at	UP	PREDICTED: Canis familiaris similar to tripartite motif protein 32 (predicted) (LOC491233), mRNA	BX255925
CLA	CfaAffx.4438.1.S1_at	UP	PREDICTED: Canis familiaris similar to FERM and PDZ domain containing 1 (LOC481614), mRNA	AB023184
CLA	CfaAffx.6670.1.S1_at	UP	PREDICTED: Canis familiaris similar to microtubule associated monoxygenase, calponin and LIM domain containing 1 (LOC481958), mRNA	BC009972
CLA	CfaAffx.7326.1.S1_s_at	DOWN	PREDICTED: Canis familiaris similar to F-box and leucine-rich repeat protein 13 (LOC609997), mRNA	NM_145032

Table 3. Genomic effect of feeding Prescription Diet® Canine j/d to arthritic dogs

2383 records for d15_AR vs d0_AR FC cutoff: 1.1; P-val cutofff: .05; Q-val cutoff: 0.3
#samples in group-1 (D15 Arth.): 30 group-2 (D0 Arth.): 31
Fold change > 1 implies probes are UP regulated in D15 Arth. samples.

Probe	P-Value	Q-Value	Fold-Change	1/Fold-Change	Top BLAST Annot.	Match Perc.	Human Accn.	Top Hit Accn.	Gene Symbol	Gene Desc.
007.1.A1_s_at	1.967210E-02	2.908241E-01	1.11	.90	PREDICTED: Canis familiaris similar to Thioredoxin; mitochondrial precursor (Mt-Trx) (MTRX) (Thioredoxin-2) (LOC474519); mRNA	76.1	AL359504	XM_531748	TXN2	thioredoxin 2
043.1.A1_at	1.757830E-02	2.762583E-01	1.12	.89	Sus scrofa clone Clu_148790.scr.msk.p1.Contig3; mRNA sequence	84.9	AF086094	AY609520		
048.1.A1_at	7.628860E-04	5.666965E-02	1.21	.83	Mouse cytomegalovirus 1 strain W8211 m157 gene; complete cds	6.3	AC002127	AY228679		
085.1.A1_at	7.481830E-04	5.619207E-02	0.87	1.15	Rattus norvegicus cDNA clone IMAGE:7305115	57.5	AC009630	BC092601		
086.1.A1_at	6.561530E-03	1.737695E-01	1.16	.86	PREDICTED: Bos taurus hypothetical LOC535045 (LOC535045); mRNA	14.2	EF015893	XM_615023		
099.1.S1_at	3.697720E-03	1.303481E-01	0.87	1.15	PREDICTED: Canis familiaris similar to suppressor of G2 allele of SKP1 (LOC609605); mRNA	94.1	CR607917	XM_846893	SUGT1	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)
101.1.A1_s_at	2.811470E-04	3.252463E-02	0.88	1.14	PREDICTED: Canis familiaris similar to single-stranded DNA binding protein 1 isoform 1 (LOC608727); mRNA	99.0	NM_003143	XM_845839	LOC608727	similar to single-stranded DNA binding protein 1 isoform 1
115.1.A1_at	1.305830E-02	2.403610E-01	1.1	.91	Mus musculus activated spleen cDNA; RIKEN full-length enriched library; clone:F830022E09 product:unclassifiable; full insert sequence	4.5	AC023043	AK156447		

Cfa.10128.1.A1_at	7.064230E-03	1.798871E-01	1.12	.89	PREDICTED: Canis familiaris similar to alpha-synuclein isoform NACP140; transcript variant 5 (LOC478478); mRNA	99.6	NULL	XM_855879	SNCA	synuclein, alpha (non A4 component of amyloid precursor)
Cfa.10151.1.A1_at	1.943470E-02	2.895647E-01	0.82	1.22	null	null	null	null		
Cfa.10178.2.S1_s_at	5.523940E-03	1.592432E-01	1.12	.90	PREDICTED: Canis familiaris heterogenous nuclear ribonucleoprotein K; transcript variant 19 (HNRPK); mRNA	99.8	NULL	XM_852199	HNRNPK	heterogeneous nuclear ribonucleoprotein K
Cfa.10214.2.A1_s_at	2.350390E-05	7.691952E-03	0.87	1.15	PREDICTED: Canis familiaris similar to U2 small nuclear ribonucleoprotein B; transcript variant 1 (LOC477148); mRNA	99.2	NULL	XM_534338	LOC477148	similar to U2 small nuclear ribonucleoprotein B
Cfa.10216.1.A1_a_at	7.141380E-03	1.804793E-01	0.85	1.17	PREDICTED: Canis familiaris similar to CG10581-PA; transcript variant 1 (LOC607237); mRNA	100.0	AL831755	XM_843650	LOC607237	similar to CG10581-PA
Cfa.10220.1.S1_at	4.949140E-03	1.497440E-01	1.11	.90	PREDICTED: Macaca mulatta hypothetical protein LOC712701 (LOC712701); mRNA	48.2	AC055872	XM_001102861	LOC712701	hypothetical protein LOC712701
Cfa.10235.1.A1_at	4.818410E-05	1.133116E-02	1.18	.84	Rattus norvegicus glial cell line derived neurotrophic factor family receptor alpha 2 (Gfra2); mRNA >gi|2282023|gb|U97143.1|RNU97143 Rattus norvegicus RET ligand 2 (RETL2) mRNA; complete cds	14.5	BC033096	NM_012750	Gfra2	glial cell line derived neurotrophic factor family receptor alpha 2
Cfa.10239.1.S1_at	2.096880E-02	2.978695E-01	0.88	1.13	PREDICTED: Canis familiaris hypothetical LOC486738 (LOC486738); mRNA	99.3	AF161448	XM_543865	LOC486738	hypothetical LOC486738
Cfa.10250.1.A1_at	2.937060E-03	1.170600E-01	0.87	1.16	PREDICTED: Canis familiaris similar to Protein C10orf70 (LOC479212); mRNA	99.8	NM_018464	XM_536355	CISD1	CDGSH iron sulfur domain 1
Cfa.10259.1.S1_at	9.239870E-03	2.040214E-01	0.85	1.18	PREDICTED: Canis familiaris similar to polymerase (DNA directed); eta (LOC474915); mRNA	60.2	BC015742	XM_532150	POLH	polymerase (DNA directed), eta
Cfa.10268.1.A1_at	1.221370E-02	2.339614E-01	0.87	1.14	PREDICTED: Equus caballus similar to Brix domain containing 2 (LOC100053899); mRNA	63.8	AK307492	XM_001500161	LOC100053899	similar to Brix domain containing 2

Cfa.10268.1.A1_s_at	9.548810E-03	2.077548E-01	0.9	1.12	PREDICTED: *Canis familiaris* similar to Brix domain containing protein 2 (Ribosome biogenesis protein Brix) (LOC479365); mRNA	39.5	CR593646	XM_536504	LOC479365	similar to Brix domain containing protein 2 (Ribosome biogenesis protein Brix)
Cfa.10278.1.A1_at	5.998420E-05	1.280276E-02	0.73	1.36	PREDICTED: Canis familiaris similar to ribosomal protein L24-like (LOC478313); mRNA	93.7	AB171708	XM_535488	LOC478313	similar to ribosomal protein L24-like
Cfa.10288.2.A1_a_at	3.480740E-03	1.274454E-01	0.89	1.13	PREDICTED: Canis familiaris similar to DC2 protein; transcript variant 2 (LOC477512); mRNA	73.0	AK312185	XM_846200	LOC477512	similar to DC2 protein
Cfa.10318.1.A1_at	3.963000E-03	1.348203E-01	0.85	1.18	NULL	null	AC087639	NULL		
Cfa.10342.1.A1_at	1.114300E-02	2.226272E-01	0.86	1.16	Human unidentified mRNA; partial sequence	5.6	AC091955	U43604		
Cfa.104.1.S1_at	5.106250E-03	1.525288E-01	1.11	.90	Sus scrofa tyrosinase (TYR); mRNA >gi|67513980|dbj|AB207239.1| Sus scrofa TYR mRNA for tyrosinase; complete cds	18.5	AJ323719	NM_001025212	TYR	tyrosinase
Cfa.10404.1.S1_at	6.863570E-03	1.771094E-01	1.1	.91	Homo sapiens phosphatidic acid phosphatase type 2 (PAP2D); transcript variant 1; mRNA	66.2	AL590110	NM_001037317	PAP2D	phosphatidic acid phosphatase type 2
Cfa.10458.1.S1_at	1.427790E-02	2.509538E-01	0.89	1.12	PREDICTED: Canis familiaris similar to CG14199-PA (LOC610083); mRNA	99.8	AC005255	XM_847481	TMEM167A	transmembrane protein 167A
Cfa.10463.1.S1_at	8.068390E-03	1.912022E-01	0.84	1.20	PREDICTED: Bos taurus similar to cell growth regulator CGR19; transcript variant 1 (LOC534344); mRNA	48.1	AL359792	XM_614089	CGRRF1	cell growth regulator with ring finger domain 1
Cfa.10495.1.A1_at	3.577820E-03	1.278354E-01	0.9	1.11	PREDICTED: Canis familiaris similar to gamma isoform of regulatory subunit B56; protein phosphatase 2A isoform b; transcript variant 9 (LOC480436); mRNA	100.0	AC009263	XM_863471	PPP2R5C	protein phosphatase 2, regulatory subunit B', gamma isoform
Cfa.10504.3.A1_at	9.764800E-03	2.100091E-01	1.1	.91	PREDICTED: Canis familiaris similar to CG30152-PA; transcript variant 6 (LOC478335); mRNA	96.0	AC104465	XM_860383	LOC478335	similar to CG30152-PA

Cfa.10509.1.S1_at	1.973240E-02	2.912153E-01	0.88	1.14	PREDICTED: Canis familiaris similar to GRINL1A combined protein isoform 1 (LOC478318); mRNA	50.0	NM_001018102	XM_535493	GCOM1	GRINL1A complex locus
Cfa.10526.1.A1_at	1.430150E-03	8.108894E-02	0.87	1.15	Homo sapiens hypothetical protein FLJ11506; mRNA (cDNA clone IMAGE:3458978); partial cds	5.3	AL136715	BC001975	FLJ11506	hypothetical protein FLJ11506
Cfa.10531.1.S1_at	1.478790E-02	2.555166E-01	0.89	1.13	PREDICTED: Canis familiaris similar to RPB5-mediating protein isoform a (LOC476501); mRNA	91.9	NM_134447	XM_533709	LOC476501	similar to RPB5-mediating protein isoform a
Cfa.10562.1.S1_at	1.493390E-02	2.565357E-01	0.86	1.17	PREDICTED: Bos taurus similar to Translin associated protein X (LOC789058); mRNA	55.3	NM_005999	XM_001255924	LOC789058	similar to translin-associated protein X
Cfa.106.1.S1_s_at	1.985880E-02	2.916359E-01	0.86	1.16	Canis lupus familiaris amyloid beta (A4) precursor protein (peptidase nexin-II; Alzheimer disease) (APP); mRNA >gi|40950171|gb|AY498706.1| Canis familiaris beta amyloid precursor protein isoform APP770 (beta APP) mRNA; complete cds; alternatively spliced	99.4	CR618347	NM_001006601	APP	amyloid beta (A4) precursor protein
Cfa.10631.1.S1_at	1.146670E-05	4.771175E-03	1.2	.83	PREDICTED: Pan troglodytes gamma-aminobutyric acid A receptor; gamma 1; transcript variant 2 (GABRG1); mRNA	13.4	NM_173536	XM_526775	GABRG1	gamma-aminobutyric acid (GABA) A receptor, gamma 1
Cfa.10635.1.S1_at	1.712530E-02	2.741519E-01	1.11	.90	PREDICTED: Pan troglodytes gamma-aminobutyric acid (GABA) A receptor; beta 2; transcript variant 3 (GABRB2); mRNA	67.6	AC022120	XM_001143967	GABRB2	gamma-aminobutyric acid (GABA) A receptor, beta 2
Cfa.10692.1.A1_at	3.261700E-03	1.229135E-01	1.13	.88	*Pisum sativum* cultivar Sparkle Ca2+ and calmodulin-dependent protein kinase (SYM9) gene; partial cds	4.1	AL049861	AY502069		
Cfa.10711.1.A1_at	6.280990E-03	1.703278E-01	0.9	1.11	PREDICTED: Pan troglodytes similar to beta-sarcoglycan; transcript variant 1 (SGCB); mRNA	28.1	AC093858	XM_001149596	SGCB	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)
Cfa.10759.1.S1_at	8.873630E-03	2.010117E-01	1.11	.90	Bos taurus prolylcarboxypeptidase (angiotensinase C) (PRCP); mRNA >gi|83405389|gb|BC111171.1| Bos taurus similar to Lysosomal Pro-X carboxypeptidase precursor (Prolylcarboxypeptidase) (PRCP) (Proline carboxypeptidase) (Angiotensinase C)	18.4	AL591074	NM_001038164	PRCP	prolylcarboxypeptidase (angiotensinase C)

					(Lysosomal carboxypeptidase C); mRNA (cDNA clone MGC:134276 IMAGE:8051015); complete cds					
Cfa.10761.1.S1_s_at	5.847970E-03	1.641666E-01	1.1	.91	Canis lupus familiaris keratin 1 (epidermolytic hyperkeratosis) (KRT1); mRNA >gi|34979906|gb|AY318945.1| Canis familiaris epithelial keratin 1 (Ker1) mRNA; complete cds	60.7	NULL	NM_001003392	KRT1	keratin 1
Cfa.10792.1.A1_a_at	1.377810E-02	2.461334E-01	0.88	1.14	PREDICTED: *Canis familiaris similar to* NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 2; 8kDa (LOC478032); mRNA	99.4	NM_002488	XM_535211	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa
Cfa.10814.1.A1_at	1.117960E-02	2.231512E-01	0.86	1.16	null	null	null	null		
Cfa.10839.1.A1_at	9.867590E-03	2.111891E-01	0.91	1.10	Homo sapiens zinc metallopeptidase (STE24 homolog; S. cerevisiae) (ZMPSTE24); mRNA	82.1	NM_005857	NM_005857	ZMPSTE24	zinc metallopeptidase (STE24 homolog, S. cerevisiae)
Cfa.10854.2.S1_at	2.380310E-03	1.047144E-01	1.21	.83	PREDICTED: Canis familiaris similar to lipin 1; transcript variant 4 (LOC475670); mRNA	47.3	AC012456	XM_851910	LPIN1	lipin 1
Cfa.1086.2.A1_a_at	2.545840E-03	1.077288E-01	0.8	1.24	PREDICTED: Canis familiaris similar to Geminin (LOC478739); mRNA	96.1	AF067855	XM_535906	GMNN	geminin, DNA replication inhibitor
Cfa.10866.1.S1_at	3.910370E-03	1.343231E-01	0.83	1.21	PREDICTED: Canis familiaris similar to EF-hand calcium binding domain 2 (LOC611783); mRNA	96.4	NM_032328	XM_849494	EFCAB2	EF-hand calcium binding domain 2
Cfa.10879.2.S1_at	2.372070E-06	2.171958E-03	1.36	.73	Penicillium chrysogenum mitochondrial gene for S5 ribosomal protein; complete cds	32.9	AC005232	D13859		
Cfa.10889.1.S1_s_at	1.180990E-04	1.985309E-02	0.84	1.19	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L33 (LOC611180); mRNA	94.1	AJ420485	XM_848822	LOC611180	similar to mitochondrial ribosomal protein L33
Cfa.10920.2.S1_at	1.779860E-03	9.151151E-02	1.17	.85	null	null	null	null		
Cfa.10923.1.A1_a_at	1.157310E-	7.176799E-	1.16	.86	PREDICTED: Macaca mulatta similar to calcium/calmodulin-dependent protein	46.4	AB073352	XM_001095396	LOC706977	similar to calcium/calmodulin-dependent protein kinase IIB

	03	02			kinase IIB isoform 1 (LOC706977); mRNA					isoform 1
Cfa.10938.1.A1_at	1.771390E-02	2.772064E-01	1.1	.91	PREDICTED: Canis familiaris similar to Secretogranin-1 precursor (Secretogranin I) (SgI) (Chromogranin B) (CgB) (LOC477165); mRNA	100.0	AK289386	XM_534354	CHGB	chromogranin B (secretogranin 1)
Cfa.10980.1.A1_at	1.683120E-03	8.920329E-02	1.2	.83	Homo sapiens transmembrane protein 155 (TMEM155); mRNA	82.9	NM_152399	NM_152399	TMEM155	transmembrane protein 155
Cfa.11007.1.A1_at	2.189490E-04	2.897822E-02	1.19	.84	NULL	null	AC092620	NULL		
Cfa.11018.1.A1_at	1.361520E-02	2.446472E-01	1.11	.90	PREDICTED: Macaca mulatta similar to doublecortin and CaM kinase-like 1 (LOC722071); mRNA	83.0	AL139083	XM_001118268	LOC722071	similar to doublecortin and CaM kinase-like 1
Cfa.11020.1.A1_at	1.812270E-04	2.557083E-02	0.83	1.21	PREDICTED: Macaca mulatta 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble) (HMGCS1); mRNA	90.0	NM_002130	XM_001090857	HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)
Cfa.11029.1.A1_at	2.746550E-04	3.223357E-02	0.9	1.11	PREDICTED: Canis familiaris similar to Protein C6orf115 (LOC476222); mRNA	100.0	AL136522	XM_533427	LOC476222	similar to Protein C6orf115
Cfa.11029.1.A1_s_at	2.329820E-03	1.033647E-01	0.86	1.16	PREDICTED: Canis familiaris similar to Protein C6orf115 (LOC476222); mRNA	99.2	NM_021243	XM_533427	LOC476222	similar to Protein C6orf115
Cfa.11074.1.A1_at	1.248980E-02	2.357450E-01	1.15	.87	PREDICTED: Pan troglodytes protein inhibitor of activated STAT X; transcript variant 3 (PIAS2); mRNA	37.5	AC090241	XM_001147067	PIAS2	protein inhibitor of activated STAT, 2
Cfa.11107.1.A1_at	8.492640E-03	1.971402E-01	0.88	1.14	Mus musculus Mor 5-prime Beta5; MOR 5-prime Beta4; MOR 5-prime beta3; MOR 5-prime beta2; and MOR 5-prime beta1 genes; complete cds; and Hbb gene; Hbb-D allele; locus control region	4.8	AL355075	AF071080		
Cfa.11127.1.A1_at	7.008290E-06	3.548256E-03	0.74	1.35	PREDICTED: Canis familiaris similar to Activated RNA polymerase II transcriptional coactivator p15 (Positive cofactor 4) (PC4) (p14) (LOC479283); mRNA	95.5	AB170806	XM_536425	LOC479283	similar to Activated RNA polymerase II transcriptional coactivator p15 (Positive cofactor 4) (PC4) (p14)

Cfa.11147.1.A1_at	1.734910E-05	6.274105E-03	0.84	1.19	PREDICTED: Canis familiaris similar to CBF1 interacting corepressor isoform 2; transcript variant 2 (LOC478804); mRNA	100.0	NM_004882	XM_535968	LOC478804	similar to CBF1 interacting corepressor isoform 2
Cfa.11167.1.A1_at	7.553520E-03	1.848014E-01	1.12	.89	Homo sapiens transcription factor FOXL2 mutant 3 (FOXL2) mRNA; complete cds	51.6	AC092947	DQ089672	FOXL2	forkhead box L2
Cfa.11172.1.A1_at	1.672460E-02	2.715507E-01	0.9	1.12	PREDICTED: Pan troglodytes similar to QKI; transcript variant 3 (LOC472181); mRNA	87.1	NM_206853	XM_001154915	QKI	quaking homolog, KH domain RNA binding (mouse)
Cfa.11186.1.A1_at	7.040390E-03	1.795988E-01	1.17	.86	PREDICTED: Equus caballus similar to delta-notch-like EGF repeat-containing transmembrane; (LOC100063115); mRNA	40.6	BC035009	XM_001494467	DNER	delta/notch-like EGF repeat containing
Cfa.11197.1.A1_s_at	2.108710E-02	2.988389E-01	0.86	1.16	PREDICTED: Canis familiaris similar to secretogranin III (LOC478307); mRNA	100.0	AK290175	XM_535482	SCG3	secretogranin III
Cfa.11202.1.S1_at	1.903900E-02	2.869854E-01	1.14	.88	PREDICTED: Pan troglodytes NGFRAP1-like 1 (NGFRAP1L1); mRNA	27.8	Z70719	XM_521186	BEX5	BEX family member 5
Cfa.11206.1.A1_at	9.680240E-03	2.091311E-01	1.15	.87	PREDICTED: Canis familiaris similar to Gamma-aminobutyric-acid receptor beta-3 subunit precursor (GABA(A) receptor) (LOC606913); mRNA	99.8	NM_021912	XM_843389	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3
Cfa.11209.1.A1_at	3.894670E-04	4.009740E-02	0.79	1.26	PREDICTED: Macaca mulatta similar to ecotropic viral integration site 2A isoform 2; transcript variant 2 (LOC713110); mRNA	33.7	M55267	XM_001112112	LOC713110	similar to ecotropic viral integration site 2A isoform 2
Cfa.11220.1.A1_at	4.759670E-03	1.476361E-01	0.88	1.13	PREDICTED: Canis familiaris similar to transmembrane protein 14A (LOC474937); mRNA	93.9	NM_014051	XM_532172	TMEM14A	transmembrane protein 14A
Cfa.11246.1.A1_at	4.081010E-04	4.143002E-02	1.18	.85	Homo sapiens cDNA clone IMAGE:3507779; partial cds	23.9	BC106032	BC001512		
Cfa.11247.1.S1_at	1.464600E-02	2.544573E-01	0.89	1.12	PREDICTED: Canis familiaris similar to FK506-binding protein 3 (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (25 kDa FKBP) (FKBP-25) (Rapamycin-selective 25 kDa immunophilin) (LOC610412); mRNA	100.0	NULL	XM_847912	LOC610412	similar to FK506-binding protein 3 (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (25 kDa FKBP) (FKBP-25) (Rapamycin-selective 25 kDa immunophilin)

Cfa.11264.1.A1_at	8.537140E-03	1.976309E-01	0.84	1.19	PREDICTED: Pan troglodytes similar to fungal sterol-C5-desaturase homolog; transcript variant 3 (LOC451624); mRNA	9.0	AL109809	XM_001167285	SC5DL	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like
Cfa.11277.1.A1_at	4.498330E-05	1.087560E-02	0.77	1.30	PREDICTED: Canis familiaris similar to Ribonuclease UK114 (14.5 kDa translational inhibitor protein) (p14.5) (UK114 antigen homolog); transcript variant 1 (LOC475043); mRNA	99.3	BC012592	XM_532278	HRSP12	heat-responsive protein 12
Cfa.1129.1.S1_at	3.851700E-03	1.336757E-01	0.89	1.13	PREDICTED: Canis familiaris similar to optic atrophy 1 isoform 8 (LOC477129); mRNA	100.0	BC025160	XM_534321	OPA1	optic atrophy 1 (autosomal dominant)
Cfa.1129.1.S1_s_at	1.221590E-02	2.339614E-01	0.9	1.11	PREDICTED: Canis familiaris similar to optic atrophy 1 isoform 8 (LOC477129); mRNA	100.0	AB385350	XM_534321	OPA1	optic atrophy 1 (autosomal dominant)
Cfa.11297.1.A1_s_at	1.717420E-02	2.741519E-01	1.16	.86	PREDICTED: Canis familiaris similar to netrin-G1 ligand (LOC607997); mRNA	81.6	NM_022143	XM_844368	LRRC4	leucine rich repeat containing 4
Cfa.11345.1.A1_s_at	2.835970E-05	8.594787E-03	0.84	1.20	PREDICTED: Canis familiaris similar to Mago nashi protein homolog; transcript variant 1 (LOC479562); mRNA	99.1	BC018211	XM_536702	MAGOH	mago-nashi homolog, proliferation-associated (Drosophila)
Cfa.11434.1.A1_at	1.744300E-02	2.752693E-01	0.83	1.20	PREDICTED: Canis familiaris similar to DPCD protein; transcript variant 3 (LOC477800); mRNA	100.0	AC025754	XM_856978	LOC477800	similar to DPCD protein
Cfa.11452.1.A1_at	1.267050E-03	7.521034E-02	0.88	1.13	PREDICTED: Canis familiaris similar to smoothelin isoform c; transcript variant 3 (LOC477542); mRNA	99.0	AK225648	XM_860837	SMTN	smoothelin
Cfa.11461.1.A1_at	1.372910E-02	2.457703E-01	1.14	.87	Homo sapiens Fanconi anemia; complementation group C (FANCC) gene; complete cds	5.2	AL359085	AY220878		
Cfa.11471.1.A1_s_at	1.603160E-02	2.649462E-01	0.9	1.11	PREDICTED: Canis familiaris similar to COX15 homolog isoform 1 precursor (LOC477792); mRNA	99.5	NULL	XM_534986	LOC477792	similar to COX15 homolog isoform 1 precursor
Cfa.11478.1.A1_at	6.916250E-03	1.781214E-01	1.16	.86	PREDICTED: Bos taurus hypothetical protein LOC782909 (LOC782909); mRNA	36.0	NULL	XM_001251564	LOC782909	similar to chromosome 9 open reading frame 79

Cfa.11496.1.A1_at	1.459120E-03	8.221204E-02	1.14	.88	Sclerotinia sclerotiorum 1980 predicted protein (SS1G_10801) partial mRNA	4.4	CT823560	XM_001588304	SS1G_10801	hypothetical protein
Cfa.11507.1.A1_at	8.960540E-04	6.245444E-02	0.79	1.27	PREDICTED: Canis familiaris similar to thyroid autoantigen; transcript variant 2 (LOC474485); mRNA	100.0	Z83840	XM_852799	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6
Cfa.11513.1.S1_at	1.691610E-03	8.942092E-02	0.87	1.15	PREDICTED: Canis familiaris similar to Enhancer of rudimentary homolog (LOC480371); mRNA	99.4	XM_001251924	XM_537493	ERH	enhancer of rudimentary homolog (Drosophila)
Cfa.11513.2.A1_at	3.207320E-04	3.539154E-02	0.83	1.20	PREDICTED: Canis familiaris similar to Enhancer of rudimentary homolog (LOC480371); mRNA	96.3	XM_001495052	XM_537493	ERH	enhancer of rudimentary homolog (Drosophila)
Cfa.11524.1.S1_at	1.663600E-02	2.707754E-01	0.89	1.12	PREDICTED: Macaca mulatta similar to ATP binding domain 1 family; member C (LOC709300); mRNA	42.1	NM_016301	XM_001107255	LOC709300	similar to ATP binding domain 1 family, member C
Cfa.1155.1.S1_at	3.845880E-03	1.336757E-01	0.91	1.10	PREDICTED: Canis familiaris similar to G+C-rich promoter-binding protein; transcript variant 7 (LOC478062); mRNA	98.2	NULL	XM_854791	GPBP1	GC-rich promoter binding protein 1
Cfa.11579.1.A1_s_at	2.726730E-03	1.120772E-01	1.15	.87	PREDICTED: Canis familiaris similar to anaphase-promoting complex subunit 5; transcript variant 6 (LOC477471); mRNA	100.0	BC001950	XM_855845	ANAPC5	anaphase promoting complex subunit 5
Cfa.11587.1.A1_at	7.578360E-03	1.848702E-01	0.77	1.29	PREDICTED: Canis familiaris similar to kinesin family member 9 isoform 2; transcript variant 1 (LOC476642); mRNA	100.0	AK292547	XM_533847	KIF9	kinesin family member 9
Cfa.11596.1.A1_s_at	1.781960E-03	9.151151E-02	0.88	1.14	Vulpes vulpes mRNA for sperm protein 13 (SP13)	97.7	AK313243	AJ421969		
Cfa.11604.1.A1_s_at	1.110410E-02	2.223862E-01	0.9	1.11	PREDICTED: Canis familiaris similar to RNA-binding protein 10 (RNA binding motif protein 10) (DXS8237E); transcript variant 1 (LOC480895); mRNA	97.3	NM_152856	XM_538013	RBM10	RNA binding motif protein 10
Cfa.11616.1.A1_at	3.502010E-04	3.758122E-02	1.21	.82	PREDICTED: Canis familiaris similar to Phosphatidylinositol 3-kinase regulatory gamma subunit (PI3-kinase p85-gamma subunit) (PtdIns-3-kinase p85-gamma) (p55PIK); transcript variant 2 (LOC482512);	100.0	AL358075	XM_856294	PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)

					mRNA					
Cfa.11617.1.A1_at	2.095500E-03	9.845149E-02	1.13	.88	NULL	null	AC019051	NULL		
Cfa.11619.1.A1_at	7.277400E-05	1.456665E-02	1.17	.86	PREDICTED: Bos taurus similar to OTTHUMP00000022587 (LOC514124); mRNA	3.9	AC073896	XM_591925		
Cfa.11625.1.A1_s_at	8.940330E-03	2.017033E-01	0.84	1.19	PREDICTED: Canis familiaris similar to 3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMG-CoA reductase); transcript variant 1 (LOC479182); mRNA	100.0	M11058	XM_536323	HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase
Cfa.11676.1.A1_at	6.535860E-03	1.734098E-01	0.86	1.16	Homo sapiens clone 24841 mRNA sequence	22.1	AC012457	AF131834	EFR3B	EFR3 homolog B (S. cerevisiae)
Cfa.11769.1.A1_s_at	1.981200E-02	2.914904E-01	0.84	1.20	PREDICTED: Canis familiaris similar to protein containing single MORN motif in testis (LOC475733); mRNA	100.0	AY367766	XM_532942	LOC475733	similar to protein containing single MORN motif in testis
Cfa.11771.1.A1_at	3.823930E-04	3.946351E-02	1.15	.87	PREDICTED: Strongylocentrotus purpuratus hypothetical LOC583843 (LOC583843); mRNA	4.8	AC008861	XM_783736	LOC583843	hypothetical LOC583843
Cfa.11774.1.S1_at	1.674490E-03	8.918524E-02	0.88	1.14	PREDICTED: Canis familiaris similar to CG18659-PA; isoform A (LOC609706); mRNA	84.1	NM_020946	XM_847020	DENND1A	DENN/MADD domain containing 1A
Cfa.11777.1.S1_at	8.373900E-03	1.951638E-01	1.14	.87	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 6; 14kDa (LOC474483); mRNA	100.0	AC213220	XM_531712	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa
Cfa.11777.2.A1_s_at	1.085590E-04	1.861289E-02	0.82	1.21	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 6; 14kDa (LOC474483); mRNA	100.0	AK291874	XM_531712	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa
Cfa.11779.1.A1_at	1.371100E-02	2.457530E-01	0.9	1.11	PREDICTED: Canis familiaris hypothetical LOC479517; transcript variant 1 (LOC479517); mRNA	100.0	BC153132	XM_536655	ZSWIM7	zinc finger, SWIM-type containing 7
Cfa.11789.1.A1_at	5.711590E-	1.620292E-	1.11	.90	PREDICTED: Pan troglodytes polymerase (RNA) III (DNA directed) polypeptide A;	5.2	BC041089	XM_507865	POLR3A	polymerase (RNA) III (DNA

	03	01			155kDa (POLR3A); mRNA					directed) polypeptide A, 155kDa
Cfa.11878.1.A1_at	1.477380E-03	8.256134E-02	1.16	.86	Bos taurus transmembrane protein 201 (TMEM201); mRNA >gi|79158726|gb|BC108140.1| Bos taurus similar to CG7744-PA; mRNA (cDNA clone MGC:128856 IMAGE:8119715); complete cds	15.8	AL954705	NM_001037451	TMEM201	transmembrane protein 201
Cfa.11892.2.A1_s_at	1.444460E-02	2.522842E-01	1.12	.89	PREDICTED: Pan troglodytes similar to glycosyl-phosphatidylinositol-anchored molecule-like protein (LOC472878); mRNA	35.5	NM_002066	XM_528249	GML	glycosylphosphatidylinositol anchored molecule like protein
Cfa.11893.1.A1_at	1.163080E-02	2.283447E-01	0.88	1.14	PREDICTED: Canis familiaris hypothetical protein LOC612595 (LOC612595); mRNA	23.0	AL160275	XM_850328	LOC612595	hypothetical protein LOC612595
Cfa.119.1.S1_at	4.206620E-04	4.208376E-02	1.18	.85	PREDICTED: Equus caballus similar to connexin 43 (LOC100067229); mRNA	91.4	AB169817	XM_001504197	CX43	connexin 43
Cfa.11901.1.A1_at	1.636380E-02	2.677628E-01	1.1	.91	Xenopus tropicalis Ras-related associated with diabetes; mRNA (cDNA clone MGC:121896 IMAGE:7587816); complete cds	4.3	AP003499	BC135196	rrad	Ras-related associated with diabetes
Cfa.11922.1.A1_at	1.404100E-02	2.485621E-01	1.2	.83	PREDICTED: Pan troglodytes similar to MEIS1 protein; transcript variant 8 (LOC459288); mRNA	91.9	AC007392	XM_001167056	MEIS1	Meis homeobox 1
Cfa.1200.1.S1_s_at	1.175080E-02	2.293204E-01	1.11	.90	Canis lupus familiaris secreted frizzled-related protein 2 (SFRP2); mRNA >gi|30519781|emb|AJ560716.1|CFA560716 Canis familiaris mRNA for putative secreted frizzled related protein 2 (sfrp2 gene)	100.0	AF311912	NM_001002987	SFRP2	secreted frizzled-related protein 2
Cfa.12004.1.A1_at	1.225910E-04	2.029117E-02	1.18	.85	Homo sapiens visual system homeobox 2 (VSX2); mRNA	28.0	NM_182894	NM_182894	VSX2	visual system homeobox 2
Cfa.1201.1.A1_s_at	6.295300E-04	5.125131E-02	0.87	1.15	Canis lupus familiaris Ribosomal protein S17 (RPS17); mRNA >gi|5441540|emb|AJ388523.1|CFA388523 Canis familiaris mRNA for Ribosomal protein S17 (rpS17 gene)	99.6	AB174364	NM_001003099	RPS17	Ribosomal protein S17

Cfa.1201.1.A1_x_at	7.369050E-03	1.825717E-01	0.88	1.13	Canis lupus familiaris Ribosomal protein S17 (RPS17); mRNA >gi|5441540|emb|AJ388523.1|CFA388523 Canis familiaris mRNA for Ribosomal protein S17 (rpS17 gene)	90.9	NULL	NM_001003099	RPS17	Ribosomal protein S17
Cfa.1201.2.S1_at	5.819370E-04	4.968980E-02	0.78	1.29	PREDICTED: Equus caballus hypothetical protein LOC100071774 (LOC100071774); mRNA	79.3	BC018386	XM_001501623		
Cfa.12032.1.A1_at	1.210340E-02	2.333646E-01	1.13	.89	PREDICTED: Bos taurus hypothetical LOC508943; transcript variant 6 (LOC508943); mRNA	62.8	AC015651	XM_880929	MAP3K3	mitogen-activated protein kinase kinase kinase 3
Cfa.12053.1.A1_at	2.572980E-03	1.085819E-01	1.12	.89	PREDICTED: Canis familiaris similar to olfactory receptor; family 2; subfamily A; member 25 (LOC482724); mRNA	99.6	NULL	XM_539840	LOC482724	similar to olfactory receptor, family 2, subfamily A, member 25
Cfa.12056.1.A1_s_at	3.279890E-07	5.227780E-04	0.79	1.27	PREDICTED: Canis familiaris similar to Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 (Rotamase Pin4) (PPIase Pin4) (LOC607878); mRNA	100.0	NR_003571	XM_844726	PIN4	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)
Cfa.12114.1.A1_at	4.731500E-03	1.473373E-01	1.12	.89	PREDICTED: Canis familiaris similar to Melanoma-associated antigen B3 (MAGE-B3 antigen) (LOC480870); mRNA	99.6	NULL	XM_537986	MAGEB5	melanoma antigen family B, 5
Cfa.12115.3.A1_s_at	6.199680E-03	1.691578E-01	0.86	1.16	PREDICTED: Canis familiaris similar to Splicing factor; arginine/serine-rich 5 (Pre-mRNA splicing factor SRP40) (Insulin-induced growth response protein CL-4) (Delayed-early protein HRS); transcript variant 16 (LOC490754); mRNA	100.0	NULL	XM_862114	SFRS5	splicing factor, arginine/serine-rich 5
Cfa.12171.1.A1_at	5.896010E-04	4.994779E-02	0.85	1.18	PREDICTED: Canis familiaris similar to CG4679-PA (LOC475765); mRNA	100.0	AC090814	XM_532975	PTCD3	Pentatricopeptide repeat domain 3
Cfa.12185.1.A1_at	1.145750E-03	7.155705E-02	1.2	.83	Homo sapiens; clone IMAGE:3049181; mRNA	44.5	BC020554	BC020554		
Cfa.12196.1.A1_at	1.315380E-04	2.104364E-02	0.82	1.22	Bos taurus chromosome 12 open reading frame 31 ortholog (C12orf31); mRNA >gi|83638543|gb|BC109741.1| Bos taurus similar to C49H3.3; mRNA (cDNA clone MGC:133594 IMAGE:8065236); complete	46.4	NULL	NM_001038522	C12orf31	chromosome 12 open reading frame 31 ortholog

					cds					
Cfa.1222.1.A1_at	1.044680E-02	2.157284E-01	1.11	.90	Homo sapiens mRNA; cDNA DKFZp547G133 (from clone DKFZp547G133)	37.6	AC090359	AL512695		
Cfa.12239.1.S1_at	2.063640E-02	2.958807E-01	0.91	1.10	PREDICTED: Canis familiaris similar to ribosomal protein L34 (LOC478509); mRNA	30.1	AL158217	XM_535688	LOC478509	similar to ribosomal protein L34
Cfa.12239.1.S1_s_at	2.454950E-04	3.098204E-02	0.77	1.31	PREDICTED: Canis familiaris similar to ribosomal protein L34 (LOC608033); mRNA	99.4	DQ895715	XM_845040	LOC608033	similar to ribosomal protein L34
Cfa.12247.1.A1_at	1.690900E-02	2.725368E-01	0.87	1.15	Botryotinia fuckeliana B05.10 hypothetical protein (BC1G_13095) partial mRNA	5.5	AC011378	XM_001548209	BC1G_13095	hypothetical protein
Cfa.12293.1.A1_at	1.238470E-02	2.353460E-01	1.17	.86	PREDICTED: Canis familiaris similar to nuclear receptor subfamily 2; group F; member 2; transcript variant 2 (LOC479026); mRNA	100.0	NULL	XM_844404	NR2F2	nuclear receptor subfamily 2, group F, member 2
Cfa.12305.1.A1_at	6.699920E-03	1.753839E-01	1.11	.90	Homo sapiens bone morphogenetic protein 15 precursor (BMP15) gene; exon 2 and complete cds	10.5	AF082350	AF082350		
Cfa.1235.1.S1_a_at	4.928800E-03	1.494791E-01	1.11	.90	Homo sapiens cholecystokinin (CCK) gene; complete cds	80.0	AY514491	AY514491		
Cfa.12354.1.A1_a_at	6.445750E-03	1.725080E-01	0.8	1.25	PREDICTED: Canis familiaris hypothetical LOC479986 (LOC479986); mRNA	100.0	AC084149	XM_537110	TYW3	tRNA-yW synthesizing protein 3 homolog (S. cerevisiae)
Cfa.12367.1.A1_at	1.403370E-02	2.485493E-01	0.81	1.24	Pongo pygmaeus mRNA; cDNA DKFZp469I056 (from clone DKFZp469I056)	68.3	AK293101	CR859714	GNG12	guanine nucleotide binding protein (G protein), gamma 12
Cfa.1237.1.S1_at	1.246360E-02	2.356048E-01	0.89	1.12	Sus scrofa mRNA; clone:THY010115H05; expressed in thymus	22.2	AL442071	AK239605		
Cfa.12374.1.A1_at	7.804360E-04	5.711916E-02	1.15	.87	PREDICTED: Canis familiaris similar to BAI1-associated protein 2-like 1; transcript variant 4 (LOC479748); mRNA	99.0	AL390964	XM_855969	BAIAP2L1	BAI1-associated protein 2-like 1
Cfa.1238.7.S1_s_at	2.372660E-03	1.045676E-01	1.13	.89	PREDICTED: Canis familiaris similar to Cytochrome c oxidase polypeptide VIa-heart; mitochondrial precursor (COXVIAH);	100.0	M83308	XM_851113	LOC479780	similar to Cytochrome c oxidase polypeptide VIa-heart,

					transcript variant 2 (LOC479780); mRNA					mitochondrial precursor (COXVIAH)
Cfa.12382.1.A1_at	6.383340E-04	5.125131E-02	1.12	.89	Hordeum vulgare subsp. vulgare cDNA clone: FLbaf76n24; mRNA sequence	5.7	AC115282	AK250434		
Cfa.12393.1.A1_at	1.883460E-02	2.851027E-01	1.1	.91	NULL	null	AC115282	NULL		
Cfa.12458.1.A1_at	1.816240E-02	2.799495E-01	1.14	.88	PREDICTED: Macaca mulatta integrin; alpha 9 (ITGA9); partial mRNA	5.8	EU368948	XM_001086555	ITGA9	integrin, alpha 9
Cfa.12483.1.A1_at	1.086250E-03	6.966732E-02	1.12	.89	null	null	null	null		
Cfa.12495.1.A1_at	1.912390E-03	9.452284E-02	0.88	1.14	PREDICTED: Canis familiaris similar to WD-repeat protein 43 (LOC475713); mRNA	100.0	NM_015131	XM_532920	WDR43	WD repeat domain 43
Cfa.12497.1.A1_at	5.308080E-04	4.690621E-02	1.13	.88	PREDICTED: Equus caballus hypothetical protein LOC100059523; transcript variant 2 (LOC100059523); mRNA	50.2	AB040529	XM_001497658	MAGED4	melanoma antigen family D, 4
Cfa.1250.1.S1_at	2.761360E-03	1.127513E-01	0.87	1.15	PREDICTED: Pan troglodytes similar to PI-3-kinase ATX; transcript variant 1 (LOC453961); mRNA	20.2	AC026472	XM_001151478	LOC453961	similar to PI-3-kinase ATX
Cfa.12502.1.A1_at	2.065010E-02	2.959298E-01	0.89	1.13	PREDICTED: Canis familiaris similar to G-protein-coupled receptor induced protein (LOC482039); mRNA	100.0	AK022787	XM_539160	TRIB1	tribbles homolog 1 (Drosophila)
Cfa.12513.1.A1_at	6.028460E-03	1.671616E-01	0.87	1.15	NULL	null	AC015751	NULL		
Cfa.12521.1.A1_at	1.875120E-02	2.842402E-01	0.83	1.21	Mus musculus pregnancy specific glycoprotein 16 (Psg16); mRNA	5.2	NULL	NM_007676	Psg16	pregnancy specific glycoprotein 16
Cfa.12533.1.A1_at	9.896190E-04	6.624244E-02	0.84	1.20	PREDICTED: Macaca mulatta similar to insulin induced gene 1 isoform 2 (LOC718513); mRNA	26.9	NM_005542	XM_001111307	LOC718513	similar to insulin induced gene 1 isoform 2
Cfa.12547.1.A1_at	1.922920E-02	2.882371E-01	0.85	1.18	Chaetomium globosum CBS 148.51 hypothetical protein (CHGG_06320) mRNA;	5.3	AC131934	XM_001222414	CHGG_06320	hypothetical protein

					complete cds					
Cfa.1259.1.S1_at	3.452590E-04	3.733221E-02	0.69	1.45	PREDICTED: Canis familiaris similar to Early endosome antigen 1 (Endosome-associated protein p162) (Zinc finger FYVE domain containing protein 2) (LOC475424); mRNA	100.0	NM_003566	XM_532649	EEA1	early endosome antigen 1
Cfa.1259.1.S1_s_at	3.124620E-03	1.199555E-01	0.78	1.28	PREDICTED: Canis familiaris similar to Early endosome antigen 1 (Endosome-associated protein p162) (Zinc finger FYVE domain containing protein 2) (LOC475424); mRNA	98.6	BC156545	XM_532649	EEA1	early endosome antigen 1
Cfa.12596.1.A1_x_at	4.763570E-03	1.476361E-01	0.86	1.16	Canis lupus familiaris SEC11 homolog C (S. cerevisiae) (SEC11C); mRNA >gi|164083|gb|J05069.1|DOGSPS Canine 21 kDa signal peptidase subunit mRNA; complete cds	78.8	NULL	NM_001003312	SEC11C	SEC11 homolog C (S. cerevisiae)
Cfa.12598.1.A1_at	3.551250E-03	1.277456E-01	1.11	.90	PREDICTED: Macaca mulatta voltage-gated sodium channel type 4 alpha (SCN4A); mRNA	9.9	AC127029	XM_001116451	SCN4A	sodium channel, voltage-gated, type IV, alpha subunit
Cfa.12614.1.A1_at	1.142500E-03	7.155705E-02	1.12	.90	Macaca fascicularis testis cDNA clone: QtsA-12836; similar to human tousled-like kinase 2 (TLK2); mRNA; RefSeq: NM_006852.2	4.9	AC002056	AB168531		
Cfa.12622.1.A1_at	4.167270E-03	1.384853E-01	1.11	.90	PREDICTED: Canis familiaris hypothetical LOC475314 (LOC475314); mRNA	64.2	AL358292	XM_532542	LOC475314	hypothetical LOC475314
Cfa.12629.1.A1_at	1.035560E-02	2.153015E-01	0.88	1.14	full-length cDNA clone CS0DF005YI08 of Fetal brain of Homo sapiens (human)	40.3	CR622439	CR622439		
Cfa.12650.1.S1_at	1.913600E-02	2.875239E-01	1.11	.90	PREDICTED: Canis familiaris similar to Sushi repeat-containing protein SRPX precursor (LOC491828); mRNA	100.0	AK125542	XM_548948	SRPX	sushi-repeat-containing protein, X-linked
Cfa.12673.1.A1_at	1.619090E-03	8.709692E-02	1.11	.90	NULL	null	BX004861	NULL		
Cfa.12674.1.A1_s_at	9.526830E-04	6.436219E-02	0.8	1.25	PREDICTED: Equus caballus ryanodine receptor 1 (LOC100034036); mRNA	95.9	NM_001042723	XM_001496610	LOC100034036	ryanodine receptor 1

Cfa.12713.1.A1_at	1.615580E-02	2.659171E-01	1.12	.89	PREDICTED: Canis familiaris similar to metallophosphoesterase 1 isoform a precursor; transcript variant 2 (LOC490556); mRNA	6.4	AC097522	XM_855269	MPPE1	metallophosphoesterase 1
Cfa.12739.1.A1_at	9.808550E-03	2.104242E-01	0.87	1.15	Homo sapiens phosphorylase kinase; beta (PHKB); transcript variant 2; mRNA	7.0	NM_001031835	NM_001031835	PHKB	phosphorylase kinase, beta
Cfa.12743.1.A1_at	8.896720E-03	2.012988E-01	1.13	.88	PREDICTED: Pan troglodytes SET domain; bifurcated 1 (SETDB1); mRNA	36.3	AL355860	XM_524864	SETDB1	SET domain, bifurcated 1
Cfa.12745.1.A1_at	1.282920E-04	2.075581E-02	1.15	.87	PREDICTED: Canis familiaris similar to suppressor of Ty 6 homolog; transcript variant 8 (LOC480627); mRNA	97.3	NULL	XM_863132	SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)
Cfa.12820.2.A1_a_at	7.908670E-03	1.892934E-01	1.1	.91	PREDICTED: Macaca mulatta cysteine-rich; angiogenic inducer; 61 (CYR61); mRNA	91.5	NM_001554	XM_001104992	CYR61	cysteine-rich, angiogenic inducer, 61
Cfa.12827.1.A1_at	5.109990E-03	1.525288E-01	0.84	1.19	PREDICTED: Ornithorhynchus anatinus similar to Rhpn1 protein (LOC100089618); mRNA	9.1	AC091611	XM_001518926	LOC100089618	similar to Rhpn1 protein
Cfa.12866.1.A1_at	1.634430E-02	2.675454E-01	0.87	1.15	null	null	null	null		
Cfa.12899.1.A1_at	1.632510E-02	2.673328E-01	0.89	1.13	Gryllus bimaculatus mRNA; GBcontig03523	5.0	NULL	AK256662		
Cfa.12909.1.A1_at	1.073340E-02	2.176197E-01	1.11	.90	Metarhizium anisopliae chitinase (CHI11) mRNA; complete cds	7.4	AC130887	AF036320		
Cfa.12910.1.A1_at	1.004690E-03	6.662070E-02	1.19	.84	Xenopus tropicalis cDNA clone MGC:181255 IMAGE:8917141; complete cds	4.2	AC091614	BC159326	ace	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1
Cfa.12924.1.A1_at	5.764720E-03	1.628197E-01	1.11	.90	Drosophila melanogaster Dgk CG34361-RE; transcript variant E (Dgk); mRNA	7.1	NULL	NM_001103749	Dgk	CG34361 gene product from transcript CG34361-RF
Cfa.12929.1.A1_at	2.479600E-03	1.062080E-01	1.18	.85	PREDICTED: Equus caballus similar to uKATP-1 (LOC100064325); mRNA	10.3	NM_004982	XM_001502229	LOC100064325	similar to uKATP-1
Cfa.12931.1.A1_at	8.926790E-	2.016611E-	0.82	1.22	PREDICTED: Canis familiaris similar to Dual specificity protein phosphatase 13 (Testis- and skeletal-muscle-specific DSP)	99.8	NM_001080426	XM_547482	DUSP27	dual specificity phosphatase 27

	03	01			(LOC490361); mRNA					(putative)
Cfa.12937.1.A1_at	1.101960E-03	7.015214E-02	1.21	.83	Raphanus sativus mRNA for vacuolar calcium binding protein; complete cds	6.7	AL139123	AB035900		
Cfa.12953.1.A1_s_at	6.713280E-04	5.284375E-02	0.87	1.15	PREDICTED: Canis familiaris similar to DnaJ (Hsp40) homolog; subfamily C; member 7; transcript variant 2 (LOC480519); mRNA	100.0	NULL	XM_537639	DNAJC7	DnaJ (Hsp40) homolog, subfamily C, member 7
Cfa.12969.1.A1_at	1.307470E-02	2.403652E-01	1.12	.89	Homo sapiens hypocretin receptor 2 (HCRTR2) gene; complete cds	7.1	AL359766	AY062031		
Cfa.13020.1.A1_at	1.790710E-02	2.787096E-01	0.83	1.21	PREDICTED: Canis familiaris similar to dimerization cofactor of hepatocyte nuclear factor 1 (HNF1) from muscle (LOC609970); mRNA	79.0	NM_032151	XM_847332	PCBD2	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2
Cfa.13042.1.A1_a_at	4.227280E-03	1.394031E-01	1.11	.90	NULL	null	AC023270	NULL		
Cfa.13059.1.A1_x_at	3.200090E-05	9.216261E-03	1.19	.84	NULL	null	AC151667	NULL		
Cfa.13076.2.A1_x_at	1.017450E-04	1.787182E-02	1.18	.85	PREDICTED: Rattus norvegicus leucine-rich repeat kinase 1 (predicted) (Lrrk1_predicted); mRNA	6.1	NULL	XM_001056955	Lrrk1	leucine-rich repeat kinase 1
Cfa.13080.1.A1_at	1.430660E-04	2.214693E-02	1.25	.80	Arabidopsis thaliana dem protein-related / defective embryo and meristems protein-related (AT4G33400) mRNA; complete cds	5.8	AL645996	NM_119494	AT4G33400	dem protein-related / defective embryo and meristems protein-related
Cfa.13100.1.A1_s_at	5.541050E-03	1.592432E-01	0.91	1.10	PREDICTED: Canis familiaris similar to Protein C2orf29 (LOC481334); mRNA	96.3	AC134770	XM_538455	LOC481334	similar to Protein C2orf29
Cfa.13124.1.A1_at	1.226780E-02	2.343297E-01	1.15	.87	Canis lupus familiaris selectin E (endothelial adhesion molecule 1) (SELE); mRNA >gi|349438|gb|L23087.1|DOGESELECT Canis familiaris E-selectin mRNA; complete cds	11.5	AL031733	NM_001003310	SELE	selectin E
Cfa.13127.1.A1_at	1.011860E-05	4.576229E-03	1.18	.85	PREDICTED: Canis familiaris similar to ATP-binding cassette; sub-family B (MDR/TAP);	45.3	NG_007374	XM_545512	ABCB11	ATP-binding cassette, sub-family B (MDR/TAP), member 11

					member 11 (LOC488390); mRNA					
Cfa.13139.1.A1_at	4.802890E-03	1.480925E-01	1.12	.89	PREDICTED: Canis familiaris similar to chromosome 6 open reading frame 71; transcript variant 2 (LOC476244); mRNA	99.2	NULL	XM_856900	IYD	iodotyrosine deiodinase
Cfa.1316.1.S1_at	1.703070E-02	2.735783E-01	0.85	1.17	PREDICTED: Canis familiaris similar to RNA U; small nuclear RNA export adaptor (phosphorylation regulated) (LOC479305); mRNA	98.9	NM_032177	XM_846266	RNUXA	RNA U, small nuclear RNA export adaptor (phosphorylation regulated)
Cfa.13177.1.S1_s_at	1.116110E-03	7.061974E-02	0.75	1.33	PREDICTED: Canis familiaris similar to lysophospholipase-like 1 (LOC488598); mRNA	99.4	AK309689	XM_545715	LYPLAL1	lysophospholipase-like 1
Cfa.13182.1.A1_at	3.172620E-03	1.208161E-01	1.15	.87	Synthetic construct Homo sapiens gateway clone IMAGE:100017243 5-prime read INHBA mRNA	7.7	AJ334767	CU675839		
Cfa.13203.1.S1_at	9.031450E-03	2.017118E-01	0.71	1.40	PREDICTED: Canis familiaris similar to Histamine N-methyltransferase (HMT) (LOC476133); mRNA	100.0	AL731575	XM_533340	HNMT	histamine N-methyltransferase
Cfa.13273.1.A1_x_at	1.026200E-02	2.148926E-01	1.13	.88	PREDICTED: Canis familiaris similar to Fibrinogen gamma chain precursor; transcript variant 4 (LOC475474); mRNA	93.8	NULL	XM_862780	FGG	fibrinogen gamma chain
Cfa.1332.1.S1_at	1.352830E-03	7.879598E-02	1.14	.88	PREDICTED: Pan troglodytes contactin 1; transcript variant 4 (CNTN1); mRNA	80.1	AC024900	XM_001168089	CNTN1	contactin 1
Cfa.13321.1.A1_at	1.834460E-02	2.812264E-01	0.88	1.14	null	null	null	null		
Cfa.13330.1.A1_s_at	3.812260E-05	9.943067E-03	1.2	.83	Mus musculus bone marrow macrophage cDNA; RIKEN full-length enriched library; clone:I830027K03 product:hypothetical protein; full insert sequence	97.9	NULL	AK151280	Tmem70	transmembrane protein 70
Cfa.13331.1.A1_at	3.702030E-03	1.303739E-01	1.13	.89	Homo sapiens MRE11 meiotic recombination 11 homolog A (S. cerevisiae) (MRE11A) gene; complete cds	5.5	AC015795	AY584241		

Cfa.13333.1.A1_at	7.718080E-04	5.674011E-02	1.18	.84	Mus musculus 16 days embryo head cDNA; RIKEN full-length enriched library; clone:C130072K23 product:unclassifiable; full insert sequence	5.7	AC074250	AK048551		
Cfa.13343.1.A1_at	4.408830E-05	1.071943E-02	1.21	.83	Canis lupus familiaris cytochrome P450 4A38 (CYP4A38); mRNA >gi|74325336|gb|DQ138951.1| Canis familiaris cytochrome P450 4A38 (CYP4A38) mRNA; complete cds	99.5	AC067733	NM_001048017	CYP4A38	cytochrome P450 4A38
Cfa.13395.1.A1_at	2.846640E-04	3.266804E-02	1.15	.87	Diadasia nigrifrons specimen-voucher BBSL 207985 cytochrome oxidase subunit I gene; partial cds; tRNA-Leu gene; complete sequence; and cytochrome oxidase subunit II gene; partial cds; mitochondrial genes for mitochondrial products	4.1	AL512430	AF300551		
Cfa.13412.1.A1_at	1.675100E-02	2.717223E-01	0.87	1.15	PREDICTED: Canis familiaris similar to WD repeat domain 66; transcript variant 2 (LOC477466); mRNA	94.7	NM_144668	XM_854906	WDR66	WD repeat domain 66
Cfa.13418.1.A1_at	5.913010E-04	4.999340E-02	1.13	.88	Homo sapiens WEE1 homolog 2 (S. pombe) (WEE2); mRNA	10.1	NM_001105558	NM_001105558	WEE2	WEE1 homolog 2 (S. pombe)
Cfa.13448.1.A1_at	1.441050E-02	2.521984E-01	1.11	.90	PREDICTED: Rattus norvegicus similar to 5930402A21 protein (predicted) (RGD1309368_predicted); mRNA	5.1	AL356432	XR_007788	RGD1309368	similar to 5930402A21 protein
Cfa.13455.1.A1_at	1.073520E-02	2.176197E-01	1.11	.90	Trichomonas vaginalis G3 hypothetical protein (TVAG_002620) partial mRNA	5.6	AC055854	XM_001300429	TVAG_002620	hypothetical protein
Cfa.13462.1.A1_at	1.053440E-02	2.164013E-01	1.1	.91	NULL	null	AL355500	NULL		
Cfa.13472.1.A1_at	1.243470E-02	2.355224E-01	0.82	1.21	NULL	null	AC095046	NULL		
Cfa.13476.1.A1_at	5.242690E-03	1.537963E-01	1.11	.90	Homo sapiens mRNA for neurotrypsin	16.9	NM_003619	AJ001531	PRSS12	protease, serine, 12 (neurotrypsin, motopsin)
Cfa.13478.1.A1_at	7.443620E-04	5.610538E-02	1.15	.87	Bos taurus kinesin family member 2B (KIF2B); mRNA >gi|148877385|gb|BC146113.1| Bos taurus similar to Kinesin family member 2B; mRNA	9.4	AP000437	NM_001101181	KIF2B	kinesin family member 2B

					(cDNA clone MGC:165746 IMAGE:30957263); complete cds					
Cfa.13502.1.A1_at	1.610020E-03	8.682608E-02	0.88	1.13	PREDICTED: Canis familiaris similar to nuclear receptor co-repressor 1; transcript variant 2 (LOC479515); mRNA	11.6	AC002553	XM_846392	NCOR1	nuclear receptor co-repressor 1
Cfa.13525.1.A1_at	4.951450E-03	1.497440E-01	0.76	1.31	Macaca fascicularis brain cDNA; clone: QflA-17255	37.1	AC127459	AB172237		
Cfa.13532.1.A1_at	1.072580E-02	2.176197E-01	1.25	.80	Spiroplasma citri restriction modification system S subunit (hsd1) gene; partial cds; and DNA-dependent RNA polymerase beta subunit (rpoB) gene; complete cds	9.5	AC010184	U25815		
Cfa.13563.1.A1_s_at	1.986460E-02	2.916359E-01	1.12	.89	PREDICTED: Canis familiaris similar to ATPase family; AAA domain containing 1 (LOC477584); mRNA	95.7	NULL	XM_534778	ATAD1	ATPase family, AAA domain containing 1
Cfa.13567.1.A1_at	5.771980E-03	1.628834E-01	0.85	1.17	null	null	null	null		
Cfa.1358.1.A1_at	2.545040E-03	1.077288E-01	1.16	.86	PREDICTED: Canis familiaris similar to discs large homolog-associated protein 1 isoform beta; transcript variant 14 (LOC480194); mRNA	98.2	AP002472	XM_852717	DLGAP1	discs, large (Drosophila) homolog-associated protein 1
Cfa.13588.1.A1_at	2.174210E-03	1.003052E-01	0.88	1.13	PREDICTED: Canis familiaris ras p21 (N-RAS); mRNA	53.5	CR595772	XM_843536	NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog
Cfa.13620.2.A1_at	1.749040E-02	2.754838E-01	1.14	.87	PREDICTED: Canis familiaris similar to N-acetyltransferase 5; transcript variant 2 (LOC477138); mRNA	100.0	AC114684	XM_851508	NAT5	N-acetyltransferase 5
Cfa.13639.1.A1_at	7.303430E-03	1.819937E-01	1.1	.91	PREDICTED: Canis familiaris similar to solute carrier family 22 (organic anion/cation transporter); member 9; transcript variant 1 (LOC476048); mRNA	98.6	AB074812	XM_533256	SLC22A10	solute carrier family 22, member 10
Cfa.13642.1.A1_at	9.559490E-04	6.448161E-02	1.14	.88	Escherichia coli strain Ec222 tRNA-Trp gene and pathogenicity island; complete sequence; YagU gene; complete cds; YkgJ gene; partial cds; and unknown genes	4.5	AL513164	AY151282		

Cfa.13653.1.A1_at	9.018180E-03	2.017118E-01	1.1	.91	Homo sapiens WAP domain containing protein HE4-V3 (WFDC2) mRNA; complete cds; alternatively spliced	34.8	AF330261	AF330261	WFDC2	WAP four-disulfide core domain 2
Cfa.1366.1.A1_at	2.821100E-04	3.254854E-02	1.21	.83	Bos taurus glycine receptor; beta (GLRB); mRNA >gi|115305327|gb|BC123491.1| Bos taurus glycine receptor; beta; mRNA (cDNA clone MGC:139764 IMAGE:8282291); complete cds	22.4	NM_000824	NM_174071	GLRB	glycine receptor, beta
Cfa.13675.1.A1_at	5.171920E-03	1.529715E-01	1.14	.87	NULL	null	AL357394	NULL		
Cfa.13699.1.A1_s_at	1.616480E-04	2.398801E-02	1.26	.79	PREDICTED: Canis familiaris similar to WNK lysine deficient protein kinase 1; transcript variant 1 (LOC477728); mRNA	99.6	NULL	XM_534925	WNK1	WNK lysine deficient protein kinase 1
Cfa.13703.1.A1_at	6.281170E-03	1.703278E-01	0.9	1.11	PREDICTED: Rattus norvegicus hypothetical protein LOC680386 (LOC680386); mRNA	4.1	NULL	XM_001056977	LOC680386	hypothetical protein LOC680386
Cfa.13712.1.A1_at	8.780280E-03	2.005228E-01	0.9	1.12	NULL	null	AJ418064	NULL		
Cfa.13718.1.S1_s_at	1.817880E-02	2.800402E-01	1.17	.85	PREDICTED: Canis familiaris similar to Synphilin 1 (Alpha-synuclein interacting protein) (LOC481479); mRNA	99.3	NM_005460	XM_538600	SNCAIP	synuclein, alpha interacting protein
Cfa.13740.1.A1_at	1.718620E-03	9.022485E-02	1.15	.87	Nematostella vectensis predicted protein (NEMVEDRAFT_v1g245290) partial mRNA	7.3	NULL	XM_001628892	NEMVEDRAFT_v1g245290	predicted protein
Cfa.13756.1.A1_at	4.396000E-04	4.299588E-02	1.12	.89	PREDICTED: Canis familiaris similar to transient receptor potential cation channel; subfamily M; member 3 isoform e; transcript variant 7 (LOC476326); mRNA	96.7	NULL	XM_854010	TRPM3	transient receptor potential cation channel, subfamily M, member 3
Cfa.13759.1.A1_at	1.639580E-02	2.680825E-01	1.15	.87	NULL	null	Z93020	NULL		
Cfa.13781.1.A1_at	1.040610E-02	2.154110E-01	1.17	.85	PREDICTED: Canis familiaris similar to ATP-binding cassette; sub-family F; member 1 (ATP-binding cassette 50) (TNF-alpha stimulated ABC protein) (LOC474826); mRNA	56.1	NM_001090	XM_532056	ABCF1	ATP-binding cassette, sub-family F (GCN20), member 1

Cfa.13785.1.A1_at	6.415160E-03	1.720925E-01	0.86	1.16	NULL	null	AC099791	NULL		
Cfa.13788.1.A1_at	1.071610E-02	2.176197E-01	1.1	.91	Homo sapiens cDNA FLJ37902 fis; clone CD34C3000494	5.8	AL022316	AK095221		
Cfa.13793.1.A1_at	1.689260E-02	2.724787E-01	0.88	1.14	null	null	null	null		
Cfa.13809.1.A1_at	7.205660E-03	1.810249E-01	0.91	1.10	Rattus norvegicus ATPase; Na+/K+ transporting; alpha 1 polypeptide; mRNA (cDNA clone MGC:72546 IMAGE:5598014); complete cds	94.3	NULL	BC061968	Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide
Cfa.13815.1.A1_at	4.305340E-03	1.409285E-01	0.87	1.15	PREDICTED: Macaca mulatta mannosidase; alpha; class 1A; member 2; transcript variant 3 (MAN1A2); mRNA	13.0	AC008530	XM_001113249	MAN1A2	mannosidase, alpha, class 1A, member 2
Cfa.13825.1.A1_at	1.036920E-02	2.153015E-01	1.12	.90	Lontra longicaudis cytochrome P-450 (CYPIA) gene; exons 4 through 6 and partial cds	9.0	NULL	DQ093090		
Cfa.13846.1.A1_at	5.292040E-04	4.690621E-02	1.16	.87	PREDICTED: Canis familiaris similar to GLI-Kruppel family member GLI3; transcript variant 2 (LOC483244); mRNA	98.9	AC005158	XM_851131	GLI3	GLI-Kruppel family member GLI3
Cfa.13851.1.A1_at	1.101390E-02	2.215217E-01	0.9	1.11	PREDICTED: Canis familiaris similar to proline dehydrogenase (oxidase) 1 (LOC477562); mRNA	17.2	U79754	XM_534757	PRODH	proline dehydrogenase (oxidase) 1
Cfa.13870.1.A1_at	3.552060E-03	1.277456E-01	1.11	.90	PREDICTED: Homo sapiens hypothetical protein DKFZP761M1511 (DKFZP761M1511); mRNA	71.0	AK026748	XM_001715867	LOC54492	hypothetical LOC54492
Cfa.13889.1.A1_at	1.247690E-02	2.356048E-01	0.86	1.16	Sus scrofa mRNA; clone:UTR010020B09; expressed in uterus	9.4	NULL	AK240002		
Cfa.13896.1.A1_at	3.267300E-03	1.230168E-01	0.9	1.11	null	null	null	null		
Cfa.13909.1.A1_at	2.788140E-05	8.509759E-03	1.29	.77	NULL	null	AC106799	NULL		

Cfa.1393.1.A1_at	2.432850E-03	1.054358E-01	1.2	.84	PREDICTED: Canis familiaris similar to Probable G-protein coupled receptor 37 precursor (Endothelin B receptor-like protein-1) (ETBR-LP-1) (Parkin-associated endothelin receptor-like receptor) (PAELR) (LOC482275); mRNA	97.4	AC004925	XM_539394	GPR37	G protein-coupled receptor 37 (endothelin receptor type B-like)
Cfa.14011.1.A1_at	1.975110E-03	9.561273E-02	1.11	.90	NULL	null	AL672138	NULL		
Cfa.14013.1.A1_at	6.784130E-03	1.764079E-01	1.15	.87	null	null	null	null		
Cfa.14020.1.A1_at	1.064020E-03	6.865405E-02	0.78	1.29	PREDICTED: Canis familiaris similar to insulin induced gene 1 isoform 1; transcript variant 1 (LOC475554); mRNA	100.0	AK291675	XM_532775	INSIG1	insulin induced gene 1
Cfa.14030.1.A1_at	9.238850E-03	2.040214E-01	0.85	1.17	null	null	null	null		
Cfa.14032.1.A1_at	2.092580E-02	2.976998E-01	1.12	.89	PREDICTED: Rattus norvegicus phosphoribosylglycinamide formyltransferase (Gart); mRNA	6.3	AC079235	XM_573258	Gart	phosphoribosylglycinamide formyltransferase
Cfa.14035.1.A1_at	1.039100E-03	6.765154E-02	1.15	.87	PREDICTED: Pan troglodytes NOL1/NOP2/Sun domain family; member 7; transcript variant 1 (NSUN7); mRNA	24.9	NULL	XM_001146944	NSUN7	NOL1/NOP2/Sun domain family, member 7
Cfa.1405.1.A1_at	9.951650E-03	2.124351E-01	0.82	1.23	PREDICTED: Canis familiaris similar to Sorting nexin-24 (LOC608666); mRNA	99.7	NM_014035	XM_845762	SNX24	sorting nexin 24
Cfa.14096.2.S1_s_at	1.300920E-02	2.403220E-01	0.89	1.13	PREDICTED: Canis familiaris similar to PEST-containing nuclear protein (PCNP); transcript variant 1 (LOC478546); mRNA	100.0	AK314629	XM_535723	PCNP	PEST proteolytic signal containing nuclear protein
Cfa.14136.1.A1_at	1.559950E-02	2.618390E-01	1.11	.90	null	null	null	null		
Cfa.14191.1.A1_at	2.026550E-02	2.938077E-01	1.12	.89	Trichomonas vaginalis G3 surface antigen BspA-like (TVAG_101710) partial mRNA	4.5	AC026955	XM_001580389	TVAG_101710	surface antigen BspA-like
Cfa.14194.1.A1_at	8.633700E-	1.989767E-	1.19	.84	NULL	null	AC114962	NULL		

	03	01								
Cfa.14196.1.A1_at	1.997340E-02	2.922407E-01	1.12	.89	PREDICTED: Canis familiaris similar to piwi-like 4 (LOC485123); mRNA	99.7	NULL	XM_542241	PIWIL4	piwi-like 4 (Drosophila)
Cfa.14204.1.A1_at	1.812150E-04	2.557083E-02	1.14	.88	PREDICTED: Canis familiaris similar to Wnt-8b protein precursor (LOC486841); mRNA	54.1	NULL	XM_543970	WNT8B	wingless-type MMTV integration site family, member 8B
Cfa.1422.1.S1_at	1.457370E-02	2.536107E-01	0.89	1.12	PREDICTED: Canis familiaris similar to Ras-related protein R-Ras (p23) (LOC476413); mRNA	97.7	NM_006270	XM_533617	RRAS	related RAS viral (r-ras) oncogene homolog
Cfa.14278.1.A1_at	7.282940E-03	1.819766E-01	0.83	1.20	PREDICTED: Macaca mulatta choroideremia (CHM); mRNA	10.9	NM_000390	XM_001083432	CHM	choroideremia
Cfa.14302.1.A1_at	1.531980E-02	2.602160E-01	0.86	1.17	PREDICTED: Pan troglodytes hypothetical protein LOC740889 (LOC740889); mRNA	5.3	NM_019037	XM_001154573	EXOSC4	exosome component 4
Cfa.14310.1.A1_at	1.073560E-02	2.176197E-01	0.87	1.15	insulin-like growth factor-binding protein 6 [cattle; endothelial cells; mRNA Partial; 366 nt]	3.9	NULL	S52774	IGFBP6	insulin-like growth factor binding protein 6
Cfa.14328.1.A1_at	3.058320E-04	3.432983E-02	1.15	.87	Homo sapiens clone BAC_22700 cytotoxic T-lymphocyte-associated protein 4 (CTLA4) and inducible T-cell co-stimulator (ICOS) genes; complete cds; and endogenous virus HERV-H; partial sequence	5.4	AC006270	AF411058		
Cfa.14342.3.A1_s_at	3.816150E-04	3.946351E-02	1.12	.89	PREDICTED: Canis familiaris similar to Plasma glutathione peroxidase precursor (GSHPx-P); transcript variant 2 (LOC489179); mRNA	100.0	CU690654	XM_848375	LOC489179	similar to Plasma glutathione peroxidase precursor (GSHPx-P)
Cfa.14357.1.A1_at	3.588430E-05	9.773929E-03	1.15	.87	PREDICTED: Canis familiaris similar to deleted in malignant brain tumors 1 isoform a precursor (LOC486922); mRNA	99.1	NULL	XM_544052	DMBT1	deleted in malignant brain tumors 1
Cfa.14361.1.A1_at	1.719340E-02	2.741519E-01	1.11	.90	NULL	null	AC019270	NULL		
Cfa.14364.1.A1_at	2.637210E-05	8.345024E-03	0.76	1.32	Pongo pygmaeus mRNA; cDNA DKFZp459N1339 (from clone	83.5	NM_001007025	CR858622	GOSR1	golgi SNAP receptor complex member 1

					DKFZp459N1339)					
Cfa.14366.1.S1_s_at	3.490280E-03	1.275078E-01	0.82	1.22	PREDICTED: Canis familiaris similar to allograft inflammatory factor 1 isoform 3; transcript variant 1 (LOC474841); mRNA	99.8	U19713	XM_532072	AIF1	allograft inflammatory factor 1
Cfa.14373.1.A1_at	7.079410E-03	1.799867E-01	1.12	.90	NULL	null	AC006038	NULL		
Cfa.14398.1.A1_at	1.596070E-02	2.647183E-01	1.13	.88	PREDICTED: Ornithorhynchus anatinus similar to T cell receptor gamma chain (LOC100081849); mRNA	12.3	AP005120	XM_001512542	LOC100081849	similar to T cell receptor gamma chain
Cfa.14401.1.A1_at	5.008940E-03	1.508466E-01	0.83	1.21	PREDICTED: Bos taurus similar to Chromosome 11 open reading frame 52 (LOC614490); mRNA	14.7	AL353996	XM_866023	LOC614490	hypothetical LOC614490
Cfa.14425.1.S1_at	3.131880E-03	1.199555E-01	1.14	.87	Sus scrofa mRNA; clone:LVRM10127D02; expressed in liver	88.6	NM_002151	AK233353		
Cfa.14434.1.A1_at	1.070090E-02	2.176197E-01	0.85	1.17	Ammopiptanthus mongolicus betaine aldehyde dehydrogenase mRNA; partial cds	4.6	AL807740	DQ288723		
Cfa.14462.2.S1_s_at	1.534760E-02	2.602160E-01	0.84	1.20	PREDICTED: Canis familiaris similar to eukaryotic translation initiation factor 3; subunit 6 (predicted); transcript variant 10 (LOC475070); mRNA	100.0	NULL	XM_855080	EIF3E	eukaryotic translation initiation factor 3, subunit E
Cfa.14495.2.S1_at	2.620310E-04	3.167557E-02	1.27	.79	PREDICTED: Canis familiaris similar to Complement factor I precursor (C3B/C4B inactivator); transcript variant 2 (LOC478515); mRNA	100.0	NM_000204	XM_535694	CFI	complement factor I
Cfa.14550.1.A1_s_at	3.995410E-03	1.356013E-01	0.84	1.19	PREDICTED: Canis familiaris similar to partitioning-defective protein 3 homolog (LOC477953); mRNA	99.3	NULL	XM_535141	PARD3	par-3 partitioning defective 3 homolog (C. elegans)
Cfa.14569.1.S1_at	4.226070E-03	1.394031E-01	1.2	.84	Homo sapiens KIAA0082; mRNA (cDNA clone IMAGE:3894870); partial cds	39.1	AC007297	BC010731	FTSJD2	FtsJ methyltransferase domain containing 2
Cfa.14573.1.A1_s_at	2.156740E-03	1.001244E-01	1.13	.88	PREDICTED: Equus caballus hypothetical protein LOC100052771 (LOC100052771);	88.6	BC108676	XM_001495676	TMEM195	transmembrane protein 195

					mRNA					
Cfa.14626.2.S1_s_at	8.331720E-04	5.946195E-02	1.11	.90	PREDICTED: Canis familiaris similar to Collagen alpha 1(III) chain precursor; transcript variant 12 (LOC478835); mRNA	54.6	NULL	XM_858055	COL3A1	collagen, type III, alpha 1
Cfa.14630.1.A1_at	1.996260E-02	2.922077E-01	0.9	1.11	PREDICTED: Canis familiaris similar to TAF15 RNA polymerase II; TATA box binding protein (TBP)-associated factor; transcript variant 6 (LOC491135); mRNA	99.6	NM_139215	XM_862595	TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa
Cfa.14643.1.A1_at	2.173110E-03	1.003052E-01	1.13	.89	PREDICTED: Canis familiaris similar to rhomboid family 1; transcript variant 1 (LOC490101); mRNA	29.5	DQ431198	XM_547222	RHBDF1	rhomboid 5 homolog 1 (Drosophila)
Cfa.14683.1.A1_at	1.805490E-02	2.792868E-01	1.1	.91	Mus musculus BR serine/threonine kinase 2 (Brsk2); transcript variant 1; mRNA	5.4	AL157996	NM_029426	Brsk2	BR serine/threonine kinase 2
Cfa.14702.1.A1_at	2.155620E-03	1.001244E-01	0.83	1.21	Homo sapiens tensin 1 (TNS1); mRNA	25.5	AC009469	NM_022648	TNS1	tensin 1
Cfa.14718.1.A1_s_at	2.387940E-03	1.047144E-01	1.11	.90	PREDICTED: Canis familiaris similar to chromodomain helicase DNA binding protein 6; transcript variant 3 (LOC477230); mRNA	53.2	BC012516	XM_861064	CHD6	chromodomain helicase DNA binding protein 6
Cfa.14738.1.A1_at	1.276090E-03	7.562380E-02	1.14	.87	Homo sapiens mRNA; cDNA DKFZp686C107 (from clone DKFZp686C107)	31.9	AC097515	AL832772		
Cfa.14796.1.S1_at	1.816780E-03	9.210656E-02	1.14	.87	Botryotinia fuckeliana B05.10 hypothetical protein (BC1G_15245) partial mRNA	14.7	NULL	XM_001546152	BC1G_15245	hypothetical protein
Cfa.148.1.A1_at	1.897100E-03	9.415394E-02	1.17	.86	Canis familiaris alpha-spectrin mRNA; partial cds	100.0	J05243	AY356551	LOC403447	alpha-spectrin
Cfa.14803.1.A1_at	1.209990E-03	7.344417E-02	1.14	.88	NULL	null	AC087069	NULL		
Cfa.1481.1.S1_at	4.807370E-03	1.480925E-01	0.84	1.18	PREDICTED: Canis familiaris similar to Stress 70 protein chaperone microsome-associated 60 kDa protein precursor (Microsomal stress 70 protein ATPase core)	32.4	AL355375	XM_844995	STCH	stress 70 protein chaperone, microsome-associated, 60kDa

					(LOC608091); mRNA					
Cfa.14837.1.A1_at	2.087010E-02	2.975017E-01	0.88	1.14	Passiflora alata isolate 111 glyceraldehyde-3-phosphate dehydrogenase gene; partial cds	4.3	NULL	AY858261		
Cfa.14863.1.A1_at	2.860510E-03	1.152818E-01	0.85	1.17	Sus scrofa mRNA; clone:UTR010032B04; expressed in uterus	64.6	NM_005318	AK240110		
Cfa.14884.1.A1_at	1.459060E-03	8.221204E-02	1.12	.90	null	null	null	null		
Cfa.14886.1.S1_s_at	2.085290E-02	2.974493E-01	0.9	1.11	PREDICTED: Canis familiaris hypothetical LOC479439; transcript variant 3 (LOC479439); mRNA	28.5	NULL	XM_845508	LOC479439	hypothetical LOC479439
Cfa.14895.1.A1_at	1.224600E-02	2.341211E-01	0.82	1.23	Sus scrofa proteasome activator 28 beta subunit (PSME2) gene; complete cds	63.0	AF079558	AY317125		
Cfa.14905.1.A1_a_at	1.602840E-02	2.649462E-01	0.85	1.18	Homo sapiens musashi homolog 2 (Drosophila) (MSI2); transcript variant 2; mRNA	41.3	NM_170721	NM_170721	MSI2	musashi homolog 2 (Drosophila)
Cfa.14908.1.A1_s_at	3.937300E-03	1.348203E-01	1.13	.88	PREDICTED: Canis familiaris similar to Fumarylacetoacetase (Fumarylacetoacetate hydrolase) (Beta-diketonase) (FAA) (LOC610140); mRNA	96.7	CU678021	XM_847553	FAH	fumarylacetoacetate hydrolase (fumarylacetoacetase)
Cfa.14919.1.A1_at	1.033290E-03	6.737520E-02	1.11	.90	PREDICTED: Pan troglodytes similar to Wnt-5b (LOC467191); mRNA	9.3	NM_030775	XM_522589	WNT5B	wingless-type MMTV integration site family, member 5B
Cfa.14989.3.A1_at	7.562510E-03	1.848591E-01	1.13	.89	Homo sapiens cDNA FLJ41092 fis; clone ASTRO2004877	53.7	AK123087	AK123087	DNAJC24	DnaJ (Hsp40) homolog, subfamily C, member 24
Cfa.15109.1.S1_at	7.874570E-03	1.885821E-01	0.83	1.21	Mus musculus 13 days embryo male testis cDNA; RIKEN full-length enriched library; clone:6030437N09 product:unclassifiable; full insert sequence	8.5	AC090805	AK134350		
Cfa.15119.2.A1_a_at	6.201490E-03	1.691578E-01	0.9	1.11	PREDICTED: Canis familiaris similar to zinc finger; matrin type 2; transcript variant 2 (LOC607047); mRNA	98.8	CR606569	XM_852454	ZMAT2	zinc finger, matrin type 2

Cfa.15130.1.A1_at	6.525160E-03	1.732327E-01	1.14	.87	NULL	null	AC095045	NULL		
Cfa.1514.1.S1_s_at	1.943420E-03	9.497007E-02	0.75	1.34	PREDICTED: Pan troglodytes progesterone-induced blocking factor 1; transcript variant 1 (LOC452596); mRNA	87.9	NM_006346	XM_001136288	PIBF1	progesterone immunomodulatory binding factor 1
Cfa.15157.3.A1_x_at	4.842140E-03	1.485257E-01	0.9	1.11	PREDICTED: Canis familiaris similar to phosphodiesterase 4D interacting protein isoform 2; transcript variant 3 (LOC475817); mRNA	74.2	CR626673	XM_853217	PDE4DIP	phosphodiesterase 4D interacting protein
Cfa.15158.1.A1_s_at	8.682610E-03	1.997093E-01	1.1	.91	PREDICTED: Canis familiaris similar to Actin-binding LIM protein 3 (Actin-binding LIM protein family member 3) (abLIM3) (LOC612309); mRNA	99.3	AB384009	XM_850053	ABLIM3	actin binding LIM protein family, member 3
Cfa.15167.1.S1_at	6.042490E-03	1.673549E-01	1.17	.85	PREDICTED: Pan troglodytes guanine nucleotide binding protein (G protein); alpha 13 (GNA13); mRNA	21.3	AK002117	XM_511632	GNA13	guanine nucleotide binding protein (G protein), alpha 13
Cfa.15181.1.A1_s_at	1.006330E-02	2.131608E-01	1.12	.90	PREDICTED: Canis familiaris similar to H/ACA ribonucleoprotein complex subunit 4 (Dyskerin) (Nucleolar protein family A member 4) (snoRNP protein DKC1) (Nopp140-associated protein of 57 kDa) (Nucleolar protein NAP57) (CBF5 homolog) (LOC492263); mRNA	100.0	AF157706	XM_549382	DKC1	dyskeratosis congenita 1, dyskerin
Cfa.15186.1.A1_at	1.356600E-02	2.441710E-01	1.12	.89	PREDICTED: Gallus gallus similar to G-2 and S-phase expressed 1 (LOC768356); mRNA	3.8	NULL	XM_001231202	LOC768356	similar to G-2 and S-phase expressed 1
Cfa.1519.1.A1_at	1.173330E-02	2.292824E-01	0.84	1.18	PREDICTED: Canis familiaris similar to Inhibitor of growth protein 4; transcript variant 2 (LOC477712); mRNA	97.4	NULL	XM_848563	ING4	inhibitor of growth family, member 4
Cfa.15193.2.S1_at	1.911430E-04	2.616405E-02	1.16	.86	Macaca fascicularis brain cDNA clone:QflA-14777; similar to human sorting nexin 1(SNX1) isoform a; mRNA; NM_003099.2	19.3	AC100840	AB056808		
Cfa.15196.1.A1_at	5.756180E-03	1.628197E-01	0.85	1.18	Sus scrofa mRNA; clone:AMP010034C08; expressed in alveolar macrophage	90.1	NM_017633	AK230737		

Cfa.15220.1.A1_s_at	2.030090E-02	2.940590E-01	1.17	.86	PREDICTED: Canis familiaris similar to NAD(P) transhydrogenase; mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase); transcript variant 5 (LOC479342); mRNA	98.5	BC064402	XM_862835	NNT	nicotinamide nucleotide transhydrogenase
Cfa.15237.2.S1_x_at	8.597870E-04	6.105765E-02	1.17	.85	PREDICTED: Canis familiaris similar to golgi phosphoprotein 4; transcript variant 2 (LOC478685); mRNA	46.9	AC117467	XM_856731	GOLIM4	golgi integral membrane protein 4
Cfa.15247.1.S1_at	6.967990E-03	1.785988E-01	1.17	.86	Homo sapiens mRNA; cDNA DKFZp586F0222 (from clone DKFZp586F0222); partial cds	33.3	AC109599	AL117395	HNRNPH3	heterogeneous nuclear ribonucleoprotein H3 (2H9)
Cfa.15258.1.A1_at	1.686020E-02	2.723461E-01	0.86	1.16	Homo sapiens PRKC; apoptosis; WT1; regulator (PAWR) gene; complete cds	4.0	AY300794	AY300794		
Cfa.15287.1.A1_s_at	1.003430E-03	6.662070E-02	1.11	.90	PREDICTED: Canis familiaris similar to Fetuin-B precursor (IRL685) (16G2) (LOC478665); mRNA	97.3	AK315309	XM_535835	FETUB	fetuin B
Cfa.15295.1.S1_s_at	2.090270E-02	2.975679E-01	0.88	1.14	PREDICTED: Canis familiaris similar to ATP synthase; H+ transporting; mitochondrial F0 complex; subunit f; isoform 2 (LOC612408); mRNA	100.0	NULL	XM_850142	LOC612408	similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2
Cfa.15340.1.A1_at	3.071630E-03	1.189972E-01	0.89	1.13	PREDICTED: Canis familiaris similar to arginase; type I (LOC474823); mRNA	21.8	AB170863	XM_532053	ARG1	arginase, liver
Cfa.15347.1.A1_x_at	1.527970E-02	2.602160E-01	0.86	1.16	Bos taurus protocadherin gamma subfamily B; 4 (PCDHGB4); mRNA >gi|151556919|gb|BC149018.1| *Bos taurus* protocadherin gamma subfamily B; 4; mRNA (cDNA clone MGC:152143 IMAGE:8398704); complete cds	55.1	BC150172	NM_001102513	PCDHGB4	protocadherin gamma subfamily B, 4
Cfa.15350.1.A1_at	6.831530E-03	1.767452E-01	0.88	1.14	PREDICTED: Pan troglodytes hypothetical protein LOC741574; transcript variant 1 (LOC741575); mRNA	43.4	AC217768	XM_001164930	LOC741575	hypothetical protein LOC741575
Cfa.15385.1.A1_at	3.480400E-06	2.482760E-03	1.26	.79	null	null	null	null		

Cfa.15393.1.A1_at	4.755620E-04	4.515395E-02	0.73	1.38	Sus scrofa mRNA; clone:OVRM10085A07; expressed in ovary	27.8	AF217403	AK235468		
Cfa.15401.1.A1_at	2.659990E-04	3.170988E-02	1.15	.87	PREDICTED: Canis familiaris hypothetical protein LOC612191 (LOC612191); mRNA	100.0	NM_199337	XM_849926	TMEM179B	transmembrane protein 179B
Cfa.15407.1.A1_s_at	3.537010E-03	1.277456E-01	1.11	.90	PREDICTED: Canis familiaris similar to a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif; 19 preproprotein (LOC609347); mRNA	100.0	AK122622	XM_846592	LOC609347	similar to a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 19 preproprotein
Cfa.15449.1.A1_at	1.071530E-02	2.176197E-01	1.11	.90	PREDICTED: Canis familiaris hypothetical protein LOC610234 (LOC610234); mRNA	99.5	AC009970	XM_847677	LOC610234	hypothetical protein LOC610234
Cfa.15461.1.A1_at	3.744210E-03	1.315364E-01	1.13	.89	Tetrahymena thermophila SB210 hypothetical protein (TTHERM_00628350) partial mRNA	7.4	AJ310932	XM_001019521	TTHERM_00628350	hypothetical protein
Cfa.15466.1.S1_s_at	3.429830E-03	1.265890E-01	0.89	1.12	PREDICTED: Canis familiaris similar to step II splicing factor SLU7 (LOC479308); mRNA	68.9	AK314564	XM_536446	SLU7	SLU7 splicing factor homolog (S. cerevisiae)
Cfa.15483.1.A1_s_at	4.524200E-04	4.366644E-02	0.89	1.12	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 3; 12kDa (LOC478869); mRNA	100.0	NM_002491	XM_536029	NDUFB3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
Cfa.15527.1.A1_at	1.090270E-02	2.198677E-01	1.12	.90	PREDICTED: Macaca mulatta similar to sorbin and SH3 domain containing 2 isoform 2; transcript variant 14 (LOC696139); mRNA	25.6	AC093797	XM_001088514	LOC696139	similar to sorbin and SH3 domain containing 2 isoform 2
Cfa.15571.1.A1_at	5.397690E-03	1.566387E-01	1.15	.87	null	null	null	null		
Cfa.15598.1.A1_at	1.708260E-03	8.987160E-02	0.8	1.25	Xenopus tropicalis ankyrin repeat and SOCS box-containing 6 (asb6); mRNA >gi|77627289|emb|CR761252.2| Xenopus tropicalis finished cDNA; clone TEgg109h20	5.2	AC114291	NM_001016375	asb6	ankyrin repeat and SOCS box-containing 6
Cfa.15645.1.A1_at	3.497010E-03	1.276453E-01	0.89	1.13	PREDICTED: Equus caballus similar to chromosome 11 open reading frame 68; (LOC100057770); mRNA	14.5	NM_031450	XM_001490996	LOC100057770	similar to chromosome 11 open reading frame 68

Cfa.15647.1.A1_s_at	1.993280E-02	2.921297E-01	1.12	.89	Mus musculus 18-day embryo whole body cDNA; RIKEN full-length enriched library; clone:1110029A09 product:hypothetical protein; full insert sequence	70.8	NULL	AK003950	D4Bwg0951e	DNA segment, Chr 4, Brigham & Women's Genetics 0951 expressed
Cfa.15675.1.A1_at	2.005710E-02	2.923975E-01	0.76	1.31	PREDICTED: Bos taurus similar to Notch3 (LOC789485); mRNA	36.6	AC004663	XR_028762	LOC789485	similar to Notch homolog 3
Cfa.15716.1.A1_s_at	1.621100E-02	2.662062E-01	0.9	1.12	PREDICTED: Canis familiaris hypothetical LOC476430 (LOC476430); mRNA	64.9	AK146297	XM_533637	CCDC61	coiled-coil domain containing 61
Cfa.15727.1.A1_at	2.026990E-02	2.938077E-01	1.14	.88	PREDICTED: Canis familiaris similar to Thyroxine-binding globulin precursor (T4-binding globulin) (LOC481007); mRNA	100.0	NM_000354	XM_538128	SERPINA7	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 7
Cfa.15761.1.A1_at	4.366140E-07	6.479201E-04	1.27	.79	PREDICTED: Canis familiaris similar to ATPase; (Na+)/K+ transporting; beta 4 polypeptide (LOC481036); mRNA	100.0	NM_012069	XM_538158	ATP1B4	ATPase, (Na+)/K+ transporting, beta 4 polypeptide
Cfa.15763.1.A1_at	1.005750E-02	2.131608E-01	0.89	1.13	Bos taurus phospholipase A2; group IIF (PLA2G2F); mRNA >gi|152001066|gb|BC147912.1| Bos taurus phospholipase A2; mRNA (cDNA clone MGC:159947 IMAGE:8468062); complete cds	8.6	AC005529	NM_001102522	PLA2G2F	phospholipase A2, group IIF
Cfa.15782.2.S1_s_at	1.898080E-03	9.415394E-02	1.14	.87	PREDICTED: Canis familiaris janus kinase 1; transcript variant 8 (JAK1); mRNA	98.1	M64174	XM_860114	JAK1	Janus kinase 1 (a protein tyrosine kinase)
Cfa.15782.3.S1_at	2.507770E-05	8.114427E-03	1.15	.87	PREDICTED: Homo sapiens similar to T12D8.4 (LOC645432); mRNA	7.3	AC006538	XM_940152		
Cfa.15788.1.S1_at	2.710130E-03	1.120772E-01	1.13	.88	PREDICTED: Canis familiaris similar to tropomyosin 2 (beta) isoform 2; transcript variant 17 (LOC481598); mRNA	74.1	NULL	XM_861514	TPM2	tropomyosin 2 (beta)
Cfa.15865.1.S1_s_at	2.278620E-03	1.022528E-01	1.11	.90	PREDICTED: Canis familiaris cOR51C4 olfactory receptor family 51 subfamily C-like (cOR51C4); mRNA	100.0	NULL	XM_542357	cOR51C4	cOR51C4 olfactory receptor family 51 subfamily C-like
Cfa.15878.1.A1_at	1.669510E-02	2.713269E-01	1.12	.89	PREDICTED: Bos taurus similar to putative SH3BGR protein (LOC617797); mRNA	12.7	AF121897	XM_870116		

Cfa.15925.1.S1_at	1.682640E-03	8.920329E-02	0.78	1.29	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L13 (LOC482029); mRNA	92.7	NM_014078	XM_539150	MRPL13	mitochondrial ribosomal protein L13
Cfa.15965.1.A1_at	1.815330E-07	3.396640E-04	1.37	.73	PREDICTED: Pan troglodytes adenylate kinase 3 (AK3); mRNA	52.8	AL356212	XM_513462	AK3L1	adenylate kinase 3-like 1
Cfa.15978.1.A1_at	5.573940E-03	1.592792E-01	1.13	.89	PREDICTED: Canis familiaris similar to synaptosomal-associated protein 25; transcript variant 2 (LOC477158); mRNA	44.3	NULL	XM_534347	SNAP25	synaptosomal-associated protein, 25kDa
Cfa.15982.1.A1_at	3.289730E-06	2.440923E-03	1.27	.79	NULL	null	AC084854	NULL		
Cfa.15985.1.A1_at	1.273460E-02	2.377586E-01	0.84	1.20	PREDICTED: Canis familiaris similar to Poly(rC)-binding protein 2 (Alpha-CP2) (Putative heterogeneous nuclear ribonucleoprotein X) (hnRNP X) (CTBP) (CBP); transcript variant 20 (LOC477596); mRNA	98.1	NULL	XM_852902	PCBP2	poly(rC) binding protein 2
Cfa.16000.1.S1_at	2.019570E-03	9.649705E-02	1.11	.90	PREDICTED: Macaca mulatta similar to Tyrosine-protein phosphatase non-receptor type 5 (Protein-tyrosine phosphatase striatum-enriched) (STEP) (Neural-specific protein-tyrosine phosphatase) (LOC708151); mRNA	43.0	NM_001039970	XM_001096604	LOC708151	similar to Tyrosine-protein phosphatase non-receptor type 5 (Protein-tyrosine phosphatase striatum-enriched) (STEP) (Neural-specific protein-tyrosine phosphatase)
Cfa.16020.1.S1_at	2.046760E-02	2.949843E-01	0.87	1.14	Xenopus tropicalis BAC clone ISB1-283J3 containing neuroD1 gene; complete cds; complete sequence	25.7	AC068985	AC151466		
Cfa.16058.1.A1_x_at	9.373840E-08	2.521270E-04	1.25	.80	null	null	null	null		
Cfa.16066.1.S1_at	4.856770E-03	1.485961E-01	1.11	.90	Homo sapiens cDNA FLJ78419 complete cds; highly similar to Homo sapiens methionine sulfoxide reductase B3; mRNA	17.0	AL833622	AK293084	MSRB3	methionine sulfoxide reductase B3
Cfa.16082.1.A1_at	6.186970E-11	2.662563E-06	1.31	.77	Macaca fascicularis brain cDNA; clone: QmoA-12220	42.4	AB074172	AB170694		
Cfa.16152.1.S1_at	4.161810E-	1.384107E-	1.1	.91	NULL	null	AC009446	NULL		

	03	01								
Cfa.16189.1.A1_s_at	1.012010E-02	2.132265E-01	0.88	1.13	PREDICTED: Canis familiaris similar to COMM domain containing 6 isoform b (LOC476946); mRNA	100.0	NM_203495	XM_534146	COMMD6	COMM domain containing 6
Cfa.16195.1.S1_at	2.045940E-02	2.949843E-01	0.87	1.16	PREDICTED: Macaca mulatta similar to Activated RNA polymerase II transcriptional coactivator p15 (SUB1 homolog) (Positive cofactor 4) (PC4) (p14) (SUB1); mRNA	15.9	AC008766	XR_010385	SUB1	similar to Activated RNA polymerase II transcriptional coactivator p15 (SUB1 homolog) (Positive cofactor 4) (PC4) (p14)
Cfa.16212.1.S1_at	1.320510E-02	2.410015E-01	0.87	1.14	Pongo pygmaeus mRNA; cDNA DKFZp459B0431 (from clone DKFZp459B0431)	15.7	AL080250	CR859205	TMEM30A	transmembrane protein 30A
Cfa.16219.1.S1_at	1.904900E-03	9.433530E-02	1.11	.90	Canis familiaris 11 beta-hydroxysteroid dehydrogenase 2 mRNA; partial cds	100.0	NULL	AY832857	HSD11B2	hydroxysteroid (11-beta) dehydrogenase 2
Cfa.16238.1.S1_at	1.542640E-03	8.426286E-02	1.14	.88	null	null	null	null		
Cfa.16243.1.S1_s_at	2.890670E-03	1.157402E-01	1.13	.88	Canis lupus familiaris endothelin receptor type A (EDNRA); mRNA >gi|60650135|dbj|AB183284.2| Canis familiaris EDNRA mRNA for endothelin receptor type A; complete cds	100.0	AB178996	NM_001031632	EDNRA	endothelin receptor type A
Cfa.16244.1.A1_at	3.003210E-03	1.183545E-01	1.16	.86	Canis familiaris runt-related transcription factor 2 mRNA; partial cds	100.0	NM_001024630	AY738265	RUNX2	runt-related transcription factor 2
Cfa.16244.1.S1_s_at	5.354210E-03	1.560046E-01	1.19	.84	Canis familiaris runt-related transcription factor 2 mRNA; partial cds	100.0	NM_001024630	AY738265	RUNX2	runt-related transcription factor 2
Cfa.1630.1.A1_at	1.275690E-04	2.071672E-02	1.18	.85	null	null	null	null		
Cfa.16305.1.S1_at	1.338070E-02	2.424583E-01	1.1	.91	PREDICTED: Canis familiaris similar to Enigma homolog (Enigma-like PDZ and LIM domains protein); transcript variant 9 (LOC478482); mRNA	94.0	AC093778	XM_856582	PDLIM5	PDZ and LIM domain 5
Cfa.16315.1.S1_at	1.520200E-	8.376672E-	1.13	.89	PREDICTED: Canis familiaris similar to protein tyrosine phosphatase type IVA; member 3 isoform 2; transcript variant 5	70.2	NULL	XM_851414	PTP4A3	protein tyrosine phosphatase type

	03	02			(LOC606961); mRNA					IVA, member 3
Cfa.16362.2.S1_at	1.030750E-02	2.152272E-01	1.11	.90	PREDICTED: Canis familiaris similar to DNA polymerase delta subunit 3 (DNA polymerase delta subunit p66); transcript variant 1 (LOC476806); mRNA	76.3	AB168150	XM_534010	POLD3	polymerase (DNA-directed), delta 3, accessory subunit
Cfa.16368.1.S1_at	2.034640E-02	2.945198E-01	1.16	.86	PREDICTED: Equus caballus hypothetical protein LOC100066589 (LOC100066589); mRNA	80.6	AL022726	XM_001496814		
Cfa.16390.1.S1_s_at	1.325810E-02	2.417637E-01	0.88	1.13	PREDICTED: Canis familiaris similar to 3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMG-CoA reductase); transcript variant 7 (LOC479182); mRNA	99.2	M11058	XM_855403	HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase
Cfa.16405.1.S1_s_at	3.116890E-04	3.466030E-02	0.8	1.25	PREDICTED: Canis familiaris similar to SMC5 protein; transcript variant 1 (LOC476327); mRNA	100.0	NM_015110	XM_533529	SMC5	structural maintenance of chromosomes 5
Cfa.1641.1.A1_at	4.752470E-03	1.476361E-01	1.16	.87	Rattus norvegicus chloride channel CLIC-like 1 (Clcc1); mRNA >gi|14278954|dbj|AB052922.1| Rattus norvegicus rMCLC-1 mRNA for Mid-1-related chloride channel 1; complete cds	4.8	AC078824	NM_133414	Clcc1	chloride channel CLIC-like 1
Cfa.16487.1.A1_at	1.500310E-03	8.331076E-02	1.14	.88	NULL	null	AC096576	NULL		
Cfa.16493.1.A1_at	4.128320E-03	1.379365E-01	0.79	1.27	PREDICTED: Canis familiaris similar to 40S ribosomal protein S20 (LOC477887); mRNA	100.0	AL512783	XM_535079	RPS20	ribosomal protein S20
Cfa.16513.1.S1_at	5.055620E-04	4.604700E-02	1.12	.89	Canis lupus familiaris defensin; beta 102 (DEFB102); mRNA >gi|66968817|gb|DQ011971.1| Canis familiaris beta-defensin 102 (CBD102) mRNA; complete cds	29.5	U91325	NM_001113715	DEFB4	defensin, beta 4
Cfa.16551.1.S1_at	1.531660E-02	2.602160E-01	0.84	1.18	PREDICTED: Canis familiaris similar to CG13570-PA; transcript variant 3 (LOC477631); mRNA	99.0	AC004241	XM_846432	RPAP3	RNA polymerase II associated protein 3
Cfa.16551.1.S1_s_at	1.231290E-	2.347743E-	0.83	1.21	PREDICTED: Canis familiaris similar to CG13570-PA; transcript variant 1	97.4	NM_024604	XM_534826	RPAP3	RNA polymerase II associated

	02	01			(LOC477631); mRNA					protein 3
Cfa.16590.1.S1_s_at	1.254540E-03	7.498490E-02	0.69	1.44	Canis lupus familiaris chemokine (C-X-C motif) ligand 10 (CXCL10); mRNA >gi|57157733|dbj|AB183191.1| Canis familiaris CXCL10 mRNA for CXC chemokine ligand 10; complete cds	99.6	BC010954	NM_001010949	CXCL10	chemokine (C-X-C motif) ligand 10
Cfa.16590.1.S2_at	2.761470E-03	1.127513E-01	0.71	1.42	Mustela putorius furo chemokine C-X-C motif ligand 10 (CXCL10) mRNA; complete cds	51.8	BC010954	EF492058		
Cfa.16603.1.A1_x_at	4.917000E-04	4.550604E-02	1.18	.85	PREDICTED: Canis familiaris similar to yippee protein homolog; transcript variant 2 (LOC475714); mRNA	83.5	BC047237	XM_857398	YPEL5	yippee-like 5 (Drosophila)
Cfa.1661.1.S1_at	3.445950E-03	1.267607E-01	0.89	1.12	Sus scrofa mRNA; clone:THY010126H05; expressed in thymus	25.3	AC026866	AK239742	LOC100153090	similar to Cathepsin S
Cfa.16612.1.S2_s_at	1.127060E-02	2.244471E-01	0.89	1.12	Canis lupus familiaris capping protein (actin filament) muscle Z-line; alpha 2 (CAPZA2); mRNA	97.0	AB169582	NM_001012995	CAPZA2	capping protein (actin filament) muscle Z-line, alpha 2
Cfa.16637.2.S1_at	1.461420E-03	8.221204E-02	1.14	.88	PREDICTED: Canis familiaris hypothetical protein LOC608839; transcript variant 2 (LOC608839); mRNA	58.0	NULL	XM_857051	LOC608839	hypothetical protein LOC608839
Cfa.1668.1.S1_s_at	1.596460E-02	2.647183E-01	0.85	1.18	PREDICTED: Canis familiaris similar to ELMO domain containing 2 (LOC476075); mRNA	99.0	NM_153702	XM_533284	ELMOD2	ELMO/CED-12 domain containing 2
Cfa.16700.1.S1_at	5.224540E-03	1.537963E-01	0.76	1.32	Sus scrofa mRNA; clone:OVRM10011A06; expressed in ovary	33.1	AF086448	AK234722		
Cfa.16734.1.S1_at	5.504640E-03	1.589880E-01	1.11	.90	NULL	null	AC073173	NULL		
Cfa.1674.1.A1_at	1.062960E-04	1.829779E-02	1.26	.80	PREDICTED: Macaca mulatta similar to TATA box binding protein-associated factor; RNA polymerase II; Q (LOC702772); mRNA	23.9	NM_024885	XM_001092487	LOC702772	similar to TATA box binding protein-associated factor, RNA polymerase II, Q
Cfa.16748.2.S1_a_at	7.838890E-	1.882515E-	0.88	1.14	PREDICTED: Canis familiaris similar to postsynaptic protein CRIPT; transcript	98.2	AK291298	XM_846811	CRIPT	cysteine-rich PDZ-binding protein

	03	01			variant 1 (LOC609976); mRNA					
Cfa.16748.2.S1_s_at	5.209620E-03	1.536170E-01	0.85	1.17	PREDICTED: Canis familiaris similar to postsynaptic protein CRIPT; transcript variant 1 (LOC609976); mRNA	97.0	AK291298	XM_846811	CRIPT	cysteine-rich PDZ-binding protein
Cfa.16823.1.S1_at	7.463840E-03	1.839506E-01	0.88	1.14	PREDICTED: Canis familiaris similar to CG9166-PA (LOC611116); mRNA	96.9	AC005082	XM_848757	LOC611116	similar to CG9166-PA
Cfa.16864.1.S1_at	5.762460E-03	1.628197E-01	1.26	.79	Bos taurus coiled-coil domain containing 126 (CCDC126); mRNA >gi|126010607|gb|BC133498.1| Bos taurus similar to glycosyltransferase; mRNA (cDNA clone MGC:142980 IMAGE:8316619); complete cds	82.9	AK289911	NM_001082472	CCDC126	coiled-coil domain containing 126
Cfa.16864.1.S1_s_at	5.004320E-03	1.508466E-01	1.29	.77	Macaca fascicularis brain cDNA clone: QmoA-11194; similar to human alpha-1;3(6)-mannosylglycoproteinbeta-1;6-N-acetyl-glucosaminyltransferase-like(LOC90693); mRNA; RefSeq: NM_138771.2	91.7	AB170507	AB170507		
Cfa.1689.1.A1_at	1.310880E-02	2.403652E-01	1.23	.81	NULL	null	NG_007455	NULL		
Cfa.16949.2.S1_at	4.380460E-05	1.071943E-02	0.77	1.30	Sus scrofa mRNA; clone:AMP010044F05; expressed in alveolar macrophage	28.5	AK307720	AK230794	ATXN3	ataxin 3
Cfa.1695.1.S1_at	1.951730E-02	2.898299E-01	0.86	1.17	Homo sapiens chromosome 21 open reading frame 91 (C21orf91); transcript variant 3; mRNA	27.2	AK023825	NM_001100421	C21orf91	chromosome 21 open reading frame 91
Cfa.16990.1.S1_at	8.992520E-03	2.017118E-01	1.1	.91	PREDICTED: Canis familiaris similar to Dysferlin (Dystrophy associated fer-1-like protein) (Fer-1 like protein 1) (LOC483121); mRNA	100.0	DQ267935	XM_540237	DYSF	dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive)
Cfa.17015.1.S1_at	9.897500E-04	6.624244E-02	1.1	.91	PREDICTED: Canis familiaris similar to ADP-ribosylation factor 4-like (LOC490950); mRNA	90.1	CR597066	XM_548073	ARL4D	ADP-ribosylation factor-like 4D
Cfa.17019.1.S1_at	9.990790E-	6.662070E-	0.76	1.32	NULL	null	AC104332	NULL		

	04	02								
Cfa.1714.1.A1_at	1.171260E-02	2.291770E-01	0.91	1.10	PREDICTED: Macaca mulatta similar to coiled-coil domain containing 45; transcript variant 3 (LOC718348); mRNA	60.3	CR936721	XM_001116623	LOC718348	similar to coiled-coil domain containing 45
Cfa.17166.1.S1_at	1.428690E-02	2.509538E-01	0.89	1.13	PREDICTED: Canis familiaris similar to mitochondrial phosphoenolpyruvate carboxykinase 2 isoform 1 precursor; transcript variant 8 (LOC480255); mRNA	100.0	CR611857	XM_854675	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
Cfa.1719.1.S1_at	2.115470E-03	9.895571E-02	0.81	1.24	PREDICTED: Canis familiaris similar to Eukaryotic translation initiation factor 4E (eIF4E) (eIF-4E) (mRNA cap-binding protein) (eIF-4F 25 kDa subunit); transcript variant 3 (LOC487870); mRNA	94.9	AC093836	XM_857135	EIF4E	eukaryotic translation initiation factor 4E
Cfa.17254.1.S1_at	4.970790E-03	1.502233E-01	1.11	.90	PREDICTED: Canis familiaris similar to protein phosphatase 1; regulatory (inhibitor) subunit 5 (LOC477766); mRNA	97.3	NM_005398	XM_534961	PPP1R3C	protein phosphatase 1, regulatory (inhibitor) subunit 3C
Cfa.1727.1.A1_at	5.166420E-03	1.529140E-01	0.89	1.12	PREDICTED: Pan troglodytes alkyldihydroxyacetone phosphate synthase; transcript variant 2 (AGPS); mRNA	50.4	AC073834	XM_001154159	AGPS	alkylglycerone phosphate synthase
Cfa.17296.1.S1_s_at	2.449250E-03	1.058268E-01	0.88	1.14	PREDICTED: Canis familiaris similar to FBJ osteosarcoma oncogene B (predicted); transcript variant 7 (LOC608412); mRNA	99.6	NULL	XM_857182	FOSL2	FOS-like antigen 2
Cfa.17298.1.S1_at	9.011470E-04	6.265083E-02	0.87	1.15	PREDICTED: Canis familiaris similar to eukaryotic translation termination factor 1 (predicted); transcript variant 5 (LOC608717); mRNA	96.6	NM_004730	XM_858404	LOC608717	similar to eukaryotic translation termination factor 1 (predicted)
Cfa.17299.1.S1_at	4.274170E-03	1.405186E-01	1.1	.91	PREDICTED: Canis familiaris similar to CG10225-PA (LOC489227); mRNA	68.3	BC017951	XM_546345	RANBP3L	RAN binding protein 3-like
Cfa.17302.1.S1_s_at	1.769650E-03	9.109676E-02	0.9	1.12	PREDICTED: Canis familiaris similar to pleckstrin homology domain containing; family G; member 3 (LOC611460); mRNA	99.3	AB385358	XM_849129	PLEKHG3	pleckstrin homology domain containing, family G (with RhoGef domain) member 3
Cfa.17378.1.S1_at	3.996140E-05	1.027795E-02	0.88	1.14	PREDICTED: Canis familiaris similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP); transcript variant 8	91.1	AC078778	XM_850858	LOC607013	similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP)

					(LOC607013); mRNA					
Cfa.17400.1.S1_at	4.456490E-03	1.428212E-01	1.18	.85	PREDICTED: Canis familiaris similar to Dual specificity protein phosphatase 24 (Map kinase phosphatase-like protein MK-STYX) (Dual specificity phosphatase inhibitor MK-STYX); transcript variant 1 (LOC489817); mRNA	98.8	AL645944	XM_546935	STYXL1	serine/threonine/tyrosine interacting-like 1
Cfa.17531.2.S1_at	4.143390E-06	2.584214E-03	1.34	.75	NULL	null	AC203603	NULL		
Cfa.17531.2.S1_x_at	6.789270E-06	3.548256E-03	1.34	.74	PREDICTED: Equus caballus similar to HSPC028 (LOC100053031); mRNA	6.7	AB169116	XM_001495936	LOC100053031	similar to Basic leucine zipper and W2 domain-containing protein 2
Cfa.17538.1.S1_s_at	4.861700E-03	1.485961E-01	1.13	.88	PREDICTED: Canis familiaris similar to D-aspartate oxidase (DASOX) (DDO) (LOC475026); mRNA	99.4	AK293029	XM_532262	DDO	D-aspartate oxidase
Cfa.17547.1.S1_at	1.049290E-02	2.162123E-01	0.86	1.16	Sus scrofa cathepsin D (CTSD) gene; complete cds	9.7	AC147651	EF157854		
Cfa.1759.1.S1_at	1.788950E-02	2.786886E-01	0.89	1.12	PREDICTED: Canis familiaris similar to phosducin-like 3; transcript variant 2 (LOC474553); mRNA	17.6	NULL	XM_858229	PDCL3	phosducin-like 3
Cfa.17618.1.S1_s_at	1.970260E-03	9.559204E-02	1.12	.89	PREDICTED: Canis familiaris similar to dymeclin; transcript variant 1 (LOC480222); mRNA	100.0	NULL	XM_537347	DYM	dymeclin
Cfa.17654.1.S1_at	8.635890E-03	1.989767E-01	1.28	.78	Mus musculus adult male colon cDNA; RIKEN full-length enriched library; clone:9030016F17 product:unclassifiable; full insert sequence	14.1	AL512449	AK078843		
Cfa.17696.1.S1_at	3.851180E-06	2.555108E-03	1.2	.83	PREDICTED: Canis familiaris similar to FYVE and coiled-coil domain containing 1 (LOC476649); mRNA	87.6	NM_024513	XM_533853	FYCO1	FYVE and coiled-coil domain containing 1
Cfa.177.1.S1_at	1.262620E-02	2.367619E-01	1.17	.86	Canis lupus familiaris collagen; type IV; alpha 5 (Alport syndrome) (COL4A5); mRNA >gi|46372000|gb|AF470624.2| Canis familiaris type IV collagen alpha 5 (COL4A5)	100.0	BC151846	NM_001002979	COL4A5	collagen, type IV, alpha 5

					mRNA; complete cds				
Cfa.17719.1.S1_s_at	3.695290E-03	1.303481E-01	1.13	.88	PREDICTED: Canis familiaris similar to transmembrane protein 38A (LOC610207); mRNA	98.8	AK292764	XM_847645	TMEM38A	transmembrane protein 38A
Cfa.17735.1.S1_at	9.931610E-05	1.773472E-02	1.25	.80	PREDICTED: Canis familiaris beta-actin; transcript variant 4 (ACTB); mRNA	100.0	M10277	XM_856587	ACTA1	actin, alpha 1, skeletal muscle
Cfa.17747.2.S1_at	5.661900E-04	4.897046E-02	1.11	.90	Pongo pygmaeus mRNA; cDNA DKFZp469N0332 (from clone DKFZp469N0332)	50.4	AC021016	CR857322	TMBIM1	transmembrane BAX inhibitor motif containing 1
Cfa.17759.1.S1_at	1.928150E-03	9.472367E-02	1.18	.85	Homo sapiens cDNA FLJ77455 complete cds; highly similar to Homo sapiens dystrobrevin; alpha (DTNA); transcript variant 5; mRNA	84.9	AK291156	AK291156	DTNA	dystrobrevin, alpha
Cfa.1776.2.S1_s_at	1.559890E-02	2.618390E-01	0.88	1.14	PREDICTED: Canis familiaris pre-mRNA processing factor 31-like protein; transcript variant 1 (PRPF31); mRNA	99.2	AM392866	XM_533592	PRPF31	PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)
Cfa.17880.1.S1_at	2.093550E-02	2.977393E-01	0.85	1.18	PREDICTED: Canis familiaris similar to DnaJ (Hsp40) homolog; subfamily B; member 9 (LOC475286); mRNA	100.0	AB173770	XM_532518	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9
Cfa.1794.1.S1_at	3.273210E-04	3.592623E-02	1.25	.80	PREDICTED: Canis familiaris similar to BE10.2 (LOC475247); mRNA	54.8	NM_001004320	XM_532481	TMEM195	transmembrane protein 195
Cfa.1794.1.S1_s_at	3.486870E-03	1.274915E-01	1.12	.89	PREDICTED: Canis familiaris similar to BE10.2 (LOC475247); mRNA	100.0	BC108676	XM_532481	TMEM195	transmembrane protein 195
Cfa.17951.1.S1_at	6.487640E-05	1.336817E-02	0.81	1.23	Canis lupus familiaris chloride channel 3 (clcn3); mRNA >gi|70561325|emb|AM048629.1| Canis familiaris mRNA for chloride channel 3 (clcn3 gene)	100.0	NM_173872	NM_001025619	clcn3	chloride channel 3
Cfa.17952.1.S1_at	1.178890E-02	2.295635E-01	1.12	.90	PREDICTED: Bos taurus similar to Kinesin family member 21A (Kinesin-like protein KIF2) (NY-REN-62 antigen); transcript variant 2 (LOC540076); mRNA	37.4	BC032344	XM_863894	KIF21A	kinesin family member 21A

Cfa.1802.1.S1_at	1.088590E-03	6.971350E-02	0.87	1.15	PREDICTED: Canis familiaris similar to Dolichol-phosphate mannosyltransferase (Dolichol-phosphate mannose synthase) (Dolichyl-phosphate beta-D-mannosyltransferase) (Mannose-P-dolichol synthase) (MPD synthase) (DPM synthase); transcript variant 7 (LOC477264); mRNA	96.8	NULL	XM_862130	DPM1	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit
Cfa.1802.3.S1_s_at	3.970970E-04	4.065939E-02	0.82	1.23	PREDICTED: Canis familiaris similar to Dolichol-phosphate mannosyltransferase (Dolichol-phosphate mannose synthase) (Dolichyl-phosphate beta-D-mannosyltransferase) (Mannose-P-dolichol synthase) (MPD synthase) (DPM synthase); transcript variant 8 (LOC477264); mRNA	50.5	NM_003859	XM_862140	DPM1	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit
Cfa.18078.1.S1_at	1.926110E-03	9.472367E-02	1.13	.88	PREDICTED: Canis familiaris similar to RAB5B; member RAS oncogene family; transcript variant 3 (LOC474394); mRNA	51.7	AB172358	XM_851035	RAB5B	RAB5B, member RAS oncogene family
Cfa.18126.1.S1_a_at	2.228300E-04	2.915209E-02	0.69	1.46	Antirrhinum majus mRNA for YA6 (nf-YA gene)	18.9	AC091610	AM422775		
Cfa.18126.2.S1_at	1.702990E-04	2.481840E-02	0.79	1.27	Canis familiaris fast myosin heavy chain extraocular gene; complete cds	19.7	NULL	DQ227284		
Cfa.18129.1.S1_at	5.544670E-03	1.592432E-01	1.14	.87	PREDICTED: Canis familiaris similar to cAMP-dependent protein kinase; beta-catalytic subunit (PKA C-beta); transcript variant 5 (LOC479975); mRNA	51.1	NULL	XM_862395	PRKACB	protein kinase, cAMP-dependent, catalytic, beta
Cfa.18148.1.A1_at	3.636860E-03	1.290291E-01	0.83	1.21	Homo sapiens cDNA FLJ34018 fis; clone FCBBF2002801	12.8	AK091337	AK091337		
Cfa.1816.1.A1_at	1.893350E-02	2.859962E-01	0.89	1.12	PREDICTED: Canis familiaris similar to Copper homeostasis protein cutC homolog (LOC477793); mRNA	100.0	NM_015960	XM_534987	CUTC	cutC copper transporter homolog (E. coli)
Cfa.1816.1.A1_s_at	4.918310E-03	1.492662E-01	0.9	1.11	PREDICTED: Canis familiaris similar to Copper homeostasis protein cutC homolog (LOC477793); mRNA	100.0	NM_015960	XM_534987	CUTC	cutC copper transporter homolog (E. coli)
Cfa.18193.1.S1_at	2.005710E-02	2.923975E-01	0.88	1.14	PREDICTED: Canis familiaris similar to 6-pyruvoyl tetrahydrobiopterin synthase precursor (PTPS) (PTP synthase)	98.3	EF445018	XM_848983	PTS	6-pyruvoyltetrahydropterin synthase

					(LOC611326); mRNA					
Cfa.18209.1.S1_s_at	3.022260E-03	1.184813E-01	1.17	.86	PREDICTED: Canis familiaris similar to ubiquitin-conjugating enzyme E2D 1; UBC4/5 homolog (LOC608578); mRNA	99.6	AK291901	XM_845637	UBE2D1	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)
Cfa.18230.1.S1_s_at	6.409710E-03	1.720925E-01	1.14	.88	PREDICTED: Canis familiaris similar to Thyroid hormone receptor-associated protein complex 150 kDa component (Trap150) (Thyroid hormone receptor associated protein 3); transcript variant 2 (LOC482476); mRNA	98.8	EU446755	XM_539593	THRAP3	thyroid hormone receptor associated protein 3
Cfa.18258.2.S1_s_at	1.086000E-03	6.966732E-02	0.9	1.11	PREDICTED: Canis familiaris similar to downregulated in renal cell carcinoma (LOC607380); mRNA	100.0	AB170850	XM_844019	LOC607380	similar to downregulated in renal cell carcinoma
Cfa.18295.1.S1_s_at	7.574620E-04	5.649459E-02	0.74	1.36	PREDICTED: Canis familiaris similar to K02F3.10 (LOC608758); mRNA	99.8	NM_198450	XM_845869	APOOL	apolipoprotein O-like
Cfa.18331.1.S1_s_at	6.905530E-03	1.779518E-01	1.12	.90	PREDICTED: Canis familiaris similar to RNA binding motif protein 22 (LOC489184); mRNA	99.0	AM393639	XM_546302	RBM22	RNA binding motif protein 22
Cfa.18351.1.S1_at	1.064070E-03	6.865405E-02	1.17	.85	PREDICTED: Canis familiaris similar to solute carrier family 20; member 2; transcript variant 1 (LOC482838); mRNA	83.5	CU688528	XM_539953	SLC20A2	solute carrier family 20 (phosphate transporter), member 2
Cfa.18395.1.S1_s_at	1.589330E-02	2.641811E-01	0.83	1.21	PREDICTED: Canis familiaris similar to F31D4.2 (LOC611986); mRNA	99.5	AB174060	XM_849706	LOC611986	similar to F31D4.2
Cfa.18401.1.S1_s_at	1.688430E-02	2.724469E-01	1.11	.90	PREDICTED: Canis familiaris similar to zinc finger protein 207 (LOC480611); mRNA	100.0	AF046001	XM_537731	ZNF207	zinc finger protein 207
Cfa.18416.1.S1_at	3.969780E-03	1.349443E-01	1.17	.86	Homo sapiens cDNA clone IMAGE:5738367; partial cds	20.6	AC006064	BC064410	FAM165B	family with sequence similarity 165, member B
Cfa.18417.1.S1_s_at	5.148880E-03	1.528298E-01	1.17	.85	PREDICTED: Canis familiaris similar to p30 DBC protein (LOC486122); mRNA	99.8	BC065495	XM_543248	LOC486122	similar to p30 DBC protein
Cfa.1842.1.S1_at	1.464280E-02	2.544573E-01	0.88	1.13	PREDICTED: Canis familiaris similar to Ras-related protein Rab-18; transcript variant 6	99.8	AK001555	XM_852130	RAB18	RAB18, member RAS oncogene family

					(LOC491408); mRNA					
Cfa.18440.1.S1_s_at	1.360520E-02	2.445697E-01	0.89	1.12	Homo sapiens cDNA; FLJ18767	93.5	AK311725	AK311725	APBB1	amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65)
Cfa.1856.1.S1_at	1.071910E-02	2.176197E-01	1.15	.87	Bos taurus hypothetical LOC534560 (MGC152232); mRNA >gi|117306532|gb|BC126659.1| Bos taurus hypothetical LOC534560; mRNA (cDNA clone MGC:152232 IMAGE:8413734); complete cds	25.1	AC067942	NM_001078001	MGC152232	hypothetical LOC534560
Cfa.18564.1.S1_s_at	1.037000E-02	2.153015E-01	1.15	.87	PREDICTED: Canis familiaris similar to spermatogenesis associated 18 homolog (LOC475141); mRNA	56.4	AK314799	XM_532371	SPATA18	spermatogenesis associated 18 homolog (rat)
Cfa.18578.1.S1_at	1.246540E-03	7.481848E-02	1.14	.88	Homo sapiens estrogen-related receptor gamma (ESRRG) gene; complete cds	14.0	AC135352	AY528719		
Cfa.18586.1.S1_at	6.353230E-03	1.715253E-01	1.15	.87	PREDICTED: Canis familiaris similar to regulatory subunit PR 53 of protein phosphatase 2A isoform b (LOC491303); mRNA	97.3	NULL	XM_548424	PPP2R4	protein phosphatase 2A activator, regulatory subunit 4
Cfa.18608.1.S1_at	1.326680E-02	2.418199E-01	1.11	.90	PREDICTED: Canis familiaris similar to myelin-associated oligodendrocytic basic protein; transcript variant 2 (LOC607986); mRNA	86.7	BC022471	XM_855718	MOBP	myelin-associated oligodendrocyte basic protein
Cfa.18611.1.S1_s_at	3.962290E-03	1.348203E-01	1.16	.86	Bos taurus membrane-spanning 4-domains; subfamily A; member 13 (MS4A13); mRNA >gi|82571700|gb|BC110154.1| Bos taurus similar to testis-expressed transmembrane-4 protein; mRNA (cDNA clone MGC:133919 IMAGE:8054431); complete cds	87.9	NM_001100909	NM_001075220	MS4A13	membrane-spanning 4-domains, subfamily A, member 13
Cfa.18642.1.S1_s_at	6.578990E-03	1.739023E-01	0.83	1.20	PREDICTED: Canis familiaris similar to PRP19/PSO4 homolog (Nuclear matrix protein 200) (hPso4); transcript variant 4 (LOC611552); mRNA	97.7	NM_014502	XM_862820	PRPF19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)
Cfa.1869.1.A1_at	1.858530E-02	2.823561E-01	1.12	.89	PREDICTED: Equus caballus hypothetical protein LOC100061975 (LOC100061975);	5.2	AC007298	XM_001496249	LOC100061975	hypothetical protein LOC100061975

					mRNA					
Cfa.1870.1.S1_at	3.631790E-03	1.289640E-01	0.82	1.22	PREDICTED: Canis familiaris similar to Zinc finger protein Rlf (Rearranged L-myc fusion gene protein) (Zn-15 related protein); transcript variant 1 (LOC475315); mRNA	50.0	U22377	XM_532543	RLF	rearranged L-myc fusion
Cfa.18795.1.S1_s_at	8.040270E-03	1.908511E-01	0.86	1.17	PREDICTED: Canis familiaris similar to Host cell factor 2 (HCF-2) (C2 factor); transcript variant 5 (LOC475449); mRNA	95.5	EU446491	XM_861982	HCFC2	host cell factor C2
Cfa.18916.1.S1_at	9.632280E-03	2.086186E-01	1.1	.91	PREDICTED: Canis familiaris similar to Potassium channel tetramerisation domain containing protein 5 (LOC490058); mRNA	99.8	BC007314	XM_547178	KCTD5	potassium channel tetramerisation domain containing 5
Cfa.1894.1.S1_at	2.656550E-03	1.104755E-01	0.85	1.18	Homo sapiens cDNA; FLJ98341	16.0	AK308393	AK308393		
Cfa.18953.1.S1_s_at	6.346650E-03	1.715253E-01	0.91	1.10	PREDICTED: Canis familiaris similar to Axin-1 (Axis inhibition protein 1) (Fused protein); transcript variant 2 (LOC490099); mRNA	99.1	BC035872	XM_847228	AXIN1	axin 1
Cfa.18966.1.S1_s_at	2.999220E-03	1.183056E-01	1.21	.83	PREDICTED: Canis familiaris similar to carnitine O-octanoyltransferase; transcript variant 1 (LOC482283); mRNA	95.5	AK313487	XM_539402	CROT	carnitine O-octanoyltransferase
Cfa.1900.1.S1_at	2.395730E-04	3.050303E-02	1.2	.83	NULL	null	AL445183	NULL		
Cfa.19007.1.S1_s_at	2.056400E-02	2.954807E-01	1.1	.91	PREDICTED: Canis familiaris similar to complement component 7 precursor; transcript variant 1 (LOC489221); mRNA	98.7	AK312737	XM_546339	C7	complement component 7
Cfa.19027.1.S1_s_at	2.130050E-03	9.931387E-02	0.83	1.20	PREDICTED: Canis familiaris similar to NAD-dependent malic enzyme; mitochondrial precursor (NAD-ME) (Malic enzyme 2); transcript variant 2 (LOC476198); mRNA	100.0	AK313391	XM_844437	ME2	malic enzyme 2, NAD(+)-dependent, mitochondrial
Cfa.1903.1.A1_at	1.001740E-03	6.662070E-02	1.17	.86	NULL	null	AC079256	NULL		
Cfa.19042.1.S1_at	9.002270E-	2.017118E-	0.86	1:16	Homo sapiens nitric oxide synthase 1	10.6	AY445095	AY445095		

	03	01			(neuronal) (NOS1) gene; complete cds					
Cfa.1906.1.S1_at	1.944510E-04	2.639810E-02	0.82	1.22	Equus caballus subclone 355H03 3.3 MHC class I antigen gene; complete cds	13.7	AP001823	DQ083409		
Cfa.19073.1.S1_at	9.079040E-03	2.023389E-01	0.89	1.12	Sus scrofa mRNA; clone:LVRM10052B08; expressed in liver	86.3	AC091151	AK232930		
Cfa.19126.2.S1_at	8.726950E-03	2.002010E-01	1.12	.89	Rhinogobius duospilus mitochondrial ND5 gene for NADH dehydrogenase subunit 5; partial cds	15.9	AC093389	AB190337		
Cfa.19139.1.S1_at	2.000560E-02	2.922407E-01	1.13	.89	Bos taurus sorbin and SH3 domain containing 2 (SORBS2); mRNA >gi|117306664|gb|BC126558.1| Bos taurus sorbin and SH3 domain containing 2; mRNA (cDNA clone MGC:142659 IMAGE:8387106); complete cds	46.7	AC093797	NM_001079787	SORBS2	sorbin and SH3 domain containing 2
Cfa.19142.1.S1_s_at	1.334560E-02	2.423597E-01	1.17	.85	PREDICTED: Equus caballus similar to cell division cycle 10 (LOC100070492); mRNA	95.8	AK290545	XM_001500153	SEPT7	septin 7
Cfa.1915.2.S1_at	2.721660E-03	1.120772E-01	0.84	1.19	PREDICTED: Gallus gallus similar to MGC80576 protein (LOC417569); mRNA	16.4	NULL	XM_415815	SLC46A1	solute carrier family 46, member 1
Cfa.19156.1.S1_at	1.775700E-02	2.773922E-01	0.88	1.13	PREDICTED: Canis familiaris hypothetical protein LOC611585 (LOC611585); mRNA	39.8	AC091843	XM_849268	CCDC59	coiled-coil domain containing 59
Cfa.19172.1.S1_s_at	1.273050E-02	2.377586E-01	0.82	1.22	PREDICTED: Canis familiaris similar to centrin 3 (LOC488915); mRNA	97.1	NM_004365	XM_546032	CETN3	centrin, EF-hand protein, 3 (CDC31 homolog, yeast)
Cfa.19185.1.S1_s_at	1.921720E-03	9.462382E-02	0.91	1.10	PREDICTED: Canis familiaris similar to protein kinase C; zeta; transcript variant 4 (LOC479577); mRNA	100.0	NULL	XM_852915	PRKCZ	protein kinase C, zeta
Cfa.1919.1.A1_at	1.477420E-02	2.554470E-01	1.11	.90	Macaca fascicularis brain cDNA clone: QflA-22219; similar to human bobby sox homolog (Drosophila) (BBX); mRNA; RefSeq: NM_020235.2	59.5	AC117477	AB173357		
Cfa.19204.1.S1_s_at	5.532130E-03	1.592432E-01	0.86	1.17	PREDICTED: Canis familiaris similar to CG5359-PA (LOC478601); mRNA	99.7	NM_152773	XM_535777	TCTEX1D2	Tctex1 domain containing 2

Cfa.1931.1.A1_at	1.312510E-02	2.404594E-01	1.12	.90	PREDICTED: Canis familiaris similar to SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a1 isoform a; transcript variant 19 (LOC481046); mRNA	98.1	NULL	XM_860493	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1
Cfa.19355.1.S1_s_at	5.110620E-04	4.627805E-02	0.91	1.10	PREDICTED: Canis familiaris similar to CG2906-PB; isoform B; transcript variant 1 (LOC490408); mRNA	99.4	AK000412	XM_547529	LOC490408	similar to CG2906-PB, isoform B
Cfa.19363.1.S1_at	4.132070E-04	4.164488E-02	1.16	.86	PREDICTED: Bos taurus hypothetical protein LOC784329 (LOC784329); mRNA	13.5	AC091814	XM_001252008	LOC784329	similar to RIKEN cDNA 4922502D21
Cfa.19381.1.S1_s_at	1.115600E-02	2.227835E-01	1.15	.87	PREDICTED: Canis familiaris similar to dynein; cytoplasmic; intermediate polypeptide 1; transcript variant 4 (LOC475236); mRNA	99.0	NULL	XM_856094	LOC475236	similar to dynein, cytoplasmic, intermediate polypeptide 1
Cfa.1939.1.S1_at	7.956520E-05	1.542382E-02	0.78	1.28	Sus scrofa clone Clu_26525.scr.msk.p1.Contig2; mRNA sequence	38.3	NULL	AY609700		
Cfa.19399.1.S1_at	1.037470E-02	2.153015E-01	0.85	1.18	Homo sapiens cDNA FLJ34588 fis; clone KIDNE2008824	21.2	AK091907	AK091907	EFHA1	EF-hand domain family, member A1
Cfa.19416.1.S1_at	3.288580E-03	1.233863E-01	0.86	1.16	PREDICTED: Canis familiaris similar to Sialin (Solute carrier family 17 member 5) (Sodium/sialic acid cotransporter) (AST) (Membrane glycoprotein HP59); transcript variant 1 (LOC474969); mRNA	96.3	AK075320	XM_532204	SLC17A5	solute carrier family 17 (anion/sugar transporter), member 5
Cfa.19419.1.S1_s_at	7.941260E-03	1.894628E-01	0.9	1.11	PREDICTED: Canis familiaris similar to mitochondrial translational release factor 1-like (LOC484040); mRNA	99.8	CU680091	XM_541157	MTRF1L	mitochondrial translational release factor 1-like
Cfa.19447.1.S1_at	1.417930E-02	2.500845E-01	0.88	1.13	Bos taurus lamin B1 (LMNB1); mRNA >gi|154425604|gb|BC151304.1| Bos taurus lamin B1; mRNA (cDNA clone MGC:165937 IMAGE:8182684); complete cds	88.6	NM_005573	NM_001103295	LMNB1	lamin B1
Cfa.1946.1.A1_at	3.470700E-03	1.273693E-01	1.12	.90	PREDICTED: Equus caballus similar to OTTHUMP00000065631 (LOC100052277); mRNA	38.8	AL833232	XM_001491510	LOC100052277	similar to hemicentin 1

Cfa.1949.1.S1_at	3.958890E-03	1.348203E-01	1.13	.88	null	null	null	null		
Cfa.19529.1.S1_s_at	1.444440E-02	2.522842E-01	1.11	.90	PREDICTED: Canis familiaris similar to peroxisomal integral membrane protein 47; transcript variant 1 (LOC474498); mRNA	99.5	CU675207	XM_531726	SLC25A17	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34kDa), member 17
Cfa.19548.1.S1_s_at	4.306750E-04	4.241213E-02	0.83	1.20	PREDICTED: Canis familiaris similar to zinc finger; CCHC domain containing 9; transcript variant 2 (LOC479161); mRNA	98.8	CU689516	XM_536305	ZCCHC9	zinc finger, CCHC domain containing 9
Cfa.19550.1.S1_s_at	1.473390E-02	2.548942E-01	0.75	1.33	PREDICTED: Canis familiaris similar to zinc finger protein 37 homolog (LOC474806); mRNA	100.0	BC126390	XM_532037	ZFP37	zinc finger protein 37 homolog (mouse)
Cfa.19553.1.S1_at	1.697140E-02	2.727275E-01	0.88	1.14	PREDICTED: Gallus gallus PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae) (PAN3); mRNA	6.7	AC010380	XM_417120	PAN3	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)
Cfa.19578.1.S1_s_at	1.733940E-02	2.746495E-01	0.9	1.11	PREDICTED: Canis familiaris similar to crystallin; zeta-like 1 isoform a (LOC478408); mRNA	100.0	AK315707	XM_535585	CRYZL1	crystallin, zeta (quinone reductase)-like 1
Cfa.19585.1.A1_at	1.742890E-02	2.752487E-01	0.9	1.11	PREDICTED: Bos taurus similar to UBE3A protein (LOC789623); mRNA	37.3	AC100774	XM_001256321		
Cfa.19589.1.A1_at	1.198370E-02	2.317046E-01	1.13	.88	PREDICTED: Apis mellifera similar to Glycyl-tRNA synthetase CG6778-PB; isoform B (LOC408392); mRNA	4.2	AC006118	XM_391940	LOC408392	similar to Glycyl-tRNA synthetase CG6778-PB, isoform B
Cfa.19595.1.S1_at	1.184710E-02	2.297611E-01	0.83	1.21	PREDICTED: Equus caballus hypothetical protein LOC100050439 (LOC100050439); mRNA	87.7	NR_003545	XM_001492618		
Cfa.19596.1.S1_at	2.636240E-03	1.101462E-01	1.12	.89	Mus musculus 17 days embryo kidney cDNA; RIKEN full-length enriched library; clone:I920196C02 product:glycerol kinase; full insert sequence	82.9	AC117404	AK169424	Gyk	glycerol kinase
Cfa.19662.1.S1_at	2.151220E-03	1.000841E-01	1.17	.86	PREDICTED: Canis familiaris similar to Dmx-like 1; transcript variant 1 (LOC474631); mRNA	94.5	NM_005509	XM_531861	DMXL1	Dmx-like 1

Cfa.1970.1.S1_at	1.314670E-02	2.406500E-01	0.84	1.19	PREDICTED: Pan troglodytes D-glucuronyl C5-epimerase; transcript variant 1 (GLCE); mRNA	36.0	AC026992	XM_001174876	GLCE	glucuronic acid epimerase
Cfa.19743.2.S1_at	4.345270E-03	1.413545E-01	1.11	.90	PREDICTED: Pan troglodytes similar to MGC107852 protein; transcript variant 2 (LOC748328); mRNA	5.3	AC083863	XM_001169689	LOC748328	similar to MGC107852 protein
Cfa.19789.1.S1_s_at	3.949400E-03	1.348203E-01	1.16	.86	PREDICTED: Canis familiaris similar to Sex comb on midleg-like protein 2; transcript variant 1 (LOC480855); mRNA	99.1	BC040497	XM_537972	SCML2	sex comb on midleg-like 2 (Drosophila)
Cfa.19796.2.A1_at	2.353990E-03	1.039015E-01	1.24	.81	PREDICTED: Canis familiaris similar to CXXC finger 6 (LOC479229); mRNA	99.1	NM_030625	XM_536371	TET1	tet oncogene 1
Cfa.19797.1.A1_at	1.125780E-03	7.089828E-02	1.15	.87	Pongo pygmaeus mRNA; cDNA DKFZp469B044 (from clone DKFZp469B044)	11.1	AL049646	CR857073	CLPB	ClpB caseinolytic peptidase B homolog (E. coli)
Cfa.198.1.S1_s_at	9.744400E-03	2.098850E-01	1.13	.88	Canis familiaris heart calcineurin catalytic subunit mRNA; partial cds	99.8	AK290532	AY266682	PPP3CA	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform
Cfa.19800.1.S1_s_at	9.305660E-03	2.047388E-01	0.83	1.20	PREDICTED: Canis familiaris similar to ATP-binding cassette sub-family E member 1 (RNase L inhibitor) (Ribonuclease 4 inhibitor) (RNS4I); transcript variant 4 (LOC475454); mRNA	95.9	AB062293	XM_862119	ABCE1	ATP-binding cassette, sub-family E (OABP), member 1
Cfa.19824.1.S1_at	1.181820E-02	2.296042E-01	0.88	1.14	PREDICTED: Canis familiaris similar to tetratricopeptide repeat domain 14; transcript variant 3 (LOC478641); mRNA	54.3	AC005365	XM_843349	TTC14	tetratricopeptide repeat domain 14
Cfa.1983.1.S1_at	5.930430E-03	1.652817E-01	0.9	1.11	PREDICTED: Canis familiaris similar to DEK oncogene (DNA binding) (LOC610538); mRNA	99.6	AC139014	XM_848066	DEK	DEK oncogene (DNA binding)
Cfa.19836.1.S1_at	1.334710E-02	2.423597E-01	0.9	1.12	PREDICTED: Canis familiaris similar to RIKEN cDNA 1110007C09 (LOC476359); mRNA	100.0	AC114285	XM_533560	LOC476359	similar to RIKEN cDNA 1110007C09
Cfa.19839.1.S1_s_at	9.655150E-04	6.502494E-02	1.12	.89	PREDICTED: Canis familiaris similar to stathmin-like-protein RB3; transcript variant 2 (LOC486105); mRNA	98.9	AB172014	XM_843955	STMN4	stathmin-like 4

Cfa.19850.1.S1_at	2.653190E-03	1.104755E-01	1.2	.83	PREDICTED: Bos taurus hypothetical protein LOC786437 (LOC786437); mRNA	39.9	AB171418	XM_001254109		
Cfa.19882.1.S1_s_at	1.112160E-02	2.225096E-01	0.88	1.13	PREDICTED: Canis familiaris similar to glutamate receptor; ionotropic; N-methyl D-asparate-associated protein 1 (LOC475118); mRNA	100.0	BC007843	XM_532348	GRINA	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)
Cfa.19895.1.S1_s_at	1.953380E-02	2.899748E-01	1.15	.87	PREDICTED: Canis familiaris hypothetical LOC480051 (LOC480051); mRNA	95.4	AB070007	XM_537173	LOC480051	hypothetical LOC480051
Cfa.19933.1.A1_s_at	2.192180E-03	1.004691E-01	0.84	1.19	PREDICTED: Canis familiaris similar to Protein O-mannosyl-transferase 2 (Dolichyl-phosphate-mannose--protein mannosyltransferase 2) (LOC480400); mRNA	100.0	BC031651	XM_537521	POMT2	protein-O-mannosyltransferase 2
Cfa.19935.1.S1_s_at	3.533070E-03	1.277456E-01	0.84	1.19	PREDICTED: Canis familiaris similar to CG14367-PA; transcript variant 1 (LOC474602); mRNA	98.3	CU679569	XM_531832	CCDC104	coiled-coil domain containing 104
Cfa.19939.1.S1_s_at	1.222170E-02	2.339684E-01	0.88	1.14	PREDICTED: Canis familiaris similar to ATP binding protein associated with cell differentiation (LOC474557); mRNA	99.2	BC070183	XM_531785	TXNDC9	thioredoxin domain containing 9
Cfa.19946.1.S1_at	5.765940E-03	1.628197E-01	1.18	.85	Homo sapiens mRNA; cDNA DKFZp686K0327 (from clone DKFZp686K0327)	78.5	BX648099	BX648099	CATSPER2	cation channel, sperm associated 2
Cfa.19956.1.S1_at	3.061000E-03	1.189972E-01	1.13	.89	PREDICTED: Canis familiaris similar to ecotropic viral integration site 5 (LOC479950); mRNA	100.0	AC004662	XM_537075	LOC479950	similar to ecotropic viral integration site 5
Cfa.19959.1.S1_at	6.516660E-03	1.732327E-01	0.9	1.11	PREDICTED: Canis familiaris similar to F-actin capping protein alpha-3 subunit (CapZ alpha-3) (Germ cell-specific protein 3) (LOC477680); mRNA	100.0	NM_033328	XM_534875	CAPZA3	capping protein (actin filament) muscle Z-line, alpha 3
Cfa.19970.1.S1_s_at	1.734640E-03	9.022485E-02	1.13	.88	PREDICTED: Canis familiaris similar to ADAM 32 precursor (A disintegrin and metalloprotease domain 32) (LOC475578); mRNA	100.0	CU693126	XM_532797	ADAM32	ADAM metallopeptidase domain 32

Cfa.19973.1.S1_at	1.249780E-02	2.357926E-01	0.88	1.13	PREDICTED: Canis familiaris similar to putative 40-2-3 protein (LOC609238); mRNA	100.0	AL022400	XM_846457	LOC609238	similar to putative 40-2-3 protein
Cfa.19999.1.S1_s_at	7.665850E-04	5.666965E-02	1.27	.79	PREDICTED: Canis familiaris similar to Heat shock factor protein 2 (HSF 2) (Heat shock transcription factor 2) (HSTF 2) (LOC476276); mRNA	100.0	CU675116	XM_533482	HSF2	heat shock transcription factor 2
Cfa.20054.1.S1_s_at	3.253910E-03	1.228351E-01	0.84	1.19	PREDICTED: Canis familiaris similar to Cytochrome P450 51A1 (CYPLI) (P450LI) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (LDM) (P450-14DM) (P45014DM); transcript variant 2 (LOC475225); mRNA	97.5	NULL	XM_855082	LOC475225	similar to Cytochrome P450 51A1 (CYPLI) (P450LI) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (LDM) (P450-14DM) (P45014DM)
Cfa.20063.1.S1_s_at	1.406980E-02	2.487915E-01	0.91	1.10	PREDICTED: Canis familiaris similar to kinectin 1 (LOC480332); mRNA	28.7	AB173341	XM_537455	KTN1	kinectin 1 (kinesin receptor)
Cfa.20068.1.S1_s_at	6.629910E-04	5.235196E-02	1.22	.82	PREDICTED: Canis familiaris similar to A-kinase anchor protein 3 (Protein kinase A anchoring protein 3) (PRKA3) (A-kinase anchor protein 110 kDa) (AKAP 110) (Sperm oocyte binding protein) (Fibrousheathin I) (Fibrous sheath protein of 95 kDa) (FSP95); transcript variant 1 (LOC477719); mRNA	99.2	NM_006422	XM_534916	AKAP3	A kinase (PRKA) anchor protein 3
Cfa.20126.1.S1_s_at	1.509840E-02	2.584702E-01	1.11	.90	PREDICTED: Canis familiaris similar to SH2 domain binding protein 1 (LOC476853); mRNA	99.5	AB383773	XM_534056	CTR9	Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)
Cfa.20128.1.S1_s_at	1.543830E-02	2.607485E-01	0.87	1.14	PREDICTED: Canis familiaris similar to CG7386-PA; transcript variant 3 (LOC476272); mRNA	99.5	AB179013	XM_858316	ZUFSP	zinc finger with UFM1-specific peptidase domain
Cfa.20146.1.S1_s_at	7.987580E-03	1.898098E-01	0.8	1.26	PREDICTED: Canis familiaris similar to centrosomal protein 70 kDa (LOC477084); mRNA	81.6	AB168710	XM_534279	CEP70	centrosomal protein 70kDa
Cfa.20149.1.S1_at	5.206340E-03	1.536170E-01	1.17	.85	Bos taurus chromodomain helicase DNA binding protein 1-like (CHD1L); mRNA >gi|78174363|gb|BC107534.1| Bos taurus chromodomain helicase DNA binding protein 1-like; mRNA (cDNA clone MGC:128792 IMAGE:7989310); complete	86.5	AK307400	NM_001037820	CHD1L	chromodomain helicase DNA binding protein 1-like

					cds					
Cfa.20157.1.S1_at	3.471350E-05	9.638035E-03	1.17	.85	PREDICTED: Canis familiaris similar to protein tyrosine phosphatase; receptor type; D isoform 4 precursor; transcript variant 1 (LOC475389); mRNA	100.0	NM_002840	XM_532613	PTPRF	protein tyrosine phosphatase, receptor type, F
Cfa.20166.1.S1_at	2.311920E-03	1.028541E-01	0.84	1.19	Homo sapiens PDZ-LIM protein mRNA; complete cds	4.6	AY217349	AY217349	PDLIM2	PDZ and LIM domain 2 (mystique)
Cfa.20182.1.A1_at	1.847570E-02	2.818510E-01	1.1	.91	Bos taurus chromosome 4 open reading frame 35 ortholog (H6C4ORF35); mRNA >gi|83638716|gb|BC110036.1| Bos taurus similar to testis development protein NYD-SP26; mRNA (cDNA clone MGC:133759 IMAGE:8048253); complete cds	70.6	NM_033122	NM_001040539	C6H4ORF35	chromosome 4 open reading frame 35 ortholog
Cfa.2021.1.A1_at	3.346760E-03	1.245915E-01	0.89	1.12	PREDICTED: Bos taurus similar to trans-Golgi p230 (LOC538893); mRNA	91.2	AY531221	XM_583499	GOLGA4	golgi autoantigen, golgin subfamily a, 4
Cfa.20224.1.S1_at	8.834340E-03	2.009348E-01	0.84	1.18	PREDICTED: Canis familiaris similar to Cytochrome P450 51A1 (CYPLI) (P450LI) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (LDM) (P450-14DM) (P45014DM); transcript variant 1 (LOC475225); mRNA	100.0	NULL	XM_532457	LOC475225	similar to Cytochrome P450 51A1 (CYPLI) (P450LI) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (LDM) (P450-14DM) (P45014DM)
Cfa.2024.1.S1_at	3.668740E-03	1.297542E-01	0.83	1.21	Sus scrofa mRNA; clone:THY010027C02; expressed in thymus	31.9	AC074344	AK238763	LOC100152540	hypothetical protein LOC100152540
Cfa.2024.2.S1_a_at	2.059980E-05	7.092099E-03	0.77	1.30	PREDICTED: Canis familiaris hypothetical LOC477835 (LOC477835); mRNA	100.0	AL356787	XM_535027	LOC477835	hypothetical LOC477835
Cfa.20262.1.S1_at	1.037630E-02	2.153015E-01	1.14	.87	Bos taurus Rho-related BTB domain containing 1 (RHOBTB1); mRNA >gi|126010690|gb|BC133510.1| Bos taurus hypothetical LOC540513; mRNA (cDNA clone MGC:152114 IMAGE:8395997); complete cds	60.7	NULL	NM_001082453	RHOBTB1	Rho-related BTB domain containing 1
Cfa.20269.1.A1_s_at	2.597330E-03	1.091563E-01	0.9	1.11	PREDICTED: Canis familiaris similar to zinc finger; A20 domain containing 3; transcript variant 11 (LOC479064); mRNA	97.6	NULL	XM_856136	ZFAND6	zinc finger, AN1-type domain 6

Cfa.20313.1.S1_at	8.957570E-03	2.017118E-01	1.14	.87	PREDICTED: Canis familiaris similar to SPFH domain family; member 2; transcript variant 5 (LOC607518); mRNA	100.0	NM_007175	XM_852488	ERLIN2	ER lipid raft associated 2
Cfa.20324.1.S1_at	6.942710E-03	1.783297E-01	0.9	1.11	PREDICTED: Canis familiaris similar to armadillo repeat containing 4 (LOC488444); mRNA	29.1	AC013468	XM_545566	ANKAR	ankyrin and armadillo repeat containing
Cfa.20345.1.S1_at	1.948080E-02	2.895798E-01	0.89	1.12	PREDICTED: Canis familiaris similar to 1110059P08Rik protein; transcript variant 4 (LOC612830); mRNA	47.2	BC022536	XM_855948	VTA1	Vps20-associated 1 homolog (S. cerevisiae)
Cfa.20373.1.S1_at	1.509920E-02	2.584702E-01	0.89	1.12	PREDICTED: Canis familiaris similar to active BCR-related gene isoform 1; transcript variant 5 (LOC480638); mRNA	55.7	NULL	XM_863282	ABR	active BCR-related gene
Cfa.2040.1.S1_at	5.529030E-03	1.592432E-01	1.1	.91	Mus musculus 16 days neonate cerebellum cDNA; RIKEN full-length enriched library; clone:9630044D01 product:unclassifiable; full insert sequence	4.5	NULL	AK036175		
Cfa.20406.1.S1_at	8.641510E-03	1.989767E-01	0.91	1.10	PREDICTED: Canis familiaris similar to DnaJ homolog subfamily B member 5 (Heat shock protein Hsp40-3) (Heat shock protein cognate 40) (Hsc40); transcript variant 1 (LOC474753); mRNA	97.9	NM_012266	XM_531984	DNAJB5	DnaJ (Hsp40) homolog, subfamily B, member 5
Cfa.20463.1.A1_s_at	1.915110E-04	2.616405E-02	1.12	.89	PREDICTED: Macaca mulatta similar to mitochondrial glutamate carrier 1 (LOC700463); mRNA	74.3	NM_024698	XM_001087788	LOC700463	similar to mitochondrial glutamate carrier 1
Cfa.2047.1.A1_at	4.036190E-05	1.027795E-02	0.77	1.30	PREDICTED: Canis familiaris similar to centrin 2 (LOC481078); mRNA	98.7	AY919675	XM_538198	CETN2	centrin, EF-hand protein, 2
Cfa.20474.1.S1_at	1.245010E-02	2.356048E-01	0.89	1.12	PREDICTED: Canis familiaris similar to Activating signal cointegrator 1 complex subunit 3 (ASC-1 complex subunit p200) (Trip4 complex subunit p200) (Helicase; ATP binding 1); transcript variant 1 (LOC475008); mRNA	77.3	BC130038	XM_532245	ASCC3	activating signal cointegrator 1 complex subunit 3
Cfa.20483.1.S1_at	9.229520E-03	2.040214E-01	0.87	1.16	PREDICTED: Canis familiaris similar to Electron transfer flavoprotein alpha-subunit; mitochondrial precursor (Alpha-ETF);	50.0	NULL	XM_848294	ETFA	electron-transfer-flavoprotein, alpha polypeptide

					transcript variant 1 (LOC610134); mRNA					
Cfa.20483.1.S1_s_at	3.503250E-03	1.277456E-01	0.89	1.13	PREDICTED: Canis familiaris similar to Electron transfer flavoprotein alpha-subunit; mitochondrial precursor (Alpha-ETF); transcript variant 1 (LOC610134); mRNA	100.0	NULL	XM_848294	ETFA	electron-transfer-flavoprotein, alpha polypeptide
Cfa.205.2.A1_at	1.740600E-04	2.495501E-02	1.14	.87	Homo sapiens potassium voltage-gated channel subfamily E member 2 (KCNE2) gene; complete cds	100.0	DQ784804	DQ784804		
Cfa.205.2.A1_x_at	6.009430E-05	1.280276E-02	1.15	.87	Homo sapiens potassium voltage-gated channel subfamily E member 2 (KCNE2) gene; complete cds	100.0	DQ784804	DQ784804		
Cfa.20524.2.S1_a_at	2.039550E-02	2.949329E-01	0.9	1.12	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1016295	71.2	AJ420538	AJ420538	C6orf130	chromosome 6 open reading frame 130
Cfa.20614.1.A1_at	4.214340E-04	4.208376E-02	0.81	1.23	Homo sapiens mixed lineage kinase-related kinase MRK-beta mRNA; complete cds	41.8	AF480462	AF480462	ZAK	sterile alpha motif and leucine zipper containing kinase AZK
Cfa.20636.1.S1_at	1.615300E-05	5.941405E-03	1.19	.84	PREDICTED: Canis familiaris similar to protein phosphatase 1; regulatory (inhibitor) subunit 1B isoform 1 (LOC608394); mRNA	99.4	NM_181505	XM_845423	PPP1R1B	protein phosphatase 1, regulatory (inhibitor) subunit 1B
Cfa.20677.2.S1_at	7.406010E-03	1.831711E-01	0.74	1.36	PREDICTED: Canis familiaris similar to UDP-glucose pyrophosphorylase 2 isoform a; transcript variant 1 (LOC474615); mRNA	96.6	AF086113	XM_531845	UGP2	UDP-glucose pyrophosphorylase 2
Cfa.20680.1.S1_s_at	1.163140E-03	7.191915E-02	0.9	1.11	PREDICTED: Canis familiaris similar to kinesin family member 1C (LOC489453); mRNA	98.4	AB384512	XM_546571	KIF1C	kinesin family member 1C
Cfa.20697.1.A1_at	3.060510E-03	1.189972E-01	1.15	.87	Kutzneria sp. 744 regulator gene; partial cds; ornithine cyclodeaminase; adenylation domain protein; radical-SAM; acyl-CoA-like dehydrogenase; thioesterase; and regulator genes; complete cds; kutznerides biosynthetic gene cluster; complete sequence; and transporter; penicillin acylase; and permease genes; complete cds	4.8	AC090426	EU074211		

Cfa.207.1.S1_s_at	1.752420E-03	9.066885E-02	1.13	.88	PREDICTED: Canis familiaris melan-A (MLANA); mRNA	100.0	AK312149	XM_848155	MLANA	melan-A
Cfa.20716.1.S1_s_at	6.289530E-03	1.704471E-01	1.15	.87	PREDICTED: Canis familiaris similar to Microtubule-associated protein RP/EB family member 2 (APC-binding protein EB2) (End-binding protein 2) (EB2) (LOC490487); mRNA	100.0	AB169699	XM_547609	MAPRE2	microtubule-associated protein, RP/EB family, member 2
Cfa.20768.1.S1_at	5.498650E-06	3.197762E-03	1.2	.83	PREDICTED: Canis familiaris similar to CG10809-PA; transcript variant 1 (LOC481261); mRNA	45.5	NULL	XM_538382	ANKRD54	ankyrin repeat domain 54
Cfa.20780.1.S1_at	2.048470E-02	2.950332E-01	0.88	1.14	PREDICTED: Canis familiaris similar to dystrobrevin binding protein 1 isoform a (LOC610315); mRNA	95.4	AK310590	XM_847791	DTNBP1	dystrobrevin binding protein 1
Cfa.20786.2.S1_s_at	5.831930E-03	1.640145E-01	0.77	1.30	PREDICTED: Canis familiaris similar to Ubiquitin-conjugating enzyme E2 E1 (Ubiquitin-protein ligase E1) (Ubiquitin carrier protein E1) (UbcM3); transcript variant 1 (LOC477048); mRNA	100.0	BC009139	XM_534245	UBE2E1	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
Cfa.20799.1.S1_at	3.524280E-03	1.277456E-01	0.89	1.13	Bos taurus general transcription factor IIE; polypeptide 2; beta 34kDa (GTF2E2); mRNA >gi|86821358|gb|BC105362.1| Bos taurus general transcription factor IIE; polypeptide 2; beta 34kDa; mRNA (cDNA clone MGC:127990 IMAGE:30957520); complete cds	89.7	AB174380	NM_001046065	GTF2E2	general transcription factor IIE, polypeptide 2, beta 34kDa
Cfa.20799.1.S1_s_at	2.972310E-03	1.176756E-01	0.9	1.11	PREDICTED: Canis familiaris similar to *Transcription initiation factor IIE beta* subunit (TFIIE-beta) (LOC475597); mRNA	97.5	AB174380	XM_532814	GTF2E2	general transcription factor IIE, polypeptide 2, beta 34kDa
Cfa.20813.1.S1_s_at	5.120060E-04	4.627805E-02	1.12	.89	PREDICTED: Canis familiaris butylcholinesterase (BCHE); mRNA	82.9	CU676204	XM_545267	BCHE	butyrylcholinesterase
Cfa.20827.1.S1_at	3.503830E-04	3.758122E-02	0.86	1.16	PREDICTED: Canis familiaris similar to Protein C14orf111 (LOC612615); mRNA	99.2	AC068776	XM_850348	LOC612615	similar to Protein C14orf111
Cfa.20828.1.S1_s_at	2.756350E-04	3.223357E-02	1.18	.85	PREDICTED: Canis familiaris similar to serine/cysteine proteinase inhibitor; clade I; member 2 isoform 1 (LOC609110); mRNA	100.0	CU693298	XM_846314	SERPINI2	serpin peptidase inhibitor, clade I (pancpin), member 2

Cfa.20854.1.S1_at	1.830960E-02	2.812111E-01	0.9	1.11	PREDICTED: Canis familiaris similar to protein phosphatase 1; regulatory (inhibitor) subunit 11 isoform 1; transcript variant 1 (LOC608919); mRNA	100.0	AB171371	XM_844699	PPP1R11	protein phosphatase 1, regulatory (inhibitor) subunit 11
Cfa.20889.1.S1_at	9.393920E-03	2.059436E-01	0.91	1.10	PREDICTED: Canis familiaris similar to Kinesin heavy chain (Ubiquitous kinesin heavy chain) (UKHC); transcript variant 6 (LOC477968); mRNA	98.0	AL161932	XM_854433	KIF5B	kinesin family member 5B
Cfa.20892.1.S1_s_at	1.744090E-04	2.495501E-02	1.15	.87	PREDICTED: Canis familiaris similar to Ectonucleoside triphosphate diphosphohydrolase 6 (NTPDase6) (CD39 antigen-like 2) (LOC485564); mRNA	99.2	NM_001114089	XM_542683	ENTPD6	ectonucleoside triphosphate diphosphohydrolase 6 (putative function)
Cfa.20967.1.S1_s_at	5.933780E-03	1.652817E-01	0.87	1.15	PREDICTED: Canis familiaris similar to CCAAT/enhancer binding protein zeta; transcript variant 2 (LOC483035); mRNA	95.4	BC034475	XM_858367	CEBPZ	CCAAT/enhancer binding protein zeta
Cfa.20981.1.S1_at	1.845870E-02	2.818510E-01	1.12	.89	PREDICTED: Canis familiaris similar to Parvalbumin alpha; transcript variant 3 (LOC481278); mRNA	100.0	Z82184	XM_538399	PVALB	parvalbumin
Cfa.21001.1.S1_at	4.174040E-03	1.384964E-01	0.84	1.20	PREDICTED: Canis familiaris similar to Sulfotransferase 1C2 (SULT1C) (SULT1C#2) (LOC474542); mRNA	99.3	BC125043	XM_531771	SULT1C4	sulfotransferase family, cytosolic, 1C, member 4
Cfa.21002.1.S1_s_at	5.119030E-03	1.525288E-01	0.87	1.14	PREDICTED: Canis familiaris similar to family with sequence similarity 62 (C2 *domain containing); member A* (LOC474397); mRNA	85.5	NM_015292	XM_531630	LOC474397	similar to family with sequence similarity 62 (C2 domain containing), member A
Cfa.21021.1.S1_s_at	2.811360E-03	1.141386E-01	1.22	.82	PREDICTED: Canis familiaris similar to solute carrier family 35; member F5 (LOC476123); mRNA	98.2	AK315719	XM_533330	SLC35F5	solute carrier family 35, member F5
Cfa.2103.2.A1_at	1.951700E-02	2.898299E-01	1.2	.84	Homo sapiens suppressor of cytokine signaling 6 (SOCS6); mRNA	82.4	NM_004232	NM_004232	SOCS6	suppressor of cytokine signaling 6
Cfa.21050.1.S1_at	9.523590E-03	2.075233E-01	1.14	.88	PREDICTED: Canis familiaris similar to T-cell differentiation antigen CD6 precursor (T12) (TP120) (LOC483804); mRNA	100.0	AK292704	XM_540925	CD6	CD6 molecule

Cfa.21061.1.S1_at	3.584700E-04	3.800811E-02	1.18	.85	PREDICTED: Equus caballus sperm-membrane associated protein P47 (LOC100033943); mRNA	28.7	NM_005928	XM_001499480	LOC100033943	sperm-membrane associated protein P47
Cfa.21102.1.S1_s_at	1.590550E-02	2.641811E-01	1.11	.90	PREDICTED: Canis familiaris similar to Translation initiation factor eIF-2B alpha subunit (eIF-2B GDP-GTP exchange factor); transcript variant 3 (LOC477447); mRNA	100.0	AB169786	XM_852815	EIF2B1	eukaryotic translation initiation factor 2B, subunit 1 alpha, 26kDa
Cfa.21115.1.S1_s_at	8.772010E-03	2.005228E-01	1.11	.90	PREDICTED: Canis familiaris Insulin-responsive glucose transporter (GLUT4); mRNA	100.0	NM_001042	XM_536618	SLC2A4	solute carrier family 2 (facilitated glucose transporter), member 4
Cfa.2114.1.S1_at	7.532730E-04	5.627969E-02	0.84	1.19	PREDICTED: Canis familiaris similar to CG15027-PA (LOC475487); mRNA	96.6	NM_018352	XM_532710	LOC475487	similar to CG15027-PA
Cfa.21159.1.S1_at	5.753250E-06	3.301215E-03	1.18	.85	Bos taurus regulator of G-protein signaling 5 (RGS5); mRNA >gi|74354560|gb|BC102265.1| Bos taurus regulator of G-protein signaling 5; mRNA (cDNA clone MGC:127135 IMAGE:7943795); complete cds	35.3	NM_003617	NM_001034707	RGS5	regulator of G-protein signaling 5
Cfa.21180.1.S1_at	2.534210E-03	1.074480E-01	1.13	.89	PREDICTED: Canis familiaris similar to centromere protein C 1 (LOC475158); mRNA	98.4	AC010201	XM_532388	CENPC1	centromere protein C 1
Cfa.21240.1.S1_at	1.376590E-02	2.460894E-01	0.88	1.13	PREDICTED: Canis familiaris similar to cAMP-specific 3;5-cyclic phosphodiesterase 4C (DPDE1) (PDE21) (LOC609938); mRNA	98.8	NULL	XM_847290	PDE4C	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila)
Cfa.21263.1.S1_at	3.793670E-05	9.943067E-03	0.85	1.17	PREDICTED: Canis familiaris similar to skeletal muscle specific actinin; alpha 3; transcript variant 11 (LOC483707); mRNA	100.0	NULL	XM_860570	ACTN3	actinin, alpha 3
Cfa.21296.1.S1_s_at	4.604250E-05	1.099109E-02	0.77	1.29	PREDICTED: Canis familiaris similar to Eukaryotic translation initiation factor 4E (eIF4E) (eIF-4E) (mRNA cap-binding protein) (eIF-4F 25 kDa subunit); transcript variant 1 (LOC487870); mRNA	97.2	AB168785	XM_544992	EIF4E	eukaryotic translation initiation factor 4E
Cfa.21300.1.S1_at	1.656240E-02	2.701029E-01	1.13	.89	PREDICTED: Canis familiaris hypothetical protein LOC607225 (LOC607225); mRNA	100.0	AC092960	XM_852399	LOC607225	hypothetical protein LOC607225

Cfa.21322.1.A1_at	1.181550E-02	2.296042E-01	1.23	.82	Bos taurus regulator of G-protein signaling 5 (RGS5); mRNA >gi|74354560|gb|BC102265.1| Bos taurus regulator of G-protein signaling 5; mRNA (cDNA clone MGC:127135 IMAGE:7943795); complete cds	29.8	AB008109	NM_001034707	RGS5	regulator of G-protein signaling 5
Cfa.21324.1.S1_at	1.084650E-02	2.190423E-01	1.18	.85	PREDICTED: Canis familiaris similar to Prolactin-inducible protein precursor (Secretory actin-binding protein) (SABP) (Gross cystic disease fluid protein 15) (GCDFP-15) (gp17) (LOC608856); mRNA	100.0	AC011243	XM_845994	PIP	prolactin-induced protein
Cfa.21352.1.S1_at	9.100670E-03	2.025064E-01	1.11	.90	PREDICTED: Canis familiaris similar to cardiomyopathy associated 5 (LOC479170); mRNA	98.7	AC109488	XM_536312	CMYA5	cardiomyopathy associated 5
Cfa.21360.1.S1_s_at	1.747680E-03	9.061616E-02	1.15	.87	PREDICTED: Canis familiaris similar to Bleomycin hydrolase (BLM hydrolase) (BMH) (BH) (LOC480635); mRNA	96.9	AK312896	XM_537755	BLMH	bleomycin hydrolase
Cfa.2137.2.S1_at	7.146200E-03	1.804793E-01	1.15	.87	PREDICTED: Canis familiaris similar to MYST histone acetyltransferase 1 (predicted); transcript variant 2 (LOC479777); mRNA	100.0	NULL	XM_851853	LOC479777	similar to MYST histone acetyltransferase 1 (predicted)
Cfa.21377.1.S1_s_at	5.952420E-03	1.656074E-01	0.91	1.10	PREDICTED: Canis familiaris similar to Thimet oligopeptidase (Endopeptidase 24.15) (MP78) (LOC476748); mRNA	98.9	EU176234	XM_533954	THOP1	thimet oligopeptidase 1
Cfa.21378.1.S1_s_at	3.863670E-03	1.337675E-01	1.13	.89	PREDICTED: Canis familiaris similar to Ubiquitin-protein ligase E3C; transcript variant 1 (LOC482822); mRNA	99.4	AK127280	XM_539937	UBE3C	ubiquitin protein ligase E3C
Cfa.21382.1.S1_s_at	4.798570E-03	1.480925E-01	0.81	1.23	Canis lupus familiaris zinc finger CCCH-type containing 15 (ZC3H15); mRNA	49.0	AB171327	NM_001114605	ZC3H15	zinc finger CCCH-type containing 15
Cfa.21470.1.S1_s_at	1.514600E-03	8.376266E-02	1.11	.90	PREDICTED: Canis familiaris similar to SYT; transcript variant 2 (SS18); mRNA	100.0	XM_001494132	XM_861846	SS18	synovial sarcoma translocation, chromosome 18
Cfa.21488.1.S1_s_at	6.584100E-03	1.739023E-01	1.12	.89	PREDICTED: Canis familiaris similar to hydroxyacyl dehydrogenase; subunit A; transcript variant 3 (LOC475687); mRNA	99.4	U04627	XM_854396	HADHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional

										protein), alpha subunit
Cfa.21540.1.S1_at	1.585460E-02	2.639469E-01	0.9	1.11	PREDICTED: Canis familiaris similar to Protein C11orf2 (Another new gene 2 protein) (LOC476028); mRNA	98.5	BC010540	XM_533237	LOC476028	similar to Protein C11orf2 (Another new gene 2 protein)
Cfa.21551.1.S1_s_at	1.632980E-03	8.751593E-02	1.16	.86	PREDICTED: Canis familiaris similar to Adseverin (Scinderin) (LOC475245); mRNA	99.6	NULL	XM_532479	LOC475245	similar to Adseverin (Scinderin)
Cfa.21566.1.S1_s_at	1.971580E-02	2.911700E-01	0.89	1.12	PREDICTED: Canis familiaris similar to Glucosidase II beta subunit precursor (Protein kinase C substrate; 60.1 kDa protein; heavy chain) (PKCSH) (80K-H protein) (LOC484941); mRNA	100.0	J03075	XM_542057	PRKCSH	protein kinase C substrate 80K-H
Cfa.21577.1.S1_at	1.072620E-02	2.176197E-01	0.88	1.14	PREDICTED: Canis familiaris similar to Y106G6H.15 (LOC491691); mRNA	94.8	AL136132	XM_548812	LOC491691	similar to Y106G6H.15
Cfa.2164.1.A1_at	1.851260E-02	2.822139E-01	0.87	1.16	Homo sapiens von Hippel-Lindau tumor suppressor (VHL) gene; complete cds	7.9	AP001136	AF010238		
Cfa.2168.1.A1_at	3.859530E-03	1.337675E-01	1.12	.89	PREDICTED: Pan troglodytes hypothetical LOC452791 (LOC452791); mRNA	22.9	AK096128	XR_024627	LOC452791	hypothetical LOC452791
Cfa.2179.1.A1_at	4.063250E-03	1.367753E-01	1.1	.91	PREDICTED: Gallus gallus hypothetical LOC426454 (LOC426454); mRNA	62.3	NULL	XM_424099	GPR155	G protein-coupled receptor 155
Cfa.2189.1.A1_at	8.180420E-04	5.906785E-02	1.13	.88	PREDICTED: Monodelphis domestica similar to interleukin-16; transcript variant 1 (LOC100015795); mRNA	4.3	NULL	XM_001365875	LOC100015795	similar to interleukin-16
Cfa.22.1.S1_at	2.741660E-03	1.123689E-01	0.87	1.15	Canis lupus familiaris BCL2-associated X protein (BAX); mRNA >gi|27372189|dbj|AB080230.1| Canis familiaris mRNA for Bax; complete cds	100.0	NM_138763	NM_001003011	BAX	BCL2-associated X protein
Cfa.2206.1.A1_at	1.363350E-05	5.238551E-03	1.17	.86	Gallus gallus finished cDNA; clone ChEST736p18	99.8	CU675355	CR406524		
Cfa.2213.1.A1_at	1.549640E-02	2.613375E-01	1.12	.89	Gallus gallus finished cDNA; clone ChEST59h14	99.8	NULL	CR406493		

Cfa.2250.1.A1_at	7.305430E-04	5.564410E-02	1.13	.89	PREDICTED: Gallus gallus similar to Ferric-chelate reductase 1 (LOC429082); mRNA	70.9	AK131302	XM_426638	FRRS1	ferric-chelate reductase 1
Cfa.2251.1.A1_at	3.706870E-03	1.304376E-01	1.14	.88	PREDICTED: Bos taurus hypothetical protein LOC786280 (LOC786280); mRNA	3.9	NULL	XM_001252773		
Cfa.2254.1.A1_at	2.883980E-03	1.156683E-01	1.1	.91	Plasmodium chabaudi chabaudi hypothetical protein (PC104902.00.0) partial mRNA	6.3	AC009974	XM_739535	PC104902.00.0	hypothetical protein
Cfa.2256.1.A1_at	6.714310E-03	1.754404E-01	1.1	.91	PREDICTED: Gallus gallus phospholipid scramblase 1; transcript variant 1 (PLSCR1); mRNA	100.0	CR607459	XM_001231236	PLSCR1	phospholipid scramblase 1
Cfa.2273.1.S1_at	6.501720E-03	1.732327E-01	1.2	.84	Homo sapiens solute carrier family 39 (zinc transporter); member 12 (SLC39A12); mRNA	7.4	BC047635	NM_152725	SLC39A12	solute carrier family 39 (zinc transporter), member 12
Cfa.2296.1.A1_s_at	8.709830E-03	2.001215E-01	0.91	1.10	PREDICTED: Canis familiaris similar to malignant T cell amplified sequence 1; transcript variant 1 (LOC481038); mRNA	99.8	NM_014060	XM_538160	MCTS1	malignant T cell amplified sequence 1
Cfa.2300.1.A1_at	1.218570E-02	2.337430E-01	0.88	1.13	PREDICTED: Bos taurus hypothetical protein LOC785707 (LOC785707); mRNA	15.7	AC002314	XM_001253642		
Cfa.2311.1.S1_s_at	2.043180E-02	2.949586E-01	0.84	1.20	PREDICTED: Canis familiaris similar to Nebulette (Actin-binding Z-disk protein); transcript variant 3 (LOC477974); mRNA	80.8	CR616315	XM_844454	NEBL	nebulette
Cfa.2314.1.A1_at	2.249200E-03	1.016747E-01	1.16	.86	Mus musculus 4 days neonate male adipose cDNA; RIKEN full-length enriched library; clone:B430205N08 product:adenylate kinase 1; full insert sequence	4.6	AL133245	AK046613	Ak1	adenylate kinase 1
Cfa.2315.1.S1_s_at	6.091610E-03	1.681491E-01	0.88	1.14	PREDICTED: Canis familiaris similar to kinectin 1 (LOC480332); mRNA	96.3	NM_004986	XM_537455	KTN1	kinectin 1 (kinesin receptor)
Cfa.2360.1.A1_at	1.258250E-02	2.363264E-01	1.24	.80	NULL	null	AC011238	NULL		
Cfa.2420.1.S1_at	1.467410E-02	2.547398E-01	0.83	1.21	Tetrahymena thermophila SB210 hypothetical protein (TTHERM_00592930)	23.2	AL035467	XM_001011652	TTHERM_00592930	hypothetical protein

					partial mRNA					
Cfa.2432.1.A1_at	7.060090E-04	5.454775E-02	0.89	1.12	PREDICTED: Canis familiaris similar to Methylmalonyl-CoA mutase; mitochondrial precursor (MCM) (Methylmalonyl-CoA isomerase) (LOC474930); mRNA	100.0	NG_007100	XM_532164	MUT	methylmalonyl Coenzyme A mutase
Cfa.2443.1.A1_at	9.312740E-03	2.047899E-01	1.15	.87	PREDICTED: Canis familiaris similar to G-protein coupled receptor family C group 5 member B precursor (Retinoic acid induced gene 2 protein) (RAIG-2) (A-69G12.1) (LOC479823); mRNA	98.4	AC004131	XM_536950	GPRC5B	G protein-coupled receptor, family C, group 5, member B
Cfa.25.1.S1_at	1.752910E-03	9.066885E-02	0.89	1.12	Canis familiaris mRNA for partial hypothetical protein; clone V2.89	55.2	AC104115	AJ388552	LOC403526	hypothetical protein LOC403526
Cfa.2557.1.S1_at	1.250260E-03	7.483302E-02	1.21	.83	Human DNA sequence from clone RP11-321C24 on chromosome 13 Contains a novel gene; the 5-prime end of the GTF2F2 gene for general transcription factor IIF; polypeptide 2; 30kDa; a novel gene similar to RIKEN cDNA 2210017A09 gene and a CpG island; complete sequence	13.5	AL138693	AL138693		
Cfa.2589.1.A1_at	3.576680E-04	3.800811E-02	0.91	1.10	PREDICTED: Pan troglodytes similar to KIAA1219 protein (LOC458242); mRNA	90.9	AL035419	XM_514640	LOC458242	similar to KIAA1219 protein
Cfa.2591.1.S1_at	2.308610E-03	1.028541E-01	1.11	.90	PREDICTED: Pan troglodytes hook homolog 1; transcript variant 1 (HOOK1); mRNA	12.4	AL355178	XM_001156392	HOOK1	hook homolog 1 (Drosophila)
Cfa.2598.1.S1_at	1.402490E-02	2.485493E-01	1.23	.81	PREDICTED: Canis familiaris similar to radixin; transcript variant 1 (LOC479446); mRNA	100.0	EF445024	XM_536581	RDX	radixin
Cfa.262.1.A1_at	9.886090E-03	2.114552E-01	1.11	.90	PREDICTED: Bos taurus similar to brain-specific angiogenesis inhibitor 1 (LOC524070); mRNA	47.2	NM_001702	XM_602388		
Cfa.2668.1.A1_at	4.215900E-04	4.208376E-02	1.13	.89	Synthetic construct Homo sapiens gateway clone IMAGE:100022857 5-prime read TBC1D3C mRNA	4.7	AC026475	CU687138		
Cfa.2707.1.A1_at	1.224430E-	2.341211E-	1.15	.87	PREDICTED: Nasonia vitripennis similar to conserved hypothetical protein	7.4	AC021058	XM_001604269	LOC100120711	similar to conserved hypothetical

	02	01			(LOC100120711); mRNA					protein
Cfa.2750.1.A1_at	2.376400E-04	3.046955E-02	1.2	.83	NULL	null	AC214170	NULL		
Cfa.2775.1.A1_at	4.466130E-04	4.328827E-02	1.23	.81	Homo sapiens suppressor of hairy wing homolog 2 (Drosophila); mRNA (cDNA clone IMAGE:4815420)	49.2	BC042370	BC042370	ZNF280B	zinc finger protein 280B
Cfa.2803.1.A1_at	1.027850E-03	6.728568E-02	1.19	.84	Mus musculus adult male hypothalamus cDNA; RIKEN full-length enriched library; clone:A230017L24 product:hypothetical Arginine-rich region profile containing protein; full insert sequence	6.3	AP003102	AK138158	B930094E09Rik	RIKEN cDNA B930094E09 gene
Cfa.2820.2.S1_at	1.948700E-02	2.895798E-01	1.13	.88	NULL	null	AC097372	NULL		
Cfa.2838.1.A1_at	1.141620E-02	2.256758E-01	1.13	.89	NULL	null	AL353639	NULL		
Cfa.2853.1.A1_at	6.888230E-04	5.389727E-02	1.13	.89	NULL	null	AL109842	NULL		
Cfa.2947.1.S1_at	1.294690E-02	2.398507E-01	0.91	1.10	PREDICTED: Canis familiaris similar to TRAF interacting protein TANK isoform a (LOC608092); mRNA	96.9	NM_004180	XM_844996	TANK	TRAF family member-associated NFKB activator
Cfa.2999.1.A1_at	1.668090E-04	2.441709E-02	1.17	.85	PREDICTED: Bos taurus similar to tensin-like SH2 domain containing 1 (LOC516555); mRNA	100.0	AC114284	XM_594710	TNS3	tensin 3
Cfa.3001.1.A1_at	6.944870E-05	1.409776E-02	1.18	.84	Sus scrofa mRNA; clone:OVR010026F11; expressed in ovary	100.0	NULL	AK234200	LOC100155717	similar to SFLQ611
Cfa.301.1.A1_at	9.733700E-03	2.098850E-01	0.82	1.23	Bos taurus non-SMC element 2; MMS21 homolog (S. cerevisiae) (NSMCE2); mRNA >gi|81673677|gb|BC109850.1| Bos taurus non-SMC element 2; MMS21 homolog (S. cerevisiae); mRNA (cDNA clone MGC:133996 IMAGE:8039332); complete cds	70.6	NM_173685	NM_001075797	NSMCE2	non-SMC element 2, MMS21 homolog (S. cerevisiae)

Cfa.3023.1.A1_at	7.791140E-03	1.875233E-01	1.11	.90	Gasterosteus aculeatus clone CNB223-C12 mRNA sequence	4.0	AL138795	BT028468		
Cfa.3059.1.A1_at	3.848920E-03	1.336757E-01	1.16	.86	NULL	null	AC007954	NULL		
Cfa.3063.1.S1_at	1.965750E-02	2.908080E-01	0.88	1.14	PREDICTED: Canis familiaris similar to CG7386-PA; transcript variant 3 (LOC476272); mRNA	99.4	AB179013	XM_858316	ZUFSP	zinc finger with UFM1-specific peptidase domain
Cfa.3063.1.S1_s_at	1.687380E-02	2.723796E-01	0.87	1.15	PREDICTED: Canis familiaris similar to CG7386-PA; transcript variant 3 (LOC476272); mRNA	100.0	BC016879	XM_858316	ZUFSP	zinc finger with UFM1-specific peptidase domain
Cfa.3082.2.S1_at	2.201460E-04	2.897822E-02	1.14	.88	Sus scrofa mRNA for hypothetical protein (5-prime ; clone 5A9)	8.8	AC011461	AJ236933		
Cfa.311.2.A1_x_at	6.209660E-03	1.691578E-01	0.85	1.17	PREDICTED: Canis familiaris similar to ubiquitin and ribosomal protein S27a precursor (LOC474599); mRNA	51.3	XR_019408	XM_531829	RPS27A	ribosomal protein S27a
Cfa.311.6.A1_x_at	7.319070E-03	1.820154E-01	0.86	1.16	PREDICTED: Canis familiaris similar to ubiquitin and ribosomal protein S27a precursor (LOC474599); mRNA	51.1	XR_019408	XM_531829	RPS27A	ribosomal protein S27a
Cfa.3164.1.A1_at	3.412990E-03	1.262924E-01	1.11	.90	Paramecium tetraurelia hypothetical protein (GSPATT00028911001) partial mRNA	4.1	AL365434	XM_001425237	GSPATT00028911001	hypothetical protein
Cfa.3214.1.S1_a_at	4.359710E-04	4.273807E-02	0.76	1.32	PREDICTED: Canis familiaris similar to large subunit ribosomal protein L36a (LOC480311); mRNA	99.8	M15661	XM_537433	RPL36AL	ribosomal protein L36a-like
Cfa.3214.1.S1_s_at	6.381940E-04	5.125131E-02	0.79	1.26	PREDICTED: Canis familiaris similar to large subunit ribosomal protein L36a (LOC480311); mRNA	99.6	CU674381	XM_537433	RPL36AL	ribosomal protein L36a-like
Cfa.3214.2.S1_at	3.880840E-03	1.339310E-01	0.85	1.18	PREDICTED: Bos taurus similar to ribosomal protein L36a (LOC784454); mRNA	22.9	AC021183	XR_027432		
Cfa.3221.1.S1_at	4.493780E-03	1.433228E-01	0.88	1.14	Tetrahymena thermophila SB210 hypothetical protein (TTHERM_01538670) partial mRNA	8.1	AC024167	XM_001029402	TTHERM_01538670	hypothetical protein

Cfa.3228.1.S1_at	1.309670E-02	2.403652E-01	0.87	1.15	PREDICTED: Canis familiaris hypothetical LOC477927 (LOC477927); mRNA	98.1	NM_001099671	XM_535116	LOC477927	hypothetical LOC477927
Cfa.3244.1.A1_at	4.372480E-03	1.417274E-01	0.89	1.12	PREDICTED: Canis familiaris similar to Mediator of RNA polymerase II transcription subunit 31 (Mediator complex subunit SOH1) (hSOH1) (LOC607000); mRNA	95.8	BC012539	XM_843504	MED31	mediator complex subunit 31
Cfa.3266.1.S1_x_at	6.817660E-06	3.548256E-03	0.74	1.35	PREDICTED: Canis familiaris similar to 60S ribosomal protein L7; transcript variant 1 (LOC477912); mRNA	99.7	NULL	XM_535102	RPL7	ribosomal protein L7
Cfa.3267.1.A1_s_at	1.826710E-02	2.808187E-01	0.86	1.16	PREDICTED: Canis familiaris similar to Transcription factor 8 (NIL-2-A zinc finger protein) (Negative regulator of IL2); transcript variant 4 (LOC477966); mRNA	48.3	NULL	XM_854721	ZEB1	zinc finger E-box binding homeobox 1
Cfa.33.1.S1_at	1.346780E-02	2.433194E-01	0.86	1.17	Paramecium tetraurelia hypothetical protein (GSPATT00028544001) partial mRNA	20.2	AC053545	XM_001424870	GSPATT00028544001	hypothetical protein
Cfa.33.1.S1_s_at	8.142520E-03	1.919022E-01	0.87	1.15	Canis lupus familiaris thiopurine S-methyltransferase (TPMT); mRNA >gi|23428514|gb|AY057077.1| Canis familiaris thiopurine methyltransferase (TPMT) mRNA; complete cds; alternatively spliced	99.0	NULL	NM_001003015	TPMT	thiopurine S-methyltransferase
Cfa.3318.1.S1_s_at	2.939380E-03	1.170600E-01	0.8	1.26	PREDICTED: Canis familiaris mutS-like protein 2; transcript variant 1 (MSH2); mRNA	100.0	NG_007110	XM_538482	MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
Cfa.3343.1.A1_at	4.293740E-03	1.407487E-01	0.9	1.11	PREDICTED: Canis familiaris similar to cleavage stimulation factor subunit 3; transcript variant 2 (LOC475948); mRNA	99.6	BC059948	XM_853526	CSTF3	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa
Cfa.3363.1.S1_at	1.498160E-02	2.570706E-01	0.81	1.23	PREDICTED: Macaca mulatta similar to Forkhead box protein C1 (Forkhead-related protein FKHL7) (Forkhead-related transcription factor 3) (FREAC-3) (FOXC1); mRNA	46.8	AF048693	XM_001119000	FOXC1	forkhead box C1
Cfa.3371.1.S1_at	1.777980E-02	2.774525E-01	0.88	1.14	PREDICTED: Canis familiaris similar to D19Bwg1357e protein (LOC476337); mRNA	100.0	AC018643	XM_533539	LOC476337	similar to D19Bwg1357e protein

Cfa.3394.1.A1_at	1.892000E-03	9.412973E-02	0.81	1.23	PREDICTED: Canis familiaris similar to GTP-binding protein SAR1b (GTBPB) (LOC481509); mRNA	99.7	NM_001033503	XM_538630	SAR1B	SAR1 gene homolog B (S. cerevisiae)
Cfa.3397.1.A1_at	3.340320E-04	3.648494E-02	0.87	1.15	PREDICTED: Canis familiaris similar to Autophagy protein 5-like (APG5-like) (Apoptosis-specific protein); transcript variant 1 (LOC610868); mRNA	100.0	NULL	XM_849201	ATG5	ATG5 autophagy related 5 homolog (S. cerevisiae)
Cfa.3397.1.A1_s_at	1.140650E-03	7.155667E-02	0.89	1.12	PREDICTED: Canis familiaris similar to Autophagy protein 5-like (APG5-like) (Apoptosis-specific protein); transcript variant 3 (LOC610868); mRNA	99.6	NULL	XM_863268	ATG5	ATG5 autophagy related 5 homolog (S. cerevisiae)
Cfa.3484.1.S1_at	1.407130E-02	2.487915E-01	1.16	.86	Canis lupus familiaris progesterone receptor (PGR); mRNA >gi|9957241|gb|AF177470.1|AF177470 Canis familiaris progesterone receptor (PR) mRNA; complete cds	98.0	AP001533	NM_001003074	PGR	progesterone receptor
Cfa.3494.1.S1_s_at	7.677270E-03	1.857174E-01	0.9	1.11	Canis lupus familiaris transglutaminase 1 (K polypeptide epidermal type I; protein-glutamine-gamma-glutamyltransferase) (TGM1); mRNA >gi|10178634|gb|AF262219.1|AF262219 Canis familiaris transglutaminase 1 mRNA; complete cds	99.8	AK291350	NM_001003079	TGM1	transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine-gamma-glutamyltransferase)
Cfa.3500.1.S1_s_at	3.961500E-03	1.348203E-01	1.12	.89	Canis lupus familiaris deiodinase; iodothyronine; type I (DIO1); mRNA	98.5	NM_001039716	NM_001007126	DIO1	deiodinase, iodothyronine, type I
Cfa.3529.1.S1_at	1.775760E-02	2.773922E-01	1.14	.88	PREDICTED: Bos taurus msh homeobox 2 (MSX2); mRNA	32.2	D89377	XM_001251115		
Cfa.354.1.A1_at	2.013210E-02	2.927965E-01	1.14	.87	PREDICTED: Pan troglodytes parvin; alpha; transcript variant 1 (PARVA); mRNA	14.0	AC009806	XM_001171433	PARVA	parvin, alpha
Cfa.3547.1.A1_s_at	1.106710E-02	2.221421E-01	0.9	1.11	Canis lupus familiaris ribosomal protein L23 (RPL23); mRNA >gi|5441536|emb|AJ388521.1|CFA388521 Canis familiaris mRNA for Ribosomal protein; L17/L23 (rpL17/L23 gene)	99.2	X55954	NM_001003100	RPL23	ribosomal protein L23
Cfa.3568.1.S1_at	4.009750E-	1.359808E-	1.11	.90	Canis familiaris cyclin-dependent kinase	100.0	NM_000389	AF076469	WAF1	cyclin-dependent kinase inhibitor

	03	01			inhibitor (WAF1) mRNA; partial cds					
Cfa.3572.1.S1_s_at	1.798250E-02	2.790268E-01	1.14	.88	PREDICTED: Canis familiaris malic enzyme 1; NADP(+)-dependent; cytosolic (ME1); mRNA	99.7	AK289783	XM_532217	ME1	malic enzyme 1, NADP(+)-dependent, cytosolic
Cfa.3590.1.S1_s_at	5.008640E-03	1.508466E-01	1.12	.90	Canis familiaris endothelin B receptor (EDNRB) mRNA; partial cds	98.6	AB171733	AF276427	EDNRB	endothelin receptor type B
Cfa.3592.1.S1_at	9.786610E-04	6.570464E-02	0.83	1.20	PREDICTED: Pan troglodytes similar to retinitis pigmentosa GTPase regulator (LOC465569); mRNA	73.6	AC197892	XM_521004	LOC465569	similar to retinitis pigmentosa GTPase regulator
Cfa.3592.4.S1_s_at	1.888460E-02	2.855582E-01	0.87	1.15	Canis lupus familiaris retinitis pigmentosa GTPase regulator (RPGR); mRNA >gi|8131935|gb|AF148801.1|AF148801 Canis familiaris retinitis pigmentosa GTP-ase regulator RPGR (RPGR) mRNA; alternative splice variant; complete cds	100.0	AC197892	NM_001003126	RPGR	retinitis pigmentosa GTPase regulator
Cfa.3594.1.S1_s_at	1.482010E-02	2.558270E-01	1.13	.89	Canis lupus familiaris lactalbumin; alpha-(LALBA); mRNA >gi|7959045|dbj|AB035079.1| Canis lupus familiaris mRNA for alpha-lactalbumin; complete cds	100.0	NULL	NM_001003129	LALBA	lactalbumin, alpha-
Cfa.3628.1.S1_s_at	8.627110E-04	6.116436E-02	1.12	.89	Canis familiaris matrix metalloproteinase-13 mRNA; partial cds	100.0	AK315341	AF201729	MMP13	matrix metallopeptidase 13 (collagenase 3)
Cfa.3654.1.S1_s_at	4.593030E-03	1.451256E-01	1.11	.90	PREDICTED: Canis familiaris CE8 protein; variant 2 (CE8); mRNA	64.0	BC140342	XM_850479	LY6G5C	lymphocyte antigen 6 complex, locus G5C
Cfa.3689.1.A1_at	2.860950E-03	1.152818E-01	1.13	.89	Canis familiaris cardiotrophin-1 mRNA; partial cds	100.0	NM_001330	AF095589	CTF1	cardiotrophin 1
Cfa.3698.1.A1_at	1.914700E-02	2.875239E-01	1.13	.88	Canis familiaris angiotensin II receptor type 2 mRNA; partial cds	100.0	AK313927	DQ195093		
Cfa.3705.1.S1_at	6.205550E-03	1.691578E-01	1.23	.82	PREDICTED: Canis familiaris collagen type IV alpha 3 chain (COL4A3); mRNA	99.1	NM_031366	XM_534590	COL4A3	collagen, type IV, alpha 3 (Goodpasture antigen)
Cfa.3709.1.S1_s_at	1.428380E-	2.509538E-	0.89	1.12	Canis lupus familiaris phospholipase A2; group VII (platelet-activating factor acetylhydrolase; plasma) (PLA2G7); mRNA	100.0	EF568110	NM_001003198	PLA2G7	phospholipase A2, group VII (platelet-activating factor

	02	01			>gi|1054900|gb|U34246.1|CFU34246 Dog plasma PAF acetylhydrolase; complete cds					acetylhydrolase, plasma)
Cfa.3718.1.S1_s_at	1.841560E-03	9.250120E-02	1.13	.88	PREDICTED: Canis familiaris desmocollin type 2; transcript variant 1 (DSC2); mRNA	100.0	X56807	XM_537291	DSC2	desmocollin 2
Cfa.3725.1.A1_at	9.980180E-03	2.128330E-01	0.89	1.13	Canis familiaris clone VDJ83 immunoglobulin IgH heavy chain VDJ region mRNA; partial cds	100.0	NULL	AF067453		
Cfa.3737.2.S1_s_at	5.620600E-03	1.600811E-01	0.9	1.11	Canis lupus familiaris galactosidase; beta 1 (GLB1); mRNA >gi|76470547|gb|DQ196436.1| Canis familiaris lysosomal beta-galactosidase (GLB1) mRNA; complete cds	99.4	NULL	NM_001037641	GLB1	galactosidase, beta 1
Cfa.3758.1.S1_x_at	4.852570E-04	4.543068E-02	1.17	.85	C.familiaris mRNA for TPCR71 protein	100.0	NULL	X89663	TPCR71	putative olfactory receptor
Cfa.3759.1.S1_s_at	6.026730E-03	1.671616E-01	1.23	.81	PREDICTED: Canis familiaris similar to olfactory receptor 1411 (LOC608434); mRNA	100.0	NULL	XM_845465	LOC608434	similar to olfactory receptor 1411
Cfa.3760.1.S1_s_at	1.033410E-04	1.807837E-02	1.13	.89	C.familiaris mRNA for TPCR63 protein	100.0	AF546692	X89661	TPCR63	putative olfactory receptor
Cfa.3771.1.S1_at	2.437140E-03	1.055154E-01	0.85	1.18	Canis lupus familiaris CD34 molecule (CD34); mRNA >gi|1224105|gb|U49457.1|CFU49457 Canis familiaris hematopoietic progenitor cell marker CD34 mRNA; complete cds	43.6	AB238231	NM_001003341	CD34	CD34 molecule
Cfa.3806.1.S1_at	6.968230E-04	5.422745E-02	1.13	.88	Canis lupus familiaris calcitonin/calcitonin-related polypeptide; alpha (CALCA); mRNA	100.0	AC026305	NM_001003266	CALCA	calcitonin/calcitonin-related polypeptide, alpha
Cfa.3821.1.S1_s_at	5.709030E-04	4.913762E-02	1.14	.88	Canis lupus familiaris 5-hydroxytryptamine (serotonin) receptor 1D (HTR1D); mRNA >gi|900|emb|X14049.1|CFGPCR4 Canis familiaris RDC4 mRNA for G protein-coupled receptor	99.6	AL049576	NM_001003280	HTR1D	5-hydroxytryptamine (serotonin) receptor 1D
Cfa.3823.1.S1_s_at	5.776750E-03	1.628899E-01	1.13	.89	C.familiaris mRNA DTPCRH09 for olfactory receptor	100.0	BC156952	X64973		

Cfa.3826.1.S1_at	1.104220E-03	7.019218E-02	1.17	.85	PREDICTED: Canis familiaris hypothetical gene supported by X64971 (LOC487943); mRNA	97.0	NULL	XM_545065	OR5H2	olfactory receptor, family 5, subfamily H, member 2
Cfa.3829.1.S1_s_at	7.949370E-06	3.843833E-03	1.28	.78	PREDICTED: Canis familiaris cOR2T13 olfactory receptor family 2 subfamily T-like (cOR2T13); mRNA	100.0	NULL	XM_539348	cOR2T13	cOR2T13 olfactory receptor family 2 subfamily T-like
Cfa.3830.1.S1_at	4.557630E-05	1.095741E-02	1.17	.85	C.familiaris mRNA DOPCRH07 for olfactory receptor	100.0	AL512324	X64966		
Cfa.384.1.S1_at	6.371640E-03	1.718067E-01	0.9	1.11	PREDICTED: Canis familiaris similar to Bleomycin hydrolase (BLM hydrolase) (BMH) (BH) (LOC480635); mRNA	98.1	AK057600	XM_537755	BLMH	bleomycin hydrolase
Cfa.3872.2.S1_at	2.078970E-03	9.799395E-02	0.91	1.10	PREDICTED: Canis familiaris similar to 40S ribosomal protein S25 (LOC479412); mRNA	93.4	AB170224	XM_536549	RPS25	ribosomal protein S25
Cfa.3881.1.S1_at	1.250130E-04	2.059437E-02	1.16	.86	Xenopus tropicalis protocadherin delta 1 gene; complete cds	24.7	AC104006	EU267080		
Cfa.3898.1.S1_at	1.765090E-02	2.766981E-01	1.15	.87	Canis lupus familiaris potassium voltage-gated channel; shaker-related subfamily; member 2 (KCNA2); mRNA >gi|304651|gb|L19740.1|DOGK2DRKC Canis familiaris Kv1.2 delayed rectifier K+ channel mRNA; complete cds	100.0	NULL	NM_001003329	KCNA2	potassium voltage-gated channel, shaker-related subfamily, member 2
Cfa.3904.1.S1_at	3.173990E-06	2.396362E-03	1.19	.84	PREDICTED: Pan troglodytes glutamate receptor 6; transcript variant 1 (GRIK2); mRNA	97.0	BC063814	XM_001142208	GRIK2	glutamate receptor, ionotropic, kainate 2
Cfa.3913.1.S1_at	3.783890E-03	1.324977E-01	1.13	.88	Mus musculus platelet derived growth factor; B polypeptide (Pdgfb); mRNA >gi|31418420|gb|BC053430.1| Mus musculus platelet derived growth factor; B polypeptide; mRNA (cDNA clone MGC:59331 IMAGE:6330609); complete cds	87.4	NULL	NM_011057	Pdgfb	platelet derived growth factor, B polypeptide
Cfa.3938.1.S1_at	8.865820E-03	2.010117E-01	1.11	.90	PREDICTED: Canis familiaris similar to gamma-aminobutyric acid (GABA) A receptor; delta; transcript variant 1 (LOC489609); mRNA	95.5	AC105081	XM_546729	GABRD	gamma-aminobutyric acid (GABA) A receptor, delta

Cfa.399.1.S1_at	1.530540E-02	2.602160E-01	0.85	1.18	Sus scrofa clone Clu_6191.scr.msk.p1.Contig1; mRNA sequence	48.6	AB173885	AY610064		
Cfa.399.3.S1_at	8.876750E-03	2.010117E-01	0.85	1.17	Sus scrofa clone Clu_6191.scr.msk.p1.Contig1; mRNA sequence	46.5	AB173885	AY610064		
Cfa.4040.1.A1_at	2.098450E-02	2.978695E-01	1.11	.90	PREDICTED: Canis familiaris similar to Inactive dipeptidyl peptidase 10 (Dipeptidyl peptidase X) (Dipeptidyl peptidase-like protein 2) (DPL2) (Dipeptidyl peptidase IV-related protein-3) (DPRP-3) (LOC476121); mRNA	100.0	NM_020868	XM_533328	DPP10	dipeptidyl-peptidase 10
Cfa.413.1.S1_at	3.766970E-05	9.943067E-03	0.8	1.25	PREDICTED: Macaca mulatta similar to C1GALT1-specific chaperone 1; transcript variant 1 (LOC696662); mRNA	42.8	AK290111	XM_001086671	LOC696662	similar to C1GALT1-specific chaperone 1
Cfa.4136.1.S1_at	1.613180E-02	2.658874E-01	0.82	1.21	PREDICTED: Canis familiaris similar to SRB7 suppressor of RNA polymerase B homolog; transcript variant 2 (LOC477664); mRNA	100.0	AK309064	XM_847225	MED21	mediator complex subunit 21
Cfa.416.1.S1_at	1.680950E-03	8.920329E-02	0.82	1.23	Canis lupus familiaris high-mobility group box 1 (HMGB1); mRNA >gi|37548601|gb|AY135519.1| Canis familiaris high mobility group protein B1 mRNA; complete cds	100.0	NULL	NM_001002937	HMGB1	high-mobility group box 1
Cfa.416.1.S1_s_at	3.482650E-03	1.274454E-01	0.88	1.14	Canis lupus familiaris high-mobility group box 1 (HMGB1); mRNA >gi|37548601|gb|AY135519.1| Canis familiaris high mobility group protein B1 mRNA; complete cds	100.0	NULL	NM_001002937	HMGB1	high-mobility group box 1
Cfa.4163.2.S1_a_at	1.560630E-02	2.618390E-01	0.86	1.16	PREDICTED: Canis familiaris similar to hypoxia induced gene 1; transcript variant 2 (LOC477037); mRNA	88.8	NULL	XM_856401	HIGD1A	HIG1 domain family, member 1A
Cfa.417.1.A1_at	2.638830E-04	3.170988E-02	1.22	.82	Homo sapiens klotho gene for Klotho protein (secreted form and membrane form); complete cds	7.5	Z84483	AB009667		
Cfa.4210.2.S1_a_at	1.343220E-	2.430844E-	0.89	1.12	PREDICTED: Canis familiaris similar to ATP synthase coupling factor 6; mitochondrial precursor (ATPase subunit F6)	91.6	NULL	XM_535569	ATP5J	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit

	02	01			(LOC478393); mRNA					F6
Cfa.4213.1.S1_at	3.953480E-03	1.348203E-01	1.16	.86	PREDICTED: Macaca mulatta similar to Synaptic vesicle membrane protein VAT-1 homolog (LOC715535); mRNA	36.6	AK001256	XM_001105796	LOC715535	similar to Synaptic vesicle membrane protein VAT-1 homolog
Cfa.4230.1.A1_at	1.947930E-03	9.497007E-02	1.13	.89	Homo sapiens testis PFKFB4 (PFKFB4) gene; complete cds	6.2	AY786551	AY786551		
Cfa.4244.1.S1_at	4.571860E-03	1.446008E-01	0.83	1.20	PREDICTED: Canis familiaris similar to Cytochrome c oxidase polypeptide VIIc; mitochondrial precursor (LOC609990); mRNA	95.7	AL133545	XM_847363	LOC609990	similar to Cytochrome c oxidase polypeptide VIIc, mitochondrial precursor
Cfa.4245.1.S1_s_at	3.553900E-03	1.277456E-01	0.86	1.16	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) Fe-S protein 6; 13kDa (NADH-coenzyme Q reductase) (LOC478629); mRNA	96.7	NM_004553	XM_535802	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)
Cfa.4252.1.S1_at	7.615920E-03	1.852748E-01	0.88	1.13	PREDICTED: Canis familiaris similar to Transcription initiation factor TFIID subunit 9 (Transcription initiation factor TFIID 31 kDa subunit) (TAFII-31) (TAFII-32) (TAFII32) (STAF31/32); transcript variant 1 (LOC480815); mRNA	49.7	CU678459	XM_845521	TAF9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa
Cfa.4258.1.A1_at	8.998810E-03	2.017118E-01	0.87	1.15	Homo sapiens mRNA; cDNA DKFZp564M1162 (from clone DKFZp564M1162)	17.6	AL833887	AL833887	KCTD3	potassium channel tetramerisation domain containing 3
Cfa.4268.1.A1_at	3.821230E-03	1.332631E-01	1.14	.88	Macaca fascicularis brain cDNA; clone: QflA-21494	21.7	AC005146	AB173201		
Cfa.4284.1.S1_at	1.062770E-02	2.175160E-01	0.86	1.16	Poeciliopsis viriosa isolate VD81-47#2 NADH dehydrogenase subunit 2 (NADH2) gene; complete cds; mitochondrial gene for mitochondrial product	4.8	AC018362	AF412174		
Cfa.4285.1.A1_at	7.080690E-03	1.799867E-01	1.11	.90	PREDICTED: Macaca mulatta similar to zinc finger protein 627 (LOC716820); mRNA	7.6	AC007024	XM_001107785	LOC716820	similar to zinc finger protein 627
Cfa.4311.1.A1_at	5.311950E-03	1.551933E-01	0.88	1.14	Canis lupus familiaris prefoldin subunit 6 (PFDN6); mRNA	100.0	AB022537	NM_001048089	PFDN6	prefoldin subunit 6

Cfa.4317.1.S1_at	4.573060E-03	1.446008E-01	0.9	1.11	Bos taurus ubiquitin specific peptidase 33 (USP33); mRNA >gi|151556800|gb|BC148905.1| Bos taurus similar to ubiquitin specific protease 33; mRNA (cDNA clone MGC:140132 IMAGE:8164589); complete cds	40.7	AL050140	NM_001101139	USP33	ubiquitin specific peptidase 33
Cfa.4336.1.S1_s_at	2.229850E-03	1.014393E-01	0.79	1.26	PREDICTED: Canis familiaris similar to proteasome alpha 3 subunit isoform 2; transcript variant 1 (LOC480338); mRNA	99.7	NULL	XM_537460	PSMA3	proteasome (prosome, macropain) subunit, alpha type, 3
Cfa.4336.2.S1_a_at	9.806040E-03	2.104242E-01	0.8	1.25	PREDICTED: Canis familiaris similar to proteasome alpha 3 subunit isoform 2; transcript variant 1 (LOC480338); mRNA	98.9	NULL	XM_537460	PSMA3	proteasome (prosome, macropain) subunit, alpha type, 3
Cfa.4403.1.S1_s_at	1.524600E-02	2.602160E-01	1.12	.89	PREDICTED: Canis familiaris similar to pumilio 1 isoform 1; transcript variant 14 (LOC478158); mRNA	96.4	NULL	XM_860226	PUM1	pumilio homolog 1 (Drosophila)
Cfa.4415.1.S1_at	5.561580E-03	1.592432E-01	0.87	1.15	PREDICTED: Canis familiaris similar to NADH-ubiquinone oxidoreductase MLRQ subunit (Complex I-MLRQ) (CI-MLRQ) (LOC477682); mRNA	98.2	BC071701	XM_534877	NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa
Cfa.4417.1.S1_at	5.169480E-06	3.047515E-03	1.19	.84	PREDICTED: Canis familiaris similar to immunoglobin superfamily; member 21 (LOC478214); mRNA	100.0	AB046009	XM_535389	IGSF21	immunoglobin superfamily, member 21
Cfa.4445.1.S1_at	4.558140E-04	4.388357E-02	0.84	1.20	PREDICTED: Canis familiaris similar to Hypothetical UPF0327 protein; transcript variant 1 (LOC612968); mRNA	98.9	NM_001032363	XM_847985	LOC612968	similar to Hypothetical UPF0327 protein
Cfa.4510.1.A1_at	1.428050E-02	2.509538E-01	0.9	1.11	Canis familiaris IgH mRNA for immunogloblin heavy chain; partial cds; clone:IgH-K2-3	100.0	DQ454194	AB117109		
Cfa.4511.1.S1_at	1.846370E-03	9.250120E-02	1.15	.87	Canis familiaris IgH mRNA for immunogloblin heavy chain; partial cds; clone:IgH-K2-4	100.0	NULL	AB117110		
Cfa.4513.1.A1_at	4.193560E-05	1.056904E-02	0.9	1.11	Canis familiaris IgH mRNA for immunogloblin heavy chain; partial cds; clone:IgH-K2-7	100.0	EU303536	AB117113		

Cfa.4516.4.S1_at	1.039550E-02	2.154008E-01	1.11	.90	Canis familiaris IgH mRNA for immunogloblin heavy chain; partial cds; clone:IgH-K2-10	100.0	AC132805	AB117116		
Cfa.4534.1.S1_at	8.762670E-03	2.005228E-01	0.9	1.11	Canis familiaris IgH mRNA for immunogloblin heavy chain; partial cds; clone:IgH-K2-32	100.0	NULL	AB117138		
Cfa.4537.1.A1_at	1.426590E-02	2.509538E-01	0.84	1.18	Canis familiaris IgH mRNA for immunogloblin heavy chain; partial cds; clone:IgH-K2-37	100.0	AM079704	AB117143		
Cfa.4537.1.S1_at	1.455780E-03	8.221204E-02	1.23	.82	Canis familiaris IgH mRNA for immunogloblin heavy chain; partial cds; clone:IgH-K2-37	100.0	AM079704	AB117143		
Cfa.4553.1.A1_at	9.074810E-04	6.280335E-02	0.82	1.23	PREDICTED: Rattus norvegicus similar to dedicator of cytokinesis 8 (LOC499337); mRNA	6.1	AL607089	XM_001056091	Dock8	dedicator of cytokinesis 8
Cfa.4568.1.S1_s_at	7.779370E-03	1.874380E-01	0.79	1.26	PREDICTED: Canis familiaris heme oxygenase-1 (HO-1); mRNA	98.9	AB174601	XM_848052	HMOX1	heme oxygenase (decycling) 1
Cfa.4594.1.A1_x_at	3.080350E-03	1.189972E-01	1.1	.91	PREDICTED: Canis familiaris similar to 60S ribosomal protein L7a (LOC478479); mRNA	96.6	NULL	XM_535657	LOC478479	similar to 60S ribosomal protein L7a
Cfa.4609.1.A1_at	1.252300E-02	2.358544E-01	0.88	1.14	null	null	null	null		
Cfa.4610.1.A1_at	2.885070E-04	3.302101E-02	1.2	.83	Mus musculus adult male bone cDNA; RIKEN full-length enriched library; clone:9830141K10 product:TELOMERIC REPEAT BINDING FACTOR 1 homolog [Mus musculus]; full insert sequence	4.5	AP001688	AK036615	Terf1	telomeric repeat binding factor 1
Cfa.4622.1.A1_at	9.523840E-03	2.075233E-01	0.79	1.26	Synthetic construct Homo sapiens gateway clone IMAGE:100022803 5-prime read GLB1L3 mRNA	5.0	AL365225	CU687844		
Cfa.4623.1.A1_at	6.322480E-04	5.125131E-02	1.14	.88	Homo sapiens cDNA FLJ45896 fis; clone OCBBF3025127	84.0	AK127795	AK127795	SYT9	synaptotagmin IX

Cfa.4624.1.A1_at	1.102260E-02	2.215589E-01	1.1	.91	Tetrahymena thermophila SB210 hypothetical protein (TTHERM_00492800) partial mRNA	48.7	NULL	XM_001023172	TTHERM_00492800	hypothetical protein
Cfa.4626.1.A1_at	1.975870E-02	2.914488E-01	0.8	1.25	PREDICTED: Pan troglodytes interleukin 15 receptor; alpha; transcript variant 3 (IL15RA); mRNA	15.6	BC065506	XM_001146046	IL15RA	interleukin 15 receptor, alpha
Cfa.464.2.S1_at	1.730890E-02	2.744615E-01	1.13	.88	Candida glabrata CBS138; CAGL0G00286g partial mRNA	13.6	AC027125	XM_446377	CAGL0G00286g	hypothetical protein
Cfa.4640.1.A1_at	5.699850E-03	1.619477E-01	0.87	1.15	Homo sapiens cDNA clone IMAGE:4800000	8.9	AK123262	BC037820		
Cfa.4665.1.A1_at	3.674930E-04	3.847947E-02	1.15	.87	Homo sapiens mRNA; cDNA DKFZp686P12164 (from clone DKFZp686P12164)	37.7	CR936816	CR936816	RGNEF	Rho-guanine nucleotide exchange factor
Cfa.4688.1.A1_at	1.173790E-02	2.292824E-01	1.13	.89	Macaca fascicularis testis cDNA clone: QtsA-13676	4.0	AL035088	AB168632		
Cfa.469.1.S1_s_at	6.578000E-03	1.739023E-01	1.15	.87	PREDICTED: Canis familiaris similar to phosphoinositide-3-kinase; regulatory subunit 4; p150; transcript variant 2 (LOC477064); mRNA	99.0	AB384687	XM_858452	PIK3R4	phosphoinositide-3-kinase, regulatory subunit 4
Cfa.4696.1.A1_at	7.166930E-03	1.805765E-01	1.13	.89	Hydrangea macrophylla reductase 2 and reductase 1 genes; complete cds	6.1	AC096772	AY382664		
Cfa.4709.1.A1_at	2.349370E-03	1.038040E-01	1.13	.89	Homo sapiens ATP-binding cassette; sub-family C (CFTR/MRP); member 1 (ABCC1) gene; complete cds	7.5	AC114495	EF419769		
Cfa.4711.1.A1_at	2.854370E-03	1.152672E-01	1.11	.90	PREDICTED: Gallus gallus similar to NPAS3 (LOC423315); mRNA	6.0	AL161901	XM_421232	NPAS3	neuronal PAS domain protein 3
Cfa.475.1.A1_at	2.468740E-03	1.059811E-01	1.13	.89	Candida glabrata CBS138; CAGL0D02464g partial mRNA	3.9	AL160004	XM_445522	CAGL0D02464g	hypothetical protein
Cfa.4753.1.A1_at	2.389440E-03	1.047144E-01	1.15	.87	NULL	null	AC023095	NULL		

Cfa.4759.1.A1_at	1.742530E-02	2.752487E-01	0.86	1.17	Homo sapiens mRNA; cDNA DKFZp686G236 (from clone DKFZp686G236)	11.2	BX648219	BX648219	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)
Cfa.4808.1.A1_at	3.588900E-03	1.280666E-01	1.12	.89	PREDICTED: Apis mellifera similar to sallimus CG1915-PC; isoform C (LOC725763); mRNA	13.2	AC106738	XM_001121572	LOC725763	similar to sallimus CG1915-PC, isoform C
Cfa.4814.1.A1_at	3.960250E-03	1.348203E-01	1.15	.87	null	null	null	null		
Cfa.4818.1.A1_at	3.433910E-03	1.266309E-01	1.13	.88	NULL	null	AC104126	NULL		
Cfa.4839.1.A1_at	1.811950E-02	2.795886E-01	1.14	.88	NULL	null	AC010618	NULL		
Cfa.4840.1.A1_at	2.053970E-03	9.713472E-02	1.13	.89	Homo sapiens mRNA; cDNA DKFZp781G1012 (from clone DKFZp781G1012)	23.4	AC063963	CR627249	FANK1	fibronectin type III and ankyrin repeat domains 1
Cfa.4841.1.A1_at	1.766330E-02	2.767165E-01	1.1	.91	NULL	null	AC073520	NULL		
Cfa.4842.1.A1_at	1.990970E-03	9.584049E-02	1.11	.90	null	null	null	null		
Cfa.485.1.A1_at	1.170470E-02	2.291682E-01	1.1	.91	NULL	null	AL163209	NULL		
Cfa.4877.1.A1_at	1.474550E-03	8.251919E-02	1.11	.90	null	null	null	null		
Cfa.4891.1.A1_at	1.291890E-03	7.615957E-02	1.16	.86	NULL	null	AL662876	NULL		
Cfa.4894.1.A1_at	6.589930E-04	5.231542E-02	1.14	.88	Macaca fascicularis brain cDNA clone: QtrA-19015; similar to human KIAA1501 protein (KIAA1501); mRNA; RefSeq: XM_290799.4	6.8	AC115090	AB174722		
Cfa.4925.1.A1_at	8.876360E-04	6.201204E-02	1.16	.86	Mus musculus hemoglobin Y; beta-like embryonic chain (Hbb-y); mRNA	100.0	NULL	NM_008221	Hbb-y	hemoglobin Y, beta-like embryonic chain

Cfa.494.1.A1_at	3.131310E-03	1.199555E-01	1.14	.88	PREDICTED: Canis familiaris similar to Yip1 domain family; member 7; transcript variant 1 (LOC475137); mRNA	84.2	AC093852	XM_532367	YIPF7	Yip1 domain family, member 7
Cfa.494.2.A1_at	1.267650E-02	2.372915E-01	1.12	.89	PREDICTED: Canis familiaris similar to Yip1 domain family; member 7; transcript variant 2 (LOC475137); mRNA	98.7	NULL	XM_853520	YIPF7	Yip1 domain family, member 7
Cfa.4962.1.A1_at	1.064340E-02	2.176197E-01	1.15	.87	PREDICTED: Pan troglodytes HMG-box transcription factor 1; transcript variant 4 (HBP1); mRNA	5.3	AC112236	XM_001163640	HBP1	HMG-box transcription factor 1
Cfa.4967.1.A1_at	1.014970E-02	2.133817E-01	0.84	1.19	PREDICTED: Bos taurus hypothetical LOC537502 (LOC537502); mRNA	11.2	AF508982	XM_617670	ANKLE1	ankyrin repeat and LEM domain containing 1
Cfa.4993.1.A1_at	9.716550E-04	6.533621E-02	1.12	.89	Sus scrofa 3-hydroxy-3-methylglutaryl coenzyme A reductase (HMGR) gene; complete cds	11.5	NULL	DQ531631		
Cfa.5.1.S1_s_at	1.797100E-03	9.174164E-02	0.78	1.28	PREDICTED: Canis familiaris transducin beta-3-subunit (GNB3); mRNA	98.5	BC000115	XM_850461	GNB3	guanine nucleotide binding protein (G protein), beta polypeptide 3
Cfa.5006.1.A1_at	3.839850E-03	1.336757E-01	0.76	1.32	Mus musculus solute carrier family 26; member 4 (Slc26a4); mRNA	8.7	AL079302	NM_011867	Slc26a4	solute carrier family 26, member 4
Cfa.501.1.S1_at	1.669610E-03	8.903552E-02	0.83	1.21	Homo sapiens cDNA FLJ12832 fis; clone NT2RP2003137	37.6	NM_152277	AK022894	UBTD2	ubiquitin domain containing 2
Cfa.5039.1.A1_at	8.187750E-03	1.926516E-01	1.2	.84	Dictyostelium discoideum AX4 hypothetical protein (DDBDRAFT_0205768) mRNA; complete cds	6.1	AL391122	XM_636537	DDBDRAFT_0205768	hypothetical protein
Cfa.505.1.A1_at	6.141160E-03	1.686566E-01	0.89	1.12	PREDICTED: Pan troglodytes vacuolar protein sorting 33A; transcript variant 5 (VPS33A); mRNA	39.2	AC048338	XM_509444	VPS33A	vacuolar protein sorting 33 homolog A (S. cerevisiae)
Cfa.507.1.A1_s_at	2.298160E-03	1.028541E-01	0.87	1.15	PREDICTED: Canis familiaris similar to RAD50 homolog isoform 1 (LOC474674); mRNA	99.7	NM_005732	XM_531901	RAD50	RAD50 homolog (S. cerevisiae)
Cfa.5081.1.A1_at	3.788120E-03	1.325380E-01	0.84	1.18	PREDICTED: Strongylocentrotus purpuratus similar to ERPROT 213-21 (LOC580361);	5.5	AC004062	XM_780424	LOC580361	similar to ERPROT 213-21

					partial mRNA					
Cfa.5094.1.A1_at	1.607940E-02	2.654304E-01	1.15	.87	NULL	null	AC010236	NULL		
Cfa.5156.1.A1_at	1.542910E-03	8.426286E-02	1.15	.87	NULL	null	AL161713	NULL		
Cfa.5157.1.A1_at	6.375800E-03	1.718112E-01	1.12	.89	NULL	null	AL807743	NULL		
Cfa.5164.1.A1_at	1.430190E-02	2.509697E-01	0.89	1.12	null	null	null	null		
Cfa.5177.1.A1_at	5.158530E-04	4.634600E-02	0.89	1.13	Mus musculus ribosomal protein L7 (Rpl7); mRNA	99.5	CT476835	NM_011291	Rpl7	ribosomal protein L7
Cfa.5191.1.A1_x_at	5.386990E-03	1.566387E-01	1.12	.89	PREDICTED: Pan troglodytes similar to transmembrane protein 16A (LOC451719); mRNA	12.0	NM_018043	XR_025296	LOC451719	similar to transmembrane protein 16A
Cfa.5215.1.A1_at	1.571040E-03	8.547371E-02	1.13	.89	NULL	null	AC087276	NULL		
Cfa.5230.1.A1_at	3.025700E-03	1.184813E-01	0.84	1.19	PREDICTED: Canis familiaris similar to nitric oxide synthase trafficker (LOC478780); mRNA	100.0	AC006010	XM_535945	NOSTRIN	nitric oxide synthase trafficker
Cfa.5237.1.A1_at	1.472020E-02	2.548942E-01	0.84	1.19	PREDICTED: Canis familiaris similar to Williams Beuren syndrome chromosome region 14 isoform alpha; transcript variant 5 (LOC489807); mRNA	77.4	NM_032954	XM_852512	MLXIPL	MLX interacting protein-like
Cfa.5249.2.S1_a_at	1.851900E-03	9.267037E-02	0.9	1.11	PREDICTED: Canis familiaris similar to 40S ribosomal protein S27-like protein (LOC610569); mRNA	100.0	AL929444	XM_848098	RPS27L	ribosomal protein S27-like
Cfa.5255.1.A1_at	5.884990E-04	4.994779E-02	1.13	.88	PREDICTED: Canis familiaris similar to fibronectin type III domain containing 1 (LOC484061); mRNA	98.9	AB384644	XM_541178	FNDC1	fibronectin type III domain containing 1

Cfa.5309.1.A1_at	1.519030E-02	2.596166E-01	0.88	1.13	PREDICTED: Canis familiaris similar to Probable C->U editing enzyme APOBEC-2 (LOC481788); mRNA	99.7	AK308197	XM_538909	APOBEC2	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2
Cfa.5359.1.A1_at	4.803570E-04	4.543068E-02	1.15	.87	NULL	null	AC007560	NULL		
Cfa.5380.1.A1_at	1.397570E-02	2.479160E-01	1.12	.89	NULL	null	AC008072	NULL		
Cfa.5400.1.A1_at	1.683010E-02	2.723461E-01	1.11	.90	Homo sapiens glutathione peroxidase 6 (olfactory) (GPX6); mRNA >gi|32492912|gb|AY324826.1| Homo sapiens glutathione peroxidase 6 mRNA; complete cds	29.6	NM_182701	NM_182701	GPX6	glutathione peroxidase 6 (olfactory)
Cfa.5409.1.A1_at	1.685440E-02	2.723461E-01	1.1	.91	Homo sapiens zinc finger protein 521 (ZNF521) gene; complete cds	13.0	NG_007397	EF445043		
Cfa.541.1.S1_at	1.933550E-02	2.890251E-01	0.9	1.12	PREDICTED: Pan troglodytes zyg-11 homolog B (ZYG11B); mRNA	22.0	AK095643	XM_001139134	ZYG11B	zyg-11 homolog B (C. elegans)
Cfa.5419.1.A1_at	7.934520E-05	1.542382E-02	1.21	.83	PREDICTED: Canis familiaris similar to Fas apoptotic inhibitory molecule 2 (LOC477613); mRNA	97.8	AF190461	XM_534807	FAIM2	Fas apoptotic inhibitory molecule 2
Cfa.5419.1.A1_s_at	5.149370E-03	1.528298E-01	1.12	.89	PREDICTED: Canis familiaris similar to Fas apoptotic inhibitory molecule 2 (LOC477613); mRNA	99.6	CU674013	XM_534807	FAIM2	Fas apoptotic inhibitory molecule 2
Cfa.5435.1.A1_at	1.935790E-02	2.892595E-01	0.85	1.18	PREDICTED: Bos taurus similar to C20orf40 (LOC529294); mRNA	53.1	NM_144703	XM_607739	LSM14B	LSM14B, SCD6 homolog B (S. cerevisiae)
Cfa.5455.1.A1_at	4.691390E-03	1.466187E-01	0.9	1.11	null	null	null	null		
Cfa.5480.1.A1_s_at	9.868740E-03	2.111891E-01	0.84	1.19	PREDICTED: Canis familiaris similar to potassium channel tetramerisation domain containing 1 (LOC480170); mRNA	96.1	CU687795	XM_537294	KCTD1	potassium channel tetramerisation domain containing 1
Cfa.5486.1.A1_at	2.026250E-02	2.938077E-01	1.11	.90	PREDICTED: Macaca mulatta similar to tRNA splicing endonuclease 54 homolog (SEN54; S. cerevisiae); transcript variant 2	5.1	AC138779	XM_001097515	LOC702604	similar to tRNA splicing endonuclease 54 homolog (SEN54,

					(LOC702604); mRNA					S. cerevisiae)
Cfa.551.1.S1_at	1.843480E-04	2.575784E-02	1.13	.88	PREDICTED: Canis familiaris similar to receptor expression enhancing protein 3 (LOC479222); mRNA	31.7	AC010863	XM_536364	REEP3	receptor accessory protein 3
Cfa.5516.1.A1_at	1.186120E-03	7.311141E-02	1.2	.83	Physcomitrella patens subsp. patens predicted protein (PHYPADRAFT_108509) mRNA; complete cds	4.6	AP003029	XM_001780281	PHYPADRAFT_108509	hypothetical protein
Cfa.5527.1.S1_at	1.445850E-02	2.522842E-01	1.12	.89	PREDICTED: Canis familiaris similar to secreted modular calcium-binding protein 2; transcript variant 1 (LOC476270); mRNA	99.7	AK056700	XM_533476	SMOC2	SPARC related modular calcium binding 2
Cfa.5553.1.A1_at	1.355150E-02	2.440121E-01	1.13	.88	NULL	null	AC079255	NULL		
Cfa.5576.1.A1_at	1.894340E-02	2.860453E-01	0.86	1.16	PREDICTED: Canis familiaris similar to kidney-specific protein (KS) (LOC479822); mRNA	27.7	AC018760	XM_536949	ACSM2A	acyl-CoA synthetase medium-chain family member 2A
Cfa.5609.1.A1_at	7.301230E-03	1.819937E-01	0.9	1.11	PREDICTED: Canis familiaris similar to U11/U12 snRNP 25K protein (LOC612990); mRNA	22.0	Z69719	XM_849308	LOC612990	similar to U11/U12 snRNP 25K protein
Cfa.563.1.S1_at	5.867150E-03	1.642831E-01	0.89	1.12	Ovis aries clone TO-UP-D23-5 mRNA sequence	14.3	NG_007264	DQ239614		
Cfa.5637.1.A1_at	1.853900E-02	2.823331E-01	1.16	.86	PREDICTED: Pan troglodytes similar to 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1); transcript variant 2 (LOC741140); mRNA	6.0	AC107485	XM_001155459	LOC741140	similar to 14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)
Cfa.5658.1.A1_at	1.712620E-02	2.741519E-01	1.13	.89	NULL	null	AL138539	NULL		
Cfa.5702.1.A1_at	1.029840E-02	2.151541E-01	1.13	.89	PREDICTED: Canis familiaris similar to synaptotagmin-like 5; transcript variant 1 (LOC480877); mRNA	77.1	BC131585	XM_537994	SYTL5	synaptotagmin-like 5
Cfa.5748.1.A1_at	8.796420E-04	6.175431E-02	0.83	1.20	Homo sapiens chromosome 14 clone RP11-463C8 containing POMT2 gene; partial cds;	14.0	AC007375	AC007375		

					and unknown genes; complete sequence					
Cfa.5793.1.A1_at	1.464330E-04	2.234661E-02	1.11	.90	Homo sapiens cDNA FLJ35508 fis; clone SMINT2011958	10.4	AP000873	AK092827		
Cfa.5794.1.A1_at	7.363200E-04	5.581943E-02	1.19	.84	PREDICTED: Pan troglodytes similar to Ells1; transcript variant 3 (LOC746500); mRNA	14.2	NM_152793	XM_001165332	LOC746500	similar to Ells1
Cfa.5832.2.S1_a_at	1.247370E-02	2.356048E-01	0.78	1.29	Arabidopsis thaliana unknown protein (At5g27940) mRNA; complete cds	7.9	AL445685	BT030603	WPP3	WPP3 (WPP domain protein 3)
Cfa.584.1.S1_at	1.487430E-02	2.560075E-01	0.85	1.18	PREDICTED: Pan troglodytes similar to Nuclear transcription factor Y; beta (LOC452191); mRNA	84.8	NM_006166	XM_509327	NFYB	nuclear transcription factor Y, beta
Cfa.5846.1.A1_at	1.604780E-02	2.651121E-01	1.14	.88	PREDICTED: Equus caballus hypothetical protein LOC100064610 (LOC100064610); mRNA	36.6	AC103595	XM_001495462		
Cfa.5871.1.A1_at	1.146600E-03	7.155705E-02	1.17	.85	PREDICTED: Canis familiaris similar to ankyrin repeat domain 35 (LOC475825); mRNA	100.0	NM_144698	XM_533033	ANKRD35	ankyrin repeat domain 35
Cfa.5877.1.A1_at	1.568360E-02	2.625219E-01	0.84	1.19	PREDICTED: Canis familiaris similar to CG12795-PA; transcript variant 2 (LOC480809); mRNA	44.9	AL512448	XM_850558	ZFAND2A	zinc finger, AN1-type domain 2A
Cfa.5883.1.A1_at	6.544540E-03	1.735331E-01	0.77	1.30	NULL	null	Z82210	NULL		
Cfa.5898.1.A1_at	4.440900E-03	1.428212E-01	1.12	.89	null	null	null	null		
Cfa.5939.1.A1_at	6.772310E-03	1.762171E-01	1.12	.90	NULL	null	AC092836	NULL		
Cfa.5955.1.S1_at	1.305050E-02	2.403220E-01	0.66	1.52	PREDICTED: Canis familiaris similar to CD5 antigen-like precursor (SP-alpha) (CT-2) (IgM-associated peptide); transcript variant 3 (LOC609953); mRNA	99.8	BC033586	XM_858956	CD5L	CD5 molecule-like

Cfa.5960.1.A1_at	2.777200E-03	1.131369E-01	1.13	.88	Mus musculus G protein-coupled receptor 171; mRNA (cDNA clone MGC:36313 IMAGE:5068166); complete cds	5.4	AC022536	BC024054	Gpr171	G protein-coupled receptor 171
Cfa.6001.1.A1_at	6.274400E-03	1.703278E-01	0.88	1.14	PREDICTED: Canis familiaris similar to Nuclear cap binding protein subunit 2 (20 kDa nuclear cap binding protein) (NCBP 20 kDa subunit) (CBP20) (NCBP interacting protein 1) (NIP1) (LOC478603); mRNA	100.0	NULL	XM_535779	NCBP2	nuclear cap binding protein subunit 2, 20kDa
Cfa.6021.1.A1_at	6.326880E-03	1.711359E-01	1.13	.88	Mus musculus serine peptidase inhibitor; Kazal type 6 (Spink6); mRNA >gi|26389293|dbj|AK028032.1| Mus musculus 18-day embryo whole body cDNA; RIKEN full-length enriched library; clone:1190026I17 product:hypothetical Kazal-type serine protease inhibitor domain containing protein; full insert sequence	62.8	NM_205841	NM_001013797	Spink6	serine peptidase inhibitor, Kazal type 6
Cfa.6031.1.A1_at	2.532560E-04	3.122886E-02	1.16	.86	PREDICTED: Macaca mulatta similar to Repetin (LOC712894); mRNA	49.8	AK291301	XM_001109196	LOC712894	similar to Repetin
Cfa.6061.1.A1_at	3.511280E-03	1.277456E-01	1.18	.85	NULL	null	AC117372	NULL		
Cfa.6087.1.A1_at	3.942560E-03	1.348203E-01	1.14	.88	null	null	null	null		
Cfa.611.1.A1_at	2.093650E-03	9.845149E-02	1.18	.85	NULL	null	AC079305	NULL		
Cfa.6122.1.A1_at	2.499590E-04	3.122886E-02	1.19	.84	PREDICTED: Canis familiaris similar to solute carrier family 30 (zinc transporter); member 3; transcript variant 1 (LOC475700); mRNA	99.7	AC013413	XM_532907	SLC30A3	solute carrier family 30 (zinc transporter), member 3
Cfa.6161.1.S1_at	8.831100E-03	2.009348E-01	1.13	.88	PREDICTED: Canis familiaris similar to F-box and leucine-rich repeat protein 10 isoform b; transcript variant 3 (LOC486262); mRNA	95.8	NULL	XM_855051	FBXL10	F-box and leucine-rich repeat protein 10
Cfa.6180.1.A1_at	3.279300E-05	9.346005E-03	1.13	.88	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc); mRNA	92.0	AL772268	NM_009242	Sparc	secreted acidic cysteine rich glycoprotein

Cfa.6193.1.A1_at	4.342960E-03	1.413545E-01	1.21	.83	NULL	null	AL365272	NULL		
Cfa.6243.1.A1_at	5.251010E-03	1.539354E-01	0.83	1.20	PREDICTED: Canis familiaris hypothetical protein LOC611035 (LOC611035); mRNA	30.5	NULL	XM_862772	LOC611035	hypothetical protein LOC611035
Cfa.6274.1.S1_at	7.053880E-04	5.454775E-02	0.9	1.11	PREDICTED: Equus caballus similar to proteasome beta 7 subunit proprotein (LOC100067317); mRNA	61.5	NULL	XM_001502120	LOC100067317	similar to proteasome beta 7 subunit proprotein
Cfa.6274.1.S1_s_at	2.754910E-04	3.223357E-02	0.91	1.10	PREDICTED: Equus caballus similar to proteasome beta 7 subunit proprotein (LOC100067317); mRNA	91.1	NM_002799	XM_001502120	LOC100067317	similar to proteasome beta 7 subunit proprotein
Cfa.632.1.A1_at	1.491530E-02	2.563590E-01	1.15	.87	Rattus norvegicus cDNA clone MGC:188284 IMAGE:7380746; complete cds	6.7	AC121493	BC158832	Tcrb	T-cell receptor beta chain
Cfa.6330.1.A1_at	9.754320E-03	2.098886E-01	0.79	1.27	PREDICTED: Canis familiaris similar to Antithrombin-III precursor (ATIII); transcript variant 1 (LOC480066); mRNA	99.7	CR619869	XM_537187	SERPINC1	serpin peptidase inhibitor, clade C (antithrombin), member 1
Cfa.6360.1.A1_s_at	4.878500E-03	1.489338E-01	0.89	1.12	Sus scrofa mRNA; clone:UTR010049G01; expressed in uterus	78.0	AC092057	AK240282		
Cfa.6384.1.A1_s_at	3.355440E-03	1.246989E-01	0.89	1.12	PREDICTED: Canis familiaris similar to mucin 17 (LOC488059); mRNA	100.0	NULL	XM_545182	LOC488059	similar to mucin 17
Cfa.6393.1.A1_at	1.240010E-03	7.473926E-02	0.8	1.25	Arabidopsis thaliana protein kinase; putative (AT5G09890) mRNA; complete cds	42.9	AC091185	NM_121026	AT5G09890	protein kinase, putative
Cfa.6425.1.A1_at	4.614170E-04	4.412685E-02	0.85	1.17	PREDICTED: Canis familiaris similar to TAF9 RNA polymerase II; TATA box binding protein (TBP)-associated factor isoform 2 (LOC478087); mRNA	99.0	NULL	XM_535264	LOC478087	similar to TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor isoform 2
Cfa.6480.1.A1_at	9.920810E-03	2.118819E-01	1.14	.88	Danio rerio zgc:152745 (zgc:152745); mRNA >gi|115313314|gb|BC124110.1| Danio rerio zgc:152745; mRNA (cDNA clone MGC:152745 IMAGE:8157251); complete cds	4.7	AL391136	NM_001077583	zmynd11	zinc finger, MYND domain containing 11
Cfa.6529.1.A1_at	8.325310E-	1.945649E-	1.12	.90	NULL	null	AC002524	NULL		

	03	01								
Cfa.6533.1.A1_at	2.248880E-03	1.016747E-01	0.85	1.18	PREDICTED: Canis familiaris similar to small nuclear ribonucleoprotein E (LOC478934); mRNA	97.8	BC072433	XM_536093	SNRPE	small nuclear ribonucleoprotein polypeptide E
Cfa.6547.1.A1_at	1.959570E-02	2.904299E-01	1.12	.89	NULL	null	AC087593	NULL		
Cfa.6556.1.A1_at	8.019020E-04	5.849128E-02	1.27	.79	PREDICTED: Canis familiaris similar to expressed sequence AI591476; transcript variant 3 (LOC475265); mRNA	99.5	AC004549	XM_859880	JAZF1	JAZF zinc finger 1
Cfa.6578.1.A1_at	3.206240E-04	3.539154E-02	1.17	.85	Homo sapiens cDNA FLJ33739 fis; clone BRAWH2018601	17.2	AK091058	AK091058		
Cfa.6583.1.A1_at	1.117510E-03	7.061974E-02	1.23	.81	PREDICTED: Canis familiaris similar to radial spokehead-like 1 (LOC476432); mRNA	100.0	NM_030785	XM_533639	RSHL1	radial spokehead-like 1
Cfa.6719.1.A1_a_at	6.694210E-03	1.753410E-01	1.11	.90	PREDICTED: Canis familiaris similar to Myc-binding protein-associated protein (LOC480552); mRNA	33.9	AL139115	XM_537674	MYCBPAP	MYCBP associated protein
Cfa.6724.1.A1_a_at	4.622720E-05	1.099109E-02	1.19	.84	PREDICTED: Homo sapiens hypothetical LOC643338 (LOC643338); mRNA	24.4	XR_041737	XM_927997		
Cfa.6729.1.A1_at	1.801670E-03	9.182039E-02	1.14	.88	Sus scrofa mRNA; clone:LVRM10091G04; expressed in liver	31.9	XM_001721840	AK233156		
Cfa.673.2.S1_s_at	8.448770E-04	6.009799E-02	0.76	1.32	PREDICTED: Canis familiaris similar to RNA processing factor 1 (LOC479972); mRNA	95.7	CU677559	XM_537096	BXDC5	brix domain containing 5
Cfa.6793.1.A1_at	3.015700E-03	1.184813E-01	1.11	.90	Hirudo medicinalis intermediate filament gliarin mRNA; complete cds	4.9	AC005996	AF101065		
Cfa.6806.1.A1_at	4.611550E-03	1.452841E-01	1.2	.83	PREDICTED: Canis familiaris similar to testis expressed sequence 13A (LOC492058); mRNA	47.8	BC120875	XM_549178	TEX13A	testis expressed 13A
Cfa.6819.1.A1_at	5.241160E-	1.537963E-	0.8	1.25	PREDICTED: Canis familiaris hypothetical	96.7	AC004540	XM_549425	LOC475262	hypothetical LOC475262

	03	01			LOC475262 (LOC475262); mRNA					
Cfa.6853.2.S1_at	6.213310E-05	1.312209E-02	1.22	.82	Lithognathus mormyrus clone lithmor665 mRNA sequence	25.0	AP000426	DQ850295		
Cfa.6856.1.S1_at	1.461770E-02	2.541708E-01	0.9	1.11	PREDICTED: Canis familiaris similar to Nucleolar autoantigen No55 (LOC607731); mRNA	99.0	NM_006455	XM_844515	LOC607731	similar to Nucleolar autoantigen No55
Cfa.6883.1.A1_at	7.365130E-03	1.825717E-01	1.11	.90	Homo sapiens cDNA; FLJ99510	36.0	AK309469	AK309469	ERG	v-ets erythroblastosis virus E26 oncogene homolog (avian)
Cfa.6898.1.A1_at	6.931720E-03	1.781999E-01	1.17	.85	PREDICTED: Canis familiaris similar to actinin; alpha 2; transcript variant 4 (LOC479191); mRNA	50.6	NULL	XM_851062	ACTN2	actinin, alpha 2
Cfa.6910.1.A1_at	9.301110E-03	2.047388E-01	1.1	.91	PREDICTED: Canis familiaris similar to Ribose-phosphate pyrophosphokinase II (Phosphoribosyl pyrophosphate synthetase II) (PRS-II); transcript variant 6 (LOC476855); mRNA	71.6	CU691885	XM_851653	PRPS2	phosphoribosyl pyrophosphate synthetase 2
Cfa.6934.1.A1_at	3.891480E-03	1.340823E-01	1.19	.84	Magnaporthe grisea 70-15 hypothetical protein (MGG_00704) partial mRNA	3.9	AC093583	XM_368540	MGG_00704	hypothetical protein
Cfa.6967.1.A1_at	7.674660E-04	5.666965E-02	1.16	.86	Mus musculus microtubule associated monoxygenase; calponin and LIM domain containing 3; mRNA (cDNA clone IMAGE:30637988); partial cds	11.6	AC011322	BC090651	Mical3	microtubule associated monoxygenase, calponin and LIM domain containing 3
Cfa.697.1.A1_at	1.693420E-02	2.725368E-01	1.12	.89	PREDICTED: Macaca mulatta sodium channel; voltage-gated; type VII; alpha (SCN7A); mRNA	71.6	AC074101	XR_012702	SCN7A	sodium channel, voltage-gated, type VII, alpha
Cfa.6971.1.A1_at	1.354140E-02	2.439323E-01	0.88	1.14	PREDICTED: Canis familiaris similar to Glutathione reductase; mitochondrial precursor (GR) (GRase) (LOC475596); mRNA	17.0	NULL	XM_532813	GSR	glutathione reductase
Cfa.6973.1.A1_at	1.101850E-03	7.015214E-02	1.14	.87	PREDICTED: Gallus gallus similar to bromodomain and WD repeat domain containing 3 variant BRWD3-A (LOC422281); mRNA	5.9	AC040162	XR_027097	LOC422281	similar to bromodomain and WD repeat domain containing 3 variant BRWD3-A

Cfa.7005.1.A1_at	2.530420E-04	3.122886E-02	0.77	1.30	PREDICTED: Rattus norvegicus similar to t-complex 11 protein (LOC684311); mRNA	6.3	AC010369	XM_001069833	LOC679989	similar to t-complex 11 protein
Cfa.7007.1.A1_x_at	1.770520E-02	2.771711E-01	1.14	.88	Homo sapiens mucin 5AC; oligomeric mucus/gel-forming (MUC5AC) gene; complete cds	5.8	EU127454	EU127454		
Cfa.7039.1.A1_at	1.553380E-02	2.613375E-01	0.89	1.12	PREDICTED: Rattus norvegicus similar to jumonji domain containing 2D (LOC684198); mRNA	5.2	AC019133	XM_001068840	LOC689582	similar to jumonji domain containing 2D
Cfa.7060.1.A1_at	5.999760E-03	1.665804E-01	1.15	.87	PREDICTED: Canis familiaris hypothetical LOC479698 (LOC479698); mRNA	96.7	NULL	XM_549677	LOC479698	hypothetical LOC479698
Cfa.707.4.A1_x_at	1.225970E-03	7.420481E-02	0.9	1.11	PREDICTED: Canis familiaris similar to 60S ribosomal protein L32; transcript variant 2 (LOC607481); mRNA	99.8	NULL	XM_854019	RPL32	ribosomal protein L32
Cfa.7093.1.A1_at	3.910930E-03	1.343231E-01	0.84	1.19	null	null	null	null		
Cfa.7093.1.A1_s_at	4.057060E-04	4.137336E-02	0.8	1.25	PREDICTED: Canis familiaris similar to cat eye syndrome critical region protein 1 isoform a precursor (LOC484249); mRNA	95.7	EU446517	XM_849704	LOC484249	similar to cat eye syndrome critical region protein 1 isoform a precursor
Cfa.7110.1.A1_at	7.783240E-03	1.874380E-01	0.89	1.13	PREDICTED: Canis familiaris similar to Myc-induced mitochondria protein (LOC478067); mRNA	94.8	AK291296	XM_535246	NDUFAF2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2
Cfa.7110.1.A1_s_at	2.047720E-03	9.710601E-02	0.86	1.17	PREDICTED: Canis familiaris similar to Myc-induced mitochondria protein (LOC478067); mRNA	99.4	AK291296	XM_535246	NDUFAF2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2
Cfa.7198.1.A1_at	1.380310E-04	2.167943E-02	1.18	.84	PREDICTED: Pan troglodytes hypothetical LOC453012; transcript variant 3 (LOC453012); mRNA	15.1	AL442663	XM_001149216	RBM25	RNA binding motif protein 25
Cfa.7238.1.A1_at	1.095780E-03	6.996572E-02	1.12	.89	Sus scrofa insulin-like growth factor binding protein 2 (IGFBP2); mRNA >gi|4927688|gb|AF120326.1| Sus scrofa insulin-like growth factor binding protein 2 mRNA; complete cds	23.9	CR625740	NM_214003	IGFBP2	insulin-like growth factor binding protein 2

Cfa.7273.2.A1_a_at	1.076390E-02	2.180906E-01	1.12	.90	PREDICTED: Bos taurus hypothetical protein LOC781143 (LOC781143); mRNA	38.5	AC011389	XM_001249520		
Cfa.7296.1.A1_at	1.302970E-02	2.403220E-01	1.12	.89	NULL	null	AC108084	NULL		
Cfa.734.1.A1_s_at	1.067060E-03	6.874390E-02	0.88	1.14	PREDICTED: Canis familiaris similar to neural precursor cell expressed; developmentally down-regulated gene 8 (LOC480265); mRNA	98.6	NM_006156	XM_537389	NEDD8	neural precursor cell expressed, developmentally down-regulated 8
Cfa.734.2.A1_a_at	1.876580E-03	9.347063E-02	0.88	1.13	PREDICTED: Canis familiaris similar to neural precursor cell expressed; developmentally down-regulated gene 8 (LOC480265); mRNA	100.0	BC104664	XM_537389	NEDD8	neural precursor cell expressed, developmentally down-regulated 8
Cfa.7359.1.A1_at	9.210540E-03	2.040018E-01	1.12	.89	Mus musculus complement component 3a receptor 1 (C3ar1) gene; complete cds	12.9	AL359916	EU007909		
Cfa.7388.1.A1_a_at	1.415730E-02	2.500039E-01	1.12	.89	PREDICTED: Canis familiaris similar to protein phosphatase 1; regulatory (inhibitor) subunit 14B; transcript variant 4 (LOC476035); mRNA	9.4	AC092765	XM_862120	PPP1R14B	protein phosphatase 1, regulatory (inhibitor) subunit 14B
Cfa.7400.1.A1_s_at	1.008640E-04	1.778968E-02	1.19	.84	PREDICTED: Macaca mulatta similar to ATP/GTP binding protein-like 3 (LOC707147); mRNA	91.6	AB169069	XM_001104528	LOC707147	similar to ATP/GTP binding protein-like 3
Cfa.7405.1.A1_at	1.002350E-02	2.131608E-01	1.11	.90	null	null	null	null		
Cfa.7435.1.A1_at	1.045340E-05	4.576229E-03	1.17	.86	PREDICTED: Canis familiaris similar to sterolin 2 (LOC474571); mRNA	99.6	NM_022437	XM_531799	ABCG8	ATP-binding cassette, sub-family G (WHITE), member 8
Cfa.7451.1.A1_at	9.879440E-05	1.771507E-02	1.14	.88	PREDICTED: Canis familiaris similar to Ral guanine nucleotide dissociation stimulator (RalGEF) (RalGDS) (LOC482936); mRNA	42.6	NULL	XM_540051	LOC482936	similar to Ral guanine nucleotide dissociation stimulator (RalGEF) (RalGDS)
Cfa.7488.1.A1_at	4.648130E-03	1.456945E-01	0.91	1.10	PREDICTED: Strongylocentrotus purpuratus hypothetical LOC589810 (LOC589810); mRNA	7.9	NULL	XM_001179389	LOC589810	hypothetical LOC589810

Cfa.75.1.S1_at	2.373940E-03	1.045676E-01	0.81	1.23	Canis lupus familiaris superoxide dismutase 1; soluble (amyotrophic lateral sclerosis 1 (adult)) (SOD1); mRNA >gi|18150345|gb|AF346417.1| Canis familiaris Cu/Zn superoxide dismutase (SOD1) mRNA; complete cds	91.8	AB220492	NM_001003035	SOD1	superoxide dismutase 1, soluble
Cfa.7504.1.A1_at	4.100280E-04	4.151895E-02	1.17	.85	PREDICTED: Canis familiaris similar to heparanase 2; transcript variant 4 (LOC486831); mRNA	96.2	AL139243	XM_856134	HPSE2	heparanase 2
Cfa.7506.1.A1_at	2.008430E-02	2.924196E-01	1.11	.90	NULL	null	AP003472	NULL		
Cfa.7539.1.A1_at	1.329120E-02	2.419572E-01	0.89	1.12	PREDICTED: Canis familiaris similar to acyl-Coenzyme A binding domain containing 4; transcript variant 2 (LOC490928); mRNA	100.0	NULL	XM_850592	ACBD4	acyl-Coenzyme A binding domain containing 4
Cfa.7573.1.A1_at	1.053100E-02	2.164013E-01	1.11	.90	NULL	null	AC025750	NULL		
Cfa.758.1.S1_at	2.305060E-03	1.028541E-01	0.83	1.21	PREDICTED: Canis familiaris annexin I (ANXA1); mRNA	97.3	CR607819	XM_533524	ANXA1	annexin A1
Cfa.7600.1.A1_at	1.963910E-03	9.539150E-02	0.87	1.15	Nematostella vectensis predicted protein (NEMVEDRAFT_v1g215187) partial mRNA	5.9	AL645504	XM_001626609	NEMVEDRAFT_v1g215187	predicted protein
Cfa.7628.1.A1_at	5.158270E-04	4.634600E-02	1.11	.90	Mus musculus prolyl 4-hydroxylase; beta polypeptide (P4hb); mRNA	4.4	NULL	NM_011032	P4hb	prolyl 4-hydroxylase, beta polypeptide
Cfa.7629.1.A1_at	7.380700E-03	1.827551E-01	1.13	.88	Mus musculus tetratricopeptide repeat domain 16 (Ttc16); mRNA >gi|26389312|dbj|AK028040.1| Mus musculus adult male lung cDNA; RIKEN full-length enriched library; clone:1200002K10 product:hypothetical Tetratricopeptide repeat (TPR) structure containing protein; full insert sequence	48.3	AB071046	NM_177384	Ttc16	tetratricopeptide repeat domain 16
Cfa.7657.1.A1_at	6.329090E-04	5.125131E-02	1.14	.88	Trichomonas vaginalis G3 hypothetical protein (TVAG_086170) partial mRNA	6.8	AC096729	XM_001310007	TVAG_086170	hypothetical protein
Cfa.7660.1.A1_at	2.662090E-	1.104755E-	1.16	.86	Homo sapiens cDNA FLJ76935 complete cds	4.6	AC008945	AK292354	FAM47A	family with sequence similarity 47,

	03	01								member A
Cfa.768.1.S1_at	6.628400E-04	5.235196E-02	0.82	1.22	Canis lupus familiaris zinc finger CCCH-type containing 15 (ZC3H15); mRNA	100.0	NM_018471	NM_001114605	ZC3H15	zinc finger CCCH-type containing 15
Cfa.7694.1.A1_at	5.024440E-04	4.604700E-02	1.13	.89	PREDICTED: Canis familiaris similar to melanoma antigen family A; 10 (LOC492221); mRNA	16.9	AY829643	XM_549341	LOC492221	similar to melanoma antigen family A, 10
Cfa.7699.1.A1_at	9.274690E-03	2.045804E-01	1.1	.91	PREDICTED: Canis familiaris similar to loss of heterozygosity; 11; chromosomal region 2; gene A homolog (LOC478206); mRNA	100.0	AL020998	XM_535381	LOC478206	similar to loss of heterozygosity, 11, chromosomal region 2, gene A homolog
Cfa.7708.1.A1_at	9.106800E-03	2.025381E-01	0.9	1.11	Homo sapiens cDNA clone IMAGE:40148063	18.9	BC151216	BC151216	RASGRP4	RAS guanyl releasing protein 4
Cfa.7724.1.A1_at	2.929620E-03	1.169538E-01	1.14	.87	NULL	null	AL445648	NULL		
Cfa.7731.1.A1_at	4.453280E-03	1.428212E-01	1.12	.89	NULL	null	AL355483	NULL		
Cfa.7753.1.A1_at	1.582880E-02	2.636643E-01	1.12	.89	NULL	null	AC112251	NULL		
Cfa.7771.1.A1_at	8.950660E-03	2.017118E-01	0.86	1.16	PREDICTED: Canis familiaris similar to pericentrin 1; transcript variant 1 (LOC475913); mRNA	18.1	AC022211	XM_533121	NUP85	nucleoporin 85kDa
Cfa.7779.1.A1_at	1.512130E-02	2.587456E-01	1.11	.90	PREDICTED: Canis familiaris similar to Receptor tyrosine-protein kinase erbB-4 precursor (p180erbB4) (Tyrosine kinase-type cell surface receptor HER4) (LOC488508); mRNA	100.0	NM_005235	XM_545629	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)
Cfa.7812.1.A1_at	1.684280E-02	2.723461E-01	0.77	1.30	Homo sapiens kinesin family member 19 (KIF19); mRNA	33.8	NM_153209	NM_153209	KIF19	kinesin family member 19
Cfa.7822.1.A1_s_at	1.189010E-02	2.303874E-01	0.88	1.14	PREDICTED: Canis familiaris similar to DnaJ (Hsp40) homolog; subfamily C; member 3 (LOC476966); mRNA	99.6	CU690538	XM_534166	DNAJC3	DnaJ (Hsp40) homolog, subfamily C, member 3

Cfa.7830.2.A1_s_at	4.834300E-04	4.543068E-02	0.88	1.14	PREDICTED: Canis familiaris similar to RUN and TBC1 domain containing 1 (LOC480654); mRNA	100.0	AB385325	XM_537773	SGSM2	small G protein signaling modulator 2
Cfa.7862.1.A1_at	1.360470E-02	2.445697E-01	1.13	.89	NULL	null	AC005090	NULL		
Cfa.7886.1.A1_at	7.171030E-03	1.805765E-01	1.12	.89	NULL	null	AC021242	NULL		
Cfa.7917.1.A1_at	4.892710E-04	4.547684E-02	1.12	.89	Homo sapiens integrin alpha 2 (ITGA2) gene; ITGA2-1 allele; exons 6-9; and partial cds	4.9	AF512556	AF035968		
Cfa.7918.1.A1_at	1.605030E-03	8.670122E-02	1.14	.88	NULL	null	AC009108	NULL		
Cfa.7924.1.A1_s_at	1.602160E-03	8.670122E-02	0.9	1.11	PREDICTED: Canis familiaris similar to DnaJ (Hsp40) homolog; subfamily C; member 7; transcript variant 2 (LOC480519); mRNA	98.9	NM_003315	XM_537639	DNAJC7	DnaJ (Hsp40) homolog, subfamily C, member 7
Cfa.7939.1.A1_at	1.817090E-03	9.210656E-02	1.16	.86	Entamoeba dispar SAW760 hypothetical protein EDI_163750 mRNA; complete cds	5.5	AC084251	XM_001741728	EDI_163750	hypothetical protein
Cfa.7953.1.A1_at	6.659970E-03	1.748699E-01	1.11	.90	Coccidioides immitis RS hypothetical protein (CIMG_00602) mRNA; complete cds	5.6	AF107257	XM_001246830	CIMG_00602	hypothetical protein
Cfa.7969.1.A1_at	6.759260E-03	1.760804E-01	1.11	.90	PREDICTED: Canis familiaris similar to olfactory receptor 627 (LOC609179); mRNA	97.1	NULL	XM_846390	LOC609179	similar to olfactory receptor 627
Cfa.7969.1.A1_s_at	2.228660E-04	2.915209E-02	1.14	.87	PREDICTED: Canis familiaris similar to olfactory receptor 627 (LOC609179); mRNA	97.9	NULL	XM_846390	LOC609179	similar to olfactory receptor 627
Cfa.7976.1.A1_at	7.915960E-03	1.893626E-01	1.11	.90	Mus musculus solute carrier family 36 (proton/amino acid symporter); member 1 (Slc36a1); mRNA	11.2	AL713870	NM_153139	Slc36a1	solute carrier family 36 (proton/amino acid symporter), member 1
Cfa.7985.1.A1_at	1.523890E-04	2.301074E-02	1.25	.80	PREDICTED: Equus caballus similar to vacuolar protein sorting 37D (LOC100061734); mRNA	95.5	AK158287	XM_001493575	LOC100061734	similar to vacuolar protein sorting 37D

Cfa.8010.1.S1_s_at	1.856110E-02	2.823561E-01	1.16	.86	PREDICTED: Canis familiaris similar to chromosome 1 open reading frame 14 (LOC480033); mRNA	99.3	BC132764	XM_537155	LOC480033	similar to chromosome 1 open reading frame 14
Cfa.8021.1.A1_a_at	8.099970E-03	1.915287E-01	1.21	.83	NULL	null	AL513008	NULL		
Cfa.8028.1.S1_s_at	1.141300E-02	2.256758E-01	0.88	1.13	PREDICTED: Canis familiaris similar to Small nuclear ribonucleoprotein F (snRNP-F) (Sm protein F) (Sm-F) (SmF) (LOC482609); mRNA	100.0	NULL	XM_539726	SNRPF	small nuclear ribonucleoprotein polypeptide F
Cfa.806.1.A1_at	9.101910E-04	6.280335E-02	1.12	.89	Homo sapiens testicular cell adhesion molecule 1 homolog (mouse) (TCAM1) on chromosome 17 >gi|12248906|dbj|AB026156.1| Homo sapiens TCAM-1 pseudogene mRNA for testicular cell adhesion molecule 1	15.8	AC015651	NR_002947	TCAM1	testicular cell adhesion molecule 1 homolog (mouse)
Cfa.8068.1.A1_at	2.498340E-03	1.064105E-01	1.12	.89	PREDICTED: Canis familiaris hypothetical LOC476029 (LOC476029); mRNA	99.5	XM_001716523	XM_533238	LOC476029	hypothetical LOC476029
Cfa.8089.1.A1_at	6.125350E-03	1.686529E-01	1.13	.88	PREDICTED: Gallus gallus hypothetical LOC427648 (LOC427648); mRNA	5.9	AL031005	XM_425221	LOXHD1	lipoxygenase homology domains 1
Cfa.8113.1.A1_at	5.679920E-04	4.898504E-02	1.16	.86	PREDICTED: Pan troglodytes hypothetical protein LOC748323 (LOC748323); mRNA	28.4	AK055418	XM_001160732	LOC748323	hypothetical protein LOC748323
Cfa.8149.1.A1_at	2.512440E-03	1.067395E-01	1.11	.90	PREDICTED: Canis familiaris similar to Cytokine receptor-like factor 1 precursor (Cytokine-like factor-1) (CLF-1) (ZcytoR5) (LOC484818); mRNA	67.2	AC003112	XM_541934	CRLF1	cytokine receptor-like factor 1
Cfa.8154.1.A1_at	7.161570E-04	5.493728E-02	1.15	.87	PREDICTED: Canis familiaris similar to Myosin-5B (Myosin Vb) (LOC480220); mRNA	14.0	AC092705	XM_537345	MYO5B	myosin VB
Cfa.8160.1.A1_at	4.496010E-03	1.433228E-01	1.14	.88	NULL	null	AC105268	NULL		
Cfa.82.1.S1_s_at	2.227980E-03	1.014393E-01	1.12	.89	Canis lupus familiaris retinitis pigmentosa 1 (autosomal dominant) (RP1); mRNA >gi|21303188|gb|AY034786.1| Canis familiaris retinitis pigmentosa 1 protein	100.0	AC090151	NM_001003040	RP1	retinitis pigmentosa 1 (autosomal dominant)

					(RP1) mRNA; complete cds					
Cfa.8202.1.A1_at	2.012010E-02	2.927209E-01	0.86	1.17	PREDICTED: Canis familiaris similar to mitochondrial intermediate peptidase (LOC477338); mRNA	100.0	AK291923	XM_534532	MIPEP	mitochondrial intermediate peptidase
Cfa.8205.1.A1_at	1.855330E-02	2.823561E-01	1.14	.88	PREDICTED: Macaca mulatta cartilage intermediate layer protein 2; transcript variant 2 (CILP2); mRNA	9.4	AY279381	XM_001100671	CILP2	cartilage intermediate layer protein 2
Cfa.8224.1.A1_at	2.533860E-03	1.074480E-01	1.11	.90	Canis familiaris cardiomyocyte alpha-spectrin mRNA; partial cds	5.6	AC010904	AY263394	SPTAN1	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)
Cfa.8227.1.A1_at	8.376150E-03	1.951638E-01	1.12	.89	PREDICTED: Canis familiaris similar to CG3625-PB; isoform B; transcript variant 4 (LOC478722); mRNA	14.9	AC006241	XM_852747	LOC478722	similar to CG3625-PB, isoform B
Cfa.8246.1.A1_at	4.739690E-03	1.474856E-01	1.12	.89	null	null	null	null		
Cfa.8280.1.A1_at	8.783220E-04	6.175431E-02	1.14	.88	PREDICTED: Macaca mulatta similar to Type I inositol-1;4;5-trisphosphate 5-phosphatase (5PTase) (LOC719508); partial mRNA	17.7	AP001836	XM_001113817	LOC719508	similar to Type I inositol-1,4,5-trisphosphate 5-phosphatase (5PTase)
Cfa.8283.1.A1_s_at	1.195300E-02	2.313978E-01	0.84	1.20	PREDICTED: Canis familiaris similar to chromosome 1 open reading frame 21 (LOC610661); mRNA	57.8	AY258286	XM_848200	LOC610661	similar to chromosome 1 open reading frame 21
Cfa.830.1.S1_at	2.468600E-03	1.059811E-01	0.79	1.26	PREDICTED: Canis familiaris similar to Coiled-coil domain containing protein 2 (Capillary morphogenesis protein-1) (CMG-1) (LOC474734); mRNA	99.4	NM_025103	XM_531964	IFT74	intraflagellar transport 74 homolog (Chlamydomonas)
Cfa.8327.1.A1_at	1.289060E-02	2.396315E-01	0.83	1.20	null	null	null	null		
Cfa.8341.1.A1_at	3.179590E-03	1.208778E-01	1.15	.87	Homo sapiens cDNA FLJ42392 fis; clone ACTVT2000380	20.8	AL356217	AK124383	FLJ42392	hypothetical gene supported by AK124383
Cfa.8378.1.A1_at	6.255540E-03	1.700614E-01	1.12	.89	Gryllus bimaculatus mRNA; GBcontig30639	4.2	AC025423	AK283778		

Cfa.8381.1.A1_at	9.555900E-03	2.078010E-01	0.83	1.21	PREDICTED: Canis familiaris similar to thyroid hormone receptor interactor 10 (LOC476726); mRNA	99.0	AB168510	XM_533930	TRIP10	thyroid hormone receptor interactor 10
Cfa.8383.1.A1_at	1.297750E-06	1.429676E-03	1.29	.78	PREDICTED: Canis familiaris similar to Ets translocation variant 1 (ER81 protein); transcript variant 6 (LOC475246); mRNA	100.0	NULL	XM_857150	ETV1	ets variant gene 1
Cfa.8404.1.A1_at	5.155280E-03	1.528997E-01	1.11	.90	NULL	null	AC100873	NULL		
Cfa.8433.1.A1_s_at	1.859410E-02	2.823561E-01	1.2	.84	PREDICTED: Canis familiaris potassium voltage-gated channel; Shal-related subfamily; member 3; transcript variant 1 (KCND3); mRNA	99.7	AL049557	XM_540343	KCND3	potassium voltage-gated channel, Shal-related subfamily, member 3
Cfa.8440.1.A1_at	4.083190E-03	1.371883E-01	1.12	.89	Oryza sativa (japonica cultivar-group) Os02g0447300 (Os02g0447300) mRNA; complete cds	4.2	AL590004	NM_001053288	Os02g0447300	Os02g0447300
Cfa.8478.1.A1_at	3.133030E-03	1.199555E-01	1.13	.89	PREDICTED: Canis familiaris similar to myosin IIIB (LOC478790); mRNA	99.6	BC040019	XM_535955	LOC478790	similar to myosin IIIB
Cfa.8500.1.A1_at	8.493040E-03	1.971402E-01	1.13	.88	PREDICTED: Canis familiaris similar to vesicle-associated membrane protein 8; transcript variant 3 (LOC609784); mRNA	96.2	NM_003761	XM_860375	VAMP8	vesicle-associated membrane protein 8 (endobrevin)
Cfa.8521.1.A1_at	5.816330E-05	1.251529E-02	1.17	.85	PREDICTED: Canis familiaris similar to melanoma antigen family A; 10 (LOC492221); mRNA	23.4	AC005585	XM_549341	LOC492221	similar to melanoma antigen family A, 10
Cfa.8534.1.A1_at	1.446230E-02	2.522842E-01	1.25	.80	Mus musculus 13 days embryo male testis cDNA; RIKEN full-length enriched library; clone:6030432E05 product:zinc finger protein 106; full insert sequence	20.4	AL449983	AK031440	Bnc2	basonuclin 2
Cfa.8534.2.A1_s_at	7.238810E-03	1.812229E-01	1.11	.90	PREDICTED: Canis familiaris similar to basonuclin 2 (LOC612979); mRNA	100.0	BC156477	XM_848855	BNC2	basonuclin 2
Cfa.8547.1.A1_at	6.832700E-04	5.356015E-02	1.13	.89	Homo sapiens SCG10 like-protein; helicase-like protein NHL; M68; and ADP-ribosylation factor related protein 1 (ARFRP1) genes; complete cds	6.5	AC092319	AF217796		

Cfa.8579.1.A1_at	8.994520E-03	2.017118E-01	1.11	.90	Bos taurus POU class 5 homeobox 1 (POU5F1); mRNA	5.9	AC011525	NM_174580	POU5F1	POU class 5 homeobox 1
Cfa.8588.1.A1_at	2.276870E-03	1.022528E-01	1.14	.88	NULL	null	AC018950	NULL		
Cfa.8640.1.A1_at	4.064780E-03	1.367753E-01	1.12	.89	Plasmodium yoelii yoelii str. 17XNL hypothetical protein (PY04935) partial mRNA	5.7	AC044784	XM_720220	PY04935	hypothetical protein
Cfa.8665.1.A1_at	1.184310E-02	2.297611E-01	1.11	.90	PREDICTED: Canis familiaris similar to flap structure-specific endonuclease 1; transcript variant 1 (LOC476063); mRNA	49.4	NG_007092	XM_533271	FEN1	flap structure-specific endonuclease 1
Cfa.8666.1.A1_at	1.650270E-04	2.423869E-02	0.78	1.28	Mus musculus 9 days embryo whole body cDNA; RIKEN full-length enriched library; clone:D030060P04 product:hypothetical Nucleic acid-binding proteins structure containing protein; full insert sequence	16.9	AL592436	AK083659	Eif1ad	eukaryotic translation initiation factor 1A domain containing
Cfa.8670.1.A1_at	1.778210E-05	6.377106E-03	1.21	.83	NULL	null	AC008798	NULL		
Cfa.8684.1.A1_at	4.910980E-03	1.492091E-01	0.86	1.17	PREDICTED: Pan troglodytes hypothetical protein LOC739903 (LOC739903); mRNA	68.5	NM_015872	XM_001141590	LOC739903	hypothetical protein LOC739903
Cfa.869.1.A1_s_at	1.228010E-02	2.344606E-01	1.1	.91	PREDICTED: Canis familiaris similar to solute carrier family 35; member A5 (LOC478565); mRNA	98.6	BC013046	XM_535741	SLC35A5	solute carrier family 35, member A5
Cfa.8697.1.A1_at	1.534930E-02	2.602160E-01	1.12	.89	Homo sapiens HLCS gene for holocarboxylase synthetase; complete cds	8.9	AP001727	AB063285		
Cfa.87.1.A1_at	1.231650E-03	7.444390E-02	1.12	.89	Canis familiaris partial mRNA for connexin 26 (cx26 gene)	100.0	NULL	AJ439693	GJB2	gap junction protein, beta 2, 26kDa
Cfa.8729.1.A1_at	4.784980E-03	1.479322E-01	1.14	.88	Xenopus laevis cDNA clone MGC:154835 IMAGE:8329546; complete cds	9.1	AC010655	BC124978	LOC100158399	hypothetical protein LOC100158399
Cfa.8732.1.A1_s_at	1.940380E-02	2.893634E-01	1.1	.91	PREDICTED: Canis familiaris similar to klotho beta like (LOC479110); mRNA	100.0	BC113653	XM_536257	KLB	klotho beta

Cfa.8733.1.A1_at	8.437050E-03	1.963702E-01	0.88	1.14	PREDICTED: Canis familiaris hypothetical LOC475958 (LOC475958); mRNA	100.0	BC047775	XM_533168	LOC475958	hypothetical LOC475958
Cfa.8752.1.A1_at	1.715340E-02	2.741519E-01	0.82	1.22	Bos taurus cDNA clone IMAGE:8034102	11.2	AC160862	BC142434		
Cfa.8761.1.A1_a_at	6.188020E-03	1.691578E-01	1.12	.89	PREDICTED: Macaca mulatta similar to CXXC finger 6 (LOC707759); mRNA	9.1	AC066612	XM_001107194	LOC707759	similar to CXXC finger 6
Cfa.8766.1.A1_at	1.731560E-02	2.744666E-01	0.9	1.11	NULL	null	AL031594	NULL		
Cfa.8796.1.A1_at	1.955650E-02	2.901146E-01	1.11	.90	Synthetic construct Homo sapiens clone IMAGE:100062163; MGC:190186 ATPase type 13A5 (ATP13A5) mRNA; encodes complete protein	4.3	AC022509	BC156652	ATP13A5	ATPase type 13A5
Cfa.8806.1.S1_s_at	1.305370E-03	7.684276E-02	0.91	1.10	PREDICTED: Canis familiaris similar to UPF0054 protein C21orf57 homolog; transcript variant 1 (LOC606842); mRNA	99.5	NM_058181	XM_843149	LOC606842	similar to UPF0054 protein C21orf57 homolog
Cfa.8807.1.A1_at	1.596860E-02	2.647183E-01	1.11	.90	Mus musculus activated spleen cDNA; RIKEN full-length enriched library; clone:F830224K14 product:unclassifiable; full insert sequence	5.0	AC093911	AK157579		
Cfa.8825.1.A1_at	1.479010E-02	2.555166E-01	1.13	.88	Xenopus laevis hypothetical protein LOC443620; mRNA (cDNA clone IMAGE:5079378); partial cds	45.2	AF295017	BC108769	LOC443620	hypothetical protein LOC443620
Cfa.8831.1.A1_at	1.997270E-03	9.603633E-02	1.12	.89	NULL	null	AC063960	NULL		
Cfa.8849.1.A1_at	1.188420E-04	1.990025E-02	1.18	.85	Mus musculus neural precursor cell expressed; developmentally down-regulated gene 8 (Nedd8); mRNA	100.0	NULL	NM_008683	Nedd8	neural precursor cell expressed, developmentally down-regulated gene 8
Cfa.8850.1.A1_at	2.483400E-03	1.062080E-01	1.16	.87	PREDICTED: Canis familiaris similar to axonemal dynein light chain (LOC482473); mRNA	100.0	AK077109	XM_539590	DNALI1	dynein, axonemal, light intermediate chain 1
Cfa.8932.1.A1_at	1.790210E-	2.787096E-	1.13	.88	Tetrahymena thermophila SB210 HECT domain and RCC1-like domain-containing	6.3	AC006431	XM_001017227	TTHERM_00194740	HECT domain and RCC1-like

	02	01			protein (TTHERM_00194740) partial mRNA					domain-containing protein
Cfa.8954.1.A1_at	1.037270E-02	2.153015E-01	0.91	1.10	PREDICTED: Canis familiaris similar to Adapter-related protein complex 4 beta 1 subunit (Beta subunit of AP-4) (AP-4 adapter complex beta subunit); transcript variant 1 (LOC483125); mRNA	100.0	NULL	XM_540241	AP4B1	adaptor-related protein complex 4, beta 1 subunit
Cfa.8963.1.A1_s_at	1.216480E-02	2.337430E-01	1.17	.85	PREDICTED: Canis familiaris similar to intersectin 2 isoform 3; transcript variant 2 (LOC475683); mRNA	100.0	NM_006277	XM_844198	ITSN2	intersectin 2
Cfa.8970.1.A1_at	1.629670E-02	2.672662E-01	1.15	.87	Oryza sativa Japonica Group cDNA clone:J013069K12; full insert sequence	4.5	AC087828	AK066489		
Cfa.8986.1.A1_at	1.395420E-03	8.003077E-02	0.74	1.35	Paramecium tetraurelia hypothetical protein (GSPATT00013141001) partial mRNA	40.4	AC092357	XM_001445013	GSPATT00013141001	hypothetical protein
Cfa.8986.1.A1_s_at	1.195720E-03	7.311141E-02	0.76	1.31	PREDICTED: Canis familiaris similar to testis-specific protein TSP-NY isoform a (LOC477458); mRNA	99.0	AK292466	XM_534656	CCDC62	coiled-coil domain containing 62
Cfa.9012.1.A1_at	1.978930E-02	2.914488E-01	1.14	.88	Bos taurus transmembrane protein 16D (TMEM16D); mRNA >gi|151556375|gb|BC147937.1| Bos taurus similar to TMEM16D protein; mRNA (cDNA clone MGC:159874 IMAGE:8631099); complete cds	54.2	AB093660	NM_001102050	ANO4	anoctamin 4
Cfa.9050.1.A1_at	3.510030E-03	1.277456E-01	1.11	.90	Macaca fascicularis brain cDNA; clone:QccE-18334	19.6	AL365361	AB051136		
Cfa.9055.1.S1_at	3.087730E-03	1.191753E-01	0.87	1.15	PREDICTED: Canis familiaris similar to vacuolar protein sorting 54 isoform 2; transcript variant 1 (LOC474616); mRNA	97.8	NULL	XM_531846	VPS54	vacuolar protein sorting 54 homolog (S. cerevisiae)
Cfa.9058.1.A1_at	2.066140E-03	9.760300E-02	1.13	.88	PREDICTED: Macaca mulatta similar to CG14446-PA (LOC716854); mRNA	20.5	AC107033	XM_001107847	LOC716854	similar to CG14446-PA
Cfa.9075.1.A1_at	8.427460E-03	1.962531E-01	1.16	.86	NULL	null	AL136160	NULL		

Cfa.9095.1.A1_at	1.499110E-03	8.331076E-02	1.25	.80	Chaetomium globosum CBS 148.51 hypothetical protein (CHGG_04799) mRNA; complete cds	4.7	AC008281	XM_001224012	CHGG_04799	hypothetical protein
Cfa.9112.1.A1_at	3.448600E-03	1.267607E-01	1.21	.83	PREDICTED: Canis familiaris similar to cofactor required for Sp1 transcriptional activation; subunit 2; 150kDa; transcript variant 4 (LOC480884); mRNA	100.0	AC186198	XM_856088	MED14	mediator complex subunit 14
Cfa.913.2.A1_at	2.024150E-03	9.649705E-02	0.82	1.22	PREDICTED: Equus caballus similar to Glycogen synthase kinase 3 beta; transcript variant 2 (LOC100061033); mRNA	100.0	DQ895714	XM_001502477	GSK3B	glycogen synthase kinase 3 beta
Cfa.9133.1.A1_at	8.218090E-03	1.930489E-01	1.11	.90	PREDICTED: Canis familiaris similar to ST8 alpha-N-acetyl-neuraminide alpha-2;8-sialyltransferase 3 (LOC612940); mRNA	95.6	AC090208	XM_847888	ST8SIA3	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3
Cfa.9135.1.A1_at	1.896620E-02	2.862718E-01	1.14	.87	PREDICTED: Ornithorhynchus anatinus similar to quinone oxidoreductase-like 1 (LOC100083233); mRNA	4.9	AL356479	XM_001513766	LOC100083233	similar to quinone oxidoreductase-like 1
Cfa.9139.1.A1_at	4.625000E-03	1.454948E-01	0.89	1.12	PREDICTED: Pan troglodytes step II splicing factor SLU7; transcript variant 4 (LOC737318); mRNA	25.1	NM_006425	XM_001143136	SLU7	SLU7 splicing factor homolog (S. cerevisiae)
Cfa.9173.1.A1_at	2.841820E-03	1.150496E-01	1.19	.84	Homo sapiens cDNA FLJ10266 fis; clone HEMBB1001024	69.8	AK001128	AK001128		
Cfa.9174.1.A1_at	1.938500E-02	2.893630E-01	0.88	1.13	NULL	null	AC001226	NULL		
Cfa.9175.1.S1_at	2.847880E-03	1.151866E-01	0.77	1.30	PREDICTED: Canis familiaris similar to squalene monooxygenase; transcript variant 2 (LOC608021); mRNA	99.7	D78130	XM_856851	SQLE	squalene epoxidase
Cfa.9189.1.A1_at	1.826230E-02	2.808187E-01	1.11	.90	Homo sapiens cDNA FLJ45171 fis; clone BRAWH3045625	13.3	NM_014702	AK127114	KIAA0408	KIAA0408
Cfa.922.1.A1_at	1.027150E-02	2.148926E-01	0.88	1.14	PREDICTED: Canis familiaris similar to Kinesin heavy chain (Ubiquitous kinesin heavy chain) (UKHC); transcript variant 6 (LOC477968); mRNA	68.5	AL161932	XM_854433	KIF5B	kinesin family member 5B

Cfa.9230.1.A1_at	2.189490E-03	1.004528E-01	1.17	.86	full-length cDNA clone CS0DC017YJ15 of Neuroblastoma Cot 25-normalized of Homo sapiens (human)	31.4	BC063015	CR614651	GALNT17	polypeptide N-acetylgalactosaminyltransferase 17
Cfa.9240.1.S1_at	7.281750E-03	1.819766E-01	0.75	1.34	PREDICTED: Canis familiaris similar to secreted phosphoprotein 1 (LOC478471); mRNA	88.0	NULL	XM_535649	SPP1	secreted phosphoprotein 1
Cfa.9271.1.A1_at	4.656760E-03	1.457481E-01	1.13	.89	PREDICTED: Canis familiaris similar to Carbonic anhydrase-related protein 10 (Carbonic anhydrase-related protein X) (CARP X) (CA-RP X); transcript variant 3 (LOC609477); mRNA	98.9	CR749607	XM_861214	CA10	carbonic anhydrase X
Cfa.9308.1.A1_at	1.843900E-03	9.250120E-02	0.85	1.17	PREDICTED: Canis familiaris similar to CG9324-PA (LOC477325); mRNA	89.2	NM_015932	XM_534518	POMP	proteasome maturation protein
Cfa.9337.1.A1_at	1.188800E-03	7.311141E-02	0.88	1.14	Homo sapiens synaptojanin 2 binding protein (SYNJ2BP); mRNA	14.4	NM_018373	NM_018373	SYNJ2BP	synaptojanin 2 binding protein
Cfa.9340.1.A1_at	1.255050E-02	2.360624E-01	1.13	.89	NULL	null	AC097641	NULL		
Cfa.9342.1.A1_at	1.364200E-03	7.900740E-02	1.19	.84	Bos taurus solute carrier family 30 (zinc transporter); member 3 (SLC30A3); mRNA >gi|115304748|gb|BC123455.1| Bos taurus similar to solute carrier family 30 (zinc transporter); member 3; mRNA (cDNA clone MGC:139533 IMAGE:8217615); complete cds	24.4	U76010	NM_001076843	SLC30A3	solute carrier family 30 (zinc transporter), member 3
Cfa.9345.2.A1_at	1.009310E-02	2.131774E-01	0.88	1.14	PREDICTED: Canis familiaris similar to Kelch repeat and BTB domain containing protein 10 (Kelch-related protein 1) (Kel-like protein 23) (Sarcosin); transcript variant 3 (LOC478784); mRNA	13.5	NULL	XM_854076	KBTBD10	kelch repeat and BTB (POZ) domain containing 10
Cfa.9352.1.A1_at	4.159300E-03	1.384107E-01	1.14	.88	PREDICTED: Canis familiaris similar to gamma-aminobutyric acid (GABA-B) receptor binding protein; transcript variant 4 (LOC478054); mRNA	100.0	AB011127	XM_854140	JAKMIP2	janus kinase and microtubule interacting protein 2
Cfa.9374.1.S1_at	1.914050E-04	2.616405E-02	1.12	.89	PREDICTED: Pan troglodytes progestin and adipoQ receptor family member VI;	88.9	AB055289	XM_001164692	PAQR6	progestin and adipoQ receptor family member VI

					transcript variant 5 (PAQR6); mRNA					
Cfa.9386.1.S1_at	4.769130E-03	1.476543E-01	1.1	.91	NULL	null	AC007040	NULL		
Cfa.9392.1.A1_at	1.395740E-02	2.477957E-01	0.89	1.12	Xenopus laevis hypothetical LOC495415; mRNA (cDNA clone MGC:80888 IMAGE:5515338); complete cds	5.1	NULL	BC084924	LOC495415	hypothetical LOC495415
Cfa.9394.1.S1_at	4.446030E-03	1.428212E-01	0.82	1.22	PREDICTED: Canis familiaris similar to Tetratricopeptide repeat protein KIAA0103 (LOC612810); mRNA	100.0	NM_014673	XM_845168	TTC35	tetratricopeptide repeat domain 35
Cfa.9406.1.A1_at	1.833810E-02	2.812264E-01	1.11	.90	PREDICTED: Macaca mulatta similar to Fibroblast growth factor 12 (FGF-12) (Fibroblast growth factor homologous factor 1) (FHF-1) (LOC705813); mRNA	48.5	NM_004113	XM_001094765	LOC705813	similar to Fibroblast growth factor 12 (FGF-12) (Fibroblast growth factor homologous factor 1) (FHF-1)
Cfa.942.1.S1_at	1.196170E-03	7.311141E-02	1.17	.86	PREDICTED: Pan troglodytes similar to soluble coxsackie-adenovirus-receptor isoform CAR2/7; transcript variant 2 (LOC743424); mRNA	8.8	XR_038797	XM_001158744	LOC743424	similar to soluble coxsackie-adenovirus-receptor isoform CAR2/7
Cfa.9425.1.A1_at	2.684130E-05	8.370401E-03	0.76	1.32	PREDICTED: Canis familiaris similar to CG1532-PA; transcript variant 1 (LOC480640); mRNA	100.0	AC108687	XM_537759	GLOD4	glyoxalase domain containing 4
Cfa.9428.3.S1_at	1.047330E-03	6.787929E-02	1.14	.87	Nematostella vectensis predicted protein (NEMVEDRAFT_v1g211310) partial mRNA	8.4	AC063922	XM_001629703	NEMVEDRAFT_v1g211310	predicted protein
Cfa.9440.1.A1_s_at	1.904860E-02	2.870296E-01	0.9	1.11	PREDICTED: Canis familiaris similar to arginine/serine-rich coiled-coil 1 (LOC477126); mRNA	86.6	AB173358	XM_534318	LOC477126	similar to arginine/serine-rich coiled-coil 1
Cfa.9442.1.A1_at	6.716750E-04	5.284375E-02	0.89	1.13	PREDICTED: Canis familiaris a disintegrin and metalloprotease domain 10; transcript variant 1 (ADAM10); mRNA	100.0	AC018904	XM_535496	ADAM10	ADAM metallopeptidase domain 10
Cfa.9453.1.A1_at	2.174340E-04	2.896988E-02	1.19	.84	Gallus gallus finished cDNA; clone ChEST164n5	4.8	AC022538	CR390117		
Cfa.9457.1.A1_at	6.200280E-	1.691578E-	0.91	1.10	PREDICTED: Mus musculus similar to beta	4.9	AL450997	XM_976893	LOC674761	similar to myosin, heavy polypeptide

	03	01			myosin heavy chain (LOC674761); mRNA					7, cardiac muscle, beta
Cfa.9464.1.S1_at	1.007280E-02	2.131608E-01	0.82	1.22	PREDICTED: Canis familiaris similar to inorganic pyrophosphatase (LOC479238); mRNA	100.0	BC001022	XM_536380	PPA1	pyrophosphatase (inorganic) 1
Cfa.9509.1.A1_at	6.285860E-04	5.125131E-02	1.18	.85	full-length cDNA clone CS0DC002YP02 of Neuroblastoma Cot 25-normalized of Homo sapiens (human)	4.6	AC010857	CR617765	CHRNB4	cholinergic receptor, nicotinic, beta 4
Cfa.9514.1.A1_at	3.305480E-03	1.236968E-01	1.12	.89	NULL	null	AC095030	NULL		
Cfa.9529.1.A1_s_at	9.702820E-06	4.489137E-03	0.81	1.24	PREDICTED: Canis familiaris similar to NADH-ubiquinone oxidoreductase 18 kDa subunit; mitochondrial precursor (Complex I-18 kDa) (CI-18 kDa) (Complex I-AQDQ) (CI-AQDQ) (LOC479335); mRNA	100.0	AC024569	XM_536474	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)
Cfa.9588.1.A1_at	1.197660E-02	2.317046E-01	1.11	.90	PREDICTED: Macaca mulatta cadherin 6; type 2; transcript variant 1 (CDH6); mRNA	33.0	AB171169	XM_001084071	CDH6	cadherin 6, type 2
Cfa.9598.1.A1_at	1.876990E-02	2.844235E-01	1.17	.86	NULL	null	AL591403	NULL		
Cfa.9602.1.A1_s_at	7.653820E-03	1.855017E-01	1.13	.89	PREDICTED: Pan troglodytes brain and acute leukemia; cytoplasmic; transcript variant 4 (BAALC); mRNA	15.2	AK093819	XM_001155628	BAALC	brain and acute leukemia, cytoplasmic
Cfa.9603.1.A1_at	2.948160E-03	1.171506E-01	0.85	1.18	Homo sapiens platelet endothelial aggregation receptor 1 (PEAR1); mRNA	10.3	AC019055	NM_001080471	PEAR1	platelet endothelial aggregation receptor 1
Cfa.9642.1.A1_at	1.648660E-03	8.824637E-02	1.14	.87	Plasmodium falciparum 3D7 hypothetical protein (PFD0435c) mRNA; complete cds	5.1	AC208872	XM_001351366	PFD0435c	hypothetical protein
Cfa.9648.1.A1_at	4.866630E-04	4.543068E-02	0.85	1.18	PREDICTED: Canis familiaris similar to CWF19-like 2; cell cycle control (LOC479454); mRNA	100.0	AL121593	XM_536589	CWF19L2	CWF19-like 2, cell cycle control (S. pombe)
Cfa.9650.1.S1_at	3.889640E-03	1.340823E-01	0.86	1.17	PREDICTED: Canis familiaris similar to RAD51 homolog C isoform 1; transcript variant 1 (LOC480573); mRNA	91.9	AC053523	XM_537695	RAD51C	RAD51 homolog C (S. cerevisiae)

Cfa.9688.1.A1_at	5.867390E-03	1.642831E-01	1.14	.88	PREDICTED: Canis familiaris similar to neurexophilin 2 (LOC476135); mRNA	99.2	AC092620	XM_533342	NXPH2	neurexophilin 2
Cfa.9692.1.A1_at	5.017610E-03	1.508965E-01	0.87	1.15	Bos taurus churchill domain containing 1 (CHURC1); mRNA >gi|88683012|gb|BC105418.1| Bos taurus similar to Churchill protein; mRNA (cDNA clone MGC:128554 IMAGE:7985210); complete cds	64.7	NM_145165	NM_001046581	CHURC1	churchill domain containing 1
Cfa.9718.1.A1_at	3.510550E-04	3.758122E-02	1.16	.86	NULL	null	AF037218	NULL		
Cfa.9730.1.A1_at	3.078790E-03	1.189972E-01	1.18	.85	Homo sapiens fibroblast growth factor 12; mRNA (cDNA clone MGC:26659 IMAGE:4794600); complete cds	18.5	BC022524	BC022524	FGF12	fibroblast growth factor 12
Cfa.9754.1.A1_at	1.621300E-02	2.662062E-01	1.19	.84	PREDICTED: Macaca mulatta similar to Glutamate receptor 4 precursor (GluR-4) (GluR4) (GluR-D) (Glutamate receptor ionotropic; AMPA 4) (AMPA-selective glutamate receptor 4); transcript variant 2 (LOC705794); mRNA	23.6	AP000673	XM_001100828	LOC705794	similar to Glutamate receptor 4 precursor (GluR-4) (GluR4) (GluR-D) (Glutamate receptor ionotropic, AMPA 4) (AMPA-selective glutamate receptor 4)
Cfa.9761.1.S1_at	3.977600E-04	4.065939E-02	0.9	1.11	PREDICTED: Canis familiaris hypothetical protein LOC608342; transcript variant 1 (LOC608342); mRNA	98.7	NULL	XM_845475	LOC608342	hypothetical protein LOC608342
Cfa.9784.1.A1_at	7.216810E-03	1.810935E-01	1.14	.88	Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1) gene; complete cds	38.5	AC022613	DQ015919		
Cfa.9804.1.A1_at	1.240740E-02	2.354288E-01	1.13	.88	null	null	null	null		
Cfa.9811.1.A1_at	9.581880E-03	2.082607E-01	0.76	1.32	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1499812	87.8	BX255925	AJ420434		
Cfa.9815.1.A1_at	9.147270E-03	2.030184E-01	0.85	1.18	Chlamydomonas reinhardtii predicted protein (CHLREDRAFT_174960) mRNA; complete cds	4.4	AL445543	XM_001695065	CHLREDRAFT_174960	hypothetical protein
Cfa.9848.1.A1_at	5.997040E-04	5.030892E-02	1.14	.88	Homo sapiens mRNA; cDNA DKFZp781P02163 (from clone	24.0	CR936711	CR936711		

					DKFZp781P02163)					
Cfa.9884.1.A1_a_at	1.176770E-02	2.294622E-01	0.89	1.13	PREDICTED: Canis familiaris similar to 28S ribosomal protein S18c; mitochondrial precursor (MRP-S18-c) (Mrps18c) (MRP-S18-1); transcript variant 2 (LOC478458); mRNA	98.6	NULL	XM_854339	MRPS18C	mitochondrial ribosomal protein S18C
Cfa.9899.1.A1_at	1.648200E-04	2.423869E-02	1.27	.79	PREDICTED: Canis familiaris similar to semaphorin 5A; transcript variant 1 (LOC478622); mRNA	100.0	NM_003966	XM_535796	SEMA5A	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A
Cfa.9913.1.S1_at	5.546970E-03	1.592432E-01	0.9	1.11	PREDICTED: Canis familiaris similar to DnaJ homolog subfamily A member 1 (Heat shock 40 kDa protein 4) (DnaJ protein homolog 2) (HSJ-2) (HSDJ); transcript variant 3 (LOC474739); mRNA	51.3	AL354807	XM_860355	LOC474739	similar to DnaJ homolog subfamily A member 1 (Heat shock 40 kDa protein 4) (DnaJ protein homolog 2) (HSJ-2) (HSDJ)
Cfa.9958.1.A1_at	1.336420E-02	2.424390E-01	1.13	.89	Homo sapiens; clone IMAGE:5802033; mRNA	37.3	AL009181	BC042916		
Cfa.9995.1.A1_at	3.076610E-03	1.189972E-01	1.14	.88	PREDICTED: Pan troglodytes alpha 1 type IX collagen; transcript variant 2 (COL9A1); mRNA	26.2	NM_001851	XM_518574	COL9A1	collagen, type IX, alpha 1
CfaAffx.10031.1.S1_at	1.502260E-03	8.331155E-02	0.83	1.21	PREDICTED: Canis familiaris similar to CG10053-PA (LOC475616); mRNA	99.7	NM_174931	XM_532830	CCDC75	coiled-coil domain containing 75
CfaAffx.10097.1.S1_s_at	1.308840E-02	2.403652E-01	0.89	1.13	PREDICTED: Canis familiaris similar to ring finger protein 137 (LOC485233); mRNA	100.0	AF360739	XM_542351	TRIM68	tripartite motif-containing 68
CfaAffx.10125.1.S1_at	1.491550E-03	8.310821E-02	0.85	1.18	PREDICTED: Canis familiaris similar to CCAAT/enhancer binding protein zeta; transcript variant 1 (LOC483035); mRNA	88.9	NM_005760	XM_540150	CEBPZ	CCAAT/enhancer binding protein zeta
CfaAffx.1013.1.S1_at	1.087390E-02	2.194926E-01	1.13	.89	PREDICTED: Canis familiaris similar to Zinc finger protein 407 (LOC476164); mRNA	100.0	AC091589	XM_533370	ZNF407	zinc finger protein 407
CfaAffx.10135.1.S1_at	1.803250E-02	2.792474E-01	1.11	.90	PREDICTED: Canis familiaris similar to protocadherin gamma subfamily A; 10 isoform 2 precursor (LOC487184); mRNA	94.9	NM_018913	XM_544312	PCDHGA10	protocadherin gamma subfamily A, 10

CfaAffx.1018.1.S1_at	1.393540E-03	8.003077E-02	1.15	.87	PREDICTED: Canis familiaris similar to Cytosolic nonspecific dipeptidase (Glutamate carboxypeptidase-like protein 1) (CNDP dipeptidase 2); transcript variant 1 (LOC476166); mRNA	67.0	NULL	XM_533372	CNDP2	CNDP dipeptidase 2 (metallopeptidase M20 family)
CfaAffx.10181.1.S1_at	4.651660E-03	1.456945E-01	1.26	.79	PREDICTED: Canis familiaris similar to Contactin 6 precursor (Neural recognition molecule NB-3) (hNB-3); transcript variant 2 (LOC484686); mRNA	100.0	AP001257	XM_857876	CNTN6	contactin 6
CfaAffx.10197.1.S1_at	7.450160E-04	5.610538E-02	1.11	.90	PREDICTED: Canis familiaris cOR52Z3 olfactory receptor family 52 subfamily Z-like (cOR52Z3); mRNA	99.4	NULL	XM_542370	cOR52Z3	cOR52Z3 olfactory receptor family 52 subfamily Z-like
CfaAffx.1023.1.S1_at	3.393980E-03	1.256970E-01	1.1	.91	PREDICTED: Equus caballus similar to F-box protein 15; (LOC100061530); mRNA	81.7	AB051122	XM_001493325	FBXO15	F-box protein 15
CfaAffx.10244.1.S1_at	2.718950E-03	1.120772E-01	1.12	.90	PREDICTED: Equus caballus hypothetical protein LOC100062457 (LOC100062457); mRNA	94.3	NM_203451	XM_001495319	LOC100062457	hypothetical protein LOC100062457
CfaAffx.10247.1.S1_at	5.808500E-03	1.635921E-01	1.14	.88	PREDICTED: Pan troglodytes similar to HOR5Beta5 (LOC450980); mRNA	86.9	NM_001005567	XM_508244	LOC450980	similar to HOR5Beta5
CfaAffx.10259.1.S1_at	1.813720E-02	2.797121E-01	0.91	1.10	PREDICTED: Canis familiaris similar to Death domain containing protein CRADD (Caspase and RIP adaptator with death domain) (RIP associated protein with a death domain) (LOC482604); mRNA	100.0	CU691520	XM_539721	CRADD	CASP2 and RIPK1 domain containing adaptor with death domain
CfaAffx.10267.1.S1_at	2.778800E-04	3.240804E-02	1.15	.87	PREDICTED: Canis familiaris cOR51K1P olfactory receptor family 51 subfamily K-like (cOR51K1P); mRNA	100.0	AC087380	XM_542385	cOR51K1P	cOR51K1P olfactory receptor family 51 subfamily K-like
CfaAffx.10278.1.S1_at	3.168980E-03	1.208161E-01	1.13	.89	PREDICTED: Canis familiaris similar to olfactory receptor 649 (LOC485270); mRNA	95.8	NULL	XM_542388	LOC485270	similar to olfactory receptor 649
CfaAffx.10280.1.S1_at	9.143340E-04	6.285681E-02	1.12	.89	PREDICTED: Canis familiaris hypothetical LOC486009 (LOC486009); mRNA	100.0	NM_017826	XM_543134	SOHLH2	spermatogenesis and oogenesis specific basic helix-loop-helix 2
CfaAffx.10299.1.S1_at	2.105890E-03	9.872220E-02	1.2	.83	PREDICTED: Canis familiaris similar to olfactory receptor 649 (LOC485279); mRNA	99.1	NULL	XM_542397	LOC485279	similar to olfactory receptor 649

CfaAffx.10317.1.S1_at	2.188140E-03	1.004528E-01	1.13	.89	Bos taurus doublecortin-like kinase 1 (DCLK1); mRNA >gi|157742950|gb|BC153836.1| Bos taurus doublecortin-like kinase 1; mRNA (cDNA clone MGC:152477 IMAGE:8414674); complete cds	100.0	CR627093	NM_001109962	DCLK1	doublecortin-like kinase 1
CfaAffx.10317.1.S1_s_at	9.424990E-04	6.396607E-02	1.12	.89	PREDICTED: Canis familiaris similar to Serine/threonine-protein kinase DCAMKL1 (Doublecortin-like and CAM kinase-like 1); transcript variant 7 (LOC477304); mRNA	100.0	AB384469	XM_853066	DCLK1	doublecortin-like kinase 1
CfaAffx.10360.1.S1_at	8.792530E-03	2.005228E-01	1.11	.90	Canis lupus familiaris coagulation factor VII (serum prothrombin conversion accelerator) (F7); mRNA >gi|77745259|gb|DQ223901.1| Canis familiaris coagulation factor VII mRNA; complete cds	99.3	AF272774	NM_001048033	F7	coagulation factor VII (serum prothrombin conversion accelerator)
CfaAffx.10363.1.S1_at	6.812690E-05	1.389498E-02	1.14	.87	PREDICTED: Equus caballus similar to olfactory receptor Olfr774 (LOC100055688); mRNA	85.7	NULL	XM_001489758	LOC100055688	similar to olfactory receptor Olfr774
CfaAffx.10364.1.S1_at	5.405090E-05	1.211500E-02	1.17	.85	NULL	null	AC015691	NULL		
CfaAffx.10365.1.S1_at	3.612250E-04	3.800811E-02	1.17	.85	PREDICTED: Equus caballus similar to olfactory receptor; family 6; subfamily C; member 6 (LOC100056791); mRNA	69.5	AB065869	XM_001490390	LOC100056791	similar to olfactory receptor, family 6, subfamily C, member 6
CfaAffx.10379.1.S1_s_at	1.004850E-02	2.131608E-01	0.83	1.20	PREDICTED: Canis familiaris similar to 26 proteasome complex subunit DSS1 (Deleted in split hand/split foot protein 1) (Split hand/foot deleted protein 1 homolog) (LOC607599); mRNA	99.5	CU689534	XM_844346	LOC607599	similar to 26 proteasome complex subunit DSS1 (Deleted in split hand/split foot protein 1) (Split hand/foot deleted protein 1 homolog)
CfaAffx.10391.1.S1_at	1.623300E-03	8.721438E-02	1.15	.87	PREDICTED: Canis familiaris cOR52H9 olfactory receptor family 52 subfamily H-like (cOR52H9); mRNA	98.3	NULL	XM_542403	cOR52H9	cOR52H9 olfactory receptor family 52 subfamily H-like
CfaAffx.10392.1.S1_s_at	6.394650E-08	2.077259E-04	1.32	.76	PREDICTED: Canis familiaris similar to olfactory receptor 825 (LOC486485); mRNA	99.7	NULL	XM_543611	LOC486485	similar to olfactory receptor 825
CfaAffx.10405.1.S1_at	1.023890E-	2.146363E-	1.15	.87	PREDICTED: Canis familiaris similar to Rho-GTPase-activating protein 26 (Oligophrenin-1 like protein) (GTPase regulator associated	100.0	NM_015071	XM_535224	ARHGAP26	Rho GTPase activating protein 26

	02	01			with focal adhesion kinase) (LOC478046); mRNA					
CfaAffx.10420.1.S1_at	6.505490E-04	5.183745E-02	1.11	.90	PREDICTED: Canis familiaris cOR52AC1 olfactory receptor family 52 subfamily AC-like (cOR52AC1); mRNA	100.0	NULL	XM_542409	cOR52AC1	cOR52AC1 olfactory receptor family 52 subfamily AC-like
CfaAffx.10444.1.S1_at	5.109920E-05	1.169710E-02	1.16	.86	PREDICTED: Canis familiaris olfactory receptor (OR26G07); mRNA	98.6	NULL	XM_543608	OR26G07	olfactory receptor
CfaAffx.10449.1.S1_s_at	3.230060E-04	3.555131E-02	0.76	1.32	PREDICTED: Canis familiaris similar to small inducible cytokine subfamily E; member 1 (LOC487893); mRNA	100.0	AB173489	XM_545016	SCYE1	small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)
CfaAffx.10458.1.S1_at	3.091610E-03	1.192181E-01	1.13	.89	Canis lupus familiaris cOR52N9 olfactory receptor family 52 subfamily N-like (cOR52N9); mRNA >gi|133711992|gb|EF451964.1| Canis lupus familiaris 52N9 olfactory receptor protein (OR52N9) mRNA; complete cds	99.7	NULL	NM_001083631	cOR52N9	cOR52N9 olfactory receptor family 52 subfamily N-like
CfaAffx.10478.1.S1_at	1.167200E-02	2.288403E-01	1.14	.88	PREDICTED: Canis familiaris similar to Olfactory receptor 52E4 (LOC485307); mRNA	97.4	BK004302	XM_542425	LOC485307	similar to Olfactory receptor 52E4
CfaAffx.10482.1.S1_at	6.957610E-07	8.806493E-04	1.46	.68	Dictyostelium discoideum AX4 SNF7 family protein (vps20) mRNA; complete cds	62.9	AL356320	XM_632346	vps20	SNF7 family protein
CfaAffx.10502.1.S1_at	1.199210E-03	7.311141E-02	1.14	.88	PREDICTED: Canis familiaris similar to Olfactory receptor 56A1 (LOC485323); mRNA	99.6	AB065821	XM_848481	LOC485323	similar to Olfactory receptor 56A1
CfaAffx.10508.1.S1_at	1.733990E-02	2.746495E-01	1.13	.89	Lodderomyces elongisporus NRRL YB-4239 DNA polymerase alpha catalytic subunit (LELG_02642) partial mRNA	40.4	Z94055	XM_001526034	LELG_02642	DNA polymerase alpha catalytic subunit
CfaAffx.10508.1.S1_s_at	8.177130E-03	1.925070E-01	1.1	.91	Schistosoma japonicum SJCHGC04721 protein mRNA; partial cds	24.7	AL138915	AY810836		
CfaAffx.10513.1.S1_at	1.054940E-02	2.165048E-01	1.11	.90	PREDICTED: Canis familiaris cOR52W2 olfactory receptor family 52 subfamily W-like (cOR52W2); mRNA	100.0	NM_001005178	XM_542449	cOR52W2	cOR52W2 olfactory receptor family 52 subfamily W-like

CfaAffx.10530.1.S1_at	1.613950E-03	8.692908E-02	0.83	1.20	PREDICTED: Canis familiaris similar to CG7139-PA; isoform A (LOC477316); mRNA	100.0	AK125067	XM_534508	N4BP2L2	NEDD4 binding protein 2-like 2
CfaAffx.10538.1.S1_at	2.955720E-03	1.173146E-01	1.13	.89	PREDICTED: Canis familiaris hypothetical LOC477172 (LOC477172); mRNA	74.7	NM_001009984	XM_534362	LOC477172	hypothetical LOC477172
CfaAffx.10554.1.S1_s_at	1.352370E-02	2.439197E-01	1.12	.89	PREDICTED: Canis familiaris similar to netrin 4 (LOC475431); mRNA	98.5	AB384963	XM_532655	NTN4	netrin 4
CfaAffx.10659.1.S1_at	1.132670E-02	2.252032E-01	0.9	1.11	PREDICTED: Pan troglodytes similar to mFLJ00251 protein (LOC748924); mRNA	83.4	AK093028	XM_001164164	LOC748924	similar to mFLJ00251 protein
CfaAffx.10668.1.S1_at	4.043300E-03	1.365804E-01	0.84	1.19	PREDICTED: Canis familiaris similar to THUMP domain containing 2 (LOC483044); mRNA	100.0	AB172066	XM_540159	THUMPD2	THUMP domain containing 2
CfaAffx.10754.1.S1_at	1.619450E-02	2.661055E-01	1.13	.89	PREDICTED: Canis familiaris similar to leiomodin 3 (fetal) (LOC476558); mRNA	99.2	AK030676	XM_549501	LMOD3	leiomodin 3 (fetal)
CfaAffx.10766.1.S1_at	1.445380E-02	2.522842E-01	0.85	1.18	PREDICTED: Canis familiaris similar to zinc finger protein 382 (LOC484559); mRNA	100.0	BC038358	XM_541673	ZNF382	zinc finger protein 382
CfaAffx.10775.1.S1_at	1.983400E-02	2.916147E-01	0.86	1.17	PREDICTED: Canis familiaris similar to IKK interacting protein isoform 2; transcript variant 3 (LOC482619); mRNA	77.0	BC051372	XM_861359	LOC482619	similar to IKK interacting protein isoform 2
CfaAffx.10778.1.S1_at	7.734090E-06	3.799443E-03	1.21	.83	Magnaporthe grisea 70-15 hypothetical protein (MGG_00883) partial mRNA	54.3	NULL	XM_368361	MGG_00883	hypothetical protein
CfaAffx.1082.1.S1_s_at	1.040870E-03	6.766441E-02	0.85	1.18	PREDICTED: Canis familiaris similar to dopamine receptor interacting protein (LOC474392); mRNA	100.0	NM_033082	XM_531625	DNAJC14	DnaJ (Hsp40) homolog, subfamily C, member 14
CfaAffx.10841.1.S1_s_at	1.365900E-03	7.900740E-02	0.89	1.12	Canis lupus familiaris high-mobility group box 1 (HMGB1); mRNA >gi|37548601|gb|AY135519.1| Canis familiaris high mobility group protein B1 mRNA; complete cds	81.5	AB168615	NM_001002937	HMGB1	high-mobility group box 1
CfaAffx.10850.1.S1_at	8.121860E-03	1.916905E-01	1.12	.89	PREDICTED: Canis familiaris similar to single-strand selective monofunctional uracil DNA glycosylase (LOC486497); mRNA	71.1	AB171004	XM_543623	SMUG1	single-strand-selective monofunctional uracil-DNA glycosylase 1

CfaAffx.10858.1.S1_at	4.857400E-04	4.543068E-02	1.18	.85	PREDICTED: Canis familiaris similar to olfactory receptor 705 (LOC485344); mRNA	99.0	NULL	XM_542462	LOC485344	similar to olfactory receptor 705
CfaAffx.10870.1.S1_at	1.729270E-02	2.744615E-01	0.86	1.16	PREDICTED: Canis familiaris similar to ubiquitin-conjugating enzyme E2 variant 2 (LOC608470); mRNA	100.0	DQ003720	XM_544068	TMEM189-UBE2V1	TMEM189-UBE2V1
CfaAffx.10870.1.S1_s_at	1.468200E-03	8.237808E-02	0.85	1.18	PREDICTED: Canis familiaris similar to ubiquitin-conjugating enzyme E2 variant 2 (LOC608470); mRNA	98.6	AB170065	XM_544068	TMEM189-UBE2V1	TMEM189-UBE2V1
CfaAffx.10891.1.S1_s_at	9.191890E-03	2.036936E-01	1.1	.91	PREDICTED: Equus caballus similar to Cell cycle exit and neuronal differentiation 1 (LOC100055133); mRNA	38.6	AK312993	XM_001494406	LOC100055133	similar to Cell cycle exit and neuronal differentiation 1
CfaAffx.10909.1.S1_x_at	6.396960E-04	5.126502E-02	0.86	1.16	PREDICTED: Canis familiaris similar to ribosomal protein L31 (LOC608415); mRNA	99.0	NULL	XM_544333	LOC608415	similar to ribosomal protein L31
CfaAffx.10916.1.S1_at	2.103390E-02	2.982517E-01	1.11	.90	PREDICTED: Equus caballus similar to m51 olfactory receptor (LOC100070370); mRNA	91.7	NULL	XM_001500024	LOC100070370	similar to m51 olfactory receptor
CfaAffx.10941.1.S1_at	3.561560E-03	1.277456E-01	0.87	1.14	PREDICTED: Canis familiaris similar to calpain; small subunit 1 (LOC612622); mRNA	100.0	AK314150	XM_850355	ALKBH6	alkB, alkylation repair homolog 6 (E. coli)
CfaAffx.11001.1.S1_at	1.508550E-04	2.291765E-02	0.77	1.29	Bos taurus ARP6 actin-related protein 6 homolog (yeast) (ACTR6); mRNA >gi|148878124|gb|BC146238.1| Bos taurus hypothetical LOC613596; mRNA (cDNA clone MGC:166308 IMAGE:8625002); complete cds	75.6	AC007371	NM_001099124	ACTR6	ARP6 actin-related protein 6 homolog (yeast)
CfaAffx.11001.1.S1_s_at	1.470880E-02	2.548942E-01	0.9	1.11	PREDICTED: Equus caballus hypothetical protein LOC100052662 (LOC100052662); mRNA	93.7	NM_022496	XM_001496172	ACTR6	ARP6 actin-related protein 6 homolog (yeast)
CfaAffx.11008.1.S1_at	2.824020E-03	1.145445E-01	1.16	.86	Homo sapiens cDNA FLJ77527 complete cds; highly similar to Homo sapiens membrane associated guanylate kinase; WW and PDZ domain containing 1 (MAGI1); transcript variant 2; mRNA	100.0	AK289803	AK289803	MAGI1	membrane associated guanylate kinase, WW and PDZ domain containing 1
CfaAffx.11012.1.S1_at	2.008580E-	2.924196E-	1.11	.90	Drosophila melanogaster GH25733 full	19.6	AC005209	AY069202	CG6971	CG6971

	02	01			length cDNA					
CfaAffx.11025.1.S1_at	1.029900E-02	2.151541E-01	1.27	.79	PREDICTED: Canis familiaris similar to dynein; cytoplasmic; light chain 2A (LOC486026); mRNA	100.0	NULL	XM_543152	LOC486026	similar to dynein, cytoplasmic, light chain 2A
CfaAffx.11025.1.S1_x_at	1.486470E-02	2.560075E-01	1.21	.82	PREDICTED: Canis familiaris similar to dynein; cytoplasmic; light chain 2A (LOC486026); mRNA	100.0	NULL	XM_543152	LOC486026	similar to dynein, cytoplasmic, light chain 2A
CfaAffx.11034.1.S1_s_at	2.029620E-05	7.043927E-03	1.14	.88	PREDICTED: Canis familiaris similar to olfactomedin-like 1 (LOC476839); mRNA	100.0	AY358591	XM_534043	OLFML1	olfactomedin-like 1
CfaAffx.11050.1.S1_at	6.516570E-04	5.183745E-02	1.14	.88	PREDICTED: Canis familiaris similar to cell division cycle 20 homolog (LOC478058); mRNA	100.0	NM_152623	XM_535236	CDC20B	cell division cycle 20 homolog B (S. cerevisiae)
CfaAffx.11134.1.S1_at	5.586520E-05	1.220385E-02	1.26	.79	Macaca fascicularis brain cDNA clone: QflA-18183; similar to human reversion-inducing-cysteine-rich protein with kazalmotifs (RECK); mRNA; RefSeq: NM_021111.1	22.7	AC126308	AB172453		
CfaAffx.11134.1.S1_s_at	2.621380E-03	1.098453E-01	1.13	.88	PREDICTED: Canis familiaris similar to solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter); member 8 (LOC482623); mRNA	47.4	AK128319	XM_539740	SLC17A8	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 8
CfaAffx.11139.1.S1_at	1.948690E-02	2.895798E-01	0.9	1.11	PREDICTED: Canis familiaris hypothetical protein LOC610050 (LOC610050); mRNA	87.3	NM_144669	XM_847440	GLT1D1	glycosyltransferase 1 domain containing 1
CfaAffx.11148.1.S1_at	2.957740E-03	1.173146E-01	0.81	1.23	PREDICTED: Canis familiaris similar to Double-strand-break repair protein rad21 homolog (Pokeweed agglutinin-binding protein 29) (PW29) (SCC1 homolog) (LOC609572); mRNA	95.6	XM_938700	XM_846853	LOC609572	similar to Double-strand-break repair protein rad21 homolog (Pokeweed agglutinin-binding protein 29) (PW29) (SCC1 homolog)
CfaAffx.11153.1.S1_s_at	3.024340E-03	1.184813E-01	1.1	.91	PREDICTED: Canis familiaris similar to olfactory receptor Olr245 (LOC485372); mRNA	100.0	AF399452	XM_848953	LOC485372	similar to olfactory receptor Olr245
CfaAffx.11155.1.S1_s_at	2.957110E-04	3.375576E-02	0.85	1.18	PREDICTED: Canis familiaris similar to Rb1-inducible coiled coil protein 1; transcript	100.0	AB059622	XM_851715	RB1CC1	RB1-inducible coiled-coil 1

					variant 4 (LOC477876); mRNA					
CfaAffx.11192.1.S1_at	1.317310E-02	2.409283E-01	1.15	.87	PREDICTED: Canis familiaris cOR10AB2 olfactory receptor family 10 subfamily AB-like (cOR10AB2); mRNA	99.7	AB065766	XM_542489	cOR10AB2	cOR10AB2 olfactory receptor family 10 subfamily AB-like
CfaAffx.1122.1.S1_at	2.961850E-03	1.173694E-01	1.14	.88	PREDICTED: Canis familiaris similar to Proliferation-associated protein 2G4 (Cell cycle protein p38-2G4 homolog) (hG4-1) (LOC474396); mRNA	95.8	NM_006191	XM_531629	PA2G4	proliferation-associated 2G4, 38kDa
CfaAffx.11231.1.S1_s_at	9.252980E-05	1.706465E-02	1.18	.85	PREDICTED: Canis familiaris similar to DEAD (Asp-Glu-Ala-Asp) box polypeptide 4 (LOC487211); mRNA	73.5	AK292417	XM_544339	DDX4	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4
CfaAffx.11248.1.S1_at	9.135770E-03	2.028678E-01	1.13	.89	Homo sapiens cDNA FLJ32561 fis; clone SPLEN1000163; moderately similar to PYRUVATE DEHYDROGENASE PROTEIN X COMPONENT; MITOCHONDRIAL PRECURSOR	31.9	AJ298105	AK057123		
CfaAffx.11284.1.S1_s_at	1.009810E-03	6.675449E-02	1.17	.85	PREDICTED: Canis familiaris similar to Potential phospholipid-transporting ATPase IB (ATPase class I type 8A member 2) (ML-1) (LOC486036); mRNA	100.0	BC156471	XM_543162	LOC486036	similar to Potential phospholipid-transporting ATPase IB (ATPase class I type 8A member 2) (ML-1)
CfaAffx.113.1.S1_at	1.267260E-08	7.906329E-05	1.49	.67	Canis familiaris olfactory receptor (CfOLF2) gene; complete cds	100.0	AP004285	U53680		
CfaAffx.11308.1.S1_s_at	1.089830E-05	4.643647E-03	1.25	.80	PREDICTED: Canis familiaris similar to solute carrier family 7; member 2 isoform 1; transcript variant 1 (LOC475614); mRNA	97.3	BC069648	XM_532828	SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2
CfaAffx.11313.1.S1_at	1.764930E-03	9.096259E-02	1.13	.88	Macaca fascicularis brain cDNA clone: QmoA-10592; similar to human ATPase; (Na+)/K+ transporting; beta 4 polypeptide(ATP1B4); mRNA; RefSeq: NM_012069.2	15.0	AL121975	AB173840		
CfaAffx.11325.1.S1_s_at	4.607720E-03	1.452698E-01	0.89	1.13	PREDICTED: Canis familiaris similar to e(y)2 protein; transcript variant 5 (LOC475074); mRNA	99.5	AK316560	XM_855218	ENY2	enhancer of yellow 2 homolog (Drosophila)

CfaAffx.11338.1.S1_at	4.398920E-03	1.421228E-01	1.11	.90	PREDICTED: Canis familiaris similar to olfactory receptor; family 13; subfamily A; member 1 (LOC486778); mRNA	71.7	NULL	XM_543905	LOC486778	similar to olfactory receptor, family 13, subfamily A, member 1
CfaAffx.11346.1.S1_at	9.621060E-03	2.084805E-01	1.12	.89	Canis familiaris beta-defensin 128 (CBD128) mRNA; complete cds	65.4	NM_001037732	DQ011997		
CfaAffx.11364.1.S1_at	1.140660E-02	2.256758E-01	1.11	.90	PREDICTED: Equus caballus similar to olfactory receptor MOR119-2 (LOC100061869); mRNA	65.1	AL512324	XM_001493660	LOC100061869	similar to olfactory receptor MOR119-2
CfaAffx.11377.1.S1_s_at	8.324610E-04	5.946195E-02	0.73	1.37	PREDICTED: Canis familiaris similar to chromosome 11 open reading frame 17 (LOC611400); mRNA	100.0	NM_182901	XM_849065	LOC611400	similar to chromosome 11 open reading frame 17
CfaAffx.11387.1.S1_at	2.073290E-03	9.783337E-02	0.86	1.16	PREDICTED: Canis familiaris similar to CG10053-PA (LOC475616); mRNA	95.8	NM_174931	XM_532830	CCDC75	coiled-coil domain containing 75
CfaAffx.11392.1.S1_s_at	3.800850E-03	1.327675E-01	1.16	.87	PREDICTED: Equus caballus similar to protein tyrosine kinase; transcript variant 1 (LOC100053254); mRNA	94.0	NULL	XM_001498502	LOC100053254	similar to protein tyrosine kinase
CfaAffx.114.1.S1_at	3.604650E-04	3.800811E-02	1.14	.88	PREDICTED: Equus caballus similar to olfactory receptor Olfr372 (LOC100069770); mRNA	87.0	BK004262	XM_001499503	LOC100069770	similar to olfactory receptor Olfr372
CfaAffx.11422.1.S1_at	1.078610E-02	2.183348E-01	0.9	1.11	PREDICTED: Canis familiaris similar to zinc finger protein 32; transcript variant 6 (LOC486784); mRNA	99.6	NULL	XM_851142	LOC486784	similar to zinc finger protein 32
CfaAffx.11424.1.S1_at	7.124530E-03	1.804793E-01	0.87	1.15	PREDICTED: Canis familiaris similar to extra spindle poles like 1 (LOC607879); mRNA	99.6	AY455930	XM_844735	ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)
CfaAffx.11439.1.S1_at	9.438470E-04	6.396607E-02	1.18	.85	PREDICTED: Canis familiaris similar to N-acetyltransferase-like protein; transcript variant 12 (LOC483431); mRNA	100.0	NULL	XM_852974	NAT10	N-acetyltransferase 10
CfaAffx.11458.1.S1_s_at	5.676190E-03	1.615574E-01	0.9	1.11	PREDICTED: Equus caballus similar to T-cell specific surface glycoprotein CD28; transcript variant 1 (LOC100062026); mRNA	91.7	M38258	XM_001504495	LOC100062026	similar to Retinoic acid receptor gamma

CfaAffx.11522.1.S1_x_at	1.844720E-03	9.250120E-02	0.81	1.24	PREDICTED: Canis familiaris similar to ribosomal protein L31; transcript variant 2 (LOC607833); mRNA	95.6	NULL	XM_854816	LOC607833	similar to ribosomal protein L31
CfaAffx.11530.1.S1_s_at	3.257480E-03	1.228621E-01	0.89	1.12	PREDICTED: Canis familiaris similar to p53 and DNA damage-regulated protein (LOC477190); mRNA	100.0	AK312021	XM_534380	PDRG1	p53 and DNA damage regulated 1
CfaAffx.11583.1.S1_at	4.286050E-04	4.230508E-02	1.15	.87	PREDICTED: Canis familiaris similar to tumor necrosis factor receptor superfamily; member 19 isoform 2 precursor (LOC486042); mRNA	100.0	AK292891	XM_543168	TNFRSF19	tumor necrosis factor receptor superfamily, member 19
CfaAffx.11584.1.S1_at	4.643130E-03	1.456945E-01	1.18	.85	PREDICTED: Equus caballus similar to ZNF382 protein (LOC100060953); mRNA	46.7	NULL	XM_001493051	LOC100060953	similar to ZNF382 protein
CfaAffx.11587.1.S1_at	4.821800E-04	4.543068E-02	1.18	.85	PREDICTED: Canis familiaris similar to ELOVL family member 7; elongation of long chain fatty acids (LOC608997); mRNA	100.0	NM_001104558	XM_846175	ELOVL7	ELOVL family member 7, elongation of long chain fatty acids (yeast)
CfaAffx.11620.1.S1_at	7.571730E-03	1.848591E-01	0.82	1.21	PREDICTED: Canis familiaris similar to Zinc finger SWIM domain containing protein 6 (LOC478068); mRNA	100.0	XM_001716154	XM_535247	ZSWIM6	zinc finger, SWIM-type containing 6
CfaAffx.11638.1.S1_at	1.068850E-02	2.176197E-01	1.13	.88	Homo sapiens pleiomorphic adenoma gene-like 2 (PLAGL2); mRNA	77.1	NM_002657	NM_002657	PLAGL2	pleiomorphic adenoma gene-like 2
CfaAffx.11659.1.S1_at	5.288160E-04	4.690621E-02	1.14	.87	Sus scrofa mRNA; clone:AMP010095G02; expressed in alveolar macrophage	15.3	AC024588	AK231115		
CfaAffx.11686.1.S1_at	2.712350E-04	3.204080E-02	1.18	.84	Canis familiaris masticatory epithelia keratin 2p (krt2p) gene; complete cds	59.3	NULL	AF293846		
CfaAffx.11709.1.S1_at	2.796640E-03	1.136482E-01	0.88	1.14	PREDICTED: Canis familiaris similar to Exportin-4 (Exp4) (LOC477344); mRNA	100.0	AL512652	XM_534538	XPO4	exportin 4
CfaAffx.11761.1.S1_at	6.120950E-04	5.075435E-02	0.86	1.16	PREDICTED: Canis familiaris similar to Keratin; type II cytoskeletal 6A (Cytokeratin 6A) (CK 6A) (K6a keratin); transcript variant 3 (LOC486523); mRNA	100.0	AK313239	XM_855364	KRT6A	keratin 6A
CfaAffx.11779.1.S1_s_at	1.886570E-	2.854731E-	1.1	.91	PREDICTED: Canis familiaris similar to ring finger protein 180; transcript variant 2	60.3	NM_001113561	XM_855650	RNF180	ring finger protein 180

	02	01			(LOC487231); mRNA					
CfaAffx.11829.1.S1_at	3.272410E-03	1.231015E-01	1.11	.90	PREDICTED: Equus caballus similar to Gap junction protein; beta 6 (LOC100053788); mRNA	91.9	NM_001110219	XM_001488823	LOC100053788	similar to Gap junction protein, beta 6
CfaAffx.11839.1.S1_at	6.787520E-04	5.330309E-02	1.2	.83	PREDICTED: Canis familiaris phenylalanine hydroxylase (PAH); mRNA	95.1	NM_000277	XM_532671	PAH	phenylalanine hydroxylase
CfaAffx.11852.1.S1_at	1.724900E-02	2.742666E-01	0.84	1.19	PREDICTED: Canis familiaris similar to Importin-7 (Imp7) (Ran-binding protein 7) (RanBP7); transcript variant 3 (LOC485383); mRNA	100.0	AL137335	XM_858719	IPO7	importin 7
CfaAffx.11865.1.S1_at	1.314270E-03	7.716181E-02	1.15	.87	Canis lupus familiaris melatonin receptor 1a (MTNR1A) gene; partial cds	100.0	EU432127	EU170444		
CfaAffx.11869.1.S1_at	9.450800E-03	2.067693E-01	1.13	.88	PREDICTED: Pan troglodytes La ribonucleoprotein domain family member 2 (LARP2); mRNA	26.8	AC040970	XM_517433	LARP2	La ribonucleoprotein domain family, member 2
CfaAffx.11904.1.S1_s_at	6.588110E-03	1.739023E-01	1.12	.89	Homo sapiens chromosome 20 open reading frame 71 (C20orf71); transcript variant 2; mRNA	71.9	NM_001042439	NM_001042439	C20orf71	chromosome 20 open reading frame 71
CfaAffx.11955.1.S1_s_at	1.215350E-02	2.337430E-01	0.88	1.13	PREDICTED: Canis familiaris similar to B5 receptor (LOC475950); mRNA	100.0	CU676385	XM_533160	EIF3M	eukaryotic translation initiation factor 3, subunit M
CfaAffx.11969.1.S1_at	1.052740E-05	4.576229E-03	1.3	.77	PREDICTED: Equus caballus similar to hCG1645384; (LOC100073196); mRNA	90.9	AK125070	XM_001503577		
CfaAffx.11987.1.S1_at	5.986740E-04	5.030892E-02	1.15	.87	NULL	null	AC117503	NULL		
CfaAffx.120.1.S1_at	2.985040E-04	3.398444E-02	1.18	.85	PREDICTED: Canis familiaris similar to Olfactory receptor 52N2 (LOC485302); mRNA	51.0	AC206475	XM_848344	LOC485302	similar to Olfactory receptor 52N2
CfaAffx.12006.1.S1_s_at	6.989450E-03	1.789357E-01	1.13	.89	PREDICTED: Canis familiaris similar to cytoplasmic polyadenylation element binding protein 3; transcript variant 2 (LOC486801); mRNA	100.0	AB384052	XM_844121	CPEB3	cytoplasmic polyadenylation element binding protein 3

CfaAffx.12018.1.S1_s_at	6.740130E-03	1.759015E-01	1.11	.90	PREDICTED: Canis familiaris similar to Asc-type amino acid transporter 1 (Asc-1) (LOC484599); mRNA	99.8	AK316594	XM_541713	SLC7A10	solute carrier family 7, (neutral amino acid transporter, y+ system) member 10
CfaAffx.12025.1.S1_s_at	7.471920E-03	1.839506E-01	0.91	1.10	PREDICTED: Canis familiaris non-gastric H+/K+-ATPase alpha-chain (ATP12A); mRNA	100.0	CU689201	XM_843185	ATP12A	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
CfaAffx.12070.1.S1_s_at	2.123370E-02	2.998990E-01	1.1	.91	PREDICTED: Canis familiaris similar to *fibronectin type III domain containing 6* (LOC610961); mRNA	90.5	BC033292	XM_848558	IL20RB	interleukin 20 receptor beta
CfaAffx.12081.1.S1_at	4.116330E-03	1.377498E-01	0.83	1.20	PREDICTED: Canis familiaris similar to Host cell factor 2 (HCF-2) (C2 factor); transcript variant 5 (LOC475449); mRNA	100.0	EU446491	XM_861982	HCFC2	host cell factor C2
CfaAffx.12110.1.S1_s_at	2.101290E-02	2.980521E-01	1.12	.89	Canis lupus familiaris paired box 6 (PAX6); mRNA >gi|134289885|gb|EF141016.1| Canis familiaris PAX6 (PAX6) mRNA; complete cds; alternatively spliced	100.0	AB171050	NM_001097544	PAX6	paired box 6
CfaAffx.12115.1.S1_at	2.244030E-05	7.486188E-03	1.24	.80	PREDICTED: Ornithorhynchus anatinus similar to KIAA0372; (LOC100085860); partial mRNA	22.9	AC008560	XM_001516054	LOC100085860	similar to KIAA0372
CfaAffx.12138.1.S1_at	2.048340E-02	2.950332E-01	1.14	.88	Synthetic construct Homo sapiens gateway clone IMAGE:100017425 3-prime read NLN mRNA	14.0	CU674807	CU674807		
CfaAffx.12178.1.S1_s_at	7.986290E-03	1.898098E-01	0.85	1.18	PREDICTED: Canis familiaris hypothetical LOC488884 (LOC488884); mRNA	100.0	NM_017676	XM_546001	GIN1	gypsy retrotransposon integrase 1
CfaAffx.122.1.S1_at	1.486510E-02	2.560075E-01	1.11	.90	PREDICTED: Canis familiaris cOR52M5 olfactory receptor family 52 subfamily M-like (cOR52M5); mRNA	99.8	AC010930	XM_542349	cOR52M5	cOR52M5 olfactory receptor family 52 subfamily M-like
CfaAffx.12238.1.S1_at	1.327330E-05	5.192425E-03	1.2	.83	Homo sapiens mRNA for KIAA1084 protein; partial cds	34.8	AB029007	AB029007	ZNF507	zinc finger protein 507
CfaAffx.12261.1.S1_at	5.044870E-03	1.515045E-01	0.82	1.22	PREDICTED: Canis familiaris similar to ATP-binding cassette sub-family E member 1 (RNase L inhibitor) (Ribonuclease 4 inhibitor) (RNS4I); transcript variant 4	100.0	NM_001040876	XM_862119	ABCE1	ATP-binding cassette, sub-family E (OABP), member 1

					(LOC475454); mRNA					
CfaAffx.1228.1.S1_at	7.785340E-07	9.306725E-04	1.36	.73	Homo sapiens gene for LIM-homeodomain protein Lhx8; partial cds	55.9	AL137021	AB050476		
CfaAffx.1230.1.S1_at	1.408600E-03	8.029020E-02	1.12	.89	PREDICTED: Canis familiaris similar to Adrenocorticotropic hormone receptor (ACTH receptor) (ACTH-R) (Melanocortin-2 receptor) (MC2-R) (Adrenocorticotropin receptor) (LOC483980); mRNA	99.7	AK315319	XM_541098	MC2R	melanocortin 2 receptor (adrenocorticotropic hormone)
CfaAffx.12302.1.S1_at	6.105950E-03	1.683341E-01	1.15	.87	Brenneria lupinicola strain EluW3L16 malate dehydrogenase (mdh) gene; partial cds	30.2	NULL	EF550766		
CfaAffx.1231.1.S1_at	4.097230E-03	1.373242E-01	1.1	.91	PREDICTED: Canis familiaris similar to melanocortin 5 receptor (LOC483981); mRNA	100.0	EF444993	XM_541099	MC5R	melanocortin 5 receptor
CfaAffx.1238.1.S1_at	1.249150E-03	7.483302E-02	1.15	.87	PREDICTED: Canis familiaris similar to heat shock protein 1; beta (LOC474634); mRNA	100.0	NULL	XM_845020	LOC474634	similar to heat shock protein 1, beta
CfaAffx.12399.1.S1_at	4.345580E-03	1.413545E-01	1.13	.88	PREDICTED: Canis familiaris cOR5B25 olfactory receptor family 5 subfamily B-like gene (cOR5B25); mRNA	98.5	BK004507	XM_540585	cOR5B25	cOR5B25 olfactory receptor family 5 subfamily B-like gene
CfaAffx.12400.1.S1_at	2.023090E-03	9.649705E-02	1.11	.90	PREDICTED: Canis familiaris olfactory receptor (OR26A01); mRNA	100.0	NULL	XM_540587	OR26A01	olfactory receptor
CfaAffx.12405.1.S1_s_at	3.374960E-04	3.676998E-02	0.77	1.29	PREDICTED: Canis familiaris similar to chromodomain helicase DNA binding protein 1; transcript variant 2 (LOC488891); mRNA	65.6	AF006513	XM_843366	CHD1	chromodomain helicase DNA binding protein 1
CfaAffx.12415.1.S1_at	2.082290E-04	2.800355E-02	1.3	.77	NULL	null	AC114399	NULL		
CfaAffx.12417.1.S1_at	1.985080E-03	9.580372E-02	1.13	.89	PREDICTED: Canis familiaris olfactory receptor (OR08G08); mRNA	99.5	NULL	XM_540594	OR08G08	olfactory receptor
CfaAffx.12421.1.S1_at	6.232540E-04	5.125131E-02	1.12	.89	PREDICTED: Canis familiaris similar to Olfactory receptor 5B2 (OST073) (Olfactory receptor OR11-240) (LOC483477); mRNA	97.3	NULL	XM_847385	LOC483477	similar to Olfactory receptor 5B2 (OST073) (Olfactory receptor OR11-240)

CfaAffx.12432.1.S1_s_at	1.112370E-03	7.050198E-02	1.2	.83	PREDICTED: Canis familiaris similar to olfactory receptor 1500 (LOC483483); mRNA	100.0	AP004247	XM_540601	LOC483483	similar to olfactory receptor 1500
CfaAffx.12432.1.S1_x_at	1.053470E-02	2.164013E-01	1.11	.90	PREDICTED: Canis familiaris similar to olfactory receptor 1500 (LOC483483); mRNA	99.6	NULL	XM_540601	LOC483483	similar to olfactory receptor 1500
CfaAffx.12435.1.S1_at	1.497100E-02	2.569912E-01	1.11	.90	PREDICTED: Macaca mulatta similar to Olfactory receptor 4K1 (LOC698752); mRNA	47.3	NULL	XM_001086899	LOC698752	similar to Olfactory receptor 4K1
CfaAffx.12438.1.S1_at	4.172150E-03	1.384964E-01	1.12	.89	PREDICTED: Macaca mulatta similar to solute carrier family 4 (anion exchanger); member 8; transcript variant 6 (LOC695616); mRNA	92.4	NULL	XM_001090067	LOC695616	similar to solute carrier family 4 (anion exchanger), member 8
CfaAffx.1244.1.S1_at	3.632030E-03	1.289640E-01	1.12	.90	null	null	null	null		
CfaAffx.12520.1.S1_at	5.138180E-03	1.527083E-01	1.12	.89	PREDICTED: Canis familiaris similar to ectonucleotide pyrophosphatase/phosphodiesterase 6 (LOC475636); mRNA	100.0	AC107222	XM_532849	ENPP6	ectonucleotide pyrophosphatase/phosphodiesterase 6
CfaAffx.12531.1.S1_at	1.234930E-02	2.349479E-01	0.84	1.19	PREDICTED: Canis familiaris similar to TFIIH basal transcription factor complex p44 subunit (Basic transcription factor 2 44 kDa subunit) (BTF2-p44) (General transcription factor IIH polypeptide 2); transcript variant 1 (LOC478089); mRNA	100.0	AB173449	XM_535266	GTF2H2	general transcription factor IIH, polypeptide 2, 44kDa
CfaAffx.12550.1.S1_at	1.365220E-02	2.450662E-01	0.84	1.19	PREDICTED: Canis familiaris similar to yippee-like 4 (LOC610168); mRNA	100.0	AK124577	XM_847589	YPEL4	yippee-like 4 (Drosophila)
CfaAffx.12595.1.S1_s_at	8.564050E-05	1.624452E-02	1.13	.88	PREDICTED: Macaca mulatta similar to heart and neural crest derivatives expressed transcript 2; transcript variant 1 (LOC696881); mRNA	91.2	AK122739	XM_001085733	LOC696881	similar to heart and neural crest derivatives expressed transcript 2
CfaAffx.12672.1.S1_at	1.159060E-02	2.276593E-01	1.14	.88	Sus scrofa mRNA; clone:UTR010086B10; expressed in uterus	48.7	AC010087	AK240513		
CfaAffx.12673.1.S1_at	3.351750E-	9.392584E-	1.25	.80	NULL	null	AL354752	NULL		

	05	03								
CfaAffx.12687.1.S1_s_at	2.513140E-07	4.326119E-04	1.25	.80	Homo sapiens glycine receptor; alpha 3 (GLRA3); transcript variant 2; mRNA	92.1	NM_001042543	NM_001042543	GLRA3	glycine receptor, alpha 3
CfaAffx.12716.1.S1_s_at	1.678560E-03	8.920329E-02	1.1	.91	PREDICTED: Canis familiaris P2X3 purinoceptor; transcript variant 1 (P2X3); mRNA	100.0	BC109287	XM_540614	P2RX3	purinergic receptor P2X, ligand-gated ion channel, 3
CfaAffx.12719.1.S1_at	3.246470E-03	1.227571E-01	1.12	.89	PREDICTED: Canis familiaris similar to CG7092-PA (LOC475774); mRNA	100.0	XR_027711	XM_532984	LOC475774	hypothetical gene supported by NM_001003142
CfaAffx.12731.1.S1_s_at	2.018660E-02	2.930939E-01	1.11	.90	PREDICTED: Canis familiaris similar to Short transient receptor potential channel 1 (TrpC1) (TRP-1 protein) (LOC485698); mRNA	99.8	XR_024392	XM_542818	TRPC1	transient receptor potential cation channel, subfamily C, member 1
CfaAffx.12742.1.S1_s_at	1.552270E-02	2.613375E-01	0.86	1.17	PREDICTED: Canis familiaris similar to CG12600-PA; transcript variant 1 (LOC482920); mRNA	70.3	NM_024949	XM_540035	WWC2	WW and C2 domain containing 2
CfaAffx.12758.1.S1_at	5.523760E-05	1.220385E-02	1.21	.83	PREDICTED: Canis familiaris similar to transmembrane protein 20 (LOC486807); mRNA	100.0	NULL	XM_543936	TMEM20	transmembrane protein 20
CfaAffx.12764.1.S1_s_at	7.029820E-03	1.795988E-01	1.12	.90	Cryptococcus neoformans var. neoformans JEC21 ER to Golgi transport-related protein (CNB00890) partial mRNA	46.3	AC097504	XM_569096	CNB00890	ER to Golgi transport-related protein
CfaAffx.12782.1.S1_at	1.051540E-03	6.804966E-02	1.15	.87	PREDICTED: Macaca mulatta similar to fatty acid desaturase 2 (LOC705393); mRNA	16.8	AL356154	XM_001093754	LOC705393	similar to fatty acid desaturase 2
CfaAffx.12792.1.S1_at	2.795700E-04	3.249746E-02	1.19	.84	PREDICTED: Canis familiaris olfactory receptor (OR04E05); mRNA	100.0	NULL	XM_540623	OR04E05	olfactory receptor
CfaAffx.12793.1.S1_at	3.153290E-03	1.205167E-01	1.12	.89	PREDICTED: Canis familiaris olfactory receptor (OR16B12); mRNA	99.6	NULL	XM_540624	OR16B12	olfactory receptor
CfaAffx.1282.1.S1_at	5.561100E-05	1.220385E-02	1.18	.84	null	null	null	null		

CfaAffx.12823.1.S1_at	4.125620E-03	1.379365E-01	1.15	.87	PREDICTED: Canis familiaris olfactory receptor OR26B08 (OR26B08); mRNA	100.0	AB065740	XM_540631	OR26B08	olfactory receptor OR26B08
CfaAffx.1283.1.S1_at	4.717050E-06	2.877211E-03	0.8	1.26	PREDICTED: Canis familiaris similar to Structural maintenance of chromosome 1-like 1 protein (SMC1alpha protein) (Chromosome segregation protein SmcB) (Sb1.8) (LOC474638); mRNA	22.8	CU689127	XM_531868	CCDC112	coiled-coil domain containing 112
CfaAffx.12849.1.S1_at	2.855230E-03	1.152672E-01	1.11	.90	PREDICTED: Canis familiaris cOR5M13P olfactory receptor family 5 subfamily M-like (cOR5M13P); mRNA	99.6	NULL	XM_540638	cOR5M13P	cOR5M13P olfactory receptor family 5 subfamily M-like
CfaAffx.12868.1.S1_at	2.014740E-03	9.649705E-02	1.14	.88	Canis lupus familiaris cOR8U2 olfactory receptor family 8 subfamily U-like (cOR8U2); mRNA	99.5	AC213240	NM_001017531	cOR8U2	cOR8U2 olfactory receptor family 8 subfamily U-like
CfaAffx.12871.1.S1_at	1.461910E-04	2.234661E-02	1.19	.84	PREDICTED: Canis familiaris olfactory receptor (OR10G10); mRNA	98.5	AC213240	XM_540647	OR10G10	olfactory receptor
CfaAffx.12874.1.S1_at	7.565420E-03	1.848591E-01	1.14	.87	PREDICTED: Macaca mulatta similar to Olfactory receptor 8K1 (LOC708388); mRNA	86.4	AB065835	XM_001103756	LOC708388	similar to Olfactory receptor 8K1
CfaAffx.12896.1.S1_s_at	4.894660E-03	1.491466E-01	0.85	1.18	PREDICTED: Macaca mulatta SAM domain; SH3 domain and nuclear localization signals; 1; transcript variant 4 (SAMSN1); mRNA	88.4	NM_022136	XM_001082905	SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1
CfaAffx.12899.1.S1_at	1.764090E-02	2.766677E-01	1.12	.89	PREDICTED: Equus caballus similar to seven transmembrane helix receptor (LOC100050556); mRNA	89.5	BK004345	XM_001504083	LOC100050556	similar to seven transmembrane helix receptor
CfaAffx.12927.1.S1_at	1.067400E-02	2.176197E-01	1.11	.90	PREDICTED: Canis familiaris similar to 40S ribosomal protein S6 (LOC475778); mRNA	97.3	NULL	XM_532987	LOC475778	similar to 40S ribosomal protein S6
CfaAffx.12939.1.S1_s_at	1.592120E-04	2.370826E-02	1.16	.86	PREDICTED: Equus caballus similar to olfactory receptor Olfr1126 (LOC100058123); partial mRNA	38.0	NULL	XM_001491213	LOC100058123	similar to olfactory receptor 1126
CfaAffx.12945.1.S1_at	6.497110E-03	1.732327E-01	0.85	1.18	PREDICTED: Canis familiaris similar to CG7220-PA; isoform A; transcript variant 1 (LOC486999); mRNA	99.6	NM_018299	XM_544128	UBE2W	ubiquitin-conjugating enzyme E2W (putative)

CfaAffx.12955.1.S1_at	5.276850E-04	4.690621E-02	1.13	.89	PREDICTED: Canis familiaris olfactory receptor (OR16D05); mRNA	99.8	AC036111	XM_540673	OR16D05	olfactory receptor
CfaAffx.12965.1.S1_at	1.743820E-04	2.495501E-02	1.31	.76	Homo sapiens methionine sulfoxide reductase gene; complete cds; alternatively spliced	77.8	AF153342	AY958432		
CfaAffx.12966.1.S1_at	1.702040E-03	8.965397E-02	1.1	.91	PREDICTED: Canis familiaris similar to olfactory receptor 1165 (LOC483559); mRNA	98.9	AB065777	XM_540679	LOC483559	similar to olfactory receptor 1165
CfaAffx.12967.1.S1_at	2.005680E-02	2.923975E-01	1.13	.89	Canis familiaris isolate cOR5D23 olfactory receptor family 5 subfamily D gene; partial cds	99.5	AF399364	AY308923		
CfaAffx.12970.1.S1_at	2.256660E-03	1.017981E-01	1.21	.83	PREDICTED: Equus caballus similar to olfactory receptor Olfr1178 (LOC100053284); mRNA	85.7	NULL	XM_001488616	LOC100053284	similar to olfactory receptor Olfr1178
CfaAffx.12980.1.S1_at	1.031250E-03	6.734422E-02	1.18	.85	PREDICTED: Canis familiaris similar to Olfactory receptor 4P4 (LOC610757); mRNA	99.2	NULL	XM_848308	LOC610757	similar to Olfactory receptor 4P4
CfaAffx.12983.1.S1_at	1.420060E-04	2.206888E-02	1.21	.83	PREDICTED: Canis familiaris cOR4Y1 olfactory receptor family 4 subfamily Y-like (cOR4Y1); mRNA	77.3	NULL	XM_540684	cOR4Y1	cOR4Y1 olfactory receptor family 4 subfamily Y-like
CfaAffx.12989.1.S1_at	1.730490E-03	9.022485E-02	1.12	.89	PREDICTED: Canis familiaris cOR4Y1 olfactory receptor family 4 subfamily Y-like (cOR4Y1); mRNA	100.0	NULL	XM_540684	cOR4Y1	cOR4Y1 olfactory receptor family 4 subfamily Y-like
CfaAffx.13031.1.S1_at	6.220300E-05	1.312209E-02	1.14	.87	PREDICTED: Equus caballus similar to olfactory receptor 1206 (LOC100064274); mRNA	82.5	NULL	XM_001495226		
CfaAffx.13032.1.S1_at	4.601150E-03	1.451690E-01	1.11	.90	PREDICTED: Canis familiaris similar to zinc finger protein of the cerebellum 4 (LOC485704); mRNA	100.0	BC126267	XM_542824	ZIC4	Zic family member 4
CfaAffx.13057.1.S1_at	8.055900E-06	3.852063E-03	1.17	.85	PREDICTED: Canis familiaris similar to olfactory receptor 1231 (LOC610972); mRNA	99.3	BK004769	XM_848572	LOC610972	similar to olfactory receptor 1231

CfaAffx.13058.1.S1_at	5.130350E-03	1.526226E-01	1.15	.87	PREDICTED: Macaca mulatta similar to olfactory receptor; family 4; subfamily A; member 15 (LOC711325); mRNA	87.4	AF399578	XM_001104583	LOC711325	similar to olfactory receptor, family 4, subfamily A, member 15
CfaAffx.13059.1.S1_at	6.271950E-05	1.316651E-02	1.2	.83	PREDICTED: Canis familiaris cOR4C1P olfactory receptor family 4 subfamily C-like (cOR4C1P); mRNA	97.1	AP005134	XM_540710	cOR4C1P	cOR4C1P olfactory receptor family 4 subfamily C-like
CfaAffx.13063.1.S1_at	3.712240E-05	9.943067E-03	1.21	.83	PREDICTED: Canis familiaris cOR4A26 olfactory receptor family 4 subfamily A-like (cOR4A26); mRNA	100.0	BK004593	XM_540711	cOR4A26	cOR4A26 olfactory receptor family 4 subfamily A-like
CfaAffx.13084.1.S1_at	3.310260E-03	1.237681E-01	1.12	.89	PREDICTED: Pan troglodytes similar to seven transmembrane helix receptor (LOC466884); mRNA	88.1	AC110057	XR_024299	LOC466884	similar to seven transmembrane helix receptor
CfaAffx.13088.1.S1_at	4.269600E-04	4.223959E-02	1.13	.88	PREDICTED: Canis familiaris cOR4C3 olfactory receptor family 4 subfamily X-like (cOR4C3); mRNA	97.9	AB065567	XM_540720	cOR4C3	cOR4C3 olfactory receptor family 4 subfamily X-like
CfaAffx.13094.1.S1_at	3.748010E-05	9.943067E-03	1.19	.84	PREDICTED: Canis familiaris similar to olfactory receptor Olr728 (LOC483599); mRNA	100.0	NULL	XM_540719	LOC483599	similar to olfactory receptor Olr728
CfaAffx.1310.1.S1_at	1.159970E-03	7.182634E-02	0.84	1.19	PREDICTED: Canis familiaris similar to transmembrane emp24 protein transport domain containing 9; transcript variant 1 (LOC481444); mRNA	100.0	NM_017510	XM_538565	TMED9	transmembrane emp24 protein transport domain containing 9
CfaAffx.13106.1.S1_at	1.307050E-03	7.684276E-02	1.14	.88	PREDICTED: Canis familiaris similar to olfactory receptor Olr737 (LOC483614); mRNA	100.0	AB065848	XM_540734	LOC483614	similar to olfactory receptor Olr737
CfaAffx.13107.1.S1_at	6.830450E-03	1.767452E-01	1.12	.89	PREDICTED: Canis familiaris olfactory receptor (OR08C02); mRNA	100.0	NULL	XM_540735	OR08C02	olfactory receptor
CfaAffx.13114.1.S1_at	1.375710E-09	2.960184E-05	1.42	.70	Elsinoe fawcettii hypothetical protein EfHP2 gene; complete cds	44.7	NG_007083	EU414200		
CfaAffx.13129.1.S1_at	1.310170E-02	2.403652E-01	1.16	.86	Bos taurus LAG1 homolog; ceramide synthase 5 (LASS5); mRNA >gi|151556237|gb|BC149597.1| Bos taurus similar to LAG1 homolog; ceramide synthase 5 (S. cerevisiae); mRNA (cDNA clone MGC:159488 IMAGE:8412174);	98.0	AC074032	NM_001102132	LASS5	LAG1 homolog, ceramide synthase 5

					complete cds				
CfaAffx.13134.1.S1_at	4.200340E-03	1.390474E-01	1.25	.80	PREDICTED: Canis familiaris similar to polymerase (RNA) III (DNA directed) polypeptide G (32kD) (LOC609731); mRNA	100.0	BC140282	XM_847057	POLR3G	polymerase (RNA) III (DNA directed) polypeptide G (32kD)
CfaAffx.13146.1.S1_at	3.894570E-03	1.340823E-01	0.8	1.25	PREDICTED: Canis familiaris similar to centrin 3 (LOC488915); mRNA	90.6	AB168852	XM_546032	CETN3	centrin, EF-hand protein, 3 (CDC31 homolog, yeast)
CfaAffx.13153.1.S1_s_at	1.725590E-03	9.022485E-02	1.1	.91	PREDICTED: Macaca mulatta similar to eukaryotic translation initiation factor 4A2 (LOC718869); mRNA	17.9	AC006000	XR_014027	LOC718869	similar to eukaryotic translation initiation factor 4A2
CfaAffx.13155.1.S1_at	2.720780E-03	1.120772E-01	1.15	.87	PREDICTED: Canis familiaris similar to Frizzled 3 precursor (Frizzled-3) (Fz-3) (hFz3); transcript variant 1 (LOC486093); mRNA	96.0	AC011132	XM_543219	FZD3	frizzled homolog 3 (Drosophila)
CfaAffx.13159.1.S1_at	7.430300E-04	5.610538E-02	1.17	.85	Candida glabrata CBS138 hypothetical protein (CAGL0M11682g) partial mRNA	18.3	AC013652	XM_449849	CAGL0M11682g	hypothetical protein
CfaAffx.13190.1.S1_s_at	1.295580E-02	2.398507E-01	0.9	1.11	PREDICTED: Canis familiaris similar to zinc finger homeodomain 4 (LOC487006); mRNA	48.4	NM_024721	XM_848173	ZFHX4	zinc finger homeobox 4
CfaAffx.13191.1.S1_at	5.232830E-04	4.677449E-02	1.19	.84	Homo sapiens cDNA; FLJ96142	33.3	AC138696	AK315167	OSBPL9	oxysterol binding protein-like 9
CfaAffx.13198.1.S1_s_at	2.055250E-02	2.954164E-01	1.1	.91	Homo sapiens mRNA; cDNA DKFZp686O1754 (from clone DKFZp686O1754)	94.0	BX640902	BX640902	FAM169A	family with sequence similarity 169, member A
CfaAffx.13210.1.S1_at	8.984160E-03	2.017118E-01	1.14	.88	NULL	null	AL356104	NULL		
CfaAffx.13214.1.S1_at	1.045910E-05	4.576229E-03	1.26	.79	NULL	null	AC013828	NULL		
CfaAffx.13252.1.S1_at	1.114590E-04	1.903428E-02	1.12	.90	PREDICTED: Canis familiaris similar to Transmembrane 4 L6 family member 4 (Intestine and liver tetraspan membrane protein) (IL-TMP) (LOC611654); mRNA	100.0	NM_004617	XM_849349	TM4SF4	transmembrane 4 L six family member 4

CfaAffx.13301.1.S1_at	4.701190E-04	4.476011E-02	1.14	.88	Bos taurus BCDIN3 domain containing (BCDIN3D); mRNA >gi|88758661|gb|BC113219.1| Bos taurus similar to CG11342-PA; mRNA (cDNA clone MGC:137886 IMAGE:8084270); complete cds	92.7	CU690987	NM_001075216	BCDIN3D	BCDIN3 domain containing
CfaAffx.13327.1.S1_at	2.312930E-03	1.028541E-01	0.86	1.17	PREDICTED: Strongylocentrotus purpuratus hypothetical LOC593637 (LOC593637); partial mRNA	42.9	AE006463	XM_001188679	LOC593637	hypothetical LOC593637
CfaAffx.13377.1.S1_at	1.278120E-02	2.383184E-01	1.13	.88	PREDICTED: Canis familiaris hypothetical LOC485714 (LOC485714); mRNA	99.8	AK093375	XM_542835	LOC485714	hypothetical LOC485714
CfaAffx.1341.1.S1_at	1.465630E-02	2.545334E-01	0.88	1.14	PREDICTED: Canis familiaris similar to mitogen-activated protein kinase kinase kinase 5 (LOC476215); mRNA	100.0	AB384845	XM_533420	MAP3K5	mitogen-activated protein kinase kinase kinase 5
CfaAffx.1342.1.S1_at	1.870960E-03	9.340692E-02	1.11	.90	PREDICTED: Canis familiaris similar to SLC26A10 (LOC481128); mRNA	100.0	AK122981	XM_538249	SLC26A10	solute carrier family 26, member 10
CfaAffx.13451.1.S1_at	1.175850E-07	2.976630E-04	0.84	1.19	Bos taurus NDRG family member 4 (NDRG4); mRNA >gi|111304966|gb|BC120117.1| Bos taurus similar to N-myc downstream regulated gene 4; mRNA (cDNA clone MGC:140660 IMAGE:8272954); complete cds	89.6	AB385436	NM_001075695	NDRG4	NDRG family member 4
CfaAffx.13475.1.S1_s_at	8.580740E-03	1.983202E-01	1.11	.90	PREDICTED: Canis familiaris similar to serine/threonine protein phosphatase with EF-hand motifs 2 isoform a (LOC487812); mRNA	27.7	AL079280	XM_544934	PPEF2	protein phosphatase, EF-hand calcium binding domain 2
CfaAffx.13493.1.S1_at	5.225720E-04	4.677449E-02	1.18	.85	Canis familiaris beta-defensin 108 (CBD108) mRNA; complete cds	100.0	AC011389	DQ011977		
CfaAffx.13557.1.S1_s_at	3.034830E-03	1.186230E-01	0.73	1.36	PREDICTED: Equus caballus similar to Kin17 (LOC100066294); mRNA	63.3	NULL	XM_001499850	LOC100066294	similar to beta amyloid precursor protein
CfaAffx.13558.1.S1_s_at	1.493850E-02	2.565357E-01	1.13	.89	PREDICTED: Canis familiaris similar to autoantigenic hnRNP-associated with lethal yellow; transcript variant 2 (LOC487025); mRNA	88.5	AF495530	XM_855936	RALYL	RALY RNA binding protein-like

CfaAffx.13570.1.S1_at	2.416000E-04	3.058016E-02	1.14	.87	Bos taurus similar to Solute carrier family 7 (cationic amino acid transporter; y+ system); member 12; mRNA (cDNA clone IMAGE:8661685); partial cds	34.3	NULL	BC151820	SLC7A13	solute carrier family 7, (cationic amino acid transporter, y+ system) member 13
CfaAffx.13608.1.S1_at	4.552350E-03	1.442639E-01	0.91	1.10	PREDICTED: Canis familiaris similar to N-myc downstream-regulated gene 3 isoform a; transcript variant 1 (LOC477220); mRNA	100.0	AK128068	XM_534411	NDRG3	NDRG family member 3
CfaAffx.13624.1.S1_at	7.294570E-03	1.819837E-01	1.12	.90	PREDICTED: Canis familiaris similar to muscleblind-like 1 isoform b; transcript variant 9 (LOC477116); mRNA	100.0	NM_207296	XM_861190	MBNL1	muscleblind-like (Drosophila)
CfaAffx.1363.1.S1_at	2.558350E-05	8.198996E-03	1.21	.82	PREDICTED: Canis familiaris similar to PERP; TP53 apoptosis effector (LOC476218); mRNA	100.0	AK314526	XM_533423	PERP	PERP, TP53 apoptosis effector
CfaAffx.13642.1.S1_s_at	4.486620E-03	1.432992E-01	1.12	.89	PREDICTED: Canis familiaris similar to Glycine receptor beta chain precursor (Glycine receptor 58 kDa subunit) (LOC475477); mRNA	99.8	U33267	XM_532701	GLRB	glycine receptor, beta
CfaAffx.13654.1.S1_s_at	1.839720E-02	2.816519E-01	0.87	1.16	PREDICTED: Canis familiaris similar to ubiquitin specific protease 16 isoform a; transcript variant 1 (LOC478398); mRNA	100.0	DQ895610	XM_535575	USP16	ubiquitin specific peptidase 16
CfaAffx.13756.1.S1_at	1.243500E-02	2.355224E-01	1.12	.89	Bos taurus major histocompatibility complex; class II; DY beta (BOLA-DYB); mRNA >gi|37653295|emb|AJ580584.1|BTA580584 Bos taurus mRNA for putative MHC class II antigen (BoLA-DYB gene)	33.9	AL844224	NM_001012679	BOLA-DYB	major histocompatibility complex, class II, DY beta
CfaAffx.13770.1.S1_s_at	4.990520E-03	1.506080E-01	0.83	1.21	PREDICTED: Canis familiaris similar to phosphoinositide-3-kinase; class 2; alpha polypeptide; transcript variant 4 (LOC485399); mRNA	100.0	NM_002645	XM_859865	PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide
CfaAffx.13781.1.S1_at	1.015920E-03	6.695271E-02	1.14	.88	PREDICTED: Canis familiaris similar to solute carrier family 39 (zinc transporter); member 13 (LOC475981); mRNA	54.5	BX647491	XM_533188	SLC39A13	solute carrier family 39 (zinc transporter), member 13
CfaAffx.13790.1.S1_s_at	6.183300E-03	1.691578E-01	0.82	1.22	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L1	98.7	AK315600	XM_535620	MRPL1	mitochondrial ribosomal protein L1

					(LOC478443); mRNA					
CfaAffx.13793.1.S1_at	6.373820E-04	5.125131E-02	1.2	.83	PREDICTED: Macaca mulatta hypothetical protein LOC721956 (LOC721956); mRNA	18.1	AL391114	XR_014682	LOC721956	hypothetical protein LOC721956
CfaAffx.13794.1.S1_at	1.584140E-06	1.585429E-03	1.41	.71	NULL	null	AC027290	NULL		
CfaAffx.13896.1.S1_at	1.316970E-03	7.721499E-02	1.26	.79	PREDICTED: Canis familiaris similar to GMP synthase [glutamine-hydrolyzing] (Glutamine amidotransferase) (GMP synthetase); transcript variant 4 (LOC477123); mRNA	86.7	D87010	XM_861324	GMPS	guanine monphosphate synthetase
CfaAffx.13903.1.S1_a_at	2.415340E-03	1.049012E-01	1.12	.89	null	null	null	null		
CfaAffx.13914.1.S1_at	2.630820E-03	1.101073E-01	1.16	.86	PREDICTED: Equus caballus similar to aldolase A; fructose-bisphosphate; (LOC100049818); mRNA	49.4	AB083610	XM_001487847	LOC100049818	similar to calcium-sensing receptor like 1
CfaAffx.13953.1.S1_s_at	1.734870E-03	9.022485E-02	1.16	.86	PREDICTED: Equus caballus similar to keratin associated protein 15-1 (LOC100065009); mRNA	51.1	AC018931	XM_001495735	LOC100065009	similar to keratin associated protein 15-1
CfaAffx.13958.1.S1_at	6.207920E-04	5.125131E-02	1.13	.88	PREDICTED: Equus caballus similar to keratin associated protein 15-1 (LOC100065009); mRNA	34.2	AP000567	XM_001495735	LOC100065009	similar to keratin associated protein 15-1
CfaAffx.13962.1.S1_at	1.129390E-02	2.247290E-01	1.1	.91	PREDICTED: Mus musculus predicted gene; EG622998 (EG622998); mRNA	18.7	NULL	XM_897455	EG622998	predicted gene, EG622998
CfaAffx.13993.1.S1_at	7.519970E-03	1.843999E-01	1.2	.83	PREDICTED: Canis familiaris similar to Progestin and adipoQ receptor family member III (LOC487820); mRNA	100.0	CU689135	XM_544942	PAQR3	progestin and adipoQ receptor family member III
CfaAffx.14025.1.S1_at	1.328590E-02	2.419572E-01	1.11	.90	PREDICTED: Canis familiaris similar to melanocortin 2 receptor accessory protein isoform alpha (LOC609708); mRNA	100.0	NULL	XM_847024	MRAP	melanocortin 2 receptor accessory protein
CfaAffx.14087.1.S1_at	2.238540E-03	1.015127E-01	1.15	.87	Plasmodium yoelii yoelii str. 17XNL hypothetical protein (PY05801) partial	28.2	AC010902	XM_721225	PY05801	hypothetical protein

					mRNA					
CfaAffx.14103.1.S1_at	3.002360E-04	3.409144E-02	1.18	.84	NULL	null	AC010260	NULL		
CfaAffx.14106.1.S1_at	1.459420E-05	5.473154E-03	1.26	.79	Phlebotomus argentipes 14 kDa salivary protein SP13 mRNA; complete cds	41.1	AL049858	DQ136159		
CfaAffx.14129.1.S1_at	9.335930E-04	6.347105E-02	1.16	.86	PREDICTED: Bos taurus similar to seven transmembrane helix receptor (LOC617415); mRNA	86.4	AC089987	XM_869667	LOC617415	similar to hCG2044647
CfaAffx.14147.1.S1_at	2.378940E-04	3.046955E-02	1.17	.85	PREDICTED: Canis familiaris olfactory receptor family 8 subfamily S (cOR8S16); mRNA	87.6	NULL	XM_846324	cOR8S16	olfactory receptor family 8 subfamily S
CfaAffx.14147.1.S1_x_at	3.168150E-04	3.513952E-02	1.19	.84	PREDICTED: Canis familiaris olfactory receptor family 8 subfamily S (cOR8S16); mRNA	87.6	NULL	XM_846324	cOR8S16	olfactory receptor family 8 subfamily S
CfaAffx.14153.1.S1_at	1.690430E-08	9.093457E-05	1.24	.81	PREDICTED: Canis familiaris similar to olfactory receptor Olr1107 (LOC609127); mRNA	99.8	NULL	XM_846335	LOC609127	similar to olfactory receptor Olr1107
CfaAffx.14175.1.S1_at	4.096350E-03	1.373242E-01	1.13	.89	Nematostella vectensis predicted protein (NEMVEDRAFT_v1g118781) partial mRNA	25.6	NULL	XM_001628754	NEMVEDRAFT_v1g118781	predicted protein
CfaAffx.14176.1.S1_at	7.609620E-03	1.852262E-01	1.12	.89	PREDICTED: Canis familiaris cOR8S9 olfactory receptor family 8 subfamily S-like (cOR8S9); mRNA	97.8	NULL	XM_543699	cOR8S9	cOR8S9 olfactory receptor family 8 subfamily S-like
CfaAffx.14177.1.S1_at	3.150040E-03	1.204995E-01	1.11	.90	PREDICTED: Canis familiaris similar to Progonadoliberin I precursor (LOC608671); mRNA	94.4	M12578	XM_845766	GNRH1	gonadotropin-releasing hormone 1 (luteinizing-releasing hormone)
CfaAffx.14181.1.S1_at	6.840710E-03	1.767452E-01	1.15	.87	NULL	null	AL358976	NULL		
CfaAffx.14182.1.S1_s_at	1.046430E-02	2.158950E-01	0.88	1.14	PREDICTED: Canis familiaris similar to Exocyst complex component Sec15B; transcript variant 3 (LOC483119); mRNA	100.0	NM_015189	XM_861551	EXOC6B	exocyst complex component 6B

CfaAffx.14197.1.S1_at	9.036840E-03	2.017118E-01	1.13	.89	PREDICTED: Canis familiaris similar to CG18675-PA; transcript variant 1 (LOC607697); mRNA	81.1	AK000474	XM_843430	LOC607697	similar to CG18675-PA
CfaAffx.14225.1.S1_at	2.177540E-05	7.378774E-03	1.15	.87	Macaca fascicularis brain cDNA clone: QmoA-11282; similar to human intersectin 2 (ITSN2); transcript variant 2; mRNA; RefSeq: NM_147152.1	17.7	AB173946	AB173946		
CfaAffx.14235.1.S1_at	8.688550E-04	6.149864E-02	1.22	.82	PREDICTED: Canis familiaris similar to Calbindin (Vitamin D-dependent calcium-binding protein; avian-type) (Calbindin D28) (D-28K) (LOC611334); mRNA	55.2	NULL	XM_848991	CALB1	calbindin 1, 28kDa
CfaAffx.1427.1.S1_s_at	1.392340E-02	2.472941E-01	0.9	1.11	PREDICTED: Canis familiaris similar to ubiquitin specific protease 15; transcript variant 1 (LOC474424); mRNA	100.0	NULL	XM_531655	USP15	ubiquitin specific peptidase 15
CfaAffx.14282.1.S1_at	2.090060E-04	2.802048E-02	1.15	.87	Paramecium tetraurelia hypothetical protein (GSPATT00037108001) partial mRNA	22.2	NULL	XM_001435684	GSPATT00037108001	hypothetical protein
CfaAffx.14312.1.S1_s_at	2.053400E-02	2.952491E-01	0.9	1.11	PREDICTED: Canis familiaris similar to exosome component 1; transcript variant 1 (LOC477787); mRNA	100.0	AK313717	XM_534981	EXOSC1	exosome component 1
CfaAffx.14355.1.S1_at	3.369520E-03	1.251141E-01	1.19	.84	Monosiga brevicollis MX1 predicted protein MONBRDRAFT_29488 mRNA; complete cds	20.4	AC080128	XM_001749966	MONBRDRAFT_29488	hypothetical protein
CfaAffx.1436.1.S1_at	1.266380E-03	7.521034E-02	1.14	.88	PREDICTED: Canis familiaris similar to laforin isoform a (LOC484022); mRNA	100.0	AF084535	XM_541139	EPM2A	epilepsy, progressive myoclonus type 2A, Lafora disease (laforin)
CfaAffx.14376.1.S1_at	6.731270E-03	1.757768E-01	1.11	.90	PREDICTED: Canis familiaris similar to tryptophan hydroxylase 1 (LOC611956); mRNA	99.5	BC106740	XM_849675	SERGEF	secretion regulating guanine nucleotide exchange factor
CfaAffx.14408.1.S1_at	1.141220E-02	2.256758E-01	1.2	.83	PREDICTED: Canis familiaris similar to CG15923-PA (LOC487049); mRNA	100.0	BC032835	XM_544178	TMEM67	transmembrane protein 67
CfaAffx.14421.1.S1_at	8.634980E-03	1.989767E-01	0.79	1.26	PREDICTED: Equus caballus similar to C21orf55 protein (LOC100052371); mRNA	89.0	AB173868	XM_001497969	LOC100052371	similar to J domain-containing protein C21orf55
CfaAffx.14435.1.S1_at	1.556380E-	2.616360E-	1.12	.89	PREDICTED: Equus caballus similar to seven transmembrane helix receptor	52.5	NULL	XM_001502392	LOC100072458	similar to olfactory receptor, family

	02	01			(LOC100072458); mRNA					5, subfamily H, member 2
CfaAffx.1444.1.S1_s_at	1.892500E-02	2.859682E-01	0.88	1.13	PREDICTED: Canis familiaris similar to SNF2 histone linker PHD RING helicase; transcript variant 1 (LOC476233); mRNA	99.3	BX648322	XM_533438	LOC476233	similar to SNF2 histone linker PHD RING helicase
CfaAffx.1445.1.S1_s_at	2.648530E-06	2.234892E-03	1.33	.75	Gallus gallus pallidin homolog (mouse) (PLDN); mRNA >gi|53135392|emb|AJ720762.1| Gallus gallus mRNA for hypothetical protein; clone 25a23	47.7	AC091173	NM_001007825	PLDN	pallidin homolog (mouse)
CfaAffx.145.1.S1_at	2.499830E-03	1.064105E-01	1.14	.88	PREDICTED: Canis familiaris similar to Olfactory receptor 2M3 (LOC482235); mRNA	87.6	NULL	XM_844645	LOC482235	similar to Olfactory receptor 2M3
CfaAffx.14521.1.S1_s_at	4.037620E-03	1.364957E-01	0.84	1.19	PREDICTED: Canis familiaris similar to tubulin cofactor a (predicted) (LOC479173); mRNA	100.0	AL451144	XM_536315	TBCA	tubulin folding cofactor A
CfaAffx.14555.1.S1_s_at	3.571000E-03	1.277456E-01	0.88	1.14	PREDICTED: Canis familiaris similar to WD repeat domain 41 (LOC610498); mRNA	98.4	AB170095	XM_848015	WDR41	WD repeat domain 41
CfaAffx.14591.1.S1_at	6.402280E-06	3.548256E-03	1.28	.78	PREDICTED: Pan troglodytes similar to KIAA1429 protein; transcript variant 5 (LOC464288); mRNA	74.6	NM_015496	XM_519860	LOC464288	similar to KIAA1429 protein
CfaAffx.14593.1.S1_at	6.303350E-07	8.684019E-04	1.28	.78	PREDICTED: Canis familiaris similar to chromodomain helicase DNA binding protein 6; transcript variant 1 (LOC477230); mRNA	53.4	NULL	XM_534421	CHD6	chromodomain helicase DNA binding protein 6
CfaAffx.146.1.S1_at	1.429910E-02	2.509697E-01	1.11	.90	PREDICTED: Equus caballus similar to seven transmembrane helix receptor (LOC100064030); mRNA	84.6	BK004500	XM_001504940	LOC100064030	similar to seven transmembrane helix receptor
CfaAffx.1460.1.S1_s_at	1.261440E-03	7.518149E-02	1.12	.89	PREDICTED: Canis familiaris similar to glutamate receptor; metabotropic 1; transcript variant 1 (LOC484024); mRNA	99.5	NM_001114329	XM_541141	GRM1	glutamate receptor, metabotropic 1
CfaAffx.14614.1.S1_s_at	6.594830E-03	1.739023E-01	1.11	.90	PREDICTED: Canis familiaris similar to activin A receptor; type IC (LOC488361); mRNA	100.0	NM_001111033	XM_545483	ACVR1C	activin A receptor, type IC

CfaAffx.1463.1.S1_s_at	5.809320E-05	1.251529E-02	1.17	.86	PREDICTED: Canis familiaris similar to CaLPain family member (clp-2) (LOC484026); mRNA	100.0	AK021951	XM_541143	LOC484026	similar to CaLPain family member (clp-2)
CfaAffx.14694.1.S1_s_at	1.012250E-02	2.132265E-01	1.12	.89	PREDICTED: Canis familiaris similar to triple functional domain (PTPRF interacting) (LOC478610); mRNA	96.3	NM_007118	XM_535785	TRIO	triple functional domain (PTPRF interacting)
CfaAffx.14696.1.S1_at	6.924660E-03	1.781248E-01	1.11	.90	PREDICTED: Canis familiaris similar to Transmembrane protein 45a (Dermal papilla derived protein 7) (LOC478543); mRNA	100.0	NULL	XM_535720	TMEM45A	transmembrane protein 45A
CfaAffx.14723.1.S1_at	9.661550E-05	1.754366E-02	0.74	1.35	PREDICTED: Canis familiaris similar to dpy-19-like 3 (LOC611671); mRNA	100.0	NM_181787	XM_849368	DPY19L4	dpy-19-like 4 (C. elegans)
CfaAffx.14726.1.S1_s_at	2.557530E-04	3.134647E-02	0.8	1.26	PREDICTED: Canis familiaris similar to Olfactomedin-like protein 3 precursor (HNOEL-iso) (hOLF44) (LOC483126); mRNA	100.0	NM_020190	XM_540242	OLFML3	olfactomedin-like 3
CfaAffx.14742.1.S1_s_at	4.437670E-03	1.428212E-01	1.18	.85	PREDICTED: Canis familiaris similar to CG5815-PA; isoform A (LOC476884); mRNA	100.0	BC056261	XM_534086	SPTY2D1	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae)
CfaAffx.1477.1.S1_at	5.535660E-05	1.220385E-02	1.18	.85	null	null	null	null		
CfaAffx.14773.1.S1_at	2.408080E-03	1.049012E-01	1.15	.87	Homo sapiens cDNA FLJ46027 fis; clone SPLEN2024922; highly similar to Homo sapiens TRK-fused gene (TFG)	43.5	AK127920	AK127920	TFG	TRK-fused gene
CfaAffx.14776.1.S1_at	4.729740E-03	1.473373E-01	1.13	.88	PREDICTED: Canis familiaris similar to death associated protein 1b (LOC607792); mRNA	98.5	NM_001017920	XM_844590	DAPL1	death associated protein-like 1
CfaAffx.14777.1.S1_at	3.521850E-03	1.277456E-01	1.12	.89	Homo sapiens cDNA; FLJ17683	36.7	AC063924	AK310641	ANO6	anoctamin 6
CfaAffx.14811.1.S1_at	1.642090E-02	2.683910E-01	0.85	1.17	PREDICTED: Canis familiaris similar to PMS1 protein homolog 1 (DNA mismatch repair protein PMS1); transcript variant 1 (LOC478840); mRNA	100.0	AC008122	XM_536002	PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)

CfaAffx.14825.1.S1_at	1.182560E-03	7.301502E-02	1.16	.86	PREDICTED: Canis familiaris similar to G protein-coupled receptor MRGX2 (LOC485410); mRNA	100.0	NM_054031	XM_542529	MRGPRX2	MAS-related GPR, member X2
CfaAffx.1484.1.S1_at	1.376980E-02	2.460894E-01	0.88	1.14	PREDICTED: Canis familiaris similar to TANK-binding kinase 1; transcript variant 1 (LOC481145); mRNA	100.0	AK002192	XM_538266	TBK1	TANK-binding kinase 1
CfaAffx.14841.1.S1_at	8.090850E-04	5.881583E-02	1.11	.90	PREDICTED: Canis familiaris similar to CG10365-PA; isoform A (LOC487504); mRNA	100.0	CR624884	XM_544628	CHAC1	ChaC, cation transport regulator homolog 1 (E. coli)
CfaAffx.14851.1.S1_at	1.777000E-07	3.396640E-04	1.47	.68	PREDICTED: Canis familiaris matrix metalloproteinase-2 (MMP-2); mRNA	93.2	AP001521	XM_535300	MMP2	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)
CfaAffx.14856.1.S1_at	1.453040E-04	2.233271E-02	1.27	.79	PREDICTED: Nasonia vitripennis similar to GA21542-PA (LOC100117390); mRNA	36.5	AL137786	XM_001601595	LOC100117390	similar to GA21542-PA
CfaAffx.14902.1.S1_s_at	5.816330E-03	1.637055E-01	0.88	1.14	PREDICTED: Canis familiaris similar to 3-hydroxyisobutyryl-Coenzyme A hydrolase isoform 1 (LOC607040); mRNA	100.0	AK313651	XM_843596	HIBCH	3-hydroxyisobutyryl-Coenzyme A hydrolase
CfaAffx.14936.1.S1_at	1.710930E-02	2.741519E-01	1.14	.88	PREDICTED: Canis familiaris similar to kelch-like 8; transcript variant 1 (LOC487847); mRNA	85.9	BX538173	XM_544969	KLHL8	kelch-like 8 (Drosophila)
CfaAffx.14952.1.S1_at	1.616450E-02	2.659171E-01	1.13	.88	PREDICTED: Canis familiaris cOR13P1 olfactory receptor family 13 subfamily P-like (cOR13P1); mRNA	95.9	NULL	XM_545793	cOR13P1	cOR13P1 olfactory receptor family 13 subfamily P-like
CfaAffx.14964.1.S1_s_at	6.636170E-03	1.744579E-01	1.2	.83	PREDICTED: Canis familiaris similar to Coagulation factor XIII A chain precursor (Coagulation factor XIIIa) (Protein-glutamine gamma-glutamyltransferase A chain) (Transglutaminase A chain); transcript variant 1 (LOC478711); mRNA	99.6	AK312735	XM_535876	F13A1	coagulation factor XIII, A1 polypeptide
CfaAffx.14982.1.S1_at	1.008470E-04	1.778968E-02	0.81	1.23	PREDICTED: Canis familiaris similar to Copper homeostasis protein cutC homolog (LOC477793); mRNA	100.0	AK314687	XM_534987	CUTC	cutC copper transporter homolog (E. coli)
CfaAffx.14999.1.S1_at	5.234510E-	1.185617E-	1.18	.85	PREDICTED: Equus caballus similar to olfactory receptor MOR111-1	78.4	NULL	XM_001504709	LOC100051018	similar to olfactory receptor, family

	05	02			(LOC100051018); mRNA					6, subfamily C, member 1
CfaAffx.15003.1.S1_s_at	8.715210E-04	6.158605E-02	1.3	.77	PREDICTED: Bos taurus similar to olfactory receptor GA_x5J8B7W6HFP-2821674-2820736 (LOC526713); mRNA	90.8	NULL	XM_605086	LOC526713	similar to olfactory receptor 769
CfaAffx.15042.1.S1_s_at	2.029270E-03	9.660358E-02	0.66	1.52	PREDICTED: Canis familiaris similar to secreted phosphoprotein 1 (LOC478471); mRNA	99.7	CU675498	XM_535649	SPP1	secreted phosphoprotein 1
CfaAffx.15051.1.S1_at	1.157360E-03	7.176799E-02	1.13	.89	PREDICTED: Equus caballus similar to membrane associated adaptor protein LAX (LOC100053861); mRNA	44.1	AK225331	XM_001488845	LOC100053861	similar to membrane associated adaptor protein LAX
CfaAffx.15175.1.S1_at	1.732800E-03	9.022485E-02	0.85	1.17	PREDICTED: Canis familiaris similar to MORC family CW-type zinc finger 3 (LOC610219); mRNA	100.0	AK292957	XM_847659	MORC3	MORC family CW-type zinc finger 3
CfaAffx.15179.1.S1_x_at	5.076380E-04	4.608903E-02	1.27	.79	PREDICTED: Canis familiaris similar to eukaryotic translation elongation factor 1 alpha 1 (LOC610824); mRNA	73.3	NULL	XM_848924	LOC610824	similar to eukaryotic translation elongation factor 1 alpha 1
CfaAffx.15235.1.S1_at	4.816930E-03	1.481191E-01	1.12	.89	PREDICTED: Canis familiaris similar to WAP four-disulfide core domain protein 8 precursor (Putative protease inhibitor WAP8) (LOC477245); mRNA	100.0	NM_181510	XM_534437	WFDC8	WAP four-disulfide core domain 8
CfaAffx.15250.1.S1_x_at	1.330050E-05	5.192425E-03	0.75	1.34	PREDICTED: Canis familiaris similar to large subunit ribosomal protein L36a; transcript variant 5 (LOC475808); mRNA	99.6	BC070204	XM_852206	LOC475808	similar to large subunit ribosomal protein L36a
CfaAffx.15287.1.S1_at	2.211310E-03	1.010231E-01	1.14	.88	PREDICTED: Homo sapiens similar to PLA2G4B protein (LOC100131005); mRNA	28.6	XM_001723659	XM_001723659	JMJD7	jumonji domain containing 7
CfaAffx.15308.1.S1_at	3.821350E-04	3.946351E-02	1.2	.84	PREDICTED: Canis familiaris similar to Synaptonemal complex protein 2 (SCP-2 protein) (Synaptonemal complex lateral element protein) (LOC609808); mRNA	64.4	NM_001040274	XM_847146	SYCP2L	synaptonemal complex protein 2-like
CfaAffx.15311.1.S1_at	3.045710E-03	1.189402E-01	1.1	.91	PREDICTED: Canis familiaris similar to nucleoplasmin 2; transcript variant 2 (LOC477386); mRNA	70.3	CR603169	XM_844509	NPM2	nucleophosmin/nucleoplasmin, 2

CfaAffx.15321.1.S1_s_at	1.545660E-02	2.609552E-01	1.11	.90	PREDICTED: Canis familiaris similar to Calsequestrin; cardiac muscle isoform precursor (Calsequestrin 2) (LOC483134); mRNA	100.0	NM_001232	XM_540252	CASQ2	calsequestrin 2 (cardiac muscle)
CfaAffx.15328.1.S1_at	3.564370E-04	3.800811E-02	1.24	.81	Homo sapiens mRNA; cDNA DKFZp779O1559 (from clone DKFZp779O1559)	26.4	AC209233	BX537783		
CfaAffx.15362.1.S1_at	4.630980E-07	6.643141E-04	1.42	.71	PREDICTED: Pan troglodytes similar to CPX chromosome region; candidate 1 (LOC735502); mRNA	35.2	AC112481	XM_001134767	LOC735502	similar to CPX chromosome region, candidate 1
CfaAffx.15382.1.S1_at	1.651460E-02	2.695130E-01	0.87	1.15	PREDICTED: Canis familiaris similar to dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A isoform 2; transcript variant 6 (LOC487755); mRNA	81.0	NULL	XM_854194	DYRK1A	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A
CfaAffx.15384.1.S1_s_at	4.035030E-03	1.364957E-01	1.15	.87	PREDICTED: Canis familiaris similar to HoloCentric chromosome binding Protein family member (hcp-6) (LOC489270); mRNA	100.0	NM_015261	XM_546388	NCAPD3	non-SMC condensin II complex, subunit D3
CfaAffx.15411.1.S1_at	2.869910E-03	1.153824E-01	1.1	.91	Mus musculus 7 days neonate cerebellum cDNA; RIKEN full-length enriched library; clone:A730082P15 product:CD9 antigen; full insert sequence	32.8	AC092578	AK080546	Cd9	CD9 antigen
CfaAffx.1543.1.S1_at	4.115630E-03	1.377498E-01	1.18	.85	PREDICTED: Canis familiaris similar to tripartite motif-containing 39 isoform 2; transcript variant 2 (LOC481703); mRNA	100.0	NULL	XM_850566	TRIM39	tripartite motif-containing 39
CfaAffx.15430.1.S1_at	1.238800E-02	2.353460E-01	1.11	.90	PREDICTED: Canis familiaris similar to transcription factor LBX1 (LOC486850); mRNA	40.4	BC069156	XM_543979	LBX1	ladybird homeobox 1
CfaAffx.1547.1.S1_at	1.046490E-02	2.158950E-01	1.13	.89	PREDICTED: Canis familiaris similar to RasGEF domain family; member 1C isoform 1 (LOC481462); mRNA	97.0	NM_175062	XM_538583	RASGEF1C	RasGEF domain family, member 1C
CfaAffx.15479.1.S1_at	3.509980E-05	9.677009E-03	1.17	.86	Homo sapiens solute carrier family 6 (neurotransmitter transporter; glycine); member 5 (SLC6A5); mRNA	85.4	NM_004211	NM_004211	SLC6A5	solute carrier family 6 (neurotransmitter transporter, glycine), member 5

CfaAffx.15487.1.S1_s_at	4.050520E-03	1.367170E-01	0.87	1.15	PREDICTED: Canis familiaris similar to CD83 antigen precursor (Cell surface protein HB15) (B-cell activation protein) (LOC610141); mRNA	100.0	AK290426	XM_847554	CD83	CD83 molecule
CfaAffx.15508.1.S1_at	5.586100E-03	1.594150E-01	1.13	.88	NULL	null	AC114806	NULL		
CfaAffx.15539.1.S1_s_at	5.461860E-03	1.581771E-01	0.87	1.16	PREDICTED: Canis familiaris similar to mucin 19 (LOC609857); mRNA	100.0	AL021528	XM_847204	MUC19	mucin 19, oligomeric
CfaAffx.15558.1.S1_s_at	5.473490E-03	1.584073E-01	0.82	1.22	PREDICTED: Canis familiaris similar to DPCD protein; transcript variant 1 (LOC477800); mRNA	100.0	NM_015448	XM_534994	LOC477800	similar to DPCD protein
CfaAffx.15573.1.S1_at	1.598620E-02	2.649080E-01	1.12	.90	PREDICTED: Canis familiaris similar to neurofascin; transcript variant 9 (LOC488565); mRNA	40.1	NULL	XM_851188	NFASC	neurofascin homolog (chicken)
CfaAffx.15578.1.S1_at	4.285620E-05	1.060852E-02	1.17	.86	PREDICTED: Canis familiaris similar to Nucleoplasmin 3 (LOC477801); mRNA	100.0	CU691104	XM_534995	NPM3	nucleophosmin/nucleoplasmin, 3
CfaAffx.15584.1.S1_s_at	2.383400E-03	1.047144E-01	1.13	.89	PREDICTED: Canis familiaris similar to gamma-aminobutyric acid (GABA) A receptor; gamma 3 (LOC488685); mRNA	54.7	BC029850	XM_545802	LOC488685	similar to gamma-aminobutyric acid (GABA) A receptor, gamma 3
CfaAffx.15627.1.S1_s_at	4.524330E-03	1.440122E-01	0.8	1.25	PREDICTED: Canis familiaris similar to mago-nashi homolog (LOC488369); mRNA	100.0	BC010905	XM_545491	LOC488369	similar to mago-nashi homolog
CfaAffx.15660.1.S1_at	1.019930E-03	6.701174E-02	0.86	1.17	PREDICTED: Canis familiaris similar to CG8379-PA; isoform A; transcript variant 1 (LOC486853); mRNA	100.0	NM_024541	XM_543983	LOC486853	similar to CG8379-PA, isoform A
CfaAffx.15746.1.S1_at	6.361170E-03	1.716319E-01	1.13	.88	PREDICTED: Canis familiaris similar to NUAK family; SNF1-like kinase; 2; transcript variant 3 (LOC488570); mRNA	98.4	CU686593	XM_851442	NUAK2	NUAK family, SNF1-like kinase, 2
CfaAffx.15747.1.S1_at	8.647210E-03	1.990014E-01	1.12	.90	PREDICTED: Canis familiaris similar to Gamma-aminobutyric-acid receptor alpha-5 subunit precursor (GABA(A) receptor) (LOC488688); mRNA	98.7	AK290453	XM_545805	GABRA5	gamma-aminobutyric acid (GABA) A receptor, alpha 5

CfaAffx.15761.1.S1_at	2.237780E-03	1.015127E-01	1.12	.89	PREDICTED: Canis familiaris similar to 60S ribosomal protein L7a (LOC612456); mRNA	45.0	NULL	XM_850185	LOC612456	similar to 60S ribosomal protein L7a
CfaAffx.15770.1.S1_s_at	3.960100E-03	1.348203E-01	0.85	1.18	Canis lupus familiaris cathepsin D (CTSD); mRNA >gi|70561317|emb|AM048627.1| Canis familiaris mRNA for cathepsin D (ctsd gene)	100.0	AK130178	NM_001025621	CTSD	cathepsin D
CfaAffx.15784.1.S1_s_at	4.410320E-03	1.423420E-01	1.14	.88	PREDICTED: Equus caballus hypothetical protein LOC100059010 (LOC100059010); mRNA	43.7	NULL	XM_001491775		
CfaAffx.15798.1.S1_at	2.048850E-03	9.710601E-02	1.16	.86	PREDICTED: Canis familiaris similar to Enigma homolog (Enigma-like PDZ and LIM domains protein); transcript variant 3 (LOC478482); mRNA	73.3	AC010198	XM_856372	PDLIM5	PDZ and LIM domain 5
CfaAffx.15809.1.S1_at	2.016950E-03	9.649705E-02	1.13	.88	PREDICTED: Pan troglodytes similar to rcRPE; transcript variant 2 (LOC450708); mRNA	84.4	NULL	XM_508010	LOC450708	rcRPE
CfaAffx.15828.1.S1_at	2.352070E-04	3.039680E-02	1.32	.76	NULL	null	AC205795	NULL		
CfaAffx.15830.1.S1_s_at	1.194530E-02	2.313528E-01	1.13	.89	PREDICTED: Canis familiaris similar to semaphorin 5A; transcript variant 2 (LOC478622); mRNA	99.8	AB384692	XM_843348	SEMA5A	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A
CfaAffx.15868.1.S1_s_at	6.457270E-07	8.684019E-04	1.2	.84	PREDICTED: Canis familiaris hypothetical LOC478943 (LOC478943); mRNA	69.1	AB049843	XM_536102	MFSD4	major facilitator superfamily domain containing 4
CfaAffx.15882.1.S1_at	1.064670E-02	2.176197E-01	1.14	.88	PREDICTED: Pan troglodytes Down syndrome cell adhesion molecule; transcript variant 2 (DSCAM); mRNA	91.9	NM_001389	XM_001171521	DSCAM	Down syndrome cell adhesion molecule
CfaAffx.15905.1.S1_at	5.005030E-04	4.604700E-02	1.2	.83	PREDICTED: Macaca mulatta similar to mucin 15; transcript variant 2 (LOC700194); mRNA	96.3	CU691285	XM_001091253	LOC700194	similar to mucin 15
CfaAffx.15952.1.S1_s_at	4.997490E-05	1.160270E-02	0.8	1.26	PREDICTED: Canis familiaris similar to NADH-ubiquinone oxidoreductase 18 kDa subunit; mitochondrial precursor (Complex I-18 kDa) (CI-18 kDa) (Complex I-AQDQ)	100.0	NULL	XM_536474	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-

					(CI-AQDQ) (LOC479335); mRNA					coenzyme Q reductase)
CfaAffx.15993.1.S1_at	2.659010E-04	3.170988E-02	0.89	1.13	PREDICTED: Canis familiaris hypothetical LOC487774 (LOC487774); mRNA	100.0	NM_015500	XM_544899	C2CD2	C2 calcium-dependent domain containing 2
CfaAffx.16002.1.S1_at	1.062820E-02	2.175160E-01	0.84	1.19	PREDICTED: Canis familiaris similar to potassium voltage-gated channel; KQT-like subfamily; member 1 isoform 2 (LOC483669); mRNA	100.0	AK290618	XM_540790	KCNQ1	potassium voltage-gated channel, KQT-like subfamily, member 1
CfaAffx.16008.1.S1_at	1.553390E-02	2.613375E-01	0.81	1.23	PREDICTED: Canis familiaris similar to Kinesin family member 18A (LOC485426); mRNA	100.0	NM_031217	XM_542544	KIF18A	kinesin family member 18A
CfaAffx.16017.1.S1_at	4.912960E-03	1.492091E-01	1.14	.87	Homo sapiens Rho GTPase-activating protein; mRNA (cDNA clone IMAGE:5580075); partial cds	97.2	BC054488	BC054488	RICS	Rho GTPase-activating protein
CfaAffx.16027.1.S1_at	6.521100E-03	1.732327E-01	1.21	.83	Mustela vison mRNA for prolactin	88.7	NULL	X63235		
CfaAffx.16045.1.S1_s_at	2.891430E-03	1.157402E-01	0.88	1.13	PREDICTED: Canis familiaris similar to solute carrier family 35; member C2; transcript variant 1 (LOC609863); mRNA	100.0	NULL	XM_847903	SLC35C2	solute carrier family 35, member C2
CfaAffx.16067.1.S1_s_at	9.744010E-03	2.098850E-01	1.14	.88	PREDICTED: Canis familiaris similar to Friend leukemia integration 1 transcription factor (Fli-1 proto-oncogene) (ERGB transcription factor); transcript variant 1 (LOC489286); mRNA	97.4	NULL	XM_546404	FLI1	Friend leukemia virus integration 1
CfaAffx.16077.1.S1_at	1.321150E-05	5.192425E-03	1.22	.82	PREDICTED: Macaca mulatta similar to musashi 1 (LOC699286); mRNA	29.5	AC003982	XM_001087753	LOC699286	similar to musashi 1
CfaAffx.16096.1.S1_at	3.541080E-03	1.277456E-01	1.1	.91	PREDICTED: Canis familiaris similar to Cytochrome P450 17A1 (CYPXVII) (P450-C17) (P450c17) (Steroid 17-alpha-monooxygenase) (Steroid 17-alpha-hydroxylase/17;20 lyase); transcript variant 3 (LOC477807); mRNA	100.0	AY888372	XM_858257	LOC477807	similar to Cytochrome P450 17A1 (CYPXVII) (P450-C17) (P450c17) (Steroid 17-alpha-monooxygenase) (Steroid 17-alpha-hydroxylase/17,20 lyase)
CfaAffx.16165.1.S1_at	2.023050E-03	9.649705E-02	1.18	.85	PREDICTED: Bos taurus similar to cyclin M2 (LOC504632); mRNA	100.0	AK023066	XM_001251265	CNNM2	cyclin M2

CfaAffx.16194.1.S1_at	1.796220E-03	9.174164E-02	0.87	1.15	Canis lupus familiaris trefoil factor 2 (spasmolytic protein 1) (TFF2); mRNA >gi|30267900|gb|AY264843.1| Canis familiaris trefoil factor 2 mRNA; complete cds	88.6	NULL	NM_001002991	TFF2	trefoil factor 2
CfaAffx.16213.1.S1_s_at	1.155780E-02	2.272224E-01	0.89	1.13	PREDICTED: Canis familiaris similar to M-phase phosphoprotein 10 (LOC612775); mRNA	98.5	BC126389	XM_844258	MPHOSPH10	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)
CfaAffx.16249.1.S1_at	1.421830E-02	2.505670E-01	0.9	1.11	PREDICTED: Canis familiaris similar to processing of precursor 5; ribonuclease P/MRP subunit isoform a; transcript variant 1 (LOC477515); mRNA	96.7	NM_015918	XM_534710	POP5	processing of precursor 5, ribonuclease P/MRP subunit (S. cerevisiae)
CfaAffx.16314.1.S1_s_at	2.023120E-03	9.649705E-02	0.81	1.23	PREDICTED: Canis familiaris similar to Geminin (LOC478739); mRNA	97.3	NULL	XM_535906	GMNN	geminin, DNA replication inhibitor
CfaAffx.16333.1.S1_at	1.001740E-02	2.131608E-01	1.13	.88	Homo sapiens alcohol dehydrogenase 5 (class III); chi polypeptide (ADH5) gene; complete cds	63.5	AC019131	AY987960		
CfaAffx.16350.1.S1_s_at	3.033810E-04	3.426772E-02	1.13	.88	PREDICTED: Canis familiaris similar to potassium channel; subfamily T; member 2 (LOC607500); mRNA	100.0	AK309729	XM_844191	KCNT2	potassium channel, subfamily T, member 2
CfaAffx.16366.1.S1_at	2.660100E-03	1.104755E-01	1.16	.86	PREDICTED: Canis familiaris similar to Sodium- and chloride-dependent transporter XTRP2 (Solute carrier family 6 member 18) (LOC478631); mRNA	100.0	NULL	XM_535804	SLC6A18	solute carrier family 6, member 18
CfaAffx.16375.1.S1_at	1.548980E-04	2.324730E-02	1.16	.86	PREDICTED: Canis familiaris similar to solute carrier family 37 member 1 (LOC487780); mRNA	69.2	BC152997	XM_544905	SLC37A1	solute carrier family 37 (glycerol-3-phosphate transporter), member 1
CfaAffx.16414.1.S1_at	8.209750E-03	1.929583E-01	1.1	.91	Homo sapiens hypothetical protein DKFZp547H025; mRNA (cDNA clone MGC:149617 IMAGE:40116809); complete cds	67.2	BC131618	BC131618	DKFZp547H025	hypothetical protein DKFZp547H025
CfaAffx.1642.1.S1_at	7.586400E-03	1.848702E-01	1.16	.87	PREDICTED: Macaca mulatta protein tyrosine phosphatase; receptor type; B; transcript variant 1 (PTPRB); mRNA	87.9	BX647238	XM_001117436	PTPRB	protein tyrosine phosphatase, receptor type, B

CfaAffx.16428.1.S1_at	2.403700E-03	1.049012E-01	0.82	1.21	PREDICTED: Canis familiaris similar to Tyrosyl-tRNA synthetase; cytoplasmic (Tyrosyl--tRNA ligase) (TyrRS); transcript variant 1 (LOC478148); mRNA	100.0	NULL	XM_535324	YARS	tyrosyl-tRNA synthetase
CfaAffx.16430.1.S1_at	6.484670E-03	1.732264E-01	1.14	.88	PREDICTED: Canis familiaris similar to potassium voltage-gated channel; subfamily H; member 7 isoform 1; transcript variant 1 (LOC478768); mRNA	97.0	AF032897	XM_535934	KCNH7	potassium voltage-gated channel, subfamily H (eag-related), member 7
CfaAffx.16446.1.S1_at	1.232450E-02	2.348729E-01	1.11	.90	PREDICTED: Canis familiaris similar to CG7568-PA (LOC477397); mRNA	100.0	NM_178821	XM_534593	WDR69	WD repeat domain 69
CfaAffx.16450.1.S1_at	1.570080E-02	2.626055E-01	1.15	.87	PREDICTED: Canis familiaris similar to leucine rich repeat containing 16 (LOC488249); mRNA	100.0	AK125696	XM_545371	LRRC16A	leucine rich repeat containing 16A
CfaAffx.1649.1.S1_at	2.051650E-03	9.713175E-02	0.87	1.14	Nicotiana benthamiana myosin XI-K mRNA; complete cds	25.0	AC005476	DQ875137		
CfaAffx.16493.1.S1_at	8.317860E-04	5.946195E-02	1.18	.85	PREDICTED: Bos taurus similar to phosphatidylinositol 4-kinase (LOC613348); mRNA	31.3	AP001979	XR_027383		
CfaAffx.16496.1.S1_at	1.444620E-02	2.522842E-01	0.9	1.11	PREDICTED: Canis familiaris similar to zinc finger and BTB domain containing 8 opposite strand; transcript variant 1 (LOC478150); mRNA	100.0	AK289480	XM_535326	ZBTB8OS	zinc finger and BTB domain containing 8 opposite strand
CfaAffx.16575.1.S1_s_at	6.052750E-03	1.675113E-01	0.83	1.21	PREDICTED: Canis familiaris similar to Regulator of G-protein signaling 1 (RGS1) (Early response protein 1R20) (B-cell activation protein BL34); transcript variant 1 (LOC488585); mRNA	98.5	AK315607	XM_545702	RGS1	regulator of G-protein signaling 1
CfaAffx.16584.1.S1_s_at	4.982370E-04	4.601208E-02	1.13	.89	PREDICTED: Canis familiaris similar to axonemal dynein heavy chain 7 (LOC488452); mRNA	60.5	BC029567	XM_545574	DNAH7	dynein, axonemal, heavy chain 7
CfaAffx.16595.1.S1_at	1.792680E-03	9.173363E-02	1.18	.85	PREDICTED: Canis familiaris similar to Growth factor receptor-bound protein 14 (GRB14 adapter protein); transcript variant 3 (LOC478770); mRNA	73.1	AC023781	XM_852507	GRB14	growth factor receptor-bound protein 14

CfaAffx.16606.1.S1_at	6.551810E-03	1.736189E-01	1.1	.91	PREDICTED: Canis familiaris similar to TP53 regulating kinase (p53-related protein kinase) (Nori-2) (LOC611235); mRNA	96.7	AB173977	XM_848873	TP53RK	TP53 regulating kinase
CfaAffx.1661.1.S1_at	1.985850E-03	9.580372E-02	0.82	1.22	PREDICTED: Canis familiaris similar to Ribonuclease UK114 (14.5 kDa translational inhibitor protein) (p14.5) (UK114 antigen homolog); transcript variant 1 (LOC475043); mRNA	100.0	AC110768	XM_532278	HRSP12	heat-responsive protein 12
CfaAffx.1661.1.S1_s_at	7.111290E-04	5.474676E-02	0.82	1.22	PREDICTED: Canis familiaris similar to Ribonuclease UK114 (14.5 kDa translational inhibitor protein) (p14.5) (UK114 antigen homolog); transcript variant 1 (LOC475043); mRNA	100.0	DQ896044	XM_532278	HRSP12	heat-responsive protein 12
CfaAffx.16691.1.S1_s_at	6.311000E-04	5.125131E-02	1.14	.88	PREDICTED: Bos taurus similar to SID1 transmembrane family; member 1 (LOC508259); mRNA	91.0	NM_017699	XM_585013	SIDT1	SID1 transmembrane family, member 1
CfaAffx.16714.1.S1_at	4.548870E-03	1.442599E-01	1.15	.87	PREDICTED: Canis familiaris similar to longevity assurance homolog 2 (LOC607925); mRNA	91.9	CU690003	XM_844788	LASS3	LAG1 homolog, ceramide synthase 3
CfaAffx.1672.1.S1_at	2.029560E-04	2.746607E-02	1.16	.87	PREDICTED: Canis familiaris similar to Corneodesmosin precursor (S protein) (LOC607062); mRNA	99.5	CU689257	XM_843636	CDSN	corneodesmosin
CfaAffx.16740.1.S1_at	7.188620E-03	1.809136E-01	1.19	.84	null	null	null	null		
CfaAffx.16798.1.S1_at	1.799310E-02	2.790268E-01	1.14	.88	PREDICTED: Canis familiaris similar to G protein-coupled receptor 55 (LOC486157); mRNA	100.0	CU689491	XM_543283	GPR55	G protein-coupled receptor 55
CfaAffx.16816.1.S1_at	6.284360E-04	5.125131E-02	1.19	.84	PREDICTED: Canis familiaris similar to System N amino acid transporter 1 (SN1) (N-system amino acid transporter 1) (Solute carrier family 38; member 3) (LOC476617); mRNA	100.0	AK313461	XM_533820	SLC38A3	solute carrier family 38, member 3
CfaAffx.16818.1.S1_at	8.850630E-04	6.193282E-02	1.18	.85	PREDICTED: Canis familiaris similar to queuine tRNA-ribosyltransferase domain containing 1; transcript variant 3	97.8	BC034559	XM_851228	QTRTD1	queuine tRNA-ribosyltransferase domain containing 1

					(LOC487983); mRNA					
CfaAffx.16842.1.S1_at	2.499850E-03	1.064105E-01	1.16	.86	Homo sapiens calpain (CAPN3) and ZFP106 (ZFP106) genes; complete cds	35.5	AF209502	AF209502		
CfaAffx.16861.1.S1_s_at	2.680780E-04	3.186944E-02	1.14	.88	PREDICTED: Canis familiaris similar to KH domain containing; RNA binding; signal transduction associated 1; transcript variant 1 (LOC487316); mRNA	100.0	BC019109	XM_544442	KHDRBS1	KH domain containing, RNA binding, signal transduction associated 1
CfaAffx.16883.1.S1_at	7.151730E-04	5.493728E-02	1.15	.87	PREDICTED: Canis familiaris similar to D(3) dopamine receptor (LOC487984); mRNA	100.0	AC092896	XM_545106	DRD3	dopamine receptor D3
CfaAffx.16890.1.S1_at	9.958150E-04	6.654487E-02	1.1	.91	PREDICTED: Canis familiaris similar to vanilloid receptor-related osmotically activated channel isoform a; transcript variant 1 (LOC486308); mRNA	100.0	BC117426	XM_543434	TRPV4	transient receptor potential cation channel, subfamily V, member 4
CfaAffx.16899.1.S1_at	1.525880E-03	8.389132E-02	1.14	.88	PREDICTED: Canis familiaris hypothetical protein LOC607178 (LOC607178); mRNA	98.7	AK024360	XM_843783	CATSPERB	cation channel, sperm-associated, beta
CfaAffx.1694.1.S1_at	1.828920E-03	9.237978E-02	1.1	.91	PREDICTED: Macaca mulatta potassium voltage-gated channel; delayed-rectifier; subfamily S; member 2 (KCNS2); mRNA	91.4	AP003355	XM_001094800	KCNS2	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 2
CfaAffx.16941.1.S1_s_at	8.165270E-04	5.906785E-02	1.14	.87	NULL	null	AL162573	NULL		
CfaAffx.16973.1.S1_at	1.931580E-05	6.869880E-03	1.22	.82	Mus musculus RAB32; member RAS oncogene family (Rab32); mRNA	29.9	AK078874	NM_026405	Rab32	RAB32, member RAS oncogene family
CfaAffx.16982.1.S1_s_at	3.015390E-03	1.184813E-01	1.12	.89	PREDICTED: Canis familiaris similar to immunoglobulin superfamily; member 11 isoform b (LOC487989); mRNA	100.0	BC034411	XM_845022	IGSF11	immunoglobulin superfamily, member 11
CfaAffx.16995.1.S1_at	2.051990E-02	2.951623E-01	0.88	1.14	PREDICTED: Canis familiaris similar to PTX1 protein; transcript variant 1 (LOC477657); mRNA	95.2	NM_016570	XM_534852	ERGIC2	ERGIC and golgi 2
CfaAffx.1700.1.S1_at	1.157630E-06	1.346449E-03	1.27	.79	Tetrahymena thermophila SB210 hypothetical protein (TTHERM_00653660) partial mRNA	28.9	NULL	XM_001013918	TTHERM_00653660	hypothetical protein

CfaAffx.17008.1.S1_at	1.137230E-02	2.254979E-01	1.12	.89	PREDICTED: Canis familiaris similar to Uroplakin-1b (Uroplakin Ib) (UPIb) (Tetraspanin-20) (Tspan-20) (LOC608131); mRNA	40.6	CU687767	XM_845047	UPK1B	uroplakin 1B
CfaAffx.17071.1.S1_at	1.518180E-03	8.376266E-02	1.1	.91	PREDICTED: Equus caballus similar to mKIAA4091 protein (LOC100051599); mRNA	34.8	NM_001105521	XM_001488141	JAKMIP3	janus kinase and microtubule interacting protein 3
CfaAffx.1714.1.S1_at	2.304700E-03	1.028541E-01	1.15	.87	PREDICTED: Macaca mulatta catenin; alpha 2; transcript variant 4 (CTNNA2); mRNA	30.9	BX537769	XM_001113096	CTNNA2	catenin (cadherin-associated protein), alpha 2
CfaAffx.17154.1.S1_at	9.031260E-03	2.017118E-01	1.11	.90	Canis familiaris tyrosine kinase receptor ron mRNA; partial cds	100.0	NM_002447	AY646195	MST1R	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
CfaAffx.17203.1.S1_s_at	8.230690E-03	1.932053E-01	0.83	1.20	PREDICTED: Canis familiaris similar to small inducible cytokine subfamily E; member 1 (LOC487893); mRNA	100.0	CU680761	XM_545016	SCYE1	small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)
CfaAffx.17206.1.S1_s_at	1.940220E-03	9.497007E-02	1.2	.83	PREDICTED: Canis familiaris similar to PTPRF interacting protein binding protein 1 isoform 1 (LOC486623); mRNA	59.5	AB384585	XM_543749	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)
CfaAffx.17236.1.S1_at	2.457700E-06	2.184509E-03	1.17	.86	PREDICTED: Canis familiaris similar to vesicle-associated calmodulin-binding protein; transcript variant 5 (LOC608098); mRNA	100.0	AK074899	XM_856485	CAMKV	CaM kinase-like vesicle-associated
CfaAffx.17239.1.S1_at	2.223580E-03	1.013684E-01	1.12	.89	PREDICTED: Bos taurus similar to olfactory receptor Olr390 (LOC788749); mRNA	88.3	NULL	XM_001255713	LOC788749	similar to olfactory receptor Olr390
CfaAffx.173.1.S1_s_at	5.855920E-03	1.642140E-01	1.11	.90	PREDICTED: Canis familiaris similar to Olfactory receptor 2T29 (LOC482243); mRNA	95.6	NM_001004696	XM_539362	LOC482243	similar to Olfactory receptor 2T29
CfaAffx.174.1.S1_at	1.626920E-02	2.670271E-01	1.15	.87	PREDICTED: Equus caballus similar to olfactory receptor Olr390 (LOC100065551); mRNA	85.4	NULL	XM_001496106	LOC100065551	similar to olfactory receptor Olr390
CfaAffx.17422.1.S1_s_at	1.716770E-02	2.741519E-01	0.83	1.20	PREDICTED: Canis familiaris similar to SRB7 suppressor of RNA polymerase B homolog; transcript variant 2 (LOC477664); mRNA	100.0	EU446930	XM_847225	MED21	mediator complex subunit 21

CfaAffx.1743.1.S1_at	2.658770E-03	1.104755E-01	1.15	.87	PREDICTED: Canis familiaris similar to olfactory receptor 768 (LOC481173); mRNA	98.3	AC122685	XM_538294	LOC481173	similar to olfactory receptor 768
CfaAffx.1745.1.S1_s_at	3.014470E-04	3.413887E-02	1.21	.83	PREDICTED: Canis familiaris similar to olfactory receptor 745 (LOC491358); mRNA	98.5	NULL	XM_548479	LOC491358	similar to olfactory receptor 745
CfaAffx.17499.1.S1_x_at	1.217750E-02	2.337430E-01	0.86	1.16	PREDICTED: Canis familiaris similar to ribosomal protein S15a; transcript variant 8 (LOC480791); mRNA	97.2	NULL	XM_857066	LOC480791	similar to ribosomal protein S15a
CfaAffx.175.1.S1_s_at	1.802910E-03	9.182039E-02	1.14	.87	null	null	null	null		
CfaAffx.17529.1.S1_s_at	1.168280E-02	2.289478E-01	1.11	.90	PREDICTED: Canis familiaris similar to Lysosomal-associated multitransmembrane protein (Retinoic acid-inducible E3 protein) (HA1520) (LOC487324); mRNA	99.1	AB383742	XM_544450	LAPTM5	lysosomal multispanning membrane protein 5
CfaAffx.17550.1.S1_at	5.103340E-03	1.525288E-01	1.12	.90	Homo sapiens gene for seven transmembrane helix receptor; complete cds; isolate:CBRC7TM_389	88.2	AB065826	AB065826		
CfaAffx.17557.1.S1_s_at	4.461170E-03	1.428212E-01	0.86	1.16	PREDICTED: Canis familiaris similar to CG3493-PA (LOC480462); mRNA	100.0	BC029524	XM_537580	CCDC46	coiled-coil domain containing 46
CfaAffx.17562.1.S1_s_at	1.444450E-02	2.522842E-01	0.9	1.12	PREDICTED: Bos taurus similar to Coiled-coil domain containing 46 (LOC615722); mRNA	94.9	NM_001037325	XM_867598	LOC615722	similar to coiled-coil domain containing 46
CfaAffx.17583.1.S1_at	8.549750E-05	1.624452E-02	1.21	.83	PREDICTED: Canis familiaris cOR8B15 olfactory receptor family 8 subfamily B-like (cOR8B15); mRNA	73.3	NG_002156	XM_847337	cOR8B15	cOR8B15 olfactory receptor family 8 subfamily B-like
CfaAffx.176.1.S1_at	6.704480E-03	1.753965E-01	1.11	.90	PREDICTED: Canis familiaris cOR8T2 olfactory receptor family 8 subfamily T-like (cOR8T2); mRNA	100.0	NULL	XM_846493	cOR8T2	cOR8T2 olfactory receptor family 8 subfamily T-like
CfaAffx.17612.1.S1_s_at	1.018910E-03	6.701174E-02	1.17	.86	C.familiaris mRNA for TPCR79 protein	100.0	AB065946	X89665	cOR8G8P	cOR8G8P olfactory receptor family 8 subfamily G pseudogene
CfaAffx.17616.1.S1_at	2.043700E-02	2.949586E-01	1.11	.90	PREDICTED: Canis familiaris similar to olfactory receptor 973 (LOC610043); mRNA	100.0	AB065943	XM_536539	LOC610043	similar to olfactory receptor 973

CfaAffx.17622.1.S1_at	1.195060E-04	1.993388E-02	1.13	.88	PREDICTED: Canis familiaris similar to olfactory receptor 967 (LOC610052); mRNA	100.0	BK004711	XM_847442	LOC610052	similar to olfactory receptor 967
CfaAffx.17642.1.S1_at	1.311700E-04	2.104364E-02	1.17	.85	White spot syndrome virus small subunit of ribonucleotide reductase gene; partial cds; large subunit of ribonucleotide reductase (RR1) gene; complete cds; and unknown genes	35.2	AC117489	AF099142		
CfaAffx.17689.1.S1_at	9.805480E-06	4.489137E-03	1.21	.83	NULL	null	AC005383	NULL		
CfaAffx.17695.1.S1_at	1.074800E-03	6.913904E-02	1.17	.86	PREDICTED: Canis familiaris similar to CG18659-PA; isoform A (LOC490259); mRNA	100.0	AK091207	XM_547378	DENND1B	DENN/MADD domain containing 1B
CfaAffx.177.1.S1_at	6.757670E-08	2.077259E-04	1.38	.73	PREDICTED: Equus caballus similar to seven transmembrane helix receptor (LOC100072447); mRNA	90.5	AL359218	XM_001502381	LOC100072447	similar to Olfactory receptor 4K1
CfaAffx.1771.1.S1_at	1.277530E-03	7.562380E-02	1.1	.91	full-length cDNA clone CS0DF027YD19 of Fetal brain of Homo sapiens (human)	27.9	NM_001080420	CR625313	SHANK3	SH3 and multiple ankyrin repeat domains 3
CfaAffx.17756.1.S1_s_at	2.046340E-02	2.949843E-01	0.87	1.15	PREDICTED: Canis familiaris similar to Protein KIAA1404 (LOC477260); mRNA	100.0	AB384600	XM_534452	ZNFX1	zinc finger, NFX1-type containing 1
CfaAffx.17758.1.S1_at	1.062940E-02	2.175160E-01	1.11	.90	PREDICTED: Canis familiaris similar to olfactory receptor 979 (LOC489340); mRNA	98.1	NULL	XM_847529	LOC489340	similar to olfactory receptor 979
CfaAffx.17788.1.S1_at	1.936150E-03	9.490002E-02	1.16	.86	PREDICTED: Equus caballus similar to seven transmembrane helix receptor (LOC100071802); mRNA	88.4	BK004315	XM_001501659	LOC100071802	similar to Olfactory receptor 6T1
CfaAffx.1779.1.S1_at	7.128770E-03	1.804793E-01	1.21	.82	null	null	null	null		
CfaAffx.17867.1.S1_at	1.982750E-03	9.580372E-02	1.15	.87	PREDICTED: Canis familiaris similar to Olfactory receptor 10T2 (LOC610659); mRNA	100.0	BC157047	XM_848198	LOC610659	similar to Olfactory receptor 10T2
CfaAffx.1791.1.S1_s_at	4.639670E-03	1.456945E-01	0.88	1.14	PREDICTED: Canis familiaris similar to K11G12.6 (LOC481188); mRNA	100.0	CU013374	XM_843334	LMF2	lipase maturation factor 2

CfaAffx.17923.1.S1_at	2.658250E-03	1.104755E-01	0.88	1.13	PREDICTED: Canis familiaris similar to germinal histone H4 gene (LOC483166); mRNA	100.0	NULL	XM_540284	LOC483166	similar to germinal histone H4 gene
CfaAffx.18048.1.S1_at	1.867710E-03	9.335296E-02	1.23	.81	NULL	null	AC113169	NULL		
CfaAffx.18048.1.S1_s_at	1.663460E-02	2.707754E-01	0.85	1.18	PREDICTED: Canis familiaris similar to Glutamyl aminopeptidase (EAP) (Aminopeptidase A) (APA) (Differentiation antigen gp160) (LOC478517); mRNA	100.0	AK313412	XM_535696	ENPEP	glutamyl aminopeptidase (aminopeptidase A)
CfaAffx.18072.1.S1_at	7.106690E-03	1.804345E-01	1.17	.86	NULL	null	AC069539	NULL		
CfaAffx.18087.1.S1_at	5.666850E-04	4.897046E-02	1.21	.83	Homo sapiens glutamate receptor; metabotropic 8 (GRM8) gene; complete cds	54.3	EU368948	EU368948		
CfaAffx.18126.1.S1_at	1.124840E-02	2.242125E-01	1.1	.91	PREDICTED: Canis familiaris similar to dehydrogenase/reductase member 2 (LOC490617); mRNA	100.0	AK017274	XM_547739	LOC490617	similar to dehydrogenase/reductase member 2
CfaAffx.18132.1.S1_at	1.017460E-02	2.136964E-01	0.87	1.15	PREDICTED: Canis familiaris similar to alpha-kinase 1 (LOC487906); mRNA	84.0	AK026715	XM_545029	ALPK1	alpha-kinase 1
CfaAffx.18147.1.S1_at	9.064910E-03	2.021287E-01	1.12	.89	PREDICTED: Canis familiaris similar to zinc finger protein Cezanne (LOC483178); mRNA	98.0	EU446827	XM_540296	OTUD7B	OTU domain containing 7B
CfaAffx.18174.1.S1_at	1.420490E-04	2.206888E-02	1.18	.85	Aspergillus clavatus NRRL 1 ribosome biogenesis (Nop4); putative (ACLA_045570); partial mRNA	50.0	AC108044	XM_001271517	ACLA_045570	ribosome biogenesis (Nop4), putative
CfaAffx.1818.1.S1_at	1.175510E-02	2.293204E-01	0.84	1.19	PREDICTED: Bos taurus hypothetical LOC614801; transcript variant 2 (LOC614801); mRNA	88.6	AP001107	XM_866432		
CfaAffx.18193.1.S1_at	6.894550E-03	1.777753E-01	0.82	1.23	NULL	null	AL591662	NULL		
CfaAffx.18216.1.S1_at	8.853370E-03	2.010117E-01	1.19	.84	PREDICTED: Canis familiaris similar to CG12058-PA (LOC478519); mRNA	36.7	AC106864	XM_535698	LARP7	La ribonucleoprotein domain family, member 7

CfaAffx.18235.1.S1_at	6.079900E-03	1.680466E-01	0.87	1.14	PREDICTED: Canis familiaris similar to mast cell antigen 32 (LOC480473); mRNA	99.5	NM_001085423	XM_537592	LOC480473	similar to mast cell antigen 32
CfaAffx.18252.1.S1_s_at	2.180040E-03	1.003931E-01	1.12	.90	PREDICTED: Canis familiaris similar to immunoglobulin superfamily; member 4B (LOC610435); mRNA	56.9	AK289541	XM_847944	CADM3	cell adhesion molecule 3
CfaAffx.18285.1.S1_at	1.218810E-03	7.387534E-02	1.13	.88	PREDICTED: Canis familiaris similar to olfactory receptor Olr1582 (LOC488626); mRNA	90.7	NULL	XM_847793	LOC488626	similar to olfactory receptor Olr1582
CfaAffx.18351.1.S1_s_at	8.319780E-03	1.945649E-01	1.11	.90	PREDICTED: Canis familiaris similar to glycoprotein M6B isoform 2 (LOC480842); mRNA	83.9	NULL	XM_537959	GPM6B	glycoprotein M6B
CfaAffx.18379.1.S1_s_at	7.510140E-03	1.842639E-01	1.12	.89	PREDICTED: Canis familiaris similar to Pancreatic lipase related protein 2 precursor (Secretory glycoprotein GP-3) (LOC486903); mRNA	99.8	NM_005396	XM_544033	PNLIPRP2	pancreatic lipase-related protein 2
CfaAffx.18424.1.S1_at	3.318410E-03	1.239069E-01	1.12	.89	PREDICTED: Equus caballus hypothetical protein LOC100068340 (LOC100068340); mRNA	89.3	AC007671	XM_001498195	LOC100068340	hypothetical protein LOC100068340
CfaAffx.18441.1.S1_at	3.292420E-03	1.234227E-01	1.12	.89	PREDICTED: Canis familiaris similar to CAAX prenyl protease 2 (Prenyl protein-specific endoprotease 2) (Farnesylated-proteins converting enzyme 2) (FACE-2) (hRCE1) (LOC483705); mRNA	97.6	NM_005133	XM_540826	RCE1	RCE1 homolog, prenyl protein peptidase (S. cerevisiae)
CfaAffx.1845.1.S1_at	7.237090E-04	5.531939E-02	1.24	.81	PREDICTED: Canis familiaris similar to MEGF10 protein (LOC474665); mRNA	67.0	AK148084	XM_531893	MEGF10	multiple EGF-like-domains 10
CfaAffx.18451.1.S1_at	1.319660E-02	2.410015E-01	1.11	.90	Brassica rapa BcABH mRNA for putative peptidyl-prolyl cis-trans isomerase; complete cds	25.3	AC116630	AB300316		
CfaAffx.18468.1.S1_at	9.499080E-03	2.074038E-01	0.88	1.14	PREDICTED: Canis familiaris similar to CG15881-PA; isoform A (LOC478583); mRNA	100.0	XM_001133823	XM_535759	CCDC58	coiled-coil domain containing 58
CfaAffx.18486.1.S1_at	4.806110E-03	1.480925E-01	1.13	.89	NULL	null	AP001929	NULL		

CfaAffx.18494.1.S1_at	1.338710E-02	2.424722E-01	0.89	1.13	PREDICTED: Bos taurus hypothetical LOC617456 (LOC617456); mRNA	14.7	CU674945	XM_869720	HJURP	Holliday junction recognition protein
CfaAffx.18500.1.S1_at	7.936460E-03	1.894628E-01	0.82	1.22	PREDICTED: Canis familiaris similar to Cg10671 like (LOC608292); mRNA	100.0	BC139911	XM_845267	LOC608292	similar to Cg10671 like
CfaAffx.18534.1.S1_at	1.037190E-02	2.153015E-01	1.11	.90	PREDICTED: Bos taurus similar to zinc finger protein EZNF; transcript variant 1 (LOC524106); mRNA	67.9	XR_041201	XM_602426	ZNF354A	zinc finger protein 354A
CfaAffx.18538.1.S1_at	3.300030E-03	1.236003E-01	1.17	.85	PREDICTED: Canis familiaris similar to phosphatidylinositol N-acetylglucosaminyltransferase subunit A isoform 1 (LOC491748); mRNA	100.0	D11466	XM_548868	PIGA	phosphatidylinositol glycan anchor biosynthesis, class A
CfaAffx.18583.1.S1_at	2.166750E-05	7.378774E-03	1.22	.82	PREDICTED: Macaca mulatta hypothetical protein LOC706163; transcript variant 1 (LOC706163); mRNA	92.0	NM_174926	XM_001106743	LOC706163	hypothetical protein LOC706163
CfaAffx.18617.1.S1_at	1.281340E-02	2.387120E-01	1.12	.89	NULL	null	AC097625	NULL		
CfaAffx.18632.1.S1_s_at	2.616010E-03	1.098341E-01	0.79	1.27	PREDICTED: Canis familiaris similar to ATP-binding cassette; sub-family B (MDR/TAP); member 11 (LOC488390); mRNA	100.0	NM_003742	XM_545512	ABCB11	ATP-binding cassette, sub-family B (MDR/TAP), member 11
CfaAffx.18644.1.S1_s_at	4.383390E-03	1.417274E-01	0.8	1.25	PREDICTED: Canis familiaris hypothetical LOC477835 (LOC477835); mRNA	96.8	CU692803	XM_535027	LOC477835	hypothetical LOC477835
CfaAffx.1865.1.S1_at	2.415640E-03	1.049012E-01	0.9	1.11	PREDICTED: Canis familiaris similar to Ubiquitin--protein ligase EDD (Hyperplastic discs protein homolog) (100 kDa protein); transcript variant 3 (LOC475055); mRNA	98.5	NM_015902	XM_853090	UBR5	ubiquitin protein ligase E3 component n-recognin 5
CfaAffx.18679.1.S1_at	9.852980E-03	2.111668E-01	0.82	1.22	PREDICTED: Canis familiaris similar to syntaxin 12 (LOC478168); mRNA	100.0	CU692349	XM_535342	STX12	syntaxin 12
CfaAffx.18684.1.S1_s_at	1.078590E-02	2.183348E-01	1.12	.89	PREDICTED: Pan troglodytes synaptotagmin XIV; transcript variant 2 (SYT14); mRNA	96.7	AJ617626	XM_001168997	SYT14	synaptotagmin XIV
CfaAffx.18693.1.S1_at	1.212430E-	2.334538E-	1.11	.90	PREDICTED: Strongylocentrotus purpuratus similar to metal response element binding transcription factor 2 (LOC590080); partial	12.8	NULL	XM_001201814	LOC590080	similar to metal response element

	02	01			mRNA					binding transcription factor 2
CfaAffx.18732.1.S1_at	1.784210E-03	9.151785E-02	1.11	.90	PREDICTED: Canis familiaris similar to membrane frizzled-related protein; transcript variant 1 (LOC489366); mRNA	99.8	BC036675	XM_546484	MFRP	membrane frizzled-related protein
CfaAffx.1875.1.S1_at	8.640690E-03	1.989767E-01	0.9	1.11	PREDICTED: Canis familiaris similar to 60S ribosomal protein L29 (P23) (LOC481990); mRNA	100.0	XM_001721013	XM_539111	LOC481990	similar to 60S ribosomal protein L29 (P23)
CfaAffx.18761.1.S1_s_at	5.165000E-03	1.529140E-01	0.87	1.15	Canis lupus familiaris cathepsin S (CTSS); mRNA >gi|27497537|gb|AY156692.1| Canis familiaris cathepsin S preproprotein (CTSS) mRNA; complete cds	99.8	AK314482	NM_001002938	CTSS	cathepsin S
CfaAffx.18765.1.S1_at	1.907370E-04	2.616405E-02	1.16	.86	NULL	null	AC114797	NULL		
CfaAffx.18766.1.S1_at	1.768170E-02	2.769039E-01	1.1	.91	Lagopus lagopus CD9 protein (CD9) mRNA; partial cds	16.1	AC037459	EF575646		
CfaAffx.1882.1.S1_at	1.751670E-02	2.755420E-01	0.88	1.13	Canis lupus familiaris HSP70 gene for heat shock protein 70; partial cds	80.6	NULL	AB013075		
CfaAffx.1893.1.S1_at	5.953170E-03	1.656074E-01	1.12	.89	Homo sapiens synaptojanin 2A mRNA; complete cds	92.3	AY152396	AY152396	SYNJ2	synaptojanin 2
CfaAffx.18940.1.S1_s_at	3.647590E-03	1.293032E-01	0.8	1.25	PREDICTED: Canis familiaris similar to amyotrophic lateral sclerosis 2 (juvenile) chromosome region; candidate 12 (LOC488474); mRNA	82.8	BC031603	XM_545595	LOC488474	similar to amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 12
CfaAffx.19000.1.S1_at	1.171370E-04	1.976859E-02	1.13	.89	Canis lupus familiaris collagen; type VI; alpha 3 (COL6A3); mRNA	99.0	NM_004369	NM_001103215	COL6A3	collagen, type VI, alpha 3
CfaAffx.19027.1.S1_at	1.004930E-04	1.778968E-02	1.17	.85	Homo sapiens soluble 29kDa NSF attachment protein (SNAP29) gene; complete cds	22.1	AC099314	AF278704		
CfaAffx.19048.1.S1_s_at	4.688980E-03	1.466187E-01	1.15	.87	PREDICTED: Canis familiaris similar to solute carrier family 7 (cationic amino acid transporter; y+ system); member 3	71.6	CU689761	XM_543630	LOC486504	similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 3

					(LOC486504); mRNA					
CfaAffx.19050.1.S1_s_at	1.385310E-03	7.987515E-02	1.13	.88	PREDICTED: Canis familiaris similar to solute carrier family 7 (cationic amino acid transporter; y+ system); member 3 (LOC486643); mRNA	48.1	NULL	XM_543770	LOC486643	similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 3
CfaAffx.19052.1.S1_at	9.235860E-03	2.040214E-01	0.9	1.11	PREDICTED: Canis familiaris similar to G patch domain containing protein 3 (LOC487350); mRNA	100.0	AK308100	XM_544476	GPATCH3	G patch domain containing 3
CfaAffx.19053.1.S1_s_at	1.595850E-03	8.649547E-02	0.85	1.18	PREDICTED: Canis familiaris similar to Protein C10orf70 (LOC479212); mRNA	100.0	AK312017	XM_536355	CISD1	CDGSH iron sulfur domain 1
CfaAffx.19055.1.S1_at	6.755700E-03	1.760804E-01	1.25	.80	Dictyostelium discoideum AX4 hypothetical protein (empA) mRNA; complete cds	15.7	AC007556	XM_631868	empA	hypothetical protein
CfaAffx.19061.1.S1_s_at	1.882980E-02	2.851027E-01	0.83	1.21	PREDICTED: Canis familiaris similar to Cytochrome c oxidase polypeptide VIIc; mitochondrial precursor (LOC609990); mRNA	100.0	X16560	XM_847363	LOC609990	similar to Cytochrome c oxidase polypeptide VIIc, mitochondrial precursor
CfaAffx.19069.1.S1_s_at	4.588010E-04	4.397439E-02	0.81	1.24	PREDICTED: Canis familiaris similar to proteasome 26S ATPase subunit 6 (LOC478522); mRNA	100.0	AK313670	XM_535701	PSMC6	proteasome (prosome, macropain) 26S subunit, ATPase, 6
CfaAffx.19087.1.S1_at	7.907990E-05	1.542382E-02	1.25	.80	Xenopus laevis African clawed frog L-myc oncogene (xL-myc1) (xL-myc1); mRNA >gi|54673679|gb|BC084925.1| Xenopus laevis African clawed frog L-myc oncogene (xL-myc1); mRNA (cDNA clone MGC:81524 IMAGE:6862458); complete cds	62.9	AL135785	NM_001087871	xL-myc1	African clawed frog L-myc oncogene (xL-myc1)
CfaAffx.1910.1.S1_at	2.338890E-06	2.171958E-03	1.21	.83	PREDICTED: Equus caballus hypothetical protein LOC100056389 (LOC100056389); mRNA	62.5	NM_030780	XM_001494337	LOC100056389	hypothetical protein LOC100056389
CfaAffx.19130.1.S1_at	9.750710E-05	1.755740E-02	1.13	.88	PREDICTED: Canis familiaris cOR51X2 olfactory receptor family 51 subfamily X-like; transcript variant 1 (cOR51X2); mRNA	100.0	NULL	XM_548754	cOR51X2	cOR51X2 olfactory receptor family 51 subfamily X-like
CfaAffx.19132.1.S1_at	8.979480E-03	2.017118E-01	1.12	.89	Sus scrofa uroplakin II gene; complete cds	32.5	AC110926	AY044189		

CfaAffx.19145.1.S1_at	1.110510E-02	2.223862E-01	1.13	.88	PREDICTED: Canis familiaris similar to Y55F3AM.9 (LOC483188); mRNA	100.0	CU689329	XM_540306	LOC483188	similar to Y55F3AM.9
CfaAffx.19168.1.S1_at	8.825330E-04	6.185636E-02	1.11	.90	PREDICTED: Canis familiaris cOR52X3 olfactory receptor family 52 subfamily X-like (cOR52X3); mRNA	84.0	NULL	XM_548762	cOR52X3	cOR52X3 olfactory receptor family 52 subfamily X-like
CfaAffx.19171.1.S1_at	1.709810E-02	2.741493E-01	0.9	1.11	PREDICTED: Canis familiaris similar to B0432.8 (LOC490284); mRNA	100.0	NM_001042553	XM_547404	TATDN3	TatD DNase domain containing 3
CfaAffx.19206.1.S1_at	2.464420E-03	1.059811E-01	0.87	1.15	Zea mays putative zinc finger protein (Z438D03.1); unknown (Z438D03.5); epsilon-COP (Z438D03.6); putative kinase (Z438D03.7); unknown (Z438D03.25); and C1-B73 (Z438D03.27) genes; complete cds	16.5	NULL	AY530950		
CfaAffx.19209.1.S1_s_at	1.023930E-02	2.146363E-01	0.8	1.25	PREDICTED: Canis familiaris similar to zinc responsive protein ZD7; transcript variant 1 (LOC476008); mRNA	73.5	AK095158	XM_533216	RBM4B	RNA binding motif protein 4B
CfaAffx.19215.1.S1_s_at	1.723640E-04	2.495501E-02	0.83	1.20	PREDICTED: Canis familiaris similar to peptidyl-prolyl isomerase G (cyclophilin G); transcript variant 3 (LOC607519); mRNA	45.1	NM_004792	XM_854236	PPIG	peptidylprolyl isomerase G (cyclophilin G)
CfaAffx.1922.1.S1_at	1.753900E-04	2.499308E-02	1.15	.87	Oryza sativa Japonica Group cDNA clone:J013000G15; full insert sequence	38.0	NULL	AK064847		
CfaAffx.19241.1.S1_at	3.063240E-04	3.432983E-02	1.17	.85	PREDICTED: Canis familiaris similar to amyotrophic lateral sclerosis 2 (juvenile) chromosome region; candidate 7 (LOC478873); mRNA	85.1	AK310050	XM_536033	PFTK2	PFTAIRE protein kinase 2
CfaAffx.19252.1.S1_at	9.281410E-04	6.330039E-02	1.21	.82	PREDICTED: Canis familiaris cOR52E13 olfactory receptor family 52 subfamily E-like (cOR52E13); mRNA	95.4	NULL	XM_548769	cOR52E13	cOR52E13 olfactory receptor family 52 subfamily E-like
CfaAffx.19281.1.S1_at	2.572010E-05	8.198996E-03	1.18	.85	Homo sapiens DLNB11 mRNA; complete cds	63.6	AB094091	AB094091	BCL9L	B-cell CLL/lymphoma 9-like
CfaAffx.19291.1.S1_at	3.475270E-03	1.273920E-01	0.87	1.14	PREDICTED: Canis familiaris similar to Cathepsin F precursor (CATSF) (LOC476010); mRNA	100.0	BC036451	XM_533219	CTSF	cathepsin F

CfaAffx.19299.1.S1_at	3.819950E-04	3.946351E-02	1.12	.89	PREDICTED: Canis familiaris similar to solute carrier family 16 (monocarboxylic acid transporters); member 9 (LOC488992); mRNA	100.0	BC130567	XM_546110	SLC16A9	solute carrier family 16, member 9 (monocarboxylic acid transporter 9)
CfaAffx.19355.1.S1_at	3.423210E-03	1.264531E-01	1.13	.88	PREDICTED: Bos taurus similar to olfactory receptor Olr87 (LOC788640); mRNA	86.4	NULL	XM_001255638	LOC788640	similar to olfactory receptor Olr87
CfaAffx.19359.1.S1_x_at	4.884960E-04	4.547684E-02	1.17	.85	PREDICTED: Canis familiaris similar to S100 calcium-binding protein A10 (LOC475851); mRNA	93.2	AK291073	XM_533060	S100A10	S100 calcium binding protein A10
CfaAffx.19365.1.S1_at	1.198110E-03	7.311141E-02	1.12	.90	PREDICTED: Canis familiaris cOR52E17 olfactory receptor family 52 subfamily E-like (cOR52E17); mRNA	96.8	NULL	XM_548771	cOR52E17	cOR52E17 olfactory receptor family 52 subfamily E-like
CfaAffx.1938.1.S1_at	2.487300E-06	2.184509E-03	1.34	.75	NULL	null	AC005510	NULL		
CfaAffx.19388.1.S1_at	8.117650E-03	1.916905E-01	1.14	.87	Paramecium tetraurelia hypothetical protein (GSPATT00030273001) partial mRNA	47.5	NULL	XM_001427000	GSPATT00030273001	hypothetical protein
CfaAffx.19408.1.S1_at	1.353090E-03	7.879598E-02	1.13	.88	Homo sapiens integrin; beta 5 (ITGB5) gene; complete cds	41.4	AC022336	EU332848		
CfaAffx.19475.1.S1_at	3.408250E-04	3.703890E-02	1.22	.82	PREDICTED: Canis familiaris similar to pleckstrin homology-like domain; family B; member 1; transcript variant 1 (LOC489381); mRNA	100.0	AB383931	XM_546499	PHLDB1	pleckstrin homology-like domain, family B, member 1
CfaAffx.19510.1.S1_at	9.278790E-05	1.706465E-02	1.17	.86	PREDICTED: Equus caballus similar to seven transmembrane helix receptor (LOC100067684); mRNA	86.2	AB065525	XM_001497654	LOC100067684	similar to seven transmembrane helix receptor
CfaAffx.19536.1.S1_at	6.591060E-03	1.739023E-01	1.1	.91	PREDICTED: Canis familiaris similar to Importin alpha-2 subunit (Karyopherin alpha-2 subunit) (SRP1-alpha) (RAG cohort protein 1); transcript variant 6 (LOC480469); mRNA	92.3	NULL	XM_857043	LOC480469	similar to Importin alpha-2 subunit (Karyopherin alpha-2 subunit) (SRP1-alpha) (RAG cohort protein 1)
CfaAffx.19544.1.S1_s_at	6.962540E-03	1.785655E-01	0.85	1.17	PREDICTED: Canis familiaris similar to PHD finger protein 7 (predicted) (LOC490639); mRNA	100.0	AB168872	XM_547761	LOC490639	similar to PHD finger protein 7 (predicted)

CfaAffx.19561.1.S1_s_at	1.915330E-02	2.875239E-01	1.1	.91	PREDICTED: Canis familiaris cOR51H4 olfactory receptor family 51 subfamily H-like (cOR51H4); mRNA	99.6	BK004773	XM_548782	cOR51H4	cOR51H4 olfactory receptor family 51 subfamily H-like
CfaAffx.19562.1.S1_x_at	2.120420E-03	9.907956E-02	1.14	.88	PREDICTED: Canis familiaris similar to olfactory receptor Olr1347 (LOC608416); mRNA	96.2	NULL	XM_534623	LOC608416	similar to olfactory receptor Olr1347
CfaAffx.19565.1.S1_at	4.037350E-06	2.555108E-03	1.32	.76	Canis familiaris isolate cOR9S20 olfactory receptor family 9 subfamily S gene; partial cds	100.0	AK090280	AY308935		
CfaAffx.19565.1.S1_x_at	1.835400E-04	2.575784E-02	1.2	.83	PREDICTED: Canis familiaris olfactory receptor family 9 subfamily S (LOC477425); mRNA	100.0	NULL	XM_534621	LOC477425	olfactory receptor family 9 subfamily S
CfaAffx.19573.1.S1_at	3.782310E-03	1.324977E-01	1.12	.89	Macaca fascicularis testis cDNA; clone: QtsA-18728	91.8	XM_001129443	AB169295		
CfaAffx.19574.1.S1_at	3.774020E-03	1.323675E-01	1.11	.90	PREDICTED: Monodelphis domestica similar to ISL2 transcription factor; LIM/homeodomain; (islet-2) (LOC100012103); mRNA	21.0	AC005585	XM_001362472	LOC100012103	similar to ISL2 transcription factor, LIM/homeodomain, (islet-2)
CfaAffx.19576.1.S1_x_at	1.491630E-02	2.563590E-01	0.87	1.15	PREDICTED: Canis familiaris similar to 60S ribosomal protein L7 (LOC480813); mRNA	100.0	NULL	XM_537929	RPL7	ribosomal protein L7
CfaAffx.19701.1.S1_at	1.987980E-03	9.580372E-02	0.88	1.14	PREDICTED: Canis familiaris similar to vesicle transport-related protein isoform a (LOC480281); mRNA	100.0	AB171946	XM_537403	SCFD1	sec1 family domain containing 1
CfaAffx.19725.1.S1_at	1.180350E-02	2.296042E-01	1.12	.89	full-length cDNA clone CS0DB002YJ10 of Neuroblastoma Cot 10-normalized of Homo sapiens (human)	72.0	CR617066	CR617066	SCFD1	sec1 family domain containing 1
CfaAffx.19725.1.S1_s_at	6.206500E-03	1.691578E-01	0.86	1.16	full-length cDNA clone CS0DB002YJ10 of Neuroblastoma Cot 10-normalized of Homo sapiens (human)	47.9	CR617066	CR617066	SCFD1	sec1 family domain containing 1
CfaAffx.19805.1.S1_at	8.155380E-03	1.921000E-01	1.1	.91	Rattus norvegicus similar to hypothetical protein FLJ21963 (predicted) (RGD1307051_predicted); mRNA	26.8	AC004550	NM_001108091	RGD1307051	similar to hypothetical protein FLJ21963

CfaAffx.19818.1.S1_at	1.745630E-02	2.753735E-01	1.11	.90	Homo sapiens epithelial V-like antigen 1 (EVA1) mRNA; complete cds	87.1	AK290326	AF304447	MPZL2	myelin protein zero-like 2
CfaAffx.19828.1.S1_at	2.500610E-07	4.326119E-04	1.2	.83	Gorilla gorilla SCML2 (SCML2) gene; partial cds	69.7	AL096763	DQ976532		
CfaAffx.19831.1.S1_x_at	8.877920E-03	2.010117E-01	0.81	1.23	PREDICTED: Canis familiaris similar to ribosomal protein L31 (LOC491760); mRNA	100.0	NULL	XM_548880	LOC491760	similar to ribosomal protein L31
CfaAffx.1984.1.S1_s_at	3.107520E-03	1.196365E-01	0.84	1.19	PREDICTED: Canis familiaris similar to eukaryotic translation initiation factor 3; subunit 6 (predicted); transcript variant 8 (LOC475070); mRNA	100.0	CU678958	XM_855004	EIF3E	eukaryotic translation initiation factor 3, subunit E
CfaAffx.19851.1.S1_at	4.633710E-03	1.456623E-01	1.12	.89	PREDICTED: Macaca mulatta hypothetical protein LOC716374 (LOC716374); mRNA	28.0	NULL	XM_001115023	LOC716374	hypothetical protein LOC716374
CfaAffx.19898.1.S1_at	2.396060E-03	1.047911E-01	1.12	.89	Bos taurus RAS-like; estrogen-regulated; growth inhibitor (RERG); mRNA >gi|111305135|gb|BC120134.1| Bos taurus similar to RAS-like; estrogen-regulated; growth inhibitor; mRNA (cDNA clone MGC:142471 IMAGE:8111069); complete cds	94.3	NULL	NM_001076198	RERG	RAS-like, estrogen-regulated, growth inhibitor
CfaAffx.19926.1.S1_s_at	2.574840E-04	3.139044E-02	0.87	1.15	PREDICTED: Canis familiaris similar to Adapter-related protein complex 4 sigma 1 subunit (Sigma subunit of AP-4) (AP-4 adapter complex sigma subunit); transcript variant 3 (LOC480283); mRNA	97.3	AY891742	XM_856027	LOC480283	similar to Adapter-related protein complex 4 sigma 1 subunit (Sigma subunit of AP-4) (AP-4 adapter complex sigma subunit)
CfaAffx.1995.1.S1_at	1.707040E-04	2.481840E-02	1.11	.90	PREDICTED: Canis familiaris similar to alpha-1;6-mannosyltransferase ALG12; transcript variant 1 (LOC481196); mRNA	100.0	NULL	XM_538317	ALG12	asparagine-linked glycosylation 12 homolog (S. cerevisiae, alpha-1,6-mannosyltransferase)
CfaAffx.20006.1.S1_at	1.540970E-02	2.605723E-01	0.8	1.25	PREDICTED: Canis familiaris similar to Cell division control protein 2 homolog (p34 protein kinase) (Cyclin-dependent kinase 1) (CDK1); transcript variant 3 (LOC488997); mRNA	100.0	AK291939	XM_844357	CDC2	cell division cycle 2, G1 to S and G2 to M
CfaAffx.2001.1.S1_s_at	1.694560E-02	2.726183E-01	0.83	1.21	PREDICTED: Canis familiaris similar to Tetratricopeptide repeat protein KIAA0103 (LOC612810); mRNA	97.6	AB384437	XM_845168	TTC35	tetratricopeptide repeat domain 35

CfaAffx.2003.1.S1_at	1.950790E-03	9.497007E-02	1.12	.90	PREDICTED: Canis familiaris similar to thyrotropin-releasing hormone receptor (LOC482007); mRNA	100.0	NM_003301	XM_539128	TRHR	thyrotropin-releasing hormone receptor
CfaAffx.20066.1.S1_at	1.564020E-02	2.621012E-01	1.24	.80	PREDICTED: Macaca mulatta similar to fibronectin type III and ankyrin repeat domains 1; transcript variant 5 (LOC696281); mRNA	77.6	AY251163	XM_001087739	LOC696281	similar to fibronectin type III and ankyrin repeat domains 1
CfaAffx.2018.1.S1_at	2.726340E-03	1.120772E-01	1.13	.89	PREDICTED: Canis familiaris similar to Chondroitin sulfate synthase 3 (Glucuronosyl-N-acetylgalactosaminyl-proteoglycan 4-beta-N-acetylgalactosaminyltransferase II) (Chondroitin synthase 2) (N-acetylgalactosaminyl-proteoglycan 3-beta-glucuronosyltransferase II) (Chondroitin g... (LOC481492); mRNA	100.0	NM_175856	XM_538613	CHSY3	chondroitin sulfate synthase 3
CfaAffx.20232.1.S1_s_at	5.516850E-03	1.592338E-01	0.9	1.11	PREDICTED: Canis familiaris similar to Tumor protein D54 (hD54) (Tumor protein D52-like 2); transcript variant 2 (LOC610715); mRNA	100.0	CU675462	XM_862574	TPD52L2	tumor protein D52-like 2
CfaAffx.20246.1.S1_at	1.263070E-03	7.518149E-02	1.14	.88	Homo sapiens protein kinase C; alpha (PRKCA) gene; complete cds	21.4	EU332865	EU332865		
CfaAffx.20258.1.S1_s_at	5.327030E-03	1.555283E-01	0.87	1.15	PREDICTED: Canis familiaris similar to cysteine string protein; transcript variant 2 (LOC485982); mRNA	61.1	AK289585	XM_862591	DNAJC5	DnaJ (Hsp40) homolog, subfamily C, member 5
CfaAffx.20285.1.S1_s_at	1.060880E-02	2.175082E-01	0.91	1.10	PREDICTED: Canis familiaris similar to Nuclear cap binding protein subunit 2 (20 kDa nuclear cap binding protein) (NCBP 20 kDa subunit) (CBP20) (NCBP interacting protein 1) (NIP1) (LOC478603); mRNA	99.8	NM_007362	XM_535779	NCBP2	nuclear cap binding protein subunit 2, 20kDa
CfaAffx.20307.1.S1_at	1.444540E-05	5.473154E-03	1.36	.73	Gallus gallus USO1 homolog; vesicle docking protein (yeast) (USO1); mRNA >gi|53126532|emb|AJ719305.1| Gallus gallus mRNA for hypothetical protein; clone 1e12	62.9	NULL	NM_001031139	USO1	USO1 homolog, vesicle docking protein (yeast)
CfaAffx.20333.1.S1_at	7.652620E-03	1.855017E-01	0.9	1.11	PREDICTED: Canis familiaris similar to basophilic leukemia expressed protein	100.0	AP006287	XM_540844	LOC483723	similar to basophilic leukemia expressed protein

					(LOC483723); mRNA					
CfaAffx.2034.1.S1_s_at	4.309310E-03	1.409285E-01	1.14	.88	PREDICTED: Canis familiaris similar to solute carrier family 22 member 3 (LOC476261); mRNA	100.0	AK314590	XM_533467	SLC22A3	solute carrier family 22 (extraneuronal monoamine transporter), member 3
CfaAffx.20347.1.S1_at	8.355750E-04	5.953472E-02	1.15	.87	null	null	null	null		
CfaAffx.20350.1.S1_at	1.434650E-03	8.123706E-02	0.89	1.12	PREDICTED: Canis familiaris similar to midline 1 (LOC609716); mRNA	100.0	NM_001007122	XM_847033	FSD2	fibronectin type III and SPRY domain containing 2
CfaAffx.20366.1.S1_at	5.274890E-03	1.544251E-01	1.12	.89	PREDICTED: Canis familiaris similar to CG4080-PA (LOC490914); mRNA	99.8	AB168516	XM_548037	MARCH10	membrane-associated ring finger (C3HC4) 10
CfaAffx.20443.1.S1_x_at	1.256770E-02	2.361795E-01	0.86	1.16	PREDICTED: Canis familiaris similar to RIKEN cDNA 1810011O16; transcript variant 1 (LOC490647); mRNA	100.0	AK000585	XM_547769	EAPP	E2F-associated phosphoprotein
CfaAffx.20465.1.S1_s_at	2.630730E-04	3.170988E-02	0.86	1.17	PREDICTED: Canis familiaris similar to CBF1 interacting corepressor isoform 2; transcript variant 2 (LOC478804); mRNA	60.3	CR599038	XM_535968	LOC478804	similar to CBF1 interacting corepressor isoform 2
CfaAffx.20486.1.S1_at	1.980240E-02	2.914488E-01	1.1	.91	PREDICTED: Canis familiaris similar to Regulator of G-protein signaling 4 (RGS4) (RGP4) (LOC488666); mRNA	100.0	AK312250	XM_545783	RGS4	regulator of G-protein signaling 4
CfaAffx.20508.1.S1_at	3.325250E-03	1.239069E-01	1.16	.86	Entamoeba histolytica HM-1:IMSS phospholipid-transporting P-type ATPase (47.t00011) partial mRNA	30.4	AC087373	XM_649568	EHI_009460	phospholipid-transporting P-type ATPase, putative
CfaAffx.20529.1.S1_at	1.805860E-02	2.792868E-01	0.81	1.23	PREDICTED: Canis familiaris similar to cell division cycle associated 1 (LOC478988); mRNA	100.0	CU678982	XM_536145	NUF2	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)
CfaAffx.20569.1.S1_at	2.926590E-06	2.376336E-03	1.33	.75	null	null	null	null		
CfaAffx.20593.1.S1_at	8.141810E-03	1.919022E-01	0.89	1.12	Oryza sativa Japonica Group cDNA; clone: J090072P08; full insert sequence	21.8	AL139100	AK288818		

CfaAffx.20634.1.S1_at	4.463680E-03	1.428212E-01	0.89	1.12	PREDICTED: Canis familiaris similar to v-rel reticuloendotheliosis viral oncogene homolog A; transcript variant 1 (LOC483729); mRNA	79.7	AB170914	XM_540850	RELA	v-rel reticuloendotheliosis viral oncogene homolog A (avian)
CfaAffx.20657.1.S1_at	2.793460E-03	1.136262E-01	1.18	.85	PREDICTED: Equus caballus similar to KIAA0806 protein (LOC100064414); mRNA	86.5	AK291031	XM_001495327	LOC100064414	similar to KIAA0806 protein
CfaAffx.20665.1.S1_at	3.322320E-05	9.392584E-03	1.19	.84	PREDICTED: Canis familiaris similar to patched domain containing 1; transcript variant 1 (LOC491775); mRNA	53.8	AC009482	XM_548895	PTCHD1	patched domain containing 1
CfaAffx.20674.1.S1_at	4.686260E-04	4.471690E-02	1.13	.89	PREDICTED: Canis familiaris similar to Monocarboxylate transporter 1 (MCT 1) (LOC487543); mRNA	95.4	AB172796	XM_544668	LOC487543	similar to Monocarboxylate transporter 1 (MCT 1)
CfaAffx.20679.1.S1_s_at	1.706440E-02	2.738595E-01	0.86	1.16	PREDICTED: Canis familiaris similar to phosphatase subunit gene g4-1; transcript variant 5 (LOC480289); mRNA	100.0	NULL	XM_856989	PPP2R3C	protein phosphatase 2 (formerly 2A), regulatory subunit B'', gamma
CfaAffx.20680.1.S1_at	6.600970E-04	5.231542E-02	1.16	.86	null	null	null	null		
CfaAffx.20690.1.S1_at	3.114150E-04	3.466030E-02	1.14	.88	PREDICTED: Canis familiaris similar to developmentally regulated protein TPO1 (LOC487527); mRNA	100.0	NM_001033517	XM_544651	SERINC4	serine incorporator 4
CfaAffx.20699.1.S1_at	1.746240E-02	2.753735E-01	0.89	1.12	PREDICTED: Macaca mulatta hypothetical protein LOC694935 (LOC694935); mRNA	91.0	XM_001723624	XM_001083105	LOC694935	hypothetical protein LOC694935
CfaAffx.20700.1.S1_at	2.010520E-02	2.926031E-01	1.21	.83	Canis familiaris DNA for bitter taste receptor; complete cds; clone: Cafa-T2R43	99.5	BC117423	AB249698		
CfaAffx.20704.1.S1_at	6.404080E-03	1.720925E-01	1.12	.89	Canis familiaris DNA for bitter taste receptor; complete cds; clone: Cafa-T2R7	100.0	NULL	AB249689		
CfaAffx.20773.1.S1_at	7.005620E-03	1.791586E-01	1.1	.91	PREDICTED: Canis familiaris similar to malate dehydrogenase 1B; NAD (soluble) (LOC478883); mRNA	100.0	AK309144	XM_536042	MDH1B	malate dehydrogenase 1B, NAD (soluble)
CfaAffx.20781.1.S1_at	1.391740E-02	2.472896E-01	1.12	.89	null	null	null	null		

CfaAffx.20788.1.S1_at	1.690010E-02	2.724975E-01	1.11	.90	PREDICTED: Canis familiaris similar to olfactory receptor 745 (LOC491358); mRNA	99.7	NULL	XM_548479	LOC491358	similar to olfactory receptor 745
CfaAffx.20789.1.S1_at	1.950820E-03	9.497007E-02	1.12	.90	PREDICTED: Canis familiaris similar to NKG2-F type II integral membrane protein (NKG2-F activating NK receptor) (NK cell receptor F) (LOC609192); mRNA	87.8	NULL	XM_846408	LOC609192	similar to NKG2-F type II integral membrane protein (NKG2-F activating NK receptor) (NK cell receptor F)
CfaAffx.20792.1.S1_at	2.254130E-03	1.017906E-01	1.12	.90	NULL	null	AC106714	NULL		
CfaAffx.20792.1.S1_s_at	1.687050E-03	8.930160E-02	1.13	.88	Canis lupus familiaris solute carrier family 5 (sodium/glucose cotransporter); member 1 (SLC5A1); mRNA >gi|54873673|gb|AY772536.1| Canis familiaris sodium-glucose cotransporter-like 1 mRNA; complete cds	52.7	NULL	NM_001007141	SLC5A1	solute carrier family 5 (sodium/glucose cotransporter), member 1
CfaAffx.20797.1.S1_at	1.130830E-03	7.104419E-02	0.83	1.20	Bos taurus chromosome 1 open reading frame 21 ortholog (H16C1ORF21); mRNA >gi|124829071|gb|BC133418.1| Bos taurus similar to C1orf21; mRNA (cDNA clone MGC:155149 IMAGE:8483680); complete cds	59.6	AY258286	NM_001081547	C16H1ORF21	chromosome 1 open reading frame 21 ortholog
CfaAffx.208.1.S1_at	7.635430E-03	1.855017E-01	1.11	.90	PREDICTED: Equus caballus similar to ASCL3 protein (LOC100071044); mRNA	85.9	BC146582	XM_001504908	LOC100071044	similar to ASCL3
CfaAffx.20808.1.S1_at	3.094570E-06	2.396362E-03	1.27	.79	PREDICTED: Canis familiaris similar to Ig lambda chain V region 4A precursor (LOC491362); mRNA	91.4	AK057174	XM_849914	LOC491362	similar to Ig lambda chain V region 4A precursor
CfaAffx.20808.1.S1_x_at	1.555530E-06	1.585429E-03	1.25	.80	PREDICTED: Canis familiaris similar to Ig lambda chain V region 4A precursor (LOC491362); mRNA	95.0	AK057174	XM_849914	LOC491362	similar to Ig lambda chain V region 4A precursor
CfaAffx.20824.1.S1_s_at	2.837870E-04	3.265447E-02	1.18	.85	PREDICTED: Canis familiaris similar to FERM domain containing 3 (LOC478282); mRNA	99.4	CU691019	XM_535456	FRMD5	FERM domain containing 5
CfaAffx.20897.1.S1_at	1.000880E-02	2.131608E-01	1.13	.88	Sus scrofa low-affinity Na-dependent glucose cotransporter (PSGLT2); mRNA >gi|164666|gb|L02900.1|PIGSGLT2X Pig Na-dependent glucose cotransporter	38.2	BC153069	NM_214182	PSGLT2	low-affinity Na-dependent glucose cotransporter

					(pSGLT2) mRNA; complete cds					
CfaAffx.20904.1.S1_x_at	1.290580E-03	7.615957E-02	1.14	.88	PREDICTED: Canis familiaris similar to Ig lambda chain V region 4A precursor (LOC612083); mRNA	47.6	NULL	XM_849810	LOC612083	similar to Ig lambda chain V region 4A precursor
CfaAffx.20920.1.S1_at	4.081870E-04	4.143002E-02	1.29	.77	PREDICTED: Canis familiaris similar to cyclin fold protein 1 (LOC488492); mRNA	100.0	XR_040725	XM_545613	CCNYL1	cyclin Y-like 1
CfaAffx.20954.1.S1_at	7.959770E-03	1.894628E-01	1.14	.88	Canis lupus familiaris 5-hydroxytryptamine (serotonin) receptor 3A (HTR3A); mRNA >gi|94537152|gb|DQ483094.1| Canis familiaris 5-hydroxytryptamine type 3A receptor (HTR3A) mRNA; complete cds	51.8	AK313896	NM_001048119	HTR3A	5-hydroxytryptamine (serotonin) receptor 3A
CfaAffx.20955.1.S1_at	2.577630E-03	1.086467E-01	0.73	1.36	PREDICTED: Canis familiaris similar to C-type lectin superfamily member 2 (Activation-induced C-type lectin) (IFN-alpha2b-inducing related protein 1) (C-type lectin domain family 2 member B) (LOC611423); mRNA	100.0	AK313916	XM_849093	CLEC2B	C-type lectin domain family 2, member B
CfaAffx.20962.1.S1_at	7.780370E-03	1.874380E-01	1.11	.90	Pan troglodytes AHSG gene for alpha2-HS glycoprotein; complete cds	24.0	AC068631	AB038690		
CfaAffx.20973.1.S1_at	4.464400E-04	4.328827E-02	1.15	.87	Canis lupus familiaris crystallin; gamma B (CRYGB); mRNA >gi|126468159|gb|EF426308.1| Canis familiaris gammaB-crystallin (Crygb) mRNA; complete cds	100.0	BC117384	NM_001110799	CRYGB	crystallin, gamma B
CfaAffx.20975.1.S1_at	4.239460E-05	1.060728E-02	1.2	.83	PREDICTED: Canis familiaris similar to 5-hydroxytryptamine (serotonin) receptor 3B precursor (LOC611236); mRNA	100.0	AK314268	XM_848874	HTR3B	5-hydroxytryptamine (serotonin) receptor 3B
CfaAffx.21027.1.S1_at	1.459800E-03	8.221204E-02	0.85	1.18	PREDICTED: Canis familiaris similar to TBP-associated factor 1A isoform 1 (LOC608850); mRNA	97.0	CR612936	XM_845987	TAF1A	TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kDa
CfaAffx.2104.1.S1_at	6.772700E-03	1.762171E-01	1.14	.88	Pongo pygmaeus SIGLEC11 gene for Siglec-11; partial cds	23.1	AL133387	AB211394		
CfaAffx.21048.1.S1_at	1.479140E-	8.256134E-	1.1	.91	PREDICTED: Canis familiaris hypothetical	100.0	XR_040922	XM_846355	LOC609145	hypothetical protein LOC609145

	03	02			protein LOC609145 (LOC609145); mRNA					
CfaAffx.2108.1.S1_s_at	1.054980E-02	2.165048E-01	1.1	.91	PREDICTED: Canis familiaris similar to butyrophilin-like 8 (LOC481727); mRNA	100.0	NULL	XM_538848	BTN3A2	butyrophilin, subfamily 3, member A2
CfaAffx.21092.1.S1_s_at	3.202570E-03	1.215367E-01	0.83	1.20	PREDICTED: Canis familiaris similar to ring finger protein 36 (predicted) (LOC478285); mRNA	100.0	NULL	XM_535459	TRIM69	tripartite motif-containing 69
CfaAffx.21104.1.S1_at	6.757430E-03	1.760804E-01	1.1	.91	PREDICTED: Canis familiaris potassium voltage-gated channel; Shal-related subfamily; member 3; transcript variant 2 (KCND3); mRNA	100.0	NM_004980	XM_845974	KCND3	potassium voltage-gated channel, Shal-related subfamily, member 3
CfaAffx.21132.1.S1_s_at	4.556650E-03	1.442939E-01	0.89	1.13	PREDICTED: Canis familiaris similar to Ras-related protein Rab-18; transcript variant 6 (LOC491408); mRNA	98.8	AF137372	XM_852130	RAB18	RAB18, member RAS oncogene family
CfaAffx.21165.1.S1_s_at	9.120970E-04	6.280335E-02	1.16	.86	PREDICTED: Canis familiaris similar to solute carrier family 25 (mitochondrial oxodicarboxylate carrier); member 21 (LOC490655); mRNA	100.0	NM_030631	XM_547777	SLC25A21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21
CfaAffx.21187.1.S1_at	6.842280E-03	1.767452E-01	1.14	.87	PREDICTED: Canis familiaris similar to transmembrane protein 7 (LOC609398); mRNA	60.9	BC131756	XM_846641	RTP3	receptor (chemosensory) transporter protein 3
CfaAffx.21188.1.S1_s_at	8.749820E-03	2.003984E-01	1.1	.91	Canis lupus familiaris dual oxidase 1 (DUOX1); mRNA >gi|8163929|gb|AF230497.1|AF230497 Canis familiaris NADPH thyroid oxidase 1 (THOX1) mRNA; complete cds	100.0	BC114938	NM_001003122	DUOX1	dual oxidase 1
CfaAffx.21193.1.S1_at	2.571220E-03	1.085819E-01	1.18	.85	null	null	null	null		
CfaAffx.21206.1.S1_at	1.404810E-03	8.018379E-02	0.91	1.10	PREDICTED: Canis familiaris similar to Nucleoprotein TPR (LOC480045); mRNA	100.0	NULL	XM_537167	TPR	translocated promoter region (to activated MET oncogene)
CfaAffx.21248.1.S1_at	1.382780E-03	7.987515E-02	1.12	.89	PREDICTED: Canis familiaris similar to CG18437-PA (LOC488505); mRNA	100.0	AC006385	XM_545626	LOC488505	similar to CG18437-PA

CfaAffx.21291.1.S1_s_at	1.827100E-02	2.808187E-01	0.89	1.12	PREDICTED: Canis familiaris similar to nucleolar protein GU2; transcript variant 2 (LOC612801); mRNA	99.8	NM_024045	XM_845081	DDX50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50
CfaAffx.21306.1.S1_at	2.729120E-05	8.390841E-03	1.23	.81	Synthetic construct DNA; clone: pF1KB1630; Homo sapiens SMARCA5 gene for SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5; complete cds; without stop codon; in Flexi system	50.0	AB384709	AB384709		
CfaAffx.2132.1.S1_at	1.598030E-05	5.928554E-03	1.16	.86	Canis familiaris MHC class II DLA DRB1 beta chain; complete cds	44.2	NULL	U47339		
CfaAffx.21330.1.S1_at	1.224350E-04	2.029117E-02	1.23	.81	PREDICTED: Canis familiaris similar to eukaryotic translation elongation factor 1 alpha 1 (LOC608732); mRNA	36.1	NULL	XM_845844	LOC608732	similar to eukaryotic translation elongation factor 1 alpha 1
CfaAffx.2135.1.S1_s_at	2.341420E-03	1.036656E-01	1.19	.84	Canis familiaris MHC class II DLA DRB1 beta chain; complete cds	100.0	AC011456	U47339		
CfaAffx.21439.1.S1_at	6.497420E-03	1.732327E-01	1.11	.90	PREDICTED: Canis familiaris similar to LanC lantibiotic synthetase component C-like 3 (LOC491823); mRNA	100.0	NM_198511	XM_548943	LANCL3	LanC lantibiotic synthetase component C-like 3 (bacterial)
CfaAffx.21480.1.S1_at	1.149200E-02	2.266536E-01	1.14	.88	PREDICTED: Canis familiaris similar to C3a anaphylatoxin chemotactic receptor (C3a-R) (C3AR) (LOC486704); mRNA	100.0	CU676681	XM_543831	C3AR1	complement component 3a receptor 1
CfaAffx.21481.1.S1_at	1.234150E-03	7.449039E-02	1.11	.90	PREDICTED: Pan troglodytes activating transcription factor 6; transcript variant 4 (ATF6); mRNA	23.9	AC016821	XM_513949	ATF6	activating transcription factor 6
CfaAffx.21535.1.S1_at	4.344520E-03	1.413545E-01	1.13	.88	PREDICTED: Canis familiaris similar to kinesin family member 18A (LOC490932); mRNA	100.0	NM_001080443	XM_548055	LOC490932	similar to kinesin family member 18A
CfaAffx.21564.1.S1_s_at	7.657760E-03	1.855017E-01	1.1	.91	PREDICTED: Canis familiaris similar to transformation related protein 63; transcript variant 3 (LOC488125); mRNA	74.3	AF075431	XM_856196	TP63	tumor protein p63
CfaAffx.2157.1.S1_at	2.801570E-04	3.249746E-02	1.17	.85	PREDICTED: Canis familiaris similar to Double-strand-break repair protein rad21 homolog (hHR21) (Nuclear matrix protein 1) (NXP-1) (SCC1 homolog); transcript	42.1	AK125620	XM_539142	RAD21	RAD21 homolog (S. pombe)

					variant 1 (LOC482021); mRNA					
CfaAffx.2159.1.S1_s_at	1.750140E-02	2.754838E-01	0.87	1.15	PREDICTED: Macaca mulatta similar to TRAP/Mediator complex component TRAP25 (LOC701367); mRNA	47.5	NM_080651	XM_001095901	LOC701367	similar to TRAP/Mediator complex component TRAP25
CfaAffx.21642.1.S1_at	1.380310E-02	2.463776E-01	1.12	.89	Mus musculus adult male testis cDNA; RIKEN full-length enriched library; clone:1700123I01 product:hypothetical protein; full insert sequence	48.6	BC106951	AK007250	1700123I01Rik	RIKEN cDNA 1700123I01 gene
CfaAffx.21665.1.S1_at	1.230820E-02	2.347743E-01	1.15	.87	PREDICTED: Canis familiaris similar to Probable leucyl-tRNA synthetase; mitochondrial precursor (Leucine--tRNA ligase) (LeuRS); transcript variant 1 (LOC476652); mRNA	100.0	AK025465	XM_533856	LARS2	leucyl-tRNA synthetase 2, mitochondrial
CfaAffx.21675.1.S1_at	9.599630E-03	2.084125E-01	0.82	1.22	PREDICTED: Canis familiaris similar to inorganic pyrophosphatase (LOC479238); mRNA	98.7	AK127102	XM_536380	PPA1	pyrophosphatase (inorganic) 1
CfaAffx.21675.1.S1_s_at	1.080040E-02	2.185215E-01	0.87	1.16	PREDICTED: Canis familiaris similar to inorganic pyrophosphatase (LOC479238); mRNA	100.0	AB169701	XM_536380	PPA1	pyrophosphatase (inorganic) 1
CfaAffx.21682.1.S1_at	1.201110E-03	7.311141E-02	1.15	.87	Cryptococcus neoformans var. neoformans JEC21 RNA helicase (CNI01550) partial mRNA	5.4	NULL	XM_572794	CNI01550	RNA helicase
CfaAffx.2172.1.S1_at	1.512400E-04	2.291765E-02	1.15	.87	Mus musculus phosphatidylinositol-5-phosphate 4-kinase; type II; gamma (Pip4k2c); mRNA >gi|18204067|gb|BC021383.1| Mus musculus phosphatidylinositol-5-phosphate 4-kinase; type II; gamma; mRNA (cDNA clone MGC:29371 IMAGE:5042933); complete cds	30.3	AC079858	NM_054097	Pip4k2c	phosphatidylinositol-5-phosphate 4-kinase, type II, gamma
CfaAffx.21753.1.S1_at	3.174360E-03	1.208161E-01	1.16	.86	Caenorhabditis vulgaris FMRFamide-like peptide-1 (Cv-flp-1A) and (Cv-flp-1B) genes; complete cds	61.8	AF041001	U05663		
CfaAffx.21762.1.S1_at	2.269120E-03	1.021460E-01	1.16	.86	PREDICTED: Bos taurus similar to olfactory receptor Olr1609 (LOC531304); mRNA	78.4	BK004626	XM_609796	LOC531304	similar to olfactory receptor Olr1609

CfaAffx.21766.1.S1 s at	1.661190E-02	2.707754E-01	1.13	.88	PREDICTED: Canis familiaris similar to BCoR protein (BCL-6 corepressor); transcript variant 4 (LOC480880); mRNA	91.8	NULL	XM 855998	BCOR	BCL6 co-repressor
CfaAffx.21806.1.S1 at	7.040070E-03	1.795988E-01	1.13	.88	PREDICTED: Canis familiaris similar to ATPase type 13A5 (LOC488128); mRNA	99.8	BC156652	XM 545252	ATP13A5	ATPase type 13A5
CfaAffx.21829.1.S1 at	7.602230E-03	1.851511E-01	1.11	.90	PREDICTED: Canis familiaris similar to Nebulin (LOC476149); mRNA	76.5	NM 004543	XM 533356	LOC476149	similar to Nebulin
CfaAffx.2183.1.S1 at	5.749220E-03	1.628197E-01	1.14	.88	PREDICTED: Canis familiaris similar to mal; T-cell differentiation protein 2 (LOC608995); mRNA	100.0	AB172185	XM 846173	MAL2	mal, T-cell differentiation protein 2
CfaAffx.21916.1.S1 at	1.472810E-02	2.548942E-01	1.11	.90	Equus caballus erythropoietin (EPO); mRNA >gi|27807633|dbj|AB100030.1| Equus caballus EPO mRNA for erythropoietin; complete cds	82.6	AC005902	NM 001081825	EPO	erythropoietin
CfaAffx.21943.1.S1 at	5.887640E-04	4.994779E-02	0.75	1.33	Homo sapiens ADP-ribosylation factor 6 (ARF6); mRNA	44.0	XR 039337	NM 001663	ARF6	ADP-ribosylation factor 6
CfaAffx.2196.1.S1 at	2.067240E-02	2.961507E-01	1.12	.89	Homo sapiens ZNRD1; PPP1R11; RNF39 genes for zinc ribbon domain containing; 1; protein phosphatase 1; regulatory (inhibitor) subunit 11; ring finger protein 39; complete cds	27.6	AB103593	AB202082		
CfaAffx.2199.1.S1 at	8.327840E-03	1.945649E-01	0.86	1.16	PREDICTED: Canis familiaris similar to CG9646-PA (LOC481210); mRNA	100.0	AB173597	XM 538331	LOC481210	similar to CG9646-PA
CfaAffx.21997.1.S1 at	3.530360E-05	9.677009E-03	1.16	.86	PREDICTED: Strongylocentrotus purpuratus hypothetical LOC592693 (LOC592693); partial mRNA	10.4	AC092045	XM 792203	LOC592693	hypothetical LOC592693
CfaAffx.22035.1.S1 s at	2.321960E-03	1.031223E-01	1.11	.90	PREDICTED: Canis familiaris similar to F-box only protein 24 (LOC608428); mRNA	100.0	AK292240	XM 845454	FBXO24	F-box protein 24
CfaAffx.22037.1.S1 s at	1.756350E-03	9.067485E-02	0.86	1.16	PREDICTED: Canis familiaris similar to constitutive photomorphogenic protein 1 (LOC480060); mRNA	100.0	AK314750	XM 537181	RFWD2	ring finger and WD repeat domain 2

CfaAffx.22050.1.S1_at	7.798510E-05	1.539490E-02	1.16	.86	PREDICTED: Canis familiaris cOR5AN3 olfactory receptor family 5 subfamily AN-like (cOR5AN3); mRNA	100.0	NULL	XM_847152	cOR5AN3	cOR5AN3 olfactory receptor family 5 subfamily AN-like
CfaAffx.22060.1.S1_s_at	2.057070E-02	2.954807E-01	1.2	.83	PREDICTED: Canis familiaris similar to radixin; transcript variant 6 (LOC479446); mRNA	68.2	AB170729	XM_857605	RDX	radixin
CfaAffx.22068.1.S1_s_at	1.373710E-02	2.458113E-01	1.1	.91	Canis lupus familiaris vanin 1 (VNN1); mRNA >gi|6649539|gb|U39663.1|CFU39663 Canis familiaris TIFF66 mRNA; complete cds	100.0	NM_004666	NM_001003372	VNN1	vanin 1
CfaAffx.22081.1.S1_at	4.083610E-03	1.371883E-01	1.22	.82	Mus musculus adult male colon cDNA; RIKEN full-length enriched library; clone:9030625E11 product:hypothetical TPR-like containing protein; full insert sequence	47.2	AC003030	AK162318	9130404D08Rik	RIKEN cDNA 9130404D08 gene
CfaAffx.22089.1.S1_s_at	1.784760E-02	2.783876E-01	0.87	1.15	PREDICTED: Canis familiaris similar to Structural maintenance of chromosomes 4-like 1 protein (Chromosome-associated polypeptide C) (hCAP-C) (XCAP-C homolog); transcript variant 1 (LOC478679); mRNA	100.0	AB179361	XM_535848	SMC4	structural maintenance of chromosomes 4
CfaAffx.22123.1.S1_s_at	3.076380E-03	1.189972E-01	1.11	.90	PREDICTED: Canis familiaris similar to transmembrane 6 superfamily member 2 (LOC609715); mRNA	65.5	AB067513	XM_847032	TM6SF2	transmembrane 6 superfamily member 2
CfaAffx.22164.1.S1_at	9.286440E-03	2.047325E-01	1.1	.91	PREDICTED: Canis familiaris beta-galactosides-binding lectin (LGALS3); mRNA	95.1	AK314929	XM_848582	LGALS3	lectin, galactoside-binding, soluble, 3
CfaAffx.22180.1.S1_at	3.280820E-04	3.592623E-02	1.23	.81	PREDICTED: Canis familiaris similar to peroxisomal trans-2-enoyl-CoA reductase; transcript variant 1 (LOC478901); mRNA	82.5	NULL	XM_536060	PECR	peroxisomal trans-2-enoyl-CoA reductase
CfaAffx.22202.1.S1_at	6.093580E-03	1.681491E-01	0.85	1.17	PREDICTED: Canis familiaris G-protein-coupled receptor GPR34; transcript variant 14 (LOC480887); mRNA	100.0	NULL	XM_856871	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)
CfaAffx.22207.1.S1_at	9.192120E-04	6.292045E-02	1.15	.87	PREDICTED: Canis familiaris olfactory receptor (OR16G03); mRNA	100.0	AC135068	XM_548629	OR16G03	olfactory receptor

CfaAffx.22229.1.S1_at	2.197610E-03	1.005039E-01	1.23	.82	Canis familiaris G-protein-coupled receptor GPR34 gene; partial cds	100.0	NULL	AY241073		
CfaAffx.22260.1.S1_s_at	3.873730E-03	1.338385E-01	0.84	1.19	PREDICTED: Canis familiaris hypothetical protein LOC608342; transcript variant 3 (LOC608342); mRNA	100.0	BC009530	XM_856703	LOC608342	hypothetical protein LOC608342
CfaAffx.22267.1.S1_s_at	2.112650E-02	2.989080E-01	0.87	1.15	PREDICTED: Macaca mulatta similar to mitogen-activated protein kinase kinase kinase kinase 5; transcript variant 1 (LOC706204); mRNA	47.5	AB173200	XM_001100409	LOC706204	similar to mitogen-activated protein kinase kinase kinase kinase 5
CfaAffx.22282.1.S1_at	1.926960E-02	2.887421E-01	1.12	.89	PREDICTED: Canis familiaris similar to sarcoma antigen 1 (LOC607344); mRNA	52.6	NULL	XM_843966	LOC607344	similar to sarcoma antigen 1
CfaAffx.22376.1.S1_s_at	6.140490E-04	5.081846E-02	0.86	1.17	Canis lupus familiaris zinc finger CCCH-type containing 15 (ZC3H15); mRNA	98.5	AB171327	NM_001114605	ZC3H15	zinc finger CCCH-type containing 15
CfaAffx.22415.1.S1_at	2.563950E-04	3.134647E-02	1.16	.86	Homo sapiens mRNA; cDNA DKFZp761F129 (from clone DKFZp761F129)	89.2	AC097381	AL834195	ABLIM2	actin binding LIM protein family, member 2
CfaAffx.22451.1.S1_at	4.756250E-03	1.476361E-01	1.12	.90	Macaca fascicularis testis cDNA clone:QtsA-21447; similar to human solute carrier family 9 isoform 11 (SLC9A11); mRNA; NM_178527	25.6	AL358939	AB072793		
CfaAffx.22457.1.S1_x_at	1.810340E-02	2.795407E-01	1.11	.90	PREDICTED: Canis familiaris cOR4C30 olfactory receptor family 4 subfamily C-like (cOR4C30); mRNA	88.7	NULL	XM_848513	cOR4C30	cOR4C30 olfactory receptor family 4 subfamily C-like
CfaAffx.2247.1.S1_at	8.518980E-03	1.973305E-01	1.12	.89	PREDICTED: Canis familiaris similar to Trafficking protein particle complex subunit 3 (BET3 homolog) (LOC612533); mRNA	88.7	XM_001725041	XM_850263	LOC612533	similar to Trafficking protein particle complex subunit 3 (BET3 homolog)
CfaAffx.22493.1.S1_at	5.997090E-04	5.030892E-02	1.17	.86	Trichomonas vaginalis G3 hypothetical protein (TVAG_081100) partial mRNA	29.6	AC107219	XM_001317706	TVAG_081100	hypothetical protein
CfaAffx.22550.1.S1_at	9.481050E-04	6.415361E-02	1.16	.86	Homo sapiens paroxysmal nonkinesigenic dyskinesia (PNKD); transcript variant 1; mRNA	96.9	NM_015488	NM_015488	PNKD	paroxysmal nonkinesigenic dyskinesia
CfaAffx.22612.1.S1_s_at	3.212360E-	9.216261E-	1.28	.78	Medicago sativa mitogen-activated protein	25.0	AC078985	DQ451007		

	05	03			kinase gene; complete cds					
CfaAffx.2262.1.S1_at	2.194560E-03	1.004712E-01	0.86	1.16	PREDICTED: Canis familiaris similar to CG7386-PA; transcript variant 1 (LOC476272); mRNA	100.0	AK307523	XM_533478	ZUFSP	zinc finger with UFM1-specific peptidase domain
CfaAffx.22622.1.S1_at	1.757240E-03	9.067485E-02	1.12	.89	PREDICTED: Canis familiaris similar to regulator of G-protein signalling 12 isoform 1; transcript variant 2 (LOC608720); mRNA	65.1	AB172036	XM_845461	RGS12	regulator of G-protein signaling 12
CfaAffx.22627.1.S1_at	1.018190E-02	2.137454E-01	1.13	.89	PREDICTED: Canis familiaris similar to Huntingtin (Huntingtons disease protein) (HD protein) (LOC479074); mRNA	100.0	NM_002111	XM_536221	HTT	huntingtin
CfaAffx.22643.1.S1_at	1.307390E-02	2.403652E-01	1.15	.87	null	null	null	null		
CfaAffx.22691.1.S1_at	1.407600E-04	2.202766E-02	0.81	1.24	PREDICTED: Canis familiaris similar to CWF19-like 2; cell cycle control (LOC479454); mRNA	100.0	NM_152434	XM_536589	CWF19L2	CWF19-like 2, cell cycle control (S. pombe)
CfaAffx.22700.1.S1_at	2.520540E-04	3.122886E-02	1.17	.86	Magnaporthe grisea 70-15 predicted protein (MGG_11753) partial mRNA	21.6	AC021016	XM_001406155	MGG_11753	hypothetical protein
CfaAffx.22720.1.S1_s_at	5.936740E-04	5.009561E-02	1.21	.82	PREDICTED: Equus caballus similar to alpha2-subunit of soluble guanylyl cyclase (LOC100069474); mRNA	83.9	BC130488	XM_001499239	LOC100069474	similar to alpha2-subunit of soluble guanylyl cyclase
CfaAffx.22747.1.S1_s_at	7.686910E-03	1.858462E-01	0.88	1.14	PREDICTED: Canis familiaris similar to ERO1-like protein alpha precursor (ERO1-Lalpha) (Oxidoreductin 1-lalpha) (Endoplasmic oxidoreductin 1-like protein) (ERO1-L) (LOC490691); mRNA	100.0	AK292839	XM_547813	ERO1L	ERO1-like (S. cerevisiae)
CfaAffx.22808.1.S1_at	1.284000E-02	2.388973E-01	0.9	1.11	PREDICTED: Canis familiaris similar to rcd1 (required for cell differentiation) homolog 1 (S. pombe) (predicted) (LOC610449); mRNA	78.8	AB179421	XM_847959	RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe)
CfaAffx.22836.1.S1_at	8.909990E-03	2.014599E-01	0.9	1.11	PREDICTED: Canis familiaris similar to ubiquitin specific protease 48; transcript variant 1 (LOC478198); mRNA	100.0	AB384973	XM_535372	USP48	ubiquitin specific peptidase 48

CfaAffx.2285.1.S1_at	1.305060E-02	2.403220E-01	0.89	1.13	Bubalus bubalis growth differentiation factor 9 mRNA; complete cds	84.0	BC096231	EF202171		
CfaAffx.22873.1.S1_at	1.044950E-03	6.782718E-02	1.2	.83	PREDICTED: Canis familiaris similar to cytochrome c oxidase; subunit 7a 3 (LOC611134); mRNA	96.0	NM_001865	XM_848778	LOC611134	similar to cytochrome c oxidase, subunit 7a 3
CfaAffx.22882.1.S1_s_at	2.996670E-03	1.183056E-01	0.84	1.20	PREDICTED: Canis familiaris similar to COP9 (constitutive photomorphogenic) homolog; subunit 2; transcript variant 3 (LOC478295); mRNA	98.8	CR604522	XM_845582	COPS2	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis)
CfaAffx.22883.1.S1_a_at	1.958840E-02	2.904299E-01	0.83	1.20	Canis lupus familiaris caspase 12 (LOC479458); mRNA >gi|81170700|gb|DQ228670.1| Canis familiaris caspase-12/a mRNA; complete cds	45.6	AY358222	NM_001077236	LOC479458	caspase 12
CfaAffx.22921.1.S1_s_at	1.631260E-02	2.673314E-01	0.9	1.11	PREDICTED: Canis familiaris similar to RING finger protein 25 (LOC478912); mRNA	98.6	AK289501	XM_536071	RNF25	ring finger protein 25
CfaAffx.22922.1.S1_s_at	7.084690E-04	5.463972E-02	1.14	.88	PREDICTED: Canis familiaris alpha-2-glycoprotein 1; zinc (AZGP1); mRNA	100.0	NULL	XM_536867	AZGP1	alpha-2-glycoprotein 1, zinc-binding
CfaAffx.22928.1.S1_at	1.930940E-02	2.889598E-01	0.88	1.14	PREDICTED: Canis familiaris similar to Pyroglutamyl-peptidase I (Pyrrolidone-carboxylate peptidase) (5-oxoprolyl-peptidase) (PGP-I) (LOC484823); mRNA	99.8	AK289968	XM_541939	PGPEP1	pyroglutamyl-peptidase I
CfaAffx.22946.1.S1_at	3.172980E-03	1.208161E-01	1.14	.88	Paramecium tetraurelia hypothetical protein (GSPATT00028864001) partial mRNA	19.6	AC208070	XM_001425190	GSPATT00028864001	hypothetical protein
CfaAffx.22960.1.S1_s_at	1.045570E-04	1.821705E-02	0.82	1.22	PREDICTED: Canis familiaris similar to Cell growth regulator with RING finger domain 1 (Cell growth regulatory gene 19 protein) (LOC480328); mRNA	99.8	NM_006568	XM_537451	CGRRF1	cell growth regulator with ring finger domain 1
CfaAffx.22964.1.S1_at	1.266970E-02	2.372674E-01	1.14	.87	PREDICTED: Canis familiaris similar to Ig lambda chain V region 4A precursor (LOC612134); mRNA	100.0	NULL	XM_849861	LOC612134	similar to Ig lambda chain V region 4A precursor
CfaAffx.23001.1.S1_at	4.096420E-03	1.373242E-01	1.1	.91	PREDICTED: Canis familiaris olfactory receptor (OR08C09); mRNA	100.0	NULL	XM_546970	OR08C09	olfactory receptor

CfaAffx.23004.1.S1_s_at	1.360570E-04	2.162691E-02	0.8	1.25	PREDICTED: Canis familiaris similar to ribosomal protein L22 like 1 (LOC488163); mRNA	100.0	NM_001099645	XM_545287	RPL22L1	ribosomal protein L22-like 1
CfaAffx.2304.1.S1_at	4.948650E-03	1.497440E-01	1.15	.87	PREDICTED: Canis familiaris similar to solute carrier family 35; member F1 (LOC484103); mRNA	100.0	AB172097	XM_541220	SLC35F1	solute carrier family 35, member F1
CfaAffx.23051.1.S1_s_at	6.644200E-03	1.745624E-01	0.9	1.11	PREDICTED: Canis familiaris similar to Phosphatidylinositol 3-kinase regulatory beta subunit (PI3-kinase p85-beta subunit) (PtdIns-3-kinase p85-beta) (LOC609956); mRNA	47.8	BC090249	XM_847313	PIK3R2	phosphoinositide-3-kinase, regulatory subunit 2 (beta)
CfaAffx.23070.1.S1_s_at	2.406770E-04	3.055320E-02	1.18	.85	PREDICTED: Canis familiaris similar to Solute carrier family 2; facilitated glucose transporter; member 2 (Glucose transporter type 2; liver) (LOC488165); mRNA	100.0	AK313622	XM_545289	SLC2A2	solute carrier family 2 (facilitated glucose transporter), member 2
CfaAffx.231.1.S1_at	8.975980E-03	2.017118E-01	1.12	.89	PREDICTED: Canis familiaris similar to olfactory receptor 437; transcript variant 1 (LOC482721); mRNA	100.0	BK004422	XM_843395	LOC482721	similar to olfactory receptor 437
CfaAffx.23117.1.S1_x_at	4.336760E-03	1.413545E-01	0.84	1.19	PREDICTED: Canis familiaris similar to ATP synthase; H+ transporting; mitochondrial F0 complex; subunit f; isoform 2 (LOC612408); mRNA	96.2	NULL	XM_850142	LOC612408	similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2
CfaAffx.23138.1.S1_s_at	1.354010E-02	2.439323E-01	1.17	.85	PREDICTED: Canis familiaris similar to Zinc finger protein 157 (HZF22) (LOC612509); mRNA	100.0	NM_003446	XM_850236	ZNF157	zinc finger protein 157
CfaAffx.2314.1.S1_at	4.715220E-03	1.472565E-01	1.14	.88	Dictyostelium discoideum AX4 hypothetical protein (DDBDRAFT_0167469) mRNA; complete cds	42.6	AC114962	XM_638670	DDBDRAFT_0167469	hypothetical protein
CfaAffx.23147.1.S1_at	4.650640E-03	1.456945E-01	1.12	.89	PREDICTED: Canis familiaris similar to ZK742.2 (LOC488812); mRNA	100.0	AC048387	XM_545930	LOC488812	similar to ZK742.2
CfaAffx.23153.1.S1_at	3.373090E-03	1.251387E-01	1.18	.85	PREDICTED: Pan troglodytes matrix metalloproteinase 13; transcript variant 2 (MMP13); mRNA	85.9	AK292211	XM_001154361	MMP13	matrix metallopeptidase 13 (collagenase 3)

CfaAffx.2316.1.S1_at	1.246430E-02	2.356048E-01	1.18	.85	Sus scrofa mRNA; clone:MLN010067H12; expressed in mesenteric lymph node	54.0	AL049758	AK233921		
CfaAffx.23162.1.S1_at	6.923000E-03	1.781248E-01	1.13	.89	PREDICTED: Canis familiaris similar to TATA box binding protein like 2 (LOC611011); mRNA	100.0	BC117159	XM_848617	TBPL2	TATA box binding protein like 2
CfaAffx.23178.1.S1_at	7.955750E-03	1.894628E-01	1.15	.87	PREDICTED: Canis familiaris similar to matrix metalloproteinase 27 (LOC489430); mRNA	100.0	BC140433	XM_546548	MMP27	matrix metallopeptidase 27
CfaAffx.2318.1.S1_at	7.573060E-03	1.848591E-01	1.1	.91	PREDICTED: Canis familiaris similar to ASF1 anti-silencing function 1 homolog A (LOC476273); mRNA	100.0	NM_014034	XM_533479	ASF1A	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)
CfaAffx.2319.1.S1_at	1.399100E-03	8.006685E-02	1.15	.87	Mus musculus adult male tongue cDNA; RIKEN full-length enriched library; clone:2310050J15 product:procollagen; type XIV; alpha 1; full insert sequence	52.6	AP005364	AK009906	Col14a1	collagen, type XIV, alpha 1
CfaAffx.23206.1.S1_s_at	6.363430E-04	5.125131E-02	1.15	.87	PREDICTED: Canis familiaris similar to Group IIC secretory phospholipase A2 precursor (Phosphatidylcholine 2-acylhydrolase GIIC) (GIIC sPLA2) (PLA2-8) (14 kDa phospholipase A2) (LOC487396); mRNA	86.6	Z98257	XM_544522	PLA2G2C	phospholipase A2, group IIC
CfaAffx.2325.1.S1_s_at	4.382860E-03	1.417274E-01	0.78	1.29	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L13 (LOC482029); mRNA	99.8	AB049640	XM_539150	MRPL13	mitochondrial ribosomal protein L13
CfaAffx.23253.1.S1_at	6.817950E-03	1.767452E-01	0.84	1.19	Canis lupus familiaris baculoviral IAP repeat-containing 3 (BIRC3); mRNA >gi|118603168|gb|EF102104.1| Canis familiaris baculoviral IAP repeat-containing protein 3 (BIRC3) mRNA; complete cds	91.3	NM_182962	NM_001080725	BIRC3	baculoviral IAP repeat-containing 3
CfaAffx.23271.1.S1_at	1.056240E-04	1.829779E-02	1.17	.86	PREDICTED: Danio rerio hypothetical LOC563491 (LOC563491); mRNA	36.5	NULL	XM_686852		
CfaAffx.23335.1.S1_at	1.390750E-02	2.472896E-01	0.9	1.11	PREDICTED: Canis familiaris similar to selectin; lymphocyte; transcript variant 1 (LOC480080); mRNA	100.0	CU676703	XM_537201	SELL	selectin L

CfaAffx.23345.1.S1_s_at	8.791870E-04	6.175431E-02	0.87	1.15	Vulpes vulpes kinectin mRNA; complete cds	99.6	AK308272	AF095786		
CfaAffx.23350.1.S1_at	6.479880E-03	1.732060E-01	0.89	1.12	Homo sapiens ubiquitously expressed transcript (UXT) mRNA; complete cds	87.8	AL009172	AF092737	UXT	ubiquitously-expressed transcript
CfaAffx.23407.1.S1_s_at	8.838610E-03	2.009348E-01	0.84	1.19	PREDICTED: Canis familiaris similar to WNK lysine deficient protein kinase 1 (LOC491427); partial mRNA	100.0	NULL	XM_548548	LOC491427	similar to WNK lysine deficient protein kinase 1
CfaAffx.2341.1.S1_s_at	3.243760E-03	1.227571E-01	1.16	.86	PREDICTED: Equus caballus hypothetical protein LOC100072923 (LOC100072923); mRNA	91.7	AK055461	XM_001503010	LOC100072923	hypothetical LOC100072923
CfaAffx.23425.1.S1_at	9.117220E-04	6.280335E-02	1.18	.85	PREDICTED: Canis familiaris similar to Thiamine transporter 1 (THTR-1) (ThTr1) (Thiamine carrier 1) (TC1) (Solute carrier family 19; member 2); transcript variant 2 (LOC490353); mRNA	74.0	AJ238413	XM_845750	SLC19A2	solute carrier family 19 (thiamine transporter), member 2
CfaAffx.23487.1.S1_s_at	2.174120E-03	1.003052E-01	1.1	.91	Synthetic construct Homo sapiens clone IMAGE:100016027; MGC:184166 transmembrane protein 16B (TMEM16B) mRNA; encodes complete protein	92.9	BC152768	BC152768	ANO2	anoctamin 2
CfaAffx.23492.1.S1_at	4.289260E-05	1.060852E-02	1.19	.84	Canis lupus familiaris T-box 19 (TBX19); mRNA >gi|52352674|gb|AY745240.1| Canis familiaris T-box transcription factor 19 mRNA; complete cds	77.5	AL009051	NM_001005758	TBX19	T-box 19
CfaAffx.23493.1.S1_at	1.393550E-07	3.146453E-04	1.3	.77	Hydrogenothermus marinus strain DSM 12046T DNA polymerase I (polA) gene; partial cds	25.9	AP001880	AY739868		
CfaAffx.23497.1.S1_x_at	6.711450E-03	1.754404E-01	1.13	.89	PREDICTED: Canis familiaris similar to olfactory receptor Olr816 (LOC491442); mRNA	100.0	NULL	XM_548563	LOC491442	similar to olfactory receptor Olr816
CfaAffx.23566.1.S1_at	9.511500E-03	2.074645E-01	1.13	.89	PREDICTED: Equus caballus similar to Thioredoxin-like 6 (LOC100070181); mRNA	86.6	XM_001718752	XM_001499845		
CfaAffx.23569.1.S1_at	1.537070E-03	8.426286E-02	1.13	.88	PREDICTED: Pan troglodytes similar to Transmembrane protein 130; transcript	98.0	AM393874	XM_001136233	TMEM130	transmembrane protein 130

					variant 1 (LOC736136); mRNA					
CfaAffx.2358.1.S1_at	5.637630E-05	1.225330E-02	1.29	.78	Mus musculus RIKEN cDNA 1110014J01 gene (1110014J01Rik); mRNA	48.9	AC144522	NM_029101	Rrp7a	ribosomal RNA processing 7 homolog A (S. cerevisiae)
CfaAffx.23585.1.S1_at	2.493860E-04	3.122886E-02	1.12	.89	PREDICTED: Canis familiaris similar to UDP glycosyltransferase 1 family; polypeptide A3 precursor (LOC491485); mRNA	98.4	AY724453	XM_548606	LOC491485	similar to UDP glycosyltransferase 1 family, polypeptide A3 precursor
CfaAffx.2367.1.S1_at	5.503240E-03	1.589880E-01	0.9	1.11	PREDICTED: Canis familiaris similar to zinc finger protein 297 (LOC607900); mRNA	69.3	AK315747	XM_844748	ZBTB22	zinc finger and BTB domain containing 22
CfaAffx.23685.1.S1_x_at	7.726200E-04	5.674011E-02	0.82	1.23	PREDICTED: Canis familiaris similar to ribosomal protein L31 (LOC610897); mRNA	67.3	NULL	XM_848464	LOC610897	similar to ribosomal protein L31
CfaAffx.2372.1.S1_at	2.114270E-02	2.989080E-01	1.11	.90	Homo sapiens heat shock transcription factor 2 (HSF2) gene; complete cds	53.4	Z99129	DQ492684		
CfaAffx.23733.1.S1_at	1.745430E-04	2.495501E-02	1.16	.86	Mus musculus 0 day neonate head cDNA; RIKEN full-length enriched library; clone:4833419B05 product:hyperpolarization-activated; cyclic nucleotide-gated K+ 1; full insert sequence	50.0	NULL	AK014722	Hcn1	hyperpolarization-activated, cyclic nucleotide-gated K+ 1
CfaAffx.23752.1.S1_s_at	4.816620E-03	1.481191E-01	0.78	1.29	PREDICTED: Canis familiaris similar to epithelial cell transforming sequence 2 oncogene protein; transcript variant 1 (LOC488172); mRNA	98.5	BC006838	XM_545296	ECT2	epithelial cell transforming sequence 2 oncogene
CfaAffx.2378.1.S1_at	8.572240E-05	1.624452E-02	1.27	.78	Homo sapiens voltage-dependent anion channel 1; mRNA (cDNA clone MGC:14782 IMAGE:4332199); complete cds	100.0	BC008482	BC008482	VDAC1	voltage-dependent anion channel 1
CfaAffx.23782.1.S1_x_at	1.561280E-02	2.618460E-01	1.12	.90	PREDICTED: Canis familiaris similar to olfactory receptor 1411 (LOC608434); mRNA	100.0	NULL	XM_845465	LOC608434	similar to olfactory receptor 1411
CfaAffx.2384.1.S1_s_at	5.580660E-03	1.593654E-01	1.28	.78	PREDICTED: Canis familiaris similar to transcription factor 7 (T-cell specific; HMG-box) isoform 2; transcript variant 4 (LOC481506); mRNA	100.0	AK310591	XM_856716	TCF7	transcription factor 7 (T-cell specific, HMG-box)

CfaAffx.23967.1.S1_s_at	2.090200E-02	2.975679E-01	0.89	1.12	PREDICTED: Canis familiaris similar to CDK-activating kinase assembly factor MAT1 (RING finger protein MAT1) (Menage a trois) (CDK7/cyclin H assembly factor) (p36) (p35) (Cyclin G1 interacting protein) (RING finger protein 66); transcript variant 1 (LOC480346); mRNA	100.0	BC000820	XM_537469	MNAT1	menage a trois homolog 1, cyclin H assembly factor (Xenopus laevis)
CfaAffx.240.1.S1_s_at	2.334990E-03	1.034874E-01	0.9	1.12	PREDICTED: Canis familiaris similar to 40S ribosomal protein S27-like protein (LOC610569); mRNA	97.5	AB170503	XM_848098	RPS27L	ribosomal protein S27-like
CfaAffx.24015.1.S1_at	2.074750E-02	2.964175E-01	0.85	1.18	PREDICTED: Canis familiaris similar to Ly1 antibody reactive clone (predicted); transcript variant 1 (LOC479095); mRNA	74.0	CU677450	XM_536242	LYAR	Ly1 antibody reactive homolog (mouse)
CfaAffx.24040.1.S1_at	2.222070E-03	1.013684E-01	0.75	1.33	PREDICTED: Canis familiaris similar to serine/threonine kinase 11 interacting protein (LOC488541); mRNA	100.0	NULL	XM_545661	STK11IP	serine/threonine kinase 11 interacting protein
CfaAffx.24097.1.S1_at	3.152260E-06	2.396362E-03	1.25	.80	PREDICTED: Canis familiaris similar to DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (LOC486745); mRNA	72.9	XM_001716130	XM_543872	DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)
CfaAffx.241.1.S1_at	3.281090E-03	1.233203E-01	1.12	.89	Ostreococcus lucimarinus CCE9901 predicted protein (OSTLU_26500) mRNA; complete cds	15.9	NULL	XM_001420276	OSTLU_26500	predicted protein
CfaAffx.24153.1.S1_s_at	6.182110E-03	1.691578E-01	1.11	.90	Canis lupus familiaris solute carrier family 6 (neurotransmitter transporter; betaine/GABA); member 12 (SLC6A12); mRNA >gi|164031|gb|M80403.1|DOGNCBTA Canis familiaris Na+- and Cl- dependent betaine transporter mRNA; complete cds	100.0	AL121998	NM_001003322	SLC6A12	solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12
CfaAffx.2418.1.S1_at	4.135470E-03	1.380682E-01	0.89	1.13	PREDICTED: Canis familiaris similar to F56A8.1 (LOC609694); mRNA	99.1	CU013034	XM_847006	CCDC134	coiled-coil domain containing 134
CfaAffx.24200.1.S1_at	1.246520E-05	5.013457E-03	1.26	.80	PREDICTED: Macaca mulatta similar to sphingosine-1-phosphatase (LOC709364); mRNA	90.4	NM_030791	XR_012031	LOC709364	similar to sphingosine-1-phosphatase
CfaAffx.24207.1.S1_at	5.174340E-	1.178189E-	1.14	.88	Rattus norvegicus rabaptin mRNA;	58.3	AC015820	U70777	Rabep1	rabaptin, RAB GTPase binding

	05	02			complete cds					effector protein 1
CfaAffx.24228.1.S1_at	1.021500E-02	2.143357E-01	0.9	1.12	PREDICTED: Canis familiaris similar to Metastasis-associated protein MTA2 (Metastasis-associated 1-like 1) (LOC476057); mRNA	100.0	BC053650	XM_533265	MTA2	metastasis associated 1 family, member 2
CfaAffx.24233.1.S1_at	3.438390E-06	2.482760E-03	1.18	.85	PREDICTED: Canis familiaris similar to Olfactory receptor 10H3 (LOC484859); mRNA	89.2	NULL	XM_847812	LOC484859	similar to Olfactory receptor 10H3
CfaAffx.24233.1.S1_x_at	5.161540E-03	1.529140E-01	1.11	.90	PREDICTED: Canis familiaris similar to Olfactory receptor 10H3 (LOC484859); mRNA	90.4	NULL	XM_847812	LOC484859	similar to Olfactory receptor 10H3
CfaAffx.24316.1.S1_at	7.783140E-05	1.539490E-02	1.21	.83	Homo sapiens janus kinase and microtubule interacting protein 1 (JAKMIP1); transcript variant 1; mRNA	64.7	NM_001099433	NM_001099433	JAKMIP1	janus kinase and microtubule interacting protein 1
CfaAffx.24327.1.S1_at	2.184300E-03	1.004288E-01	1.14	.87	PREDICTED: Canis familiaris hypothetical protein LOC611848 (LOC611848); mRNA	100.0	XM_001717264	XM_849569	LOC611848	hypothetical protein LOC611848
CfaAffx.2433.1.S1_s_at	5.448290E-03	1.579967E-01	0.8	1.25	PREDICTED: Canis familiaris similar to GTP-binding protein SAR1b (GTBPB) (LOC481509); mRNA	100.0	AL512710	XM_538630	SAR1B	SAR1 gene homolog B (S. cerevisiae)
CfaAffx.24335.1.S1_at	7.285830E-03	1.819766E-01	1.11	.90	PREDICTED: Canis familiaris similar to Pro-neuregulin-3 precursor (Pro-NRG3) (LOC479263); mRNA	71.5	AL589782	XM_536405	NRG3	neuregulin 3
CfaAffx.24361.1.S1_at	1.488740E-02	2.560669E-01	1.1	.91	PREDICTED: Canis familiaris similar to Unc-13 homolog C (Munc13-3); transcript variant 3 (LOC487564); mRNA	100.0	NM_001080534	XM_544689	UNC13C	unc-13 homolog C (C. elegans)
CfaAffx.24380.1.S1_at	1.406880E-02	2.487915E-01	0.89	1.13	PREDICTED: Canis familiaris similar to Kinesin-Like Protein family member (klp-6) (LOC490381); mRNA	99.7	AC113174	XM_547502	LOC490381	similar to Kinesin-Like Protein family member (klp-6)
CfaAffx.24384.1.S1_s_at	2.250930E-04	2.935417E-02	0.73	1.37	PREDICTED: Canis familiaris similar to ribosomal protein L24-like (LOC478313); mRNA	99.8	BC026267	XM_535488	LOC478313	similar to ribosomal protein L24-like

CfaAffx.24391.1.S1_at	7.211880E-03	1.810754E-01	1.12	.89	PREDICTED: Canis familiaris similar to cholinergic receptor; nicotinic; alpha polypeptide 9 precursor (LOC488832); mRNA	85.8	NM_017581	XM_545950	CHRNA9	cholinergic receptor, nicotinic, alpha 9
CfaAffx.24394.1.S1_s_at	1.525580E-02	2.602160E-01	1.1	.91	PREDICTED: Canis familiaris similar to cholinergic receptor; nicotinic; alpha polypeptide 9 precursor (LOC488832); mRNA	50.5	BC113549	XM_545950	CHRNA9	cholinergic receptor, nicotinic, alpha 9
CfaAffx.2454.1.S1_at	4.324080E-08	1.691698E-04	1.61	.62	HIV-1 isolate ML1881-26.2.01(2) from Kenya gag protein (gag) gene; partial cds	40.0	AL023553	EF164022		
CfaAffx.24562.1.S1_at	1.126170E-02	2.243737E-01	1.11	.90	PREDICTED: Canis familiaris similar to CDC42-binding protein kinase alpha isoform B; transcript variant 7 (LOC480107); mRNA	100.0	AB007920	XM_858531	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)
CfaAffx.24572.1.S1_at	2.081380E-02	2.970885E-01	1.13	.88	NULL	null	AC093791	NULL		
CfaAffx.24611.1.S1_s_at	6.815410E-03	1.767452E-01	1.19	.84	PREDICTED: Canis familiaris presenilin 2 (PSEN2); mRNA	98.7	CU675366	XM_547503	PSEN2	presenilin 2 (Alzheimer disease 4)
CfaAffx.24625.1.S1_at	1.566630E-02	2.623343E-01	0.9	1.11	PREDICTED: Equus caballus similar to Meiosis-specific nuclear structural 1 (LOC100068954); mRNA	91.5	NM_018365	XM_001498774	LOC100068954	similar to Meiosis-specific nuclear structural 1
CfaAffx.24676.1.S1_at	1.517910E-03	8.376266E-02	1.13	.89	PREDICTED: Canis familiaris similar to monocyte-to-macrophage differentiation factor 2 (LOC609327); mRNA	100.0	NM_198403	XM_846573	MMD2	monocyte to macrophage differentiation-associated 2
CfaAffx.24689.1.S1_at	3.387880E-03	1.255792E-01	1.12	.90	PREDICTED: Canis familiaris similar to membrane-associated guanylate kinase-related (MAGI-3) (LOC479761); mRNA	100.0	CU678809	XM_536889	LOC479761	similar to membrane-associated guanylate kinase-related (MAGI-3)
CfaAffx.24696.1.S1_at	1.551370E-02	2.613375E-01	1.13	.88	Homo sapiens cDNA FLJ43264 fis; clone HLUNG2017350; weakly similar to GAP JUNCTION ALPHA-3 PROTEIN	50.0	BC153089	AK125254	GJD3	gap junction protein, delta 3, 31.9kDa
CfaAffx.2473.1.S1_at	5.444970E-04	4.772389E-02	0.75	1.34	PREDICTED: Canis familiaris similar to squalene monooxygenase; transcript variant 2 (LOC608021); mRNA	100.0	CR599266	XM_856851	SQLE	squalene epoxidase

CfaAffx.24783.1.S1_at	1.508150E-02	2.584702E-01	0.9	1.11	PREDICTED: Canis familiaris similar to CG6451-PA; transcript variant 2 (LOC489469); mRNA	98.3	AB384293	XM_853667	LOC489469	similar to CG6451-PA
CfaAffx.24801.1.S1_s_at	4.011410E-05	1.027795E-02	0.8	1.25	PREDICTED: Canis familiaris similar to Churchill protein; transcript variant 1 (LOC609942); mRNA	100.0	AK057626	XM_847755	CHURC1	churchill domain containing 1
CfaAffx.2482.1.S1_at	5.374110E-05	1.210863E-02	1.39	.72	PREDICTED: Canis familiaris similar to enoyl Coenzyme A hydratase domain containing 1; transcript variant 2 (LOC609850); mRNA	96.2	AK021464	XM_858918	ECHDC1	enoyl Coenzyme A hydratase domain containing 1
CfaAffx.24827.1.S1_at	1.890150E-04	2.615518E-02	0.85	1.17	Bos taurus farnesyltransferase; CAAX box; beta (FNTB); mRNA >gi|133778306|gb|BC123393.1| Bos taurus farnesyltransferase; CAAX box; beta; mRNA (cDNA clone MGC:139313 IMAGE:8209333); complete cds	82.7	AK225917	NM_175805	FNTB	farnesyltransferase, CAAX box, beta
CfaAffx.24849.1.S1_at	5.547770E-04	4.832961E-02	1.13	.89	PREDICTED: Canis familiaris similar to Olfactory receptor 7A5 (Olfactory receptor TPCR92) (LOC610545); mRNA	99.8	NULL	XM_848072	LOC610545	similar to Olfactory receptor 7A5 (Olfactory receptor TPCR92)
CfaAffx.24855.1.S1_at	3.361120E-05	9.392584E-03	1.28	.78	PREDICTED: Canis familiaris similar to olfactory receptor Olr1075 (LOC610568); mRNA	99.7	NULL	XM_848097	LOC610568	similar to olfactory receptor Olr1075
CfaAffx.24855.1.S1_x_at	1.050130E-05	4.576229E-03	1.28	.78	PREDICTED: Canis familiaris similar to olfactory receptor Olr1075 (LOC610568); mRNA	99.7	NULL	XM_848097	LOC610568	similar to olfactory receptor Olr1075
CfaAffx.24863.1.S1_at	8.082310E-03	1.913213E-01	1.11	.90	PREDICTED: Canis familiaris olfactory receptor (OR12C09); mRNA	85.9	NULL	XM_542009	OR12C09	olfactory receptor
CfaAffx.2487.1.S1_s_at	1.200830E-03	7.311141E-02	0.83	1.21	Homo sapiens non-SMC element 2; MMS21 homolog (S. cerevisiae) (NSMCE2); mRNA >gi|21618546|gb|BC032797.1| Homo sapiens non-SMC element 2; MMS21 homolog (S. cerevisiae); mRNA (cDNA clone MGC:45394 IMAGE:5109691); complete cds	66.4	NM_173685	NM_173685	NSMCE2	non-SMC element 2, MMS21 homolog (S. cerevisiae)
CfaAffx.24872.1.S1_at	8.729200E-03	2.002010E-01	1.14	.87	PREDICTED: Canis familiaris olfactory receptor (OR01C09); mRNA	99.6	NULL	XM_542000	OR01C09	olfactory receptor

CfaAffx.24874.1.S1_at	2.378820E-04	3.046955E-02	1.2	.83	PREDICTED: Canis familiaris olfactory receptor (OR10A12); mRNA	96.0	NULL	XM_542001	OR10A12	olfactory receptor
CfaAffx.24874.1.S1_x_at	3.158710E-05	9.216261E-03	1.23	.81	PREDICTED: Canis familiaris olfactory receptor (OR10A12); mRNA	97.0	NULL	XM_542001	OR10A12	olfactory receptor
CfaAffx.24879.1.S1_at	2.097030E-04	2.802661E-02	1.22	.82	Canis familiaris isolate cOR7C43 olfactory receptor family 7 subfamily C gene; partial cds	98.8	NULL	AY308916		
CfaAffx.24881.1.S1_at	3.604040E-04	3.800811E-02	1.13	.89	PREDICTED: Canis familiaris similar to olfactory receptor; family 7; subfamily A; member 17 (LOC610635); mRNA	96.4	NULL	XM_848171	LOC610635	similar to olfactory receptor, family 7, subfamily A, member 17
CfaAffx.24887.1.S1_at	8.606370E-05	1.624452E-02	1.21	.83	Canis familiaris isolate cOR7C44 olfactory receptor family 7 subfamily C gene; partial cds	99.3	NULL	AY308924		
CfaAffx.24899.1.S1_at	7.199860E-04	5.513274E-02	1.18	.85	PREDICTED: Bos taurus similar to OLF4 (LOC785624); partial mRNA	72.7	NULL	XM_001253584	LOC785624	similar to olfactory receptor, family 7, subfamily A, member 17
CfaAffx.24910.1.S1_at	1.396610E-03	8.003077E-02	1.16	.87	NULL	null	AC010265	NULL		
CfaAffx.25051.1.S1_at	3.108020E-03	1.196365E-01	1.11	.90	Mus musculus potassium inwardly-rectifying channel; subfamily J; member 1 (Kcnj1); mRNA >gi|18088198|gb|BC020525.1| Mus musculus potassium inwardly-rectifying channel; subfamily J; member 1; mRNA (cDNA clone MGC:18350 IMAGE:4241262); complete cds	15.0	AC145098	NM_019659	Kcnj1	potassium inwardly-rectifying channel, subfamily J, member 1
CfaAffx.25078.1.S1_at	1.001210E-03	6.662070E-02	0.89	1.12	PREDICTED: Canis familiaris similar to Phenylethanolamine N-methyltransferase (PNMTase) (Noradrenaline N-methyltransferase) (LOC491023); mRNA	98.7	NM_002686	XM_548143	PNMT	phenylethanolamine N-methyltransferase
CfaAffx.25115.1.S1_at	9.009680E-03	2.017118E-01	0.88	1.13	PREDICTED: Canis familiaris similar to lunatic fringe homolog (LOC489891); mRNA	100.0	NM_001040167	XM_547009	LOC489891	similar to lunatic fringe homolog
CfaAffx.25140.1.S1_at	1.154800E-02	2.272224E-01	1.11	.90	Homo sapiens family with sequence similarity 120C (FAM120C); mRNA	91.5	NM_017848	NM_017848	FAM120C	family with sequence similarity 120C

CfaAffx.25159.1.S1_at	9.753980E-03	2.098886E-01	1.12	.89	Homo sapiens WNK lysine deficient protein kinase 3 (WNK3); transcript variant 2; mRNA	65.0	AB046786	NM_001002838	WNK3	WNK lysine deficient protein kinase 3
CfaAffx.25181.1.S1_s_at	1.799100E-02	2.790268E-01	0.85	1.18	PREDICTED: Canis familiaris similar to CD5 antigen-like precursor (SP-alpha) (CT-2) (IgM-associated peptide); transcript variant 3 (LOC609953); mRNA	100.0	CU689661	XM_858956	CD5L	CD5 molecule-like
CfaAffx.25207.1.S1_s_at	5.111710E-03	1.525288E-01	0.84	1.19	PREDICTED: Canis familiaris similar to Mitotic spindle assembly checkpoint protein MAD1 (Mitotic arrest deficient-like protein 1) (MAD1-like 1) (Mitotic checkpoint MAD1 protein-homolog) (HsMAD1) (hMAD1) (Tax binding protein-181) (LOC609673); mRNA	100.0	BC018870	XM_846973	MAD1L1	MAD1 mitotic arrest deficient-like 1 (yeast)
CfaAffx.25283.1.S1_at	1.156710E-02	2.273014E-01	1.14	.87	PREDICTED: Canis familiaris similar to peroxisome proliferative activated receptor; gamma; coactivator 1 alpha; transcript variant 5 (LOC479127); mRNA	70.4	NM_013261	XM_859296	PPARGC1A	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
CfaAffx.25285.1.S1_at	5.043920E-04	4.604700E-02	1.16	.86	PREDICTED: Canis familiaris similar to cytosolic beta-glucosidase (LOC488857); mRNA	100.0	AK313189	XM_545975	GBA3	glucosidase, beta, acid 3 (cytosolic)
CfaAffx.25290.1.S1_at	8.559680E-05	1.624452E-02	1.25	.80	Homo sapiens cDNA FLJ75928 complete cds; highly similar to Homo sapiens Kv channel interacting protein 4 (KCNIP4); transcript variant 4; mRNA	100.0	AK290998	AK290998	KCNIP4	Kv channel interacting protein 4
CfaAffx.25345.1.S1_s_at	1.831850E-03	9.241930E-02	0.84	1.19	PREDICTED: Canis familiaris similar to Enhancer of rudimentary homolog (LOC480371); mRNA	100.0	XM_001251924	XM_537493	ERH	enhancer of rudimentary homolog (Drosophila)
CfaAffx.2537.1.S1_s_at	1.205590E-03	7.328046E-02	1.14	.88	Monosiga brevicollis MX1 predicted protein MONBRDRAFT_32964 mRNA; complete cds	41.3	AC008661	XM_001747086	MONBRDRAFT_32964	hypothetical protein
CfaAffx.25393.1.S1_at	6.447450E-04	5.157361E-02	1.17	.85	Mus musculus SPARC related modular calcium binding 1; mRNA (cDNA clone MGC:30627 IMAGE:3673732); complete cds	87.7	AC008039	BC031804	Smoc1	SPARC related modular calcium binding 1
CfaAffx.25411.1.S1_at	1.083950E-05	4.643647E-03	1.2	.83	Nematostella vectensis predicted protein (NEMVEDRAFT_v1g220711) partial mRNA	34.9	Z98946	XM_001622390	NEMVEDRAFT_v1g220711	predicted protein

CfaAffx.2542.1.S1_at	3.471690E-03	1.273693E-01	1.13	.89	PREDICTED: Equus caballus similar to laminin; alpha 2 (merosin; congenital muscular dystrophy) (LOC100073067); mRNA	91.0	NM_001079823	XM_001503221	LAMA2	laminin, alpha 2 (merosin, congenital muscular dystrophy)
CfaAffx.25460.1.S1_s_at	7.927730E-03	1.894336E-01	0.89	1.13	PREDICTED: Canis familiaris similar to transmembrane 4 superfamily member 17 isoform b; transcript variant 5 (LOC489098); mRNA	98.6	CU688249	XM_860825	TSPAN17	tetraspanin 17
CfaAffx.25470.1.S1_at	7.634010E-03	1.855017E-01	1.12	.89	NULL	null	AC005537	NULL		
CfaAffx.25492.1.S1_at	4.023990E-05	1.027795E-02	1.16	.86	PREDICTED: Canis familiaris similar to a disintegrin and metalloproteinase domain 21 preproprotein (LOC480377); mRNA	85.4	AF158643	XM_537500	ADAM21	ADAM metallopeptidase domain 21
CfaAffx.25548.1.S1_at	5.783430E-04	4.948110E-02	1.14	.88	Xenopus laevis hypothetical protein LOC100101324 (LOC100101324); mRNA >gi|148921508|gb|BC146624.1| Xenopus laevis hypothetical protein LOC100101324; mRNA (cDNA clone MGC:160896 IMAGE:7977629); complete cds	40.8	NULL	NM_001099905	LOC100101324	hypothetical protein LOC100101324
CfaAffx.25557.1.S1_s_at	1.263370E-04	2.059437E-02	0.75	1.33	PREDICTED: Canis familiaris similar to Activated RNA polymerase II transcriptional coactivator p15 (Positive cofactor 4) (PC4) (p14) (LOC479283); mRNA	98.6	AB384907	XM_536425	LOC479283	similar to Activated RNA polymerase II transcriptional coactivator p15 (Positive cofactor 4) (PC4) (p14)
CfaAffx.2556.1.S1_s_at	8.372570E-03	1.951638E-01	1.12	.89	PREDICTED: Macaca mulatta sparc/osteonectin; cwcv and kazal-like domains proteoglycan 1 (SPOCK1); mRNA	90.6	AK094489	XM_001106476	SPOCK1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1
CfaAffx.25608.1.S1_at	3.322710E-03	1.239069E-01	1.1	.91	PREDICTED: Canis familiaris similar to diacylglycerol O-acyltransferase 2-like 4 (LOC491936); mRNA	100.0	BC153070	XM_549056	DGAT2L4	diacylglycerol O-acyltransferase 2-like 4
CfaAffx.25621.1.S1_at	7.535230E-03	1.845638E-01	0.9	1.11	PREDICTED: Canis familiaris similar to ring finger protein 3 (LOC612315); mRNA	100.0	BC107061	XM_850058	PCGF3	polycomb group ring finger 3
CfaAffx.2567.1.S1_at	4.064840E-03	1.367753E-01	1.14	.88	PREDICTED: Canis familiaris similar to Kelch-like protein 3 (LOC481523); mRNA	84.6	AB032955	XM_538644	KLHL3	kelch-like 3 (Drosophila)

CfaAffx.25708.1.S1_s_at	1.514540E-02	2.589520E-01	1.1	.91	PREDICTED: Canis familiaris similar to Pyridoxine-5-phosphate oxidase (Pyridoxamine-phosphate oxidase) (LOC480540); mRNA	100.0	NM_018129	XM_537661	PNPO	pyridoxamine 5'-phosphate oxidase
CfaAffx.25764.1.S1_at	1.713360E-05	6.248682E-03	1.17	.85	PREDICTED: Canis familiaris similar to CG5805-PA (LOC490415); mRNA	76.2	AC007227	XM_547537	SLC25A44	solute carrier family 25, member 44
CfaAffx.25844.1.S1_at	2.940440E-03	1.170600E-01	0.89	1.13	PREDICTED: Canis familiaris hypothetical LOC22889; transcript variant 4 (LOC612936); mRNA	100.0	CR602947	XM_859480	LOC612936	hypothetical LOC612936
CfaAffx.25864.1.S1_at	5.649310E-04	4.897046E-02	1.14	.88	PREDICTED: Canis familiaris similar to ATP-binding cassette; sub-family D; member 4 isoform 1; transcript variant 4 (LOC490781); mRNA	70.8	NULL	XM_862917	ABCD4	ATP-binding cassette, sub-family D (ALD), member 4
CfaAffx.25899.1.S1_x_at	2.007860E-02	2.924196E-01	1.1	.91	Magnaporthe grisea 70-15 hypothetical protein (MGG_11634) partial mRNA	9.4	AC005921	XM_001411405	MGG_11634	hypothetical protein
CfaAffx.25962.1.S1_at	8.519580E-03	1.973305E-01	0.91	1.10	PREDICTED: Canis familiaris similar to CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase); transcript variant 2 (LOC489940); mRNA	100.0	CU674709	XM_844107	CDIPT	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)
CfaAffx.25987.1.S1_s_at	1.913080E-03	9.452284E-02	1.14	.88	PREDICTED: Equus caballus similar to integrin alpha 3 (LOC100056202); mRNA	86.9	AK289961	XM_001502583	ITGA3	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)
CfaAffx.2600.1.S1_s_at	5.837560E-03	1.640145E-01	1.15	.87	PREDICTED: Equus caballus hypothetical protein LOC100072627 (LOC100072627); mRNA	65.1	CU692209	XM_001502633		
CfaAffx.26004.1.S1_at	4.219440E-04	4.208376E-02	1.23	.81	Armoracia rusticana Arcry2-3 mRNA for cryptochrome 2; complete cds	38.0	NULL	AB092683		
CfaAffx.26023.1.S1_at	9.866190E-03	2.111891E-01	1.11	.90	PREDICTED: Canis familiaris similar to Alpha-sarcoglycan precursor (Alpha-SG) (Adhalin) (50 kDa dystrophin-associated glycoprotein) (50DAG) (Dystroglycan 2) (LOC609265); mRNA	99.7	NULL	XM_846494	SGCA	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)
CfaAffx.26039.1.S1_at	2.745140E-	1.124045E-	1.14	.88	PREDICTED: Canis familiaris hypothetical	68.5	NM_153229	XM_846500	TMEM92	transmembrane protein 92

	03	01			protein LOC609270 (LOC609270); mRNA					
CfaAffx.26081.1.S1_at	3.118980E-06	2.396362E-03	1.23	.81	PREDICTED: Homo sapiens similar to Keratin; type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Cytokeratin endo A) (LOC342419); mRNA	18.2	AC007182	XR_018318		
CfaAffx.26083.1.S1_s_at	9.611150E-03	2.084125E-01	1.1	.91	PREDICTED: Canis familiaris similar to Zinc finger protein 261 (DXS6673E protein); transcript variant 4 (LOC491948); mRNA	100.0	AB002383	XM_549068	ZMYM3	zinc finger, MYM-type 3
CfaAffx.26106.1.S1_s_at	7.457250E-04	5.610538E-02	0.86	1.17	PREDICTED: Canis familiaris similar to arginyl-tRNA synthetase; transcript variant 4 (LOC609803); mRNA	99.8	NM_002887	XM_861845	RARS	arginyl-tRNA synthetase
CfaAffx.26161.1.S1_at	2.946370E-03	1.171506E-01	1.1	.91	PREDICTED: Rattus norvegicus similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (LOC307263); mRNA	39.4	NULL	XR_007312	LOC307263	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
CfaAffx.26185.1.S1_at	8.299820E-04	5.946195E-02	1.12	.89	NULL	null	AL663088	NULL		
CfaAffx.26219.1.S1_s_at	1.357710E-03	7.895818E-02	0.83	1.21	PREDICTED: Canis familiaris similar to Cyclin-dependent kinases regulatory subunit 1 (CKS-1) (Sid 1334) (LOC612237); mRNA	100.0	AK311769	XM_849974	CKS1B	CDC28 protein kinase regulatory subunit 1B
CfaAffx.26219.1.S1_x_at	2.410930E-03	1.049012E-01	0.77	1.30	PREDICTED: Canis familiaris similar to Cyclin-dependent kinases regulatory subunit 1 (CKS-1) (Sid 1334) (LOC612237); mRNA	100.0	AK311769	XM_849974	CKS1B	CDC28 protein kinase regulatory subunit 1B
CfaAffx.26220.1.S1_s_at	6.885840E-06	3.548256E-03	1.18	.85	PREDICTED: Canis familiaris similar to voltage-dependent calcium channel alpha 1G subunit isoform 8; transcript variant 17 (LOC491083); mRNA	100.0	NULL	XM_860802	CACNA1G	calcium channel, voltage-dependent, T type, alpha 1G subunit
CfaAffx.26269.1.S1_at	9.134920E-03	2.028678E-01	1.12	.89	PREDICTED: Canis familiaris similar to odd Oz/ten-m homolog 2 (LOC489137); mRNA	86.5	NM_001122679	XM_546255	LOC489137	similar to odd Oz/ten-m homolog 2
CfaAffx.26283.1.S1_at	5.014760E-05	1.160270E-02	1.17	.86	PREDICTED: Canis familiaris cOR2Y2 olfactory receptor family 2 subfamily Y-like (cOR2Y2); mRNA	61.0	NULL	XM_545435	cOR2Y2	cOR2Y2 olfactory receptor family 2 subfamily Y-like

CfaAffx.26287.1.S1 s at	1.324900E-02	2.417002E-01	1.1	.91	PREDICTED: Canis familiaris similar to Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1) (CD126 antigen) (LOC612271); mRNA	100.0	BC132686	XM 850012	IL6R	interleukin 6 receptor
CfaAffx.26349.1.S1 at	6.430810E-03	1.722153E-01	1.12	.90	PREDICTED: Equus caballus hypothetical protein LOC100059217 (LOC100059217); mRNA	92.1	BC103980	XM 001504982	ZDHHC15	zinc finger, DHHC-type containing 15
CfaAffx.26362.1.S1 at	5.117120E-03	1.525288E-01	1.17	.85	Homo sapiens cDNA; FLJ96186	100.0	NM 198904	AK315200	GABRG2	gamma-aminobutyric acid (GABA) A receptor, gamma 2
CfaAffx.26399.1.S1 at	1.041620E-02	2.155102E-01	1.11	.90	PREDICTED: Canis familiaris similar to gamma-aminobutyric acid (GABA) A receptor; beta 2 isoform 1; transcript variant 8 (LOC489146); mRNA	39.5	AC091882	XM 862047	GABRB2	gamma-aminobutyric acid (GABA) A receptor, beta 2
CfaAffx.26421.1.S1 at	2.611450E-06	2.234892E-03	0.83	1.20	PREDICTED: Canis familiaris similar to step II splicing factor SLU7 (LOC479308); mRNA	67.9	AB169852	XM 536446	SLU7	SLU7 splicing factor homolog (S. cerevisiae)
CfaAffx.2647.1.S1 at	1.208930E-02	2.331972E-01	1.14	.88	PREDICTED: Canis familiaris similar to ribosomal protein S24 isoform 3; transcript variant 4 (LOC485132); mRNA	47.5	NULL	XM 859358	LOC485132	similar to ribosomal protein S24 isoform 3
CfaAffx.26487.1.S1 s at	2.051000E-02	2.951623E-01	0.88	1.13	PREDICTED: Canis familiaris similar to zinc finger protein 617 (LOC611075); mRNA	100.0	AK290911	XM 848708	ZNF564	zinc finger protein 564
CfaAffx.26512.1.S1 at	3.284690E-03	1.233478E-01	1.11	.90	PREDICTED: Canis familiaris similar to tubulin; alpha 1 (LOC491090); mRNA	99.6	NULL	XM 847699	LOC491090	similar to tubulin, alpha 1
CfaAffx.26516.1.S1 at	4.187760E-03	1.387377E-01	1.1	.91	PREDICTED: Canis familiaris similar to kinesin protein (LOC491092); mRNA	99.8	AC019315	XM 548212	KIF2B	kinesin family member 2B
CfaAffx.26523.1.S1 at	2.393860E-03	1.047911E-01	1.14	.88	PREDICTED: Canis familiaris similar to ribosomal protein S3a; transcript variant 7 (LOC608454); mRNA	39.0	NULL	XM 856546	LOC608454	similar to ribosomal protein S3a
CfaAffx.26540.1.S1 at	8.808500E-03	2.007806E-01	0.87	1.15	PREDICTED: Canis familiaris similar to bromo domain-containing protein disrupted in leukemia (LOC491984); mRNA	87.6	NM 153252	XM 549104	BRWD3	bromodomain and WD repeat domain containing 3
CfaAffx.26559.1.S1 s at	9.035030E-	2.017118E-	1.1	.91	PREDICTED: Canis familiaris hypothetical	100.0	AB170566	XM 846961	TMEM100	transmembrane protein 100

	03	01			protein LOC609661 (LOC609661); mRNA					
CfaAffx.26569.1.S1_at	4.616230E-03	1.453251E-01	1.13	.88	Mus musculus 10 days neonate cerebellum cDNA; RIKEN full-length enriched library; clone:B930051D08 product:NONMUSCLE MYOSIN II HEAVY CHAIN-B (FRAGMENT) homolog [Homo sapiens]; full insert sequence	91.0	AK047340	AK047340	Myh10	myosin, heavy polypeptide 10, non-muscle
CfaAffx.26595.1.S1_s_at	1.113880E-02	2.226272E-01	0.81	1.23	PREDICTED: Canis familiaris similar to nucleoporin 210kDa-like (LOC490448); mRNA	100.0	NM_207308	XM_547570	NUP210L	nucleoporin 210kDa-like
CfaAffx.26638.1.S1_at	2.609460E-04	3.163327E-02	1.2	.83	NULL	null	AC097658	NULL		
CfaAffx.26684.1.S1_at	9.162700E-03	2.032561E-01	1.15	.87	Homo sapiens tetraspanin 16 (TSPAN16); mRNA	48.6	NM_012466	NM_012466	TSPAN16	tetraspanin 16
CfaAffx.26687.1.S1_at	3.120310E-05	9.216261E-03	1.21	.83	PREDICTED: Canis familiaris similar to olfactory receptor 464 (LOC609961); mRNA	57.5	NULL	XM_847316	LOC609961	similar to olfactory receptor 464
CfaAffx.26721.1.S1_at	7.652810E-03	1.855017E-01	0.91	1.10	PREDICTED: Canis familiaris similar to CG13902-PA (LOC608058); mRNA	99.8	NM_024773	XM_844945	JMJD5	jumonji domain containing 5
CfaAffx.26750.1.S1_at	1.093620E-02	2.203368E-01	0.85	1.18	PREDICTED: Canis familiaris similar to thyroid hormone receptor interactor 11 (LOC608376); mRNA	99.8	AK307489	XM_845392	LOC608376	similar to thyroid hormone receptor interactor 11
CfaAffx.26755.1.S1_at	5.044230E-03	1.515045E-01	1.1	.91	PREDICTED: Canis familiaris similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP) (LOC490827); mRNA	90.5	NULL	XM_850009	LOC490827	similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP)
CfaAffx.26769.1.S1_s_at	1.257290E-04	2.059437E-02	1.13	.89	PREDICTED: Canis familiaris similar to Protocadherin 19 precursor (LOC492013); mRNA	100.0	EF676096	XM_549133	PCDH19	protocadherin 19
CfaAffx.26800.1.S1_s_at	2.286210E-04	2.963465E-02	1.18	.85	PREDICTED: Canis familiaris fast myosin heavy chain; transcript variant 1 (MYH1); mRNA	100.0	X51592	XM_546622	MYH8	myosin, heavy chain 8, skeletal muscle, perinatal

CfaAffx.26810.1.S1_s_at	1.945070E-02	2.895647E-01	1.13	.88	PREDICTED: Canis familiaris similar to p53 inducible protein (LOC479317); mRNA	100.0	AB384575	XM_536455	CYFIP2	cytoplasmic FMR1 interacting protein 2
CfaAffx.26821.1.S1_at	9.395910E-05	1.713360E-02	1.19	.84	PREDICTED: Canis familiaris hypothetical protein LOC610018 (LOC610018); mRNA	73.3	AC005666	XM_847402	LOC610018	hypothetical protein LOC610018
CfaAffx.26848.1.S1_at	5.701190E-03	1.619477E-01	1.11	.90	Ursus americanus skeletal muscle myosin type IIa mRNA; partial cds	94.6	NM_017534	AY943173		
CfaAffx.26886.1.S1_s_at	3.625540E-05	9.812900E-03	1.12	.89	PREDICTED: Macaca mulatta similar to NADPH oxidase 1 isoform long variant; transcript variant 3 (LOC701376); mRNA	87.9	NM_013955	XM_001090025	LOC701376	similar to NADPH oxidase 1 isoform long variant
CfaAffx.269.1.S1_at	1.328850E-06	1.429676E-03	1.24	.81	PREDICTED: Canis familiaris similar to olfactory receptor Olr1414 (LOC482222); mRNA	100.0	NULL	XM_539341	LOC482222	similar to olfactory receptor Olr1414
CfaAffx.26959.1.S1_at	2.043720E-04	2.757100E-02	1.2	.83	PREDICTED: Canis familiaris similar to OTU domain; ubiquitin aldehyde binding 2 (LOC480420); mRNA	62.1	AL079302	XM_537541	OTUB2	OTU domain, ubiquitin aldehyde binding 2
CfaAffx.26960.1.S1_at	1.535780E-02	2.602160E-01	1.1	.91	Homo sapiens cDNA FLJ75585 complete cds; highly similar to Homo sapiens dystrophin related protein 2 (DRP2); mRNA	89.5	AK289825	AK289825	DRP2	dystrophin related protein 2
CfaAffx.26980.1.S1_at	1.495290E-06	1.569507E-03	1.25	.80	PREDICTED: Homo sapiens lipoxygenase homology domains 1 (LOXHD1); mRNA	25.6	AC004976	XM_001713756	LOXHD1	lipoxygenase homology domains 1
CfaAffx.27011.1.S1_at	6.760040E-06	3.548256E-03	1.36	.74	Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTLS32ZB06 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress)	37.9	NULL	BX827281		
CfaAffx.27042.1.S1_at	4.578720E-04	4.397439E-02	1.14	.88	Homo sapiens mRNA for FP3235 variant; clone: CBR07485	25.8	AK225173	AK225173	QTRT1	queuine tRNA-ribosyltransferase 1
CfaAffx.27048.1.S1_at	7.977980E-04	5.829072E-02	1.13	.88	Homo sapiens cDNA; FLJ17911	67.4	AK310869	AK310869	SERPINA5	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5
CfaAffx.27050.1.S1_s_at	6.980480E-	3.548256E-	1.21	.83	PREDICTED: Canis familiaris similar to serine (or cysteine) proteinase inhibitor; clade A (alpha-1 antiproteinase;	99.2	AK313196	XM_547962	SERPINA4	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase,

	06	03			antitrypsin); member 4 (LOC490840); mRNA					antitrypsin), member 4
CfaAffx.27092.1.S1_at	9.461260E-03	2.067879E-01	0.9	1.12	PREDICTED: Equus caballus similar to Armadillo repeat containing; X-linked 6 (LOC100060676); mRNA	89.0	CU675754	XM_001492877	LOC100060676	similar to Armadillo repeat containing, X-linked 6
CfaAffx.27158.1.S1_at	1.216410E-02	2.337430E-01	0.89	1.13	PREDICTED: Canis familiaris hypothetical LOC479813 (LOC479813); mRNA	100.0	NM_173615	XM_536940	VWA3A	von Willebrand factor A domain containing 3A
CfaAffx.27166.1.S1_at	3.868400E-07	5.945593E-04	1.35	.74	NULL	null	AP005203	NULL		
CfaAffx.27220.1.S1_s_at	4.199620E-05	1.056904E-02	1.18	.85	PREDICTED: Canis familiaris similar to ATP-binding cassette transporter sub-family A member 15 (LOC489979); mRNA	95.5	AC066692	XM_547099	LOC489979	similar to ATP-binding cassette transporter sub-family A member 15
CfaAffx.27228.1.S1_at	5.574670E-05	1.220385E-02	1.21	.83	Nematostella vectensis predicted protein (NEMVEDRAFT_v1g223487) partial mRNA	24.5	AP002956	XM_001620035	NEMVEDRAFT_v1g223487	hypothetical protein
CfaAffx.27241.1.S1_s_at	3.060640E-03	1.189972E-01	0.8	1.25	PREDICTED: Canis familiaris similar to vaccinia related kinase 1 (LOC490848); mRNA	100.0	AK290110	XM_547970	VRK1	vaccinia related kinase 1
CfaAffx.27251.1.S1_s_at	1.529950E-02	2.602160E-01	1.11	.90	PREDICTED: Canis familiaris similar to Mu-crystallin homolog (NADP-regulated thyroid-hormone binding protein); transcript variant 3 (LOC479818); mRNA	100.0	AB173432	XM_845361	CRYM	crystallin, mu
CfaAffx.2729.1.S1_at	2.000440E-02	2.922407E-01	1.11	.90	NULL	null	AC079176	NULL		
CfaAffx.27290.1.S1_at	3.559290E-03	1.277456E-01	0.81	1.23	PREDICTED: Equus caballus hypothetical protein LOC100071410 (LOC100071410); mRNA	90.4	BC156433	XM_001503800	LOC100071410	similar to phosphatidylinositol glycan, class W
CfaAffx.27300.1.S1_at	1.132950E-02	2.252032E-01	0.89	1.12	Homo sapiens tyrosine kinase 2 (TYK2) gene; complete cds	76.9	AK308360	AY549314		
CfaAffx.27320.1.S1_at	2.014410E-02	2.928487E-01	1.17	.85	PREDICTED: Canis familiaris similar to Dual specificity mitogen-activated protein kinase kinase 4 (MAP kinase kinase 4) (JNK activating kinase 1) (c-Jun N-terminal kinase kinase 1) (JNKK) (SAPK/ERK kinase	100.0	AK131544	XM_546627	MAP2K4	mitogen-activated protein kinase kinase 4

					1) (SEK1) (LOC489508); mRNA					
CfaAffx.27321.1.S1_s_at	2.403250E-03	1.049012E-01	0.88	1.14	PREDICTED: Canis familiaris similar to Non-receptor tyrosine-protein kinase TYK2 (LOC476714); mRNA	94.6	AK308360	XM_533918	TYK2	tyrosine kinase 2
CfaAffx.27349.1.S1_at	6.418230E-03	1.720925E-01	0.75	1.33	PREDICTED: Canis familiaris similar to chromosome 18 open reading frame 21; transcript variant 2 (LOC480160); mRNA	100.0	BC119766	XM_537283	LOC480160	similar to chromosome 18 open reading frame 21
CfaAffx.27359.1.S1_at	7.348000E-03	1.822600E-01	1.13	.89	PREDICTED: Canis familiaris similar to Sphingosine 1-phosphate receptor Edg-5 (S1P receptor Edg-5) (Endothelial differentiation G-protein coupled receptor 5) (Sphingosine 1-phosphate receptor 2) (S1P2) (LOC484959); mRNA	100.0	NM_004230	XM_542076	S1PR2	sphingosine-1-phosphate receptor 2
CfaAffx.27405.1.S1_s_at	1.416710E-03	8.053912E-02	1.12	.90	PREDICTED: Canis familiaris similar to solute carrier family 36 (proton/amino acid symporter); member 3 (LOC489175); mRNA	100.0	BC101095	XM_546293	SLC36A3	solute carrier family 36 (proton/amino acid symporter), member 3
CfaAffx.27455.1.S1_s_at	1.101180E-02	2.215217E-01	0.86	1.16	PREDICTED: Canis familiaris similar to exonuclease NEF-sp; transcript variant 5 (LOC479820); mRNA	100.0	AK314458	XM_856648	LOC479820	similar to exonuclease NEF-sp
CfaAffx.27472.1.S1_s_at	1.744590E-03	9.056506E-02	1.11	.90	PREDICTED: Canis familiaris similar to Y45F10A.6b; transcript variant 1 (LOC492052); mRNA	100.0	NM_017752	XM_549172	TBC1D8B	TBC1 domain family, member 8B (with GRAM domain)
CfaAffx.2751.1.S1_at	2.529610E-04	3.122886E-02	1.16	.86	PREDICTED: Bos taurus similar to olfactory receptor MOR107-1 (LOC783250); partial mRNA	89.9	NM_001001959	XM_001251887	LOC783250	similar to olfactory receptor 323
CfaAffx.27521.1.S1_at	1.141290E-04	1.933678E-02	1.2	.83	Bos taurus similar to dystrobrevin alpha; mRNA (cDNA clone MGC:140020 IMAGE:8286407); complete cds	93.0	NM_001392	BC118294	DTNA	dystrobrevin, alpha
CfaAffx.27529.1.S1_at	3.570170E-03	1.277456E-01	0.86	1.17	Homo sapiens acyl-CoA synthetase medium-chain family member 3; mRNA (cDNA clone MGC:3570 IMAGE:3617826); complete cds	39.6	EU176405	BC002790	ACSM3	acyl-CoA synthetase medium-chain family member 3

CfaAffx.27529.1.S1_s_at	1.389550E-03	7.994557E-02	0.81	1.23	PREDICTED: Canis familiaris similar to SA hypertension-associated homolog isoform 1 (LOC608888); mRNA	100.0	AB179232	XM_846027	ACSM3	acyl-CoA synthetase medium-chain family member 3
CfaAffx.27538.1.S1_at	1.253340E-02	2.359470E-01	0.89	1.13	Homo sapiens zinc finger protein 624; mRNA (cDNA clone MGC:119602 IMAGE:40008882); complete cds	79.4	BC103944	BC103943	ZNF624	zinc finger protein 624
CfaAffx.27545.1.S1_at	1.427030E-02	2.509538E-01	1.11	.90	PREDICTED: Canis familiaris similar to Acetyl-coenzyme A synthetase (Acetate--CoA ligase) (Acyl-activating enzyme) (Acetyl-CoA synthetase) (ACS) (AceCS) (LOC609009); mRNA	100.0	NM_017888	XM_846187	ACSM5	acyl-CoA synthetase medium-chain family member 5
CfaAffx.27551.1.S1_s_at	4.244340E-04	4.208645E-02	1.16	.86	PREDICTED: Canis familiaris similar to Myosin-9 (Myosin heavy chain; nonmuscle IIa) (Nonmuscle myosin heavy chain IIa) (NMHC II-a) (Cellular myosin heavy chain; type A) (Nonmuscle myosin heavy chain-A) (NMMHC-A) (LOC490493); mRNA	100.0	AK129955	XM_850292	LOC490493	similar to Myosin-9 (Myosin heavy chain, nonmuscle IIa) (Nonmuscle myosin heavy chain IIa) (NMHC II-a) (Cellular myosin heavy chain, type A) (Nonmuscle myosin heavy chain-A) (NMMHC-A)
CfaAffx.27607.1.S1_at	2.467330E-03	1.059811E-01	1.13	.88	PREDICTED: Canis familiaris similar to N-acetylglucosaminyl-phosphatidylinositol de-N-acetylase (Phosphatidylinositol-glycan biosynthesis; class L protein) (PIG-L) (LOC479514); mRNA	66.1	CU686622	XM_536652	PIGL	phosphatidylinositol glycan anchor biosynthesis, class L
CfaAffx.27608.1.S1_at	2.359330E-05	7.691952E-03	1.28	.78	PREDICTED: Equus caballus similar to collagen; type IV; alpha 5 (Alport syndrome);; transcript variant 1 (LOC100054545); mRNA	88.2	BC151846	XM_001490419	LOC100054545	similar to collagen, type IV, alpha 5 (Alport syndrome)
CfaAffx.27612.1.S1_at	1.069840E-02	2.176197E-01	1.1	.91	PREDICTED: Canis familiaris similar to eukaryotic translation elongation factor 1 alpha 1 (LOC607797); mRNA	64.9	NULL	XM_844656	LOC607797	similar to eukaryotic translation elongation factor 1 alpha 1
CfaAffx.27616.1.S1_s_at	1.442140E-02	2.522842E-01	1.15	.87	PREDICTED: Canis familiaris similar to transcriptional co-repressor Sin3A (LOC478372); mRNA	97.9	BX649162	XM_535546	SIN3A	SIN3 homolog A, transcription regulator (yeast)
CfaAffx.2768.1.S1_at	8.240080E-04	5.929964E-02	1.17	.86	PREDICTED: Canis familiaris cOR2T13 olfactory receptor family 2 subfamily T-like (cOR2T13); mRNA	100.0	XM_001713613	XM_539348	cOR2T13	cOR2T13 olfactory receptor family 2 subfamily T-like

CfaAffx.27726.1.S1_s_at	1.228620E-05	4.988203E-03	1.2	.83	PREDICTED: Canis familiaris similar to transmembrane channel-like gene family 5 (predicted) (LOC489989); mRNA	100.0	NM_001105249	XM_547109	TMC5	transmembrane channel-like 5
CfaAffx.27734.1.S1_at	5.129460E-04	4.627805E-02	1.18	.85	Kogia simus KSOR1 gene for olfactory receptor; partial cds	89.2	BK004266	AB301617		
CfaAffx.27735.1.S1_at	4.765110E-03	1.476361E-01	1.12	.89	PREDICTED: Canis familiaris olfactory receptor (OR08C06); mRNA	90.6	NULL	XM_542099	OR08C06	olfactory receptor
CfaAffx.27737.1.S1_at	5.929520E-03	1.652817E-01	1.13	.88	PREDICTED: Canis familiaris olfactory receptor (OR08C06); mRNA	99.5	NULL	XM_542099	OR08C06	olfactory receptor
CfaAffx.2774.1.S1_at	7.771990E-04	5.697915E-02	1.2	.83	PREDICTED: Canis familiaris similar to Olfactory receptor 2M3 (LOC482235); mRNA	98.0	AL592313	XM_844645	LOC482235	similar to Olfactory receptor 2M3
CfaAffx.27741.1.S1_x_at	3.062080E-04	3.432983E-02	1.16	.86	PREDICTED: Canis familiaris similar to Olfactory receptor 7G1 (Olfactory receptor 19-15) (OR19-15) (LOC611416); mRNA	99.6	NULL	XM_849085	LOC611416	similar to Olfactory receptor 7G1 (Olfactory receptor 19-15) (OR19-15)
CfaAffx.27745.1.S1_at	5.367980E-04	4.724152E-02	1.12	.89	PREDICTED: Canis familiaris olfactory receptor (OR04A12); mRNA	99.5	NULL	XM_542103	OR04A12	olfactory receptor
CfaAffx.27746.1.S1_at	2.292960E-03	1.027891E-01	1.14	.87	PREDICTED: Canis familiaris olfactory receptor (OR04A12); mRNA	99.6	NULL	XM_542103	OR04A12	olfactory receptor
CfaAffx.27747.1.S1_at	3.875050E-03	1.338385E-01	1.17	.86	PREDICTED: Bos taurus cadherin 2 (CDH2); mRNA	37.5	NULL	XM_001250829	CDH2	cadherin 2, type 1, N-cadherin (neuronal)
CfaAffx.27749.1.S1_at	2.752320E-03	1.125913E-01	1.29	.78	AGAP001787-PA (AgaP_AGAP001787) mRNA; complete cds	15.2	AC016482	XM_321281	AgaP_AGAP001787	AGAP001787-PA
CfaAffx.27750.1.S1_at	1.152950E-03	7.170116E-02	1.19	.84	PREDICTED: Canis familiaris olfactory receptor OR08F07 (OR08F07); mRNA	100.0	NULL	XM_542104	OR08F07	olfactory receptor OR08F07
CfaAffx.27751.1.S1_at	6.353550E-04	5.125131E-02	1.15	.87	PREDICTED: Canis familiaris olfactory receptor (OR08C10); mRNA	100.0	NULL	XM_542105	OR08C10	olfactory receptor
CfaAffx.27761.1.S1_at	3.613950E-03	1.285342E-01	1.11	.90	PREDICTED: Canis familiaris similar to Aquaporin 4 (WCH4) (Mercurial-insensitive water channel) (MIWC) (LOC612628);	99.5	D63412	XM_850363	AQP4	aquaporin 4

					mRNA				
CfaAffx.27762.1.S1_at	1.288980E-04	2.077575E-02	1.25	.80	PREDICTED: Canis familiaris similar to potassium channel tetramerisation domain containing 1 (LOC480170); mRNA	100.0	AC026844	XM_537294	KCTD1	potassium channel tetramerisation domain containing 1
CfaAffx.27771.1.S1_at	3.698270E-03	1.303481E-01	1.11	.90	PREDICTED: Canis familiaris similar to proteasome (prosome; macropain) subunit; alpha type; 8 isoform 2 (LOC490508); mRNA	81.3	AB168880	XM_547630	PSMA8	proteasome (prosome, macropain) subunit, alpha type, 8
CfaAffx.27784.1.S1_at	1.125380E-03	7.089828E-02	1.13	.89	PREDICTED: Gallus gallus hypothetical LOC430303 (LOC430303); mRNA	12.1	NULL	XM_427861	LOC430303	hypothetical LOC430303
CfaAffx.27790.1.S1_at	1.353730E-02	2.439323E-01	1.18	.85	NULL	null	NG_007077	NULL		
CfaAffx.27806.1.S1_x_at	5.852970E-04	4.987774E-02	1.15	.87	PREDICTED: Canis familiaris similar to Small inducible cytokine A3-like 1 precursor (Tonsillar lymphocyte LD78 beta protein) (LD78-beta(1-70)) (G0/G1 switch regulatory protein 19-2) (G0S19-2 protein) (PAT 464.2) (LOC480600); mRNA	63.4	BC148784	XM_537720	LOC480600	similar to Small inducible cytokine A3-like 1 precursor (Tonsillar lymphocyte LD78 beta protein) (LD78-beta(1-70)) (G0/G1 switch regulatory protein 19-2) (G0S19-2 protein) (PAT 464.2)
CfaAffx.2781.1.S1_at	6.777290E-05	1.388860E-02	1.13	.88	PREDICTED: Canis familiaris cOR2T23 olfactory receptor family 2 subfamily T-like; transcript variant 1 (cOR2T23); mRNA	100.0	BC148403	XM_539357	cOR2T23	cOR2T23 olfactory receptor family 2 subfamily T-like
CfaAffx.2789.1.S1_at	2.515340E-04	3.122886E-02	1.18	.85	PREDICTED: Canis familiaris similar to Olfactory receptor 2T29 (LOC482243); mRNA	97.7	NM_001004697	XM_539362	LOC482243	similar to Olfactory receptor 2T29
CfaAffx.2796.1.S1_s_at	7.260910E-04	5.540306E-02	1.13	.89	PREDICTED: Equus caballus patched (LOC100033936); mRNA	89.2	BC152919	XM_001494689	LOC100033936	patched
CfaAffx.27984.1.S1_at	2.059970E-02	2.956998E-01	1.12	.90	PREDICTED: Canis familiaris similar to Cdc42 guanine nucleotide exchange factor (GEF) 9 (LOC489191); mRNA	100.0	AK123597	XM_546309	LOC489191	similar to Cdc42 guanine nucleotide exchange factor (GEF) 9
CfaAffx.27985.1.S1_at	4.709360E-05	1.113557E-02	1.2	.84	Pseudomonas putida FadD2 (fadD2) and FadD1 (fadD1) genes; complete cds; and unknown gene	52.8	DQ105654	AF290948		

CfaAffx.27994.1.S1_at	1.243340E-02	2.355224E-01	0.9	1.11	PREDICTED: Canis familiaris similar to Notchless homolog 1 (WD-repeat protein HUSSY-07) (LOC491142); mRNA	100.0	AB179488	XM_548262	NLE1	notchless homolog 1 (Drosophila)
CfaAffx.28047.1.S1_s_at	2.512540E-03	1.067395E-01	0.9	1.11	PREDICTED: Canis familiaris similar to THO complex subunit 1 (Tho1) (Nuclear matrix protein p84); transcript variant 6 (LOC490529); mRNA	98.6	AB170312	XM_851404	THOC1	THO complex 1
CfaAffx.28081.1.S1_at	1.733110E-03	9.022485E-02	1.17	.85	PREDICTED: Pan troglodytes serotonin 5-HT4 receptor; transcript variant 3 (HTR4); mRNA	51.5	NM_001040173	XM_001162146	HTR4	5-hydroxytryptamine (serotonin) receptor 4
CfaAffx.28104.1.S1_at	1.115100E-05	4.704738E-03	1.34	.75	Homo sapiens RTS (RTS) gene; complete cds; alternatively spliced	77.8	AF305057	AF305057		
CfaAffx.28117.1.S1_at	1.201520E-02	2.319758E-01	0.85	1.18	Bos taurus hypothetical protein LOC777593 (LOC777593); mRNA >gi|111601582|gb|BC120475.1| Bos taurus hypothetical protein LOC777593; mRNA (cDNA clone MGC:151928 IMAGE:8032383); complete cds	60.7	AC013265	NM_001078140	LOC777593	hypothetical protein LOC777593
CfaAffx.28124.1.S1_at	7.089660E-03	1.801083E-01	1.13	.89	Bigelowiella natans DNA directed RNA polymerase subunit I/II/III (rbp8) mRNA; complete cds	14.7	AC026991	XM_001712912	rbp8	DNA directed RNA polymerase subunit I/II/III
CfaAffx.28129.1.S1_at	7.598550E-05	1.513906E-02	1.23	.81	Canis lupus familiaris myeloid cell leukemia sequence 1 (BCL2-related) (MCL1); mRNA >gi|26006286|dbj|AB093582.2| Canis familiaris mRNA for Mcl-1; complete cds	17.1	AC109515	NM_001003016	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)
CfaAffx.28131.1.S1_at	1.856990E-02	2.823561E-01	1.1	.91	PREDICTED: Canis familiaris similar to Endothelial cell-specific molecule 1 precursor (ESM-1 secretory protein) (ESM-1) (LOC489201); mRNA	100.0	CU680151	XM_546319	ESM1	endothelial cell-specific molecule 1
CfaAffx.2814.1.S1_s_at	8.879360E-03	2.010117E-01	0.86	1.17	PREDICTED: Canis familiaris similar to eukaryotic translation termination factor 1 (predicted); transcript variant 3 (LOC474696); mRNA	58.0	AC113403	XM_854857	LOC474696	similar to eukaryotic translation termination factor 1 (predicted)
CfaAffx.28197.1.S1_x_at	1.228650E-05	4.988203E-03	0.73	1.36	PREDICTED: Canis familiaris similar to large subunit ribosomal protein L36a	95.9	NULL	XM_538108	RPL36A	ribosomal protein L36a

					(LOC480987); mRNA					
CfaAffx.2822.1.S1_s_at	1.101560E-02	2.215217E-01	1.12	.89	PREDICTED: Canis familiaris similar to Aminopeptidase O (AP-O); transcript variant 1 (LOC484139); mRNA	36.7	BX648970	XM_541256	LOC484139	similar to Aminopeptidase O (AP-O)
CfaAffx.28233.1.S1_s_at	6.667770E-03	1.749680E-01	0.86	1.16	PREDICTED: Canis familiaris similar to mitochondrial Rho 1; transcript variant 2 (LOC480613); mRNA	100.0	AB174561	XM_862873	RHOT1	ras homolog gene family, member T1
CfaAffx.28241.1.S1_s_at	7.359540E-04	5.581943E-02	1.16	.86	Camelus dromedarius IgVH mRNA for immunoglobulin heavy chain VHDJ region; partial cds; clone:YA0540H	48.8	M25625	AB092168		
CfaAffx.28243.1.S1_at	2.122820E-09	3.045185E-05	1.52	.66	NULL	null	AC104619	NULL		
CfaAffx.28274.1.S1_at	2.129310E-03	9.931387E-02	1.19	.84	PREDICTED: Canis familiaris similar to Ig heavy chain V-III region VH26 precursor (LOC607202); mRNA	100.0	AY909713	XM_843810	LOC607202	similar to Ig heavy chain V-III region VH26 precursor
CfaAffx.283.1.S1_s_at	7.124840E-03	1.804793E-01	1.22	.82	PREDICTED: Equus caballus similar to olfactory receptor; family 6; subfamily C; member 3 (LOC100055600); mRNA	91.1	AC213208	XM_001489711	LOC100055600	similar to olfactory receptor, family 6, subfamily C, member 3
CfaAffx.28332.1.S1_at	1.751790E-02	2.755420E-01	1.11	.90	PREDICTED: Canis familiaris hypothetical protein LOC609651 (LOC609651); mRNA	100.0	AB168304	XM_846950	LOC609651	hypothetical protein LOC609651
CfaAffx.28353.1.S1_s_at	4.022460E-03	1.361971E-01	0.84	1.19	Sus scrofa clone Clu_55966.scr.msk.p1.Contig1; mRNA sequence	94.9	AK290111	AY610012		
CfaAffx.28355.1.S1_at	2.063980E-02	2.958807E-01	0.86	1.16	PREDICTED: Canis familiaris similar to mesoderm induction early response 1; transcript variant 2 (LOC479536); mRNA	100.0	NM_020948	XM_846977	MIER1	mesoderm induction early response 1 homolog (Xenopus laevis)
CfaAffx.28446.1.S1_at	1.543380E-02	2.607485E-01	1.14	.88	PREDICTED: Canis familiaris janus kinase 1; transcript variant 8 (JAK1); mRNA	96.2	NULL	XM_860114	JAK1	Janus kinase 1 (a protein tyrosine kinase)
CfaAffx.28452.1.S1_at	7.582990E-03	1.848702E-01	1.16	.86	PREDICTED: Canis familiaris similar to osmosis responsive factor (LOC479352); mRNA	100.0	AK312560	XM_536492	TTC33	tetratricopeptide repeat domain 33

CfaAffx.28455.1.S1_at	2.394600E-04	3.050303E-02	1.23	.81	Mesocricetus auratus mRNA for carboxylesterase; complete cds	37.9	AC006435	D50578		
CfaAffx.28463.1.S1_at	1.043180E-02	2.157284E-01	0.76	1.32	PREDICTED: Canis familiaris similar to Complement C3 precursor (LOC476728); mRNA	100.0	K02765	XM_533932	C3	complement component 3
CfaAffx.28464.1.S1_at	2.098450E-02	2.978695E-01	1.1	.91	PREDICTED: Canis familiaris similar to von Willebrand factor type A and cache domain containing 1 (LOC479541); mRNA	100.0	NM_020925	XM_536680	CACHD1	cache domain containing 1
CfaAffx.28495.1.S1_at	8.079810E-03	1.913213E-01	1.15	.87	Arabidopsis thaliana unknown protein (At1g48420) mRNA; complete cds	35.2	NULL	AY093325		
CfaAffx.285.1.S1_at	1.138100E-02	2.254979E-01	1.1	.91	PREDICTED: Canis familiaris similar to NADP-dependent retinol dehydrogenase/reductase (LOC488391); mRNA	89.3	NULL	XM_545513	DHRS9	dehydrogenase/reductase (SDR family) member 9
CfaAffx.2860.1.S1_at	1.526360E-03	8.389132E-02	1.16	.86	NULL	null	AC083873	NULL		
CfaAffx.28606.1.S1_s_at	6.053350E-04	5.058367E-02	1.18	.85	PREDICTED: Canis familiaris similar to BCL6 co-repressor-like 1 (LOC481047); mRNA	99.7	NM_021946	XM_538169	BCORL1	BCL6 co-repressor-like 1
CfaAffx.28627.1.S1_at	1.182300E-02	2.296042E-01	1.13	.89	PREDICTED: Canis familiaris similar to UDP glycosyltransferase 3 family; polypeptide A2 (LOC489234); mRNA	100.0	CU690025	XM_546352	UGT3A2	UDP glycosyltransferase 3 family, polypeptide A2
CfaAffx.28655.1.S1_s_at	6.033280E-04	5.051405E-02	1.15	.87	NULL	null	AP001180	NULL		
CfaAffx.28665.1.S1_s_at	1.155720E-02	2.272224E-01	1.1	.91	PREDICTED: Canis familiaris similar to KPL2 protein isoform 1; transcript variant 1 (LOC489235); mRNA	99.8	BX648691	XM_546353	SPEF2	sperm flagellar 2
CfaAffx.28671.1.S1_at	5.436880E-04	4.772389E-02	1.2	.83	PREDICTED: Mus musculus RIKEN cDNA 9030411M15 gene (9030411M15Rik); mRNA	57.2	AK127627	XM_001478778	9030411M15Rik	RIKEN cDNA 9030411M15 gene
CfaAffx.28697.1.S1_s_at	8.124630E-03	1.916905E-01	0.87	1.15	PREDICTED: Canis familiaris similar to apoptosis regulator; transcript variant 2	100.0	AK291114	XM_858095	BFAR	bifunctional apoptosis regulator

					(LOC489998); mRNA					
CfaAffx.28712.1.S1_at	5.544800E-03	1.592432E-01	0.86	1.16	Homo sapiens cDNA; FLJ97440	98.3	AK307492	AK307492	BXDC2	brix domain containing 2
CfaAffx.28727.1.S1_at	1.842450E-04	2.575784E-02	1.12	.89	PREDICTED: Canis familiaris similar to dedicator of cytokinesis 7 (LOC479548); mRNA	100.0	AB284127	XM_536687	DOCK7	dedicator of cytokinesis 7
CfaAffx.28731.1.S1_at	2.042110E-03	9.710601E-02	1.1	.91	PREDICTED: Pan troglodytes similar to olfactory receptor 1323 (LOC743834); mRNA	81.7	AL135784	XR_020926	LOC743834	similar to olfactory receptor 1323
CfaAffx.28743.1.S1_at	1.724090E-02	2.742666E-01	0.9	1.11	PREDICTED: Canis familiaris similar to retinoic acid induced 14 (LOC479368); mRNA	100.0	NULL	XM_536507	RAI14	retinoic acid induced 14
CfaAffx.28766.1.S1_s_at	1.905710E-02	2.870572E-01	1.12	.90	PREDICTED: Canis familiaris similar to InaD-like protein isoform 1; transcript variant 1 (LOC479550); mRNA	100.0	AJ224748	XM_536689	INADL	InaD-like (Drosophila)
CfaAffx.28768.1.S1_x_at	4.849630E-06	2.898664E-03	1.28	.78	Homo sapiens cDNA; FLJ92386	90.2	AK312104	AK312104	HSPE1	heat shock 10kDa protein 1 (chaperonin 10)
CfaAffx.28788.1.S1_at	1.313070E-02	2.404594E-01	1.14	.88	PREDICTED: Equus caballus hypothetical protein LOC100055746 (LOC100055746); mRNA	92.2	NM_032167	XM_001489792	LOC100055746	hypothetical protein LOC100055746
CfaAffx.28790.1.S1_at	1.887770E-02	2.855542E-01	0.72	1.38	Homo sapiens B cell maturation antigen transcript variant 4 (BCMA) mRNA; complete cds; alternatively spliced	30.8	EF152353	EF152355	TNFRSF17	tumor necrosis factor receptor superfamily, member 17
CfaAffx.288.1.S1_at	6.797880E-07	8.806493E-04	1.21	.83	PREDICTED: Canis familiaris cOR56A4 olfactory receptor family 56 subfamily A-like (cOR56A4); mRNA	99.6	BK004255	XM_542429	cOR56A4	cOR56A4 olfactory receptor family 56 subfamily A-like
CfaAffx.28803.1.S1_s_at	2.100170E-03	9.856141E-02	1.11	.90	PREDICTED: Canis familiaris similar to F-box only protein 16 (LOC608213); mRNA	100.0	AF453435	XM_845172	FBXO16	F-box protein 16
CfaAffx.28876.1.S1_at	1.970470E-02	2.911700E-01	0.88	1.13	PREDICTED: Canis familiaris similar to OMA1 homolog; zinc metallopeptidase (LOC489569); mRNA	100.0	CU680447	XM_546689	OMA1	OMA1 homolog, zinc metallopeptidase (S. cerevisiae)

CfaAffx.28915.1.S1_s_at	2.585290E-03	1.087566E-01	1.14	.88	PREDICTED: Canis familiaris similar to Disabled homolog 1 (LOC610344); mRNA	100.0	AB055282	XM_847827	DAB1	disabled homolog 1 (Drosophila)
CfaAffx.28926.1.S1_at	8.167370E-05	1.576156E-02	1.14	.87	PREDICTED: Canis familiaris similar to ubiquitin-like; containing PHD and RING finger domains; 1; transcript variant 1 (LOC611463); mRNA	41.5	AC004103	XM_849329	UHRF1	ubiquitin-like with PHD and ring finger domains 1
CfaAffx.28942.1.S1_at	1.798790E-02	2.790268E-01	1.11	.90	PREDICTED: Canis familiaris similar to Bombesin receptor subtype-3 (BRS-3) (LOC613002); mRNA	90.2	NM_001727	XM_849676	BRS3	bombesin-like receptor 3
CfaAffx.28972.1.S1_at	1.943840E-02	2.895647E-01	1.11	.90	PREDICTED: Canis familiaris similar to 5-AMP-activated protein kinase; catalytic alpha-2 chain (AMPK alpha-2 chain) (LOC489571); mRNA	96.9	NM_006252	XM_546691	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit
CfaAffx.28977.1.S1_at	1.028790E-03	6.728568E-02	1.14	.88	PREDICTED: Canis familiaris similar to G protein-coupled receptor 101 (LOC492167); mRNA	100.0	NM_054021	XM_549287	GPR101	G protein-coupled receptor 101
CfaAffx.28982.1.S1_s_at	1.082650E-02	2.187410E-01	0.9	1.12	PREDICTED: Canis familiaris similar to T25G3.1 (LOC476657); mRNA	97.4	AK289549	XM_533861	LOC476657	similar to T25G3.1
CfaAffx.28991.1.S1_at	1.609530E-02	2.655683E-01	1.12	.90	PREDICTED: Equus caballus similar to zinc-finger protein of the cerebellum 3 (LOC100054537); mRNA	42.2	NM_003413	XM_001489459	LOC100054537	similar to zinc-finger protein of the cerebellum 3
CfaAffx.29019.1.S1_s_at	4.533270E-03	1.440957E-01	1.16	.87	PREDICTED: Canis familiaris similar to Proto-oncogene DBL (Proto-oncogene MCF-2) (LOC492176); mRNA	59.8	NM_001099855	XM_549296	MCF2	MCF.2 cell line derived transforming sequence
CfaAffx.29036.1.S1_at	2.184200E-04	2.897822E-02	1.16	.86	PREDICTED: Canis familiaris similar to deleted in colorectal carcinoma (LOC611097); mRNA	100.0	AK290266	XM_848731	TMIGD1	transmembrane and immunoglobulin domain containing 1
CfaAffx.29053.1.S1_at	1.320100E-02	2.410015E-01	0.87	1.16	PREDICTED: Canis familiaris similar to golgi SNAP receptor complex member 1 isoform 2 (LOC491185); mRNA	100.0	AK291381	XM_548305	GOSR1	golgi SNAP receptor complex member 1
CfaAffx.29061.1.S1_s_at	3.519190E-06	2.482760E-03	0.89	1.13	PREDICTED: Canis familiaris similar to leucine zipper; down-regulated in cancer 1 (LOC492180); mRNA	100.0	EU446786	XM_549300	LDOC1	leucine zipper, down-regulated in cancer 1

CfaAffx.2917.1.S1_s_at	1.431300E-02	2.510024E-01	0.86	1.16	PREDICTED: Canis familiaris hypothetical protein LOC612366 (LOC612366); mRNA	100.0	CU691639	XM_850095	LOC612366	hypothetical protein LOC612366
CfaAffx.29177.1.S1_s_at	7.769280E-06	3.799443E-03	0.73	1.37	PREDICTED: Canis familiaris similar to Proteasome subunit alpha type 2 (Proteasome component C3) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3); transcript variant 3 (LOC475870); mRNA	58.7	CU690460	XM_851043	PSMA2	proteasome (prosome, macropain) subunit, alpha type, 2
CfaAffx.29198.1.S1_s_at	7.233960E-05	1.454736E-02	0.72	1.40	PREDICTED: Canis familiaris similar to CG1532-PA; transcript variant 1 (LOC480640); mRNA	100.0	CU677472	XM_537759	GLOD4	glyoxalase domain containing 4
CfaAffx.29226.1.S1_at	3.052370E-03	1.189972E-01	1.12	.90	PREDICTED: Canis familiaris similar to PAS domain containing 1 (LOC492216); mRNA	100.0	NM_173493	XM_549336	PASD1	PAS domain containing 1
CfaAffx.29249.1.S1_at	1.404870E-03	8.018379E-02	0.84	1.19	PREDICTED: Canis familiaris similar to Mago nashi protein homolog; transcript variant 1 (LOC479562); mRNA	81.9	NM_002370	XM_536702	MAGOH	mago-nashi homolog, proliferation-associated (Drosophila)
CfaAffx.29250.1.S1_s_at	1.387810E-02	2.472037E-01	0.89	1.13	PREDICTED: Canis familiaris similar to CG4646-PA (LOC479563); mRNA	100.0	BC010908	XM_536703	LOC479563	similar to CG4646-PA
CfaAffx.29254.1.S1_s_at	6.501000E-04	5.183745E-02	0.75	1.34	PREDICTED: Canis familiaris similar to centrin 2 (LOC481078); mRNA	98.6	AK311940	XM_538198	CETN2	centrin, EF-hand protein, 2
CfaAffx.29259.1.S1_at	1.403450E-02	2.485493E-01	1.1	.91	PREDICTED: Canis familiaris similar to zinc finger RNA binding protein (LOC485051); mRNA	100.0	NM_015174	XM_849721	ZFR2	zinc finger RNA binding protein 2
CfaAffx.29299.1.S1_s_at	1.148970E-03	7.155705E-02	0.87	1.15	PREDICTED: Canis familiaris similar to podocan; transcript variant 5 (LOC479564); mRNA	67.2	BX537619	XM_861039	SCP2	sterol carrier protein 2
CfaAffx.29316.1.S1_at	4.874080E-05	1.139978E-02	1.2	.84	PREDICTED: Gallus gallus similar to Cytosolic phospholipase A2 epsilon (cPLA2-epsilon) (Phospholipase A2 group IVE) (LOC771574); mRNA	19.0	AC016883	XM_001234837	LOC771574	similar to Cytosolic phospholipase A2 epsilon (cPLA2-epsilon) (Phospholipase A2 group IVE)
CfaAffx.29317.1.S1_at	1.218820E-02	2.337430E-01	0.85	1.18	PREDICTED: Canis familiaris similar to DnaJ homolog subfamily A member 3; mitochondrial precursor (Tumorous imaginal discs protein Tid56 homolog) (DnaJ protein Tid-1) (hTid-1); transcript	100.0	AK314218	XM_846658	DNAJA3	DnaJ (Hsp40) homolog, subfamily A, member 3

					variant 2 (LOC479865); mRNA					
CfaAffx.29457.1.S1_at	3.420140E-03	1.264482E-01	1.14	.88	PREDICTED: Canis familiaris similar to RUN and TBC1 domain containing 1 (LOC480654); mRNA	46.2	CR596157	XM_537773	SGSM2	small G protein signaling modulator 2
CfaAffx.29503.1.S1_at	3.112530E-04	3.466030E-02	1.14	.88	Canis lupus familiaris 1P2 olfactory receptor protein (OR1P2) mRNA; complete cds	99.8	NULL	EF451962	cOR1P2	cOR1P2 olfactory receptor family 1 subfamily P-like
CfaAffx.29510.1.S1_at	1.445530E-04	2.229691E-02	1.14	.88	PREDICTED: Canis familiaris olfactory receptor family 1 subfamily E (LOC491216); mRNA	99.8	NULL	XM_548336	LOC491216	olfactory receptor family 1 subfamily E
CfaAffx.2955.1.S1_at	2.670740E-05	8.370401E-03	1.2	.83	PREDICTED: Macaca mulatta neurotrophic tyrosine kinase; receptor; type 2; transcript variant 3 (NTRK2); mRNA	96.2	AF410901	XM_001107145	NTRK2	neurotrophic tyrosine kinase, receptor, type 2
CfaAffx.29558.1.S1_s_at	6.272970E-03	1.703278E-01	0.88	1.14	PREDICTED: Canis familiaris similar to serine/arginine repetitive matrix 2; transcript variant 2 (LOC609646); mRNA	46.5	AK025903	XM_859515	LOC609646	similar to serine/arginine repetitive matrix 2
CfaAffx.29568.1.S1_at	2.893840E-03	1.157402E-01	1.12	.89	PREDICTED: Canis familiaris similar to tryptase 4 (LOC479874); mRNA	100.0	NM_144956	XM_536999	PRSS21	protease, serine, 21 (testisin)
CfaAffx.29602.1.S1_at	1.341900E-02	2.429477E-01	0.9	1.11	PREDICTED: Canis familiaris similar to ELG protein (LOC611456); mRNA	100.0	NM_018553	XM_849124	LOC611456	similar to ELG protein
CfaAffx.29680.1.S1_at	1.502090E-07	3.146453E-04	1.18	.85	PREDICTED: Canis familiaris similar to splicing factor 3a; subunit 2; 66kDa (predicted) (LOC612188); mRNA	24.1	AK314815	XM_849923	SF3A2	splicing factor 3a, subunit 2, 66kDa
CfaAffx.29705.1.S1_s_at	1.118730E-02	2.232014E-01	0.91	1.10	PREDICTED: Canis familiaris similar to Host cell factor (HCF) (HCF-1) (C1 factor) (VP16 accessory protein) (VCAF) (CFF); transcript variant 3 (LOC492246); mRNA	100.0	L20010	XM_862360	HCFC1	host cell factor C1 (VP16-accessory protein)
CfaAffx.29748.1.S1_at	1.971290E-02	2.911700E-01	1.12	.89	PREDICTED: Pan troglodytes Williams-Beuren syndrome chromosome region 16; transcript variant 5 (WBSCR16); mRNA	63.9	AC124781	XM_519150	WBSCR16	Williams-Beuren syndrome chromosome region 16
CfaAffx.29813.1.S1_at	4.265820E-03	1.404570E-01	1.12	.89	Coccidioides immitis RS hypothetical protein (CIMG_07470) mRNA; complete cds	26.4	BX648966	XM_001240306	CIMG_07470	hypothetical protein

CfaAffx.29827.1.S1_s_at	1.068740E-02	2.176197E-01	1.12	.89	PREDICTED: Canis familiaris similar to UDP-N-acteylglucosamine pyrophosphorylase 1; like 1 (LOC491239); mRNA	100.0	AK095393	XM_548360	LOC491239	similar to UDP-N-acteylglucosamine pyrophosphorylase 1, like 1
CfaAffx.2983.1.S1_s_at	5.857290E-03	1.642140E-01	0.89	1.12	PREDICTED: Canis familiaris heterogenous nuclear ribonucleoprotein K; transcript variant 29 (HNRPK); mRNA	89.9	NULL	XM_852599	HNRNPK	heterogeneous nuclear ribonucleoprotein K
CfaAffx.3003.1.S1_s_at	1.810300E-02	2.795407E-01	1.15	.87	PREDICTED: Canis familiaris similar to casein kinase 1 epsilon; transcript variant 7 (LOC474510); mRNA	100.0	CR609912	XM_855894	CSNK1E	casein kinase 1, epsilon
CfaAffx.30030.1.S1_at	1.863640E-04	2.595526E-02	1.23	.82	PREDICTED: Pan troglodytes cardiac muscle ryanodine receptor (RYR2); mRNA	37.9	NM_001035	XM_514296	RYR2	ryanodine receptor 2 (cardiac)
CfaAffx.30037.1.S1_at	8.683760E-05	1.631902E-02	1.2	.83	PREDICTED: Canis familiaris similar to Synaptobrevin-like protein 1 (LOC612663); mRNA	81.3	AJ549301	XM_850396	VAMP7	vesicle-associated membrane protein 7
CfaAffx.30115.1.S1_x_at	1.126860E-03	7.089828E-02	0.8	1.26	PREDICTED: Canis familiaris similar to ribosomal protein L31 (LOC489638); mRNA	100.0	NULL	XM_546758	LOC489638	similar to ribosomal protein L31
CfaAffx.30155.1.S1_at	3.016950E-03	1.184813E-01	1.14	.88	PREDICTED: Canis familiaris similar to DNA-directed RNA polymerase; mitochondrial precursor (MtRPOL) (LOC485102); mRNA	72.1	XR_019047	XM_542220	POLRMT	polymerase (RNA) mitochondrial (DNA directed)
CfaAffx.3019.1.S1_at	2.455450E-03	1.058821E-01	0.89	1.12	PREDICTED: Rattus norvegicus similar to Protein C22orf5 (RGD1306591); mRNA	86.4	AK048138	XM_001076493	Tmem184b	transmembrane protein 184B
CfaAffx.30192.1.S1_at	1.323530E-03	7.738874E-02	1.16	.86	PREDICTED: Pan troglodytes similar to olfactory receptor; family 6; subfamily C; member 6 (LOC467022); mRNA	84.8	NM_001005493	XM_522422	LOC467022	similar to olfactory receptor, family 6, subfamily C, member 6
CfaAffx.30214.1.S1_at	3.612300E-03	1.285342E-01	1.15	.87	Ciona intestinalis cDNA; clone:citb006p12; full insert sequence	19.0	AC004045	AK112847		
CfaAffx.30295.1.S1_at	8.868420E-03	2.010117E-01	1.1	.91	null	null	null	null		
CfaAffx.30313.1.S1_at	4.342420E-04	4.266576E-02	1.16	.86	PREDICTED: Canis familiaris similar to Vav-2 protein (LOC608060); mRNA	100.0	S76992	XM_844947	VAV2	vav 2 guanine nucleotide exchange factor

CfaAffx.30315.1.S1_at	7.062180E-03	1.798871E-01	1.11	.90	NULL	null	AL512412	NULL		
CfaAffx.30333.1.S1_s_at	4.461260E-04	4.328827E-02	1.19	.84	PREDICTED: Danio rerio hypothetical LOC569798 (LOC569798); mRNA	45.1	AC023844	XM_693205	LOC569798	similar to LOC495387 protein
CfaAffx.30385.1.S1_s_at	3.079730E-03	1.189972E-01	1.13	.88	Homo sapiens POM121-2 mRNA for nuclear pore membrane protein 121-2; partial cds	13.8	AC026591	AB354586	POM121C	POM121 membrane glycoprotein C
CfaAffx.30442.1.S1_at	2.717530E-04	3.204080E-02	0.91	1.10	PREDICTED: Canis familiaris similar to BarH-like 1 (LOC491283); mRNA	100.0	NM_020064	XM_548404	BARHL1	BarH-like homeobox 1
CfaAffx.30542.1.S1_at	2.095540E-03	9.845149E-02	1.14	.88	Synthetic construct DNA; clone: pF1KA1624; Homo sapiens GPR107 gene for G-protein coupled receptor 107; complete cds; without stop codon; in Flexi system	33.3	AB385490	AB385490		
CfaAffx.30559.1.S1_at	1.899050E-03	9.415394E-02	1.14	.88	PREDICTED: Canis familiaris similar to leucine rich repeat containing 50 (LOC479628); mRNA	64.3	AC092980	XM_536764	LRRC50	leucine rich repeat containing 50
CfaAffx.30566.1.S1_at	2.113570E-02	2.989080E-01	1.12	.89	Small ruminant lentivirus isolate SNCR5592 pol protein (pol) gene; partial cds	15.6	U44132	AY454257		
CfaAffx.30630.1.S1_at	6.473890E-03	1.731534E-01	1.12	.89	Gryllus bimaculatus mRNA; GBcontig15650	25.3	NULL	AK268789		
CfaAffx.30691.1.S1_s_at	3.325490E-03	1.239069E-01	1.12	.89	PREDICTED: Canis familiaris similar to plasticity related gene 1 (LOC490146); mRNA	62.1	AB384482	XM_547267	LOC490146	similar to plasticity related gene 1
CfaAffx.3074.1.S1_s_at	1.372870E-02	2.457703E-01	1.11	.90	PREDICTED: Canis familiaris similar to FERM domain containing 3 (LOC484151); mRNA	100.0	EF560742	XM_541268	FRMD3	FERM domain containing 3
CfaAffx.30778.1.S1_s_at	7.001300E-04	5.438645E-02	1.19	.84	PREDICTED: Canis familiaris similar to CG1311-PA (LOC490152); mRNA	100.0	NM_001114106	XM_547273	SLC44A3	solute carrier family 44, member 3
CfaAffx.3085.1.S1_at	3.569350E-03	1.277456E-01	1.14	.88	PREDICTED: Canis familiaris hypothetical LOC474705 (LOC474705); mRNA	87.1	AK308643	XM_531931	LOC474705	hypothetical LOC474705

CfaAffx.30878.1.S1_at	3.699500E-04	3.864271E-02	1.16	.86	Mus musculus c222389 pseudogene; complete sequence; nuclear receptor 2E1 (Nr2e1) and sorting nexin 3 (Snx3) genes; complete cds; and lactation elevated 1 (Lace1) gene; partial cds	33.3	AL590552	AF520420		
CfaAffx.30887.1.S1_at	1.105970E-03	7.019973E-02	0.9	1.11	Homo sapiens LIM homeobox transcription factor 1; beta (LMX1B); mRNA	100.0	NM_002316	NM_002316	LMX1B	LIM homeobox transcription factor 1, beta
CfaAffx.309.1.S1_x_at	7.231280E-03	1.812229E-01	0.82	1.22	PREDICTED: Canis familiaris similar to ribosomal protein L31; transcript variant 1 (LOC607191); mRNA	97.9	NULL	XM_535622	LOC607191	similar to ribosomal protein L31
CfaAffx.30901.1.S1_at	2.069070E-02	2.962285E-01	1.12	.89	Mus musculus 15 days embryo head cDNA; RIKEN full-length enriched library; clone:4022427D05 product:unclassifiable; full insert sequence	26.0	AC013416	AK132347		
CfaAffx.30915.1.S1_at	1.555550E-02	2.615986E-01	1.12	.89	PREDICTED: Bos taurus hypothetical LOC505814 (LOC505814); mRNA	89.1	AK094079	XM_582165	HFM1	HFM1, ATP-dependent DNA helicase homolog (S. cerevisiae)
CfaAffx.31039.1.S1_at	1.370300E-04	2.166111E-02	1.22	.82	Physcomitrella patens subsp. patens predicted protein (PHYPADRAFT_68202) mRNA; complete cds	41.9	AL355103	XM_001755272	PHYPADRAFT_68202	hypothetical protein
CfaAffx.31042.1.S1_x_at	1.382030E-02	2.465823E-01	0.89	1.13	PREDICTED: Canis familiaris similar to 60S ribosomal protein L7; transcript variant 1 (LOC477912); mRNA	94.1	AK313365	XM_535102	RPL7	ribosomal protein L7
CfaAffx.31153.1.S1_at	1.436510E-02	2.516085E-01	1.12	.89	Equus caballus prostaglandin F receptor (FP) (PTGFR); mRNA >gi|86451130|gb|DQ385610.1| Equus caballus prostaglandin F2alpha receptor mRNA; complete cds	90.9	AK292845	NM_001081806	PTGFR	prostaglandin F receptor (FP)
CfaAffx.31177.1.S1_at	1.299860E-02	2.402898E-01	1.11	.90	PREDICTED: Pan troglodytes zinc finger; DHHC domain containing 1; transcript variant 2 (ZDHHC1); mRNA	17.4	AC009061	XM_001163435	ZDHHC1	zinc finger, DHHC-type containing 1
CfaAffx.31178.1.S1_at	1.946480E-02	2.895647E-01	1.14	.88	PREDICTED: Canis familiaris similar to zinc finger; DHHC domain containing 1 (LOC479686); mRNA	98.4	AC009061	XM_536817	LOC479686	similar to zinc finger, DHHC domain containing 1

CfaAffx.31199.1.S1_at	7.134020E-03	1.804793E-01	1.11	.90	Mus musculus 16 days neonate thymus cDNA; RIKEN full-length enriched library; clone:A130074N06 product:unclassifiable; full insert sequence	28.4	AC092640	AK138034		
CfaAffx.31199.1.S1_s_at	2.582310E-04	3.139257E-02	1.16	.86	PREDICTED: Canis familiaris similar to E2F transcription factor 4 (LOC611243); mRNA	73.9	BT019802	XM_848882	E2F4	E2F transcription factor 4, p107/p130-binding
CfaAffx.31219.1.S1_at	1.797440E-02	2.790268E-01	1.12	.89	PREDICTED: Canis familiaris similar to MutS protein homolog 4 (LOC612681); mRNA	100.0	NM_002440	XM_850410	MSH4	mutS homolog 4 (E. coli)
CfaAffx.31237.1.S1_s_at	6.525120E-03	1.732327E-01	0.83	1.21	PREDICTED: Canis familiaris similar to crystallin; zeta; transcript variant 2 (LOC611431); mRNA	45.2	AB174315	XM_862830	LOC611431	similar to crystallin, zeta
CfaAffx.31241.1.S1_at	3.352230E-03	1.246873E-01	1.1	.91	NULL	null	AL160255	NULL		
CfaAffx.31264.1.S1_at	1.103910E-02	2.217870E-01	1.1	.91	PREDICTED: Canis familiaris similar to chemokine-like factor superfamily 1 isoform 13 (LOC611367); mRNA	97.0	NM_052999	XM_849025	CMTM1	CKLF-like MARVEL transmembrane domain containing 1
CfaAffx.31268.1.S1_at	1.750760E-06	1.712363E-03	1.26	.79	NULL	null	AC099564	NULL		
CfaAffx.3133.1.S1_at	5.585530E-04	4.856026E-02	0.78	1.28	PREDICTED: Canis familiaris similar to CG6479-PA; isoform A; transcript variant 15 (LOC475194); mRNA	100.0	NM_032842	XM_532426	TMEM209	transmembrane protein 209
CfaAffx.3145.1.S1_at	9.508210E-03	2.074645E-01	0.91	1.10	PREDICTED: Canis familiaris similar to Platelet glycoprotein V precursor (GPV) (CD42D) (LOC481269); mRNA	100.0	Z94160	XM_538390	ELFN2	extracellular leucine-rich repeat and fibronectin type III domain containing 2
CfaAffx.3150.1.S1_at	5.754740E-04	4.943218E-02	1.23	.81	Vibrio parahaemolyticus Chi1 gene for chitinase; complete cds	7.1	NULL	AB299855		
CfaAffx.3152.1.S1_at	1.459160E-02	2.538195E-01	0.89	1.13	PREDICTED: Canis familiaris similar to Cytohesin 4 (LOC481270); mRNA	99.8	CU013439	XM_538391	CYTH4	cytohesin 4
CfaAffx.32019.1.S1_at	1.921660E-03	9.462382E-02	1.14	.88	Canine adenovirus type 2 E1A; E1B and IX protein genes; complete cds	62.4	EF445024	J04368		

CfaAffx.32040.1.S1_at	6.978120E-05	1.409875E-02	1.14	.88	PREDICTED: Tribolium castaneum similar to CG14064-PA (LOC659280); mRNA	4.4	NULL	XM_965605	LOC659280	similar to CG14064-PA
CfaAffx.330.1.S1_s_at	7.946350E-03	1.894628E-01	0.88	1.13	PREDICTED: Canis familiaris similar to NADH-ubiquinone oxidoreductase MWFE subunit (Complex I-MWFE) (CI-MWFE) (LOC481033); mRNA	100.0	U54993	XM_538155	LOC481033	similar to NADH-ubiquinone oxidoreductase MWFE subunit (Complex I-MWFE) (CI-MWFE)
CfaAffx.331.1.S1_at	7.501110E-04	5.623872E-02	1.27	.79	PREDICTED: Canis familiaris cardiac titin (TTN); mRNA	97.9	AJ277892	XM_535982	TTN	titin
CfaAffx.3310.1.S1_s_at	7.860380E-03	1.885571E-01	0.89	1.12	PREDICTED: Canis familiaris similar to transcription factor EB (LOC609046); mRNA	100.0	EU446667	XM_846234	TFEB	transcription factor EB
CfaAffx.3331.1.S1_at	1.962350E-02	2.906773E-01	1.23	.81	PREDICTED: Canis familiaris similar to Protein C9orf55; transcript variant 2 (LOC474721); mRNA	100.0	NM_017925	XM_846931	DENND4C	DENN/MADD domain containing 4C
CfaAffx.3351.1.S1_s_at	1.044500E-02	2.157284E-01	0.9	1.11	PREDICTED: Canis familiaris similar to cysteine and histidine rich 1 isoform 1 (LOC482097); mRNA	100.0	XM_001714906	XM_539218	LOC482097	similar to cysteine and histidine rich 1 isoform 1
CfaAffx.3363.1.S1_s_at	5.708990E-03	1.620292E-01	1.19	.84	PREDICTED: Canis familiaris similar to vacuolar protein sorting 13A isoform A (LOC476319); mRNA	82.2	NM_015186	XM_533522	VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)
CfaAffx.3375.1.S1_s_at	8.233730E-03	1.932053E-01	1.12	.89	PREDICTED: Canis familiaris similar to calumenin precursor; transcript variant 8 (LOC475201); mRNA	98.4	NULL	XM_853685	CALU	calumenin
CfaAffx.3453.1.S1_at	1.847910E-06	1.767218E-03	1.24	.80	PREDICTED: Bos taurus RNA binding motif protein 9; transcript variant 8 (RBM9); mRNA	61.8	AF229058	XM_881737		
CfaAffx.3460.1.S1_s_at	3.442770E-04	3.731980E-02	0.81	1.24	PREDICTED: Canis familiaris similar to Coiled-coil domain containing protein 2 (Capillary morphogenesis protein-1) (CMG-1) (LOC474734); mRNA	100.0	AB169310	XM_531964	IFT74	intraflagellar transport 74 homolog (Chlamydomonas)
CfaAffx.3492.1.S1_x_at	5.453240E-03	1.580338E-01	1.14	.88	PREDICTED: Canis familiaris similar to 60S ribosomal protein L37a (LOC609501); mRNA	93.8	BC014262	XM_846121	LOC609501	similar to 60S ribosomal protein L37a

CfaAffx.3512.1.S1_at	4.208180E-03	1.391999E-01	1.17	.86	PREDICTED: Canis familiaris similar to Glycine N-methyltransferase; transcript variant 1 (LOC474905); mRNA	100.0	DQ893974	XM_532140	GNMT	glycine N-methyltransferase
CfaAffx.3513.1.S1_at	1.858890E-02	2.823561E-01	1.15	.87	PREDICTED: Canis familiaris similar to Metabotropic glutamate receptor 8 precursor (mGluR8); transcript variant 2 (LOC482270); mRNA	42.1	NULL	XM_853912	GRM8	glutamate receptor, metabotropic 8
CfaAffx.3536.1.S1_s_at	2.038580E-02	2.949178E-01	1.11	.90	PREDICTED: Canis familiaris similar to F-box only protein 7 (LOC474522); mRNA	42.4	AB171373	XM_531752	FBXO7	F-box protein 7
CfaAffx.3551.1.S1_at	5.050020E-04	4.604700E-02	1.14	.88	PREDICTED: Canis familiaris similar to hyaluronoglucosaminidase 4; transcript variant 1 (LOC475212); mRNA	100.0	NM_012269	XM_532444	HYAL4	hyaluronoglucosaminidase 4
CfaAffx.3553.1.S1_at	6.263920E-04	5.125131E-02	1.14	.88	Homo sapiens cDNA; FLJ98958	30.9	AK308917	AK308917	KLHDC3	kelch domain containing 3
CfaAffx.3570.1.S1_s_at	1.954960E-03	9.506407E-02	0.77	1.30	PREDICTED: Canis familiaris annexin I (ANXA1); mRNA	68.1	NULL	XM_533524	ANXA1	annexin A1
CfaAffx.3571.1.S1_s_at	4.434350E-03	1.428212E-01	0.78	1.29	PREDICTED: Canis familiaris annexin I (ANXA1); mRNA	100.0	NULL	XM_533524	ANXA1	annexin A1
CfaAffx.3579.1.S1_at	7.395640E-03	1.830198E-01	1.15	.87	Bovine papillomavirus gene for E1 protein; partial cds	19.3	AL365445	AB035261		
CfaAffx.3609.1.S1_s_at	1.915490E-02	2.875239E-01	1.11	.90	PREDICTED: Canis familiaris similar to transmembrane channel-like gene family 1 (LOC484168); mRNA	69.3	AK307461	XM_541284	TMC1	transmembrane channel-like 1
CfaAffx.3639.1.S1_s_at	3.531760E-03	1.277456E-01	0.88	1.13	PREDICTED: Canis familiaris similar to DnaJ homolog subfamily A member 1 (Heat shock 40 kDa protein 4) (DnaJ protein homolog 2) (HSJ-2) (HSDJ); transcript variant 1 (LOC474739); mRNA	96.6	NULL	XM_531970	LOC474739	similar to DnaJ homolog subfamily A member 1 (Heat shock 40 kDa protein 4) (DnaJ protein homolog 2) (HSJ-2) (HSDJ)
CfaAffx.367.1.S1_at	7.529530E-04	5.627969E-02	1.12	.89	PREDICTED: Bos taurus similar to seven transmembrane helix receptor (LOC509369); mRNA	70.8	AP000435	XM_586311	LOC509369	similar to Olfactory receptor 5B3 (Olfactory receptor OR11-239)

CfaAffx.3673.1.S1_s_at	2.072290E-02	2.963809E-01	0.9	1.11	PREDICTED: Canis familiaris similar to BAG-family molecular chaperone regulator-1 (BCL-2 binding athanogene-1) (BAG-1) (Glucocorticoid receptor-associated protein RAP46) (LOC611781); mRNA	100.0	NM_004323	XM_849492	BAG1	BCL2-associated athanogene
CfaAffx.371.1.S1_at	1.933880E-03	9.489684E-02	1.19	.84	PREDICTED: Canis familiaris similar to olfactory receptor; family 2; subfamily AG; member 2 (LOC485343); mRNA	100.0	AB065823	XM_848692	LOC485343	similar to olfactory receptor, family 2, subfamily AG, member 2
CfaAffx.3710.1.S1_at	2.871490E-03	1.153824E-01	1.13	.89	PREDICTED: Canis familiaris hypothetical LOC482288 (LOC482288); mRNA	100.0	NM_181646	XM_539407	ZNF804B	zinc finger protein 804B
CfaAffx.3741.1.S1_at	9.147170E-05	1.704106E-02	1.27	.78	PREDICTED: Canis familiaris similar to gamma-aminobutyric acid A receptor; gamma 1 precursor (LOC482130); mRNA	99.8	NM_173536	XM_539249	GABRG1	gamma-aminobutyric acid (GABA) A receptor, gamma 1
CfaAffx.3745.1.S1_at	5.565490E-03	1.592492E-01	1.11	.90	PREDICTED: Canis familiaris similar to Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (LOC482293); mRNA	100.0	NULL	XM_539410	LOC482293	similar to Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8)
CfaAffx.3761.1.S1_s_at	1.578310E-03	8.576082E-02	0.89	1.12	PREDICTED: Canis familiaris similar to CG13957-PA (LOC474533); mRNA	82.9	AB385420	XM_531762	LOC474533	similar to CG13957-PA
CfaAffx.3775.1.S1_at	3.156780E-09	3.396301E-05	1.49	.67	PREDICTED: Gallus gallus G protein-coupled receptor 125 (GPR125); mRNA	32.4	AC000057	XM_420763	GPR125	G protein-coupled receptor 125
CfaAffx.3819.1.S1_x_at	5.727510E-03	1.623738E-01	0.82	1.22	PREDICTED: Canis familiaris similar to ribosomal protein L31 (LOC609137); mRNA	98.0	NULL	XM_846343	LOC609137	similar to ribosomal protein L31
CfaAffx.3834.1.S1_s_at	2.478780E-04	3.119132E-02	0.8	1.26	PREDICTED: Canis familiaris similar to Cytochrome P450 51A1 (CYPLI) (P450LI) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (LDM) (P450-14DM) (P45014DM); transcript variant 1 (LOC475225); mRNA	100.0	AB168372	XM_532457	LOC475225	similar to Cytochrome P450 51A1 (CYPLI) (P450LI) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (LDM) (P450-14DM) (P45014DM)
CfaAffx.3930.1.S1_at	3.033030E-03	1.186230E-01	1.26	.79	PREDICTED: Canis familiaris similar to G10 protein homolog (EDG-2); transcript variant 2 (LOC479743); mRNA	90.0	CU692727	XM_855762	BUD31	BUD31 homolog (S. cerevisiae)
CfaAffx.3936.1.S1_at	2.112480E-02	2.989080E-01	1.12	.89	Homo sapiens hypothetical protein LOC253012 (LOC253012); transcript variant	90.4	BC139906	NM_001039372	HEPACAM2	HEPACAM family member 2

					1; mRNA					
CfaAffx.394.1.S1_s_at	7.367360E-04	5.581943E-02	1.18	.85	PREDICTED: Canis familiaris similar to Olfactory receptor 10A3 (HTPCRX12) (LOC611322); mRNA	99.2	NM_001003745	XM_848979	LOC611322	similar to Olfactory receptor 10A3 (HTPCRX12)
CfaAffx.3941.1.S1_at	8.125440E-04	5.896767E-02	1.12	.89	PREDICTED: Canis familiaris similar to ubiquitin specific protease 46; transcript variant 2 (LOC475142); mRNA	77.9	EU176797	XM_844557	USP46	ubiquitin specific peptidase 46
CfaAffx.3947.1.S1_at	7.169590E-03	1.805765E-01	1.14	.87	PREDICTED: Danio rerio hypothetical protein LOC799970 (LOC799970); mRNA	53.7	AL445984	XM_001340229		
CfaAffx.3960.1.S1_at	1.642760E-02	2.683985E-01	0.87	1.15	PREDICTED: Canis familiaris similar to GRIP and coiled-coil domain-containing 2 isoform a (LOC474541); mRNA	70.9	CR936614	XM_531770	GCC2	GRIP and coiled-coil domain containing 2
CfaAffx.398.1.S1_at	2.358340E-05	7.691952E-03	1.23	.82	Canis familiaris beta-defensin 105 (CBD105) mRNA; complete cds	99.5	BC128437	DQ011974		
CfaAffx.400.1.S1_at	1.556900E-03	8.481163E-02	1.16	.86	Canis familiaris beta-defensin 107 (CBD107) mRNA; complete cds	100.0	NULL	DQ011976		
CfaAffx.4010.1.S1_s_at	1.810990E-02	2.795407E-01	1.13	.89	PREDICTED: Canis familiaris similar to regulatory factor X3 isoform b; transcript variant 4 (LOC476339); mRNA	99.8	BC022191	XM_856001	RFX3	regulatory factor X, 3 (influences HLA class II expression)
CfaAffx.4023.1.S1_at	1.842570E-02	2.818510E-01	1.11	.90	PREDICTED: Canis familiaris similar to solute carrier family 5 (choline transporter); member 7 (LOC481311); mRNA	97.7	AC009963	XM_538432	SLC5A7	solute carrier family 5 (choline transporter), member 7
CfaAffx.4050.1.S1_at	6.938990E-04	5.409772E-02	1.23	.81	Homo sapiens G protein-coupled receptor 111 (GPR111); mRNA	87.0	NM_153839	NM_153839	GPR111	G protein-coupled receptor 111
CfaAffx.4052.1.S1_at	6.132100E-03	1.686566E-01	1.1	.91	PREDICTED: Canis familiaris similar to TPA regulated locus (LOC475144); mRNA	36.0	AK290663	XM_532375	TMEM165	transmembrane protein 165
CfaAffx.4065.1.S1_at	2.446200E-03	1.058012E-01	1.12	.89	PREDICTED: Canis familiaris similar to CG11212-PA; transcript variant 4 (LOC481829); mRNA	100.0	AL161622	XM_861045	LOC481829	similar to CG11212-PA

CfaAffx.4082.1.S1_at	1.538890E-02	2.604379E-01	0.85	1.18	PREDICTED: Canis familiaris hypothetical protein LOC611271 (LOC611271); mRNA	99.6	NM_024093	XM_848918	LOC611271	hypothetical protein LOC611271
CfaAffx.4085.1.S1_at	2.075620E-02	2.964175E-01	0.86	1.16	PREDICTED: Canis familiaris similar to CD274 antigen (LOC484186); mRNA	100.0	NULL	XM_541302	CD274	CD274 molecule
CfaAffx.4087.1.S1_at	4.763540E-04	4.515395E-02	0.8	1.25	PREDICTED: Canis familiaris similar to programmed cell death 1 ligand 2 (LOC609699); mRNA	91.4	EF444806	XM_847012	PDCD1LG2	programmed cell death 1 ligand 2
CfaAffx.411.1.S1_at	5.782290E-04	4.948110E-02	1.18	.85	PREDICTED: Canis familiaris similar to CG5032-PA (LOC489718); mRNA	100.0	CU690019	XM_546838	FTSJD1	FtsJ methyltransferase domain containing 1
CfaAffx.4166.1.S1_at	1.135770E-02	2.254514E-01	0.9	1.11	PREDICTED: Canis familiaris hypothetical protein LOC610261 (LOC610261); mRNA	100.0	AL929575	XM_847717	LOC610261	hypothetical protein LOC610261
CfaAffx.4178.1.S1_at	1.256750E-02	2.361795E-01	0.84	1.19	PREDICTED: Equus caballus hypothetical protein LOC100059079 (LOC100059079); mRNA	90.2	BC019355	XM_001491820	LOC100059079	hypothetical protein LOC100059079
CfaAffx.4186.1.S1_at	2.734590E-06	2.263136E-03	1.25	.80	Trichomonas vaginalis G3 hypothetical protein (TVAG_373470) partial mRNA	12.6	AL353150	XM_001326402	TVAG_373470	hypothetical protein
CfaAffx.4188.1.S1_at	8.890240E-05	1.663441E-02	1.24	.81	PREDICTED: Canis familiaris similar to Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-related death receptor-6) (Death receptor 6) (LOC609964); mRNA	26.4	AL157936	XM_847321	TNFRSF21	tumor necrosis factor receptor superfamily, member 21
CfaAffx.4190.1.S1_at	4.397820E-05	1.071943E-02	1.27	.79	Bos taurus cDNA clone IMAGE:8025816	32.8	NULL	BC149545	LOC614269	similar to leucine rich repeat containing 37A
CfaAffx.4224.1.S1_s_at	6.425820E-03	1.721888E-01	0.86	1.16	PREDICTED: Canis familiaris similar to phosducin-like 3; transcript variant 1 (LOC474553); mRNA	99.8	AF110511	XM_531782	PDCL3	phosducin-like 3
CfaAffx.4233.1.S1_at	7.165570E-03	1.805765E-01	1.11	.90	PREDICTED: Canis familiaris similar to CG32369-PB; isoform B (LOC481336); mRNA	100.0	NM_198461	XM_538457	LONRF2	LON peptidase N-terminal domain and ring finger 2
CfaAffx.424.1.S1_at	3.723320E-05	9.943067E-03	1.18	.85	PREDICTED: Equus caballus hypothetical protein LOC100051055 (LOC100051055);	77.5	AK291180	XM_001494332		

					mRNA					
CfaAffx.4263.1.S1_at	3.248990E-03	1.227571E-01	1.17	.86	PREDICTED: Canis familiaris similar to islet cell autoantigen 1 isoform 1; transcript variant 5 (LOC475242); mRNA	83.0	AK292106	XM_856660	ICA1	islet cell autoantigen 1, 69kDa
CfaAffx.4269.1.S1_at	6.236080E-04	5.125131E-02	1.2	.84	PREDICTED: Canis familiaris similar to Neurexophilin-1 precursor (LOC610361); mRNA	86.0	NM_152745	XM_847844	NXPH1	neurexophilin 1
CfaAffx.427.1.S1_at	3.669360E-03	1.297542E-01	1.17	.86	Canis familiaris DNA for bitter taste receptor; complete cds; clone: Cafa-T2R12	99.8	AC006518	AB249693		
CfaAffx.4275.1.S1_s_at	4.294250E-03	1.407487E-01	0.82	1.22	PREDICTED: Canis familiaris similar to NADH-ubiquinone oxidoreductase MLRQ subunit (Complex I-MLRQ) (CI-MLRQ) (LOC477682); mRNA	100.0	NULL	XM_534877	NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa
CfaAffx.4287.1.S1_at	1.806050E-03	9.187159E-02	1.16	.86	PREDICTED: Canis familiaris similar to olfactory receptor 155 (LOC611988); mRNA	99.8	NULL	XM_849709	LOC611988	similar to olfactory receptor 155
CfaAffx.4288.1.S1_at	1.975130E-03	9.561273E-02	1.21	.83	Homo sapiens PHD finger protein 14; mRNA (cDNA clone MGC:176640 IMAGE:8862519); complete cds	72.6	BC152414	BC152414	PHF14	PHD finger protein 14
CfaAffx.4289.1.S1_at	1.089260E-02	2.197670E-01	1.1	.91	Ovis aries PHD finger protein 14-like protein mRNA; partial cds	24.2	AC005007	EU366485	PHF14	PHD finger protein 14
CfaAffx.4329.1.S1_at	3.942430E-03	1.348203E-01	1.11	.90	PREDICTED: Equus caballus hypothetical protein LOC100065043 (LOC100065043); mRNA	79.6	XM_936911	XM_001495758		
CfaAffx.435.1.S1_at	5.614930E-03	1.600255E-01	1.11	.90	PREDICTED: Canis familiaris similar to zinc finger protein 91 (HPF7; HTF10) (LOC484250); mRNA	83.6	AB384346	XM_848551	ZNF594	zinc finger protein 594
CfaAffx.435.1.S1_x_at	4.747240E-03	1.476138E-01	1.12	.89	PREDICTED: Canis familiaris similar to zinc finger protein 91 (HPF7; HTF10) (LOC484250); mRNA	80.0	AB384346	XM_848551	ZNF594	zinc finger protein 594
CfaAffx.4459.1.S1_at	1.886390E-04	2.615518E-02	1.22	.82	PREDICTED: Mus musculus hypothetical LOC672501 (LOC672501); mRNA	42.9	NULL	XM_001476001	672501	predicted gene, 672501

CfaAffx.4483.1.S1_at	7.545310E-03	1.847056E-01	1.11	.90	PREDICTED: Canis familiaris similar to Mitochondrial import inner membrane translocase subunit Tim23; transcript variant 1 (LOC486776); mRNA	95.0	XM_928114	XM_543903	TIMM23	translocase of inner mitochondrial membrane 23 homolog (yeast)
CfaAffx.4490.1.S1_at	1.286030E-08	7.906329E-05	1.32	.76	PREDICTED: Equus caballus hypothetical protein LOC100052771 (LOC100052771); mRNA	65.3	NM_001004320	XM_001495676	TMEM195	transmembrane protein 195
CfaAffx.4549.1.S1_at	9.378190E-03	2.057786E-01	1.12	.89	PREDICTED: Canis familiaris hypothetical protein LOC610495 (LOC610495); mRNA	100.0	NM_152731	XM_848011	LOC610495	hypothetical protein LOC610495
CfaAffx.4556.1.S1_at	7.818340E-03	1.879677E-01	1.11	.90	PREDICTED: Canis familiaris cOR6Z2 olfactory receptor family 6 subfamily Z-like (cOR6Z2); mRNA	50.3	NULL	XM_541386	cOR6Z2	cOR6Z2 olfactory receptor family 6 subfamily Z-like
CfaAffx.4564.1.S1_at	1.843250E-03	9.250120E-02	0.86	1.17	PREDICTED: Canis familiaris similar to CG12822-PA; isoform A; transcript variant 1 (LOC474773); mRNA	97.8	CU678255	XM_532004	LOC474773	similar to CG12822-PA, isoform A
CfaAffx.4577.1.S1_at	1.218270E-02	2.337430E-01	1.14	.88	PREDICTED: Canis familiaris similar to KH domain-containing; RNA-binding; signal transduction-associated protein 2 (LOC481859); mRNA	50.2	AL049544	XM_538980	KHDRBS2	KH domain containing, RNA binding, signal transduction associated 2
CfaAffx.459.1.S1_s_at	7.489830E-03	1.841842E-01	0.86	1.17	PREDICTED: Canis familiaris similar to zinc finger protein 18 (LOC479505); mRNA	96.9	CU690295	XM_536644	ZNF18	zinc finger protein 18
CfaAffx.4646.1.S1_at	1.219960E-02	2.338574E-01	1.13	.88	PREDICTED: Canis familiaris similar to putative binding protein 7a5 (LOC482343); mRNA	100.0	NM_182762	XM_539460	LOC482343	similar to putative binding protein 7a5
CfaAffx.4649.1.S1_s_at	9.354970E-05	1.713154E-02	1.15	.87	PREDICTED: Canis familiaris similar to NACHT; leucine rich repeat and PYD containing 13 (LOC484287); mRNA	95.8	BC148742	XM_541402	NLRP13	NLR family, pyrin domain containing 13
CfaAffx.466.1.S1_at	4.286740E-03	1.407169E-01	1.13	.89	PREDICTED: Bos taurus similar to RIKEN cDNA 4930425N13 gene (LOC787358); mRNA	52.6	AC009019	XM_001254778	LOC787358	similar to transmembrane protein 202
CfaAffx.4727.1.S1_at	4.111310E-04	4.153292E-02	1.13	.89	Human DNA sequence from clone RP11-190I13 on chromosome 9 Contains the 5-prime end of a novel gene (FLJ20287); a novel gene similar to RIKEN cDNA 5730528L13 gene (MGC17337); the 5-	57.9	AL353805	AL353805		

					prime end of the TMEFF1 gene for transmembrane protein with EGF-like and two follistatin-like domains 1 (H7365; C9ORF2) and four CpG islands; complete sequence					
CfaAffx.474.1.S1_at	4.936230E-03	1.495991E-01	0.81	1.23	PREDICTED: Canis familiaris similar to COMM domain containing 6 isoform b (LOC476946); mRNA	100.0	NM_203497	XM_534146	COMMD6	COMM domain containing 6
CfaAffx.4758.1.S1_at	2.881770E-03	1.156683E-01	0.87	1.14	NULL	null	AL713892	NULL		
CfaAffx.4840.1.S1_at	4.861110E-03	1.485961E-01	0.9	1.11	PREDICTED: Pan troglodytes leukocyte receptor cluster (LRC) member 8; transcript variant 2 (LENG8); mRNA	90.7	CR624593	XM_001174966	LENG8	leukocyte receptor cluster (LRC) member 8
CfaAffx.4905.1.S1_at	1.462560E-05	5.473154E-03	1.17	.85	PREDICTED: Equus caballus similar to olfactory receptor MOR262-9 (LOC100061131); mRNA	85.9	NM_001004484	XM_001493177	LOC100061131	similar to olfactory receptor MOR262-9
CfaAffx.4907.1.S1_at	1.625510E-03	8.722422E-02	1.17	.85	PREDICTED: Canis familiaris similar to olfactory receptor 270; transcript variant 2 (LOC610556); mRNA	100.0	NULL	XM_848374	LOC610556	similar to olfactory receptor 270
CfaAffx.4963.1.S1_at	7.871870E-05	1.542382E-02	1.19	.84	Mus musculus adult male corpora quadrigemina cDNA; RIKEN full-length enriched library; clone:B230215C04 product:unclassifiable; full insert sequence	18.6	AC007682	AK045606	9530019H20Rik	RIKEN cDNA 9530019H20 gene
CfaAffx.4997.1.S1_at	2.149660E-03	1.000841E-01	1.15	.87	NULL	null	AC005682	NULL		
CfaAffx.4997.1.S1_s_at	4.857590E-03	1.485961E-01	1.12	.89	PREDICTED: Rattus norvegicus similar to Solute carrier family 40 member 1 (Ferroportin-1) (LOC685585); mRNA	9.6	AC005682	XM_001064431	LOC685585	similar to Solute carrier family 40 member 1 (Ferroportin-1)
CfaAffx.5036.1.S1_at	8.234390E-04	5.929964E-02	1.15	.87	NULL	null	AC073172	NULL		
CfaAffx.5040.1.S1_at	7.495640E-03	1.841842E-01	1.11	.90	Oryza sativa (japonica cultivar-group) Os03g0431800 (Os03g0431800) mRNA; complete cds	21.7	AL136093	NM_001056964	Os03g0431800	Os03g0431800

CfaAffx.5053.1.S1_at	7.325450E-03	1.820154E-01	1.13	.89	Arabidopsis thaliana unknown protein (AT3G13510) mRNA; complete cds	56.3	AL442643	NM_112197	AT3G13510	hypothetical protein
CfaAffx.5056.1.S1_x_at	1.302070E-02	2.403220E-01	0.87	1.15	PREDICTED: Canis familiaris similar to zinc finger protein 420 (LOC484331); mRNA	79.5	AC092070	XM_541447	ZNF677	zinc finger protein 677
CfaAffx.51.1.S1_s_at	1.433860E-02	2.512466E-01	0.82	1.22	Sus scrofa mRNA; clone:OVRM10197C06; expressed in ovary	100.0	CT476837	AK236486	LOC100153932	similar to FDPS protein
CfaAffx.5102.1.S1_at	9.239860E-04	6.311704E-02	0.9	1.12	PREDICTED: Canis familiaris similar to Zinc finger protein 432; transcript variant 7 (LOC484338); mRNA	100.0	AK097156	XM_858019	LOC484338	similar to Zinc finger protein 432
CfaAffx.5121.1.S1_at	1.720780E-03	9.022485E-02	1.2	.84	Homo sapiens cDNA FLJ11627 fis; clone HEMBA1004225	39.2	AC005522	AK021689		
CfaAffx.5129.1.S1_s_at	6.109940E-03	1.683363E-01	0.86	1.16	PREDICTED: Canis familiaris similar to Zinc finger protein 268 (Zinc finger protein HZF3) (LOC611692); mRNA	100.0	CU678844	XM_849390	ZNF665	zinc finger protein 665
CfaAffx.5148.1.S1_at	1.672780E-02	2.715507E-01	1.11	.90	PREDICTED: Canis familiaris similar to Protein C6orf152 (LOC481893); mRNA	100.0	AC012155	XM_539014	LCA5	Leber congenital amaurosis 5
CfaAffx.5179.1.S1_at	1.015350E-03	6.695271E-02	1.15	.87	PREDICTED: Canis familiaris similar to CG8399-PA (LOC612466); mRNA	100.0	BC156447	XM_850196	LOC612466	similar to CG8399-PA
CfaAffx.5261.1.S1_at	3.843590E-03	1.336757E-01	1.13	.89	Oryza sativa (japonica cultivar-group) Os06g0705500 (Os06g0705500) mRNA; complete cds	36.7	AC135054	NM_001065052	Os06g0705500	Os06g0705500
CfaAffx.5295.1.S1_s_at	1.848830E-02	2.819433E-01	1.1	.91	Canis lupus familiaris kallikrein 1 (KLK1); mRNA >gi|414018|emb|X75479.1|CFKALLIK C.familiaris dKlk-2 mRNA for kallikrein	100.0	NULL	NM_001003262	KLK1	kallikrein 1
CfaAffx.5303.1.S1_at	4.886090E-03	1.490240E-01	0.84	1.19	PREDICTED: Canis familiaris similar to G-rich RNA sequence binding factor 1 (LOC475170); mRNA	100.0	AB173944	XM_532402	GRSF1	G-rich RNA sequence binding factor 1
CfaAffx.5335.1.S1_s_at	7.850930E-03	1.884355E-01	1.11	.90	PREDICTED: Canis familiaris similar to homeobox A2 protein; transcript variant 1 (LOC609592); mRNA	100.0	NULL	XM_846812	HOXA2	homeobox A2

CfaAffx.5344.1.S1_at	4.978400E-03	1.503477E-01	1.11	.90	PREDICTED: Canis familiaris similar to sodium bicarbonate cotransporter; transcript variant 1 (LOC475171); mRNA	100.0	NULL	XM_532403	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4
CfaAffx.5384.1.S1_s_at	1.337400E-02	2.424390E-01	0.86	1.16	PREDICTED: Canis familiaris similar to zinc finger protein 684 (LOC482454); mRNA	100.0	CU684036	XM_539571	ZNF684	zinc finger protein 684
CfaAffx.5397.1.S1_at	1.735940E-03	9.022485E-02	1.21	.83	PREDICTED: Canis familiaris similar to endothelial differentiation; lysophosphatidic acid G-protein-coupled receptor; 2; transcript variant 2 (LOC474800); mRNA	99.0	AK290287	XM_848441	LPAR1	lysophosphatidic acid receptor 1
CfaAffx.5406.1.S1_x_at	4.284690E-03	1.407169E-01	0.84	1.19	PREDICTED: Canis familiaris similar to zinc finger protein 684 (LOC482454); mRNA	88.5	AB169189	XM_539571	ZNF684	zinc finger protein 684
CfaAffx.5411.1.S1_at	1.946610E-03	9.497007E-02	1.12	.90	Homo sapiens T-box 18; mRNA (cDNA clone IMAGE:6023106); partial cds	53.8	BC040697	BC040697	TBX18	T-box 18
CfaAffx.5423.1.S1_s_at	1.050490E-02	2.162123E-01	1.1	.91	PREDICTED: Canis familiaris similar to stromal membrane-associated protein 1-like (LOC482458); mRNA	100.0	AK308280	XM_539575	SMAP2	stromal membrane-associated GTPase-activating protein 2
CfaAffx.5438.1.S1_at	2.653130E-04	3.170988E-02	1.13	.88	NULL	null	AC007542	NULL		
CfaAffx.5446.1.S1_at	1.805510E-04	2.557083E-02	0.82	1.22	PREDICTED: Canis familiaris similar to Zinc finger protein Rlf (Rearranged L-myc fusion gene protein) (Zn-15 related protein); transcript variant 2 (LOC475315); mRNA	97.7	NM_012421	XM_843442	RLF	rearranged L-myc fusion
CfaAffx.5446.1.S1_s_at	2.052110E-02	2.951623E-01	0.91	1.10	PREDICTED: Canis familiaris similar to Zinc finger protein Rlf (Rearranged L-myc fusion gene protein) (Zn-15 related protein); transcript variant 1 (LOC475315); mRNA	100.0	NM_012421	XM_532543	RLF	rearranged L-myc fusion
CfaAffx.546.1.S1_at	4.232470E-04	4.208376E-02	1.18	.85	PREDICTED: Canis familiaris similar to reelin isoform b; transcript variant 1 (LOC483273); mRNA	100.0	NM_005045	XM_540392	RELN	reelin
CfaAffx.547.1.S1_at	5.359130E-04	4.724152E-02	0.85	1.17	PREDICTED: Canis familiaris similar to 60S ribosomal protein L7 (LOC607231); mRNA	91.0	NULL	XM_843932	LOC607231	similar to 60S ribosomal protein L7

CfaAffx.5470.1.S1_at	1.943970E-04	2.639810E-02	1.24	.81	Bos taurus fibronectin type III domain containing 4 (FNDC4); mRNA >gi|151555814|gb|BC149374.1| Bos taurus hypothetical protein LOC781806; mRNA (cDNA clone MGC:148929 IMAGE:8253136); complete cds	38.8	AC005162	NM_001102324	FNDC4	fibronectin type III domain containing 4
CfaAffx.5521.1.S1_at	6.492270E-05	1.336817E-02	1.16	.87	Synthetic construct Homo sapiens gateway clone IMAGE:100020839 3-prime read GJB7 mRNA	86.5	CU691253	CU691253		
CfaAffx.5532.1.S1_at	2.470060E-03	1.059811E-01	1.12	.89	Taeniopygia guttata clone 0061P0025F12 C2f protein-like mRNA; complete sequence	25.0	AC097470	DQ214886		
CfaAffx.554.1.S1_at	5.476060E-04	4.789883E-02	1.16	.86	PREDICTED: Canis familiaris similar to Olfactory receptor 7A5 (Olfactory receptor TPCR92) (LOC484888); mRNA	85.7	NULL	XM_542004	LOC484888	similar to Olfactory receptor 7A5 (Olfactory receptor TPCR92)
CfaAffx.5615.1.S1_at	1.716750E-02	2.741519E-01	1.1	.91	Human growth hormone-releasing hormone receptor gene; alternatively spliced forms a; b; and c; partial cds	39.7	AC005155	U17579		
CfaAffx.5673.1.S1_at	1.039590E-02	2.154008E-01	0.89	1.12	PREDICTED: Canis familiaris similar to Kelch repeat and BTB domain containing protein 2 (BTB and kelch domain containing protein 1); transcript variant 1 (LOC482391); mRNA	59.7	NULL	XM_539508	KBTBD2	kelch repeat and BTB (POZ) domain containing 2
CfaAffx.569.1.S1_at	1.577520E-02	2.632360E-01	1.12	.89	PREDICTED: Equus caballus similar to bovine seminal plasma protein-like 2 (LOC100053046); mRNA	81.4	NULL	XM_001488543		
CfaAffx.576.1.S1_at	1.846970E-02	2.818510E-01	0.87	1.15	PREDICTED: Canis familiaris similar to expressed sequence AW209491 (LOC483243); mRNA	100.0	CU674395	XM_540362	LOC483243	similar to expressed sequence AW209491
CfaAffx.5761.1.S1_at	2.491650E-03	1.063771E-01	1.12	.90	PREDICTED: Canis familiaris similar to Solute carrier family 23; member 2 (Sodium-dependent vitamin C transporter 2) (mSVCT2) (Na(+)/L-ascorbic acid transporter 2) (Yolk sac permease-like molecule 2) (LOC482707); mRNA	100.0	XM_001132982	XM_539823	LOC482707	similar to Solute carrier family 23, member 2 (Sodium-dependent vitamin C transporter 2) (mSVCT2) (Na(+)/L-ascorbic acid transporter 2) (Yolk sac permease-like molecule 2)
CfaAffx.5774.1.S1_s_at	4.366220E-03	1.417046E-01	1.12	.89	PREDICTED: Canis familiaris similar to CCR4-NOT transcription complex; subunit 4 isoform a; transcript variant 10	100.0	NULL	XM_854588	CNOT4	CCR4-NOT transcription complex, subunit 4

					(LOC482708); mRNA					
CfaAffx.582.1.S1_at	1.504510E-03	8.332894E-02	1.13	.89	PREDICTED: Canis familiaris olfactory receptor (OR18D12); mRNA	100.0	NULL	XM_539550	OR18D12	olfactory receptor
CfaAffx.5828.1.S1_at	9.175750E-04	6.292045E-02	1.1	.91	null	null	null	null		
CfaAffx.5841.1.S1_at	9.396000E-06	4.395183E-03	0.84	1.19	PREDICTED: Canis familiaris similar to regulator of G-protein signalling 3 isoform 6 (LOC481684); mRNA	100.0	AF490838	XM_538806	LOC481684	similar to regulator of G-protein signalling 3 isoform 6
CfaAffx.5860.1.S1_at	1.330560E-02	2.421055E-01	0.88	1.14	PREDICTED: Canis familiaris similar to Nucleolar GTP-binding protein 2 (Autoantigen NGP-1); transcript variant 5 (LOC475329); mRNA	63.7	NM_013285	XM_853292	GNL2	guanine nucleotide binding protein-like 2 (nucleolar)
CfaAffx.589.1.S1_s_at	4.746880E-06	2.877211E-03	1.21	.83	PREDICTED: Canis familiaris olfactory receptor OR08B05 (OR08B05); mRNA	100.0	BK004396	XM_540676	OR08B05	olfactory receptor OR08B05
CfaAffx.590.1.S1_at	3.953640E-06	2.555108E-03	1.24	.81	PREDICTED: Canis familiaris olfactory receptor (OR16D05); mRNA	100.0	AC036111	XM_540673	OR16D05	olfactory receptor
CfaAffx.591.1.S1_at	2.729680E-05	8.390841E-03	1.19	.84	PREDICTED: Canis familiaris olfactory receptor (OR08C10); mRNA	100.0	AB065925	XM_542105	OR08C10	olfactory receptor
CfaAffx.595.1.S1_at	6.317150E-06	3.548256E-03	1.26	.79	PREDICTED: Bos taurus similar to seven transmembrane helix receptor (LOC505250); mRNA	75.6	NM_001005203	XM_581506	LOC505250	similar to hCG2044662
CfaAffx.5962.1.S1_at	7.690270E-04	5.666965E-02	1.12	.89	PREDICTED: Canis familiaris similar to Solute carrier family 13; member 4 (Na(+)/sulfate cotransporter SUT-1) (LOC610242); mRNA	72.6	AC093107	XM_847687	SLC13A4	solute carrier family 13 (sodium/sulfate symporters), member 4
CfaAffx.5977.1.S1_at	7.236720E-03	1.812229E-01	1.11	.90	Homo sapiens vascular endothelial cell growth inhibitor (VEGI) mRNA; partial cds	36.7	AL390240	AF039390	TNFSF15	tumor necrosis factor (ligand) superfamily, member 15
CfaAffx.5988.1.S1_at	4.150660E-03	1.383607E-01	0.83	1.21	PREDICTED: Canis familiaris similar to zinc finger protein 420 (LOC484365); mRNA	100.0	AC093518	XM_541480	ZNF30	zinc finger protein 30

CfaAffx.6008.1.S1_at	1.137450E-02	2.254979E-01	0.91	1.10	PREDICTED: Canis familiaris similar to SINK-homologous serine/threonine kinase (LOC482475); mRNA	99.5	AK024504	XM_539592	STK40	serine/threonine kinase 40
CfaAffx.6016.1.S1_s_at	1.999370E-02	2.922407E-01	1.13	.88	PREDICTED: Canis familiaris similar to 3-oxo-5-beta-steroid 4-dehydrogenase (Delta(4)-3-ketosteroid 5-beta-reductase) (Aldo-keto reductase family 1 member D1) (LOC482711); mRNA	98.5	AK289425	XM_539827	AKR1D1	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)
CfaAffx.6037.1.S1_at	9.663510E-03	2.089007E-01	1.13	.89	PREDICTED: Canis familiaris similar to leader-binding protein 32 isoform 1 (LOC475664); mRNA	35.2	AC010969	XM_532872	GRHL1	grainyhead-like 1 (Drosophila)
CfaAffx.6067.1.S1_at	1.392130E-07	3.146453E-04	1.27	.79	Pichia guilliermondii ATCC 6260 hypothetical protein (PGUG_01236) mRNA; complete cds	19.2	AF000113	XM_001485515	PGUG_01236	hypothetical protein
CfaAffx.6106.1.S1_at	6.083000E-04	5.073293E-02	1.17	.85	PREDICTED: Equus caballus similar to G protein-coupled receptor 63 (LOC100071441); mRNA	93.2	BC067469	XM_001501202	GPR63	G protein-coupled receptor 63
CfaAffx.613.1.S1_at	5.897130E-03	1.647941E-01	0.83	1.21	null	null	null	null		
CfaAffx.6146.1.S1_s_at	1.101210E-02	2.215217E-01	0.87	1.14	PREDICTED: Canis familiaris coenzyme Q3 (COQ3); mRNA	100.0	BC015634	XM_532241	COQ3	coenzyme Q3 homolog, methyltransferase (S. cerevisiae)
CfaAffx.6153.1.S1_s_at	4.843640E-04	4.543068E-02	0.84	1.19	PREDICTED: Canis familiaris similar to Protein C14orf111 (LOC612615); mRNA	83.5	BX248271	XM_850348	LOC612615	similar to Protein C14orf111
CfaAffx.6157.1.S1_at	3.985980E-03	1.353880E-01	1.11	.90	PREDICTED: Canis familiaris similar to EGFR-coamplified and overexpressed protein (LOC608562); mRNA	100.0	XM_001723367	XM_845618	LOC608562	similar to EGFR-coamplified and overexpressed protein
CfaAffx.6158.1.S1_at	1.900650E-02	2.865959E-01	0.88	1.13	PREDICTED: Canis familiaris hypothetical LOC475005; transcript variant 14 (LOC475005); mRNA	100.0	NULL	XM_863095	SFRS18	splicing factor, arginine/serine-rich 18
CfaAffx.6168.1.S1_at	5.302200E-04	4.690621E-02	1.13	.88	PREDICTED: Canis familiaris hypothetical protein LOC609927 (LOC609927); mRNA	99.8	AK292828	XM_847274	LOC609927	hypothetical protein LOC609927

CfaAffx.6200.1.S1_at	1.535390E-07	3.146453E-04	1.28	.78	PREDICTED: Canis familiaris olfactory receptor (OR08A11); mRNA	100.0	NULL	XM_539835	OR08A11	olfactory receptor
CfaAffx.6200.1.S1_x_at	6.704050E-06	3.548256E-03	1.19	.84	PREDICTED: Canis familiaris olfactory receptor (OR08A11); mRNA	100.0	NULL	XM_539835	OR08A11	olfactory receptor
CfaAffx.6201.1.S1_s_at	2.233800E-05	7.486188E-03	1.18	.85	PREDICTED: Canis familiaris similar to ubiquitin specific protease 45; transcript variant 1 (LOC481933); mRNA	100.0	AL832030	XM_539054	USP45	ubiquitin specific peptidase 45
CfaAffx.6206.1.S1_x_at	3.727520E-06	2.546251E-03	1.2	.83	PREDICTED: Canis familiaris putative olfactory receptor (TPCR71); mRNA	100.0	U86278	XM_532739	TPCR71	putative olfactory receptor
CfaAffx.621.1.S1_s_at	1.717450E-02	2.741519E-01	1.12	.89	PREDICTED: Canis familiaris similar to Olfactory receptor 4C6 (LOC491531); mRNA	95.0	AC210900	XM_848499	LOC491531	similar to Olfactory receptor 4C6
CfaAffx.6214.1.S1_at	1.789830E-03	9.169683E-02	0.81	1.24	PREDICTED: Canis familiaris similar to Proteasome subunit alpha type 2 (Proteasome component C3) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3); transcript variant 1 (LOC475870); mRNA	100.0	NM_002787	XM_533078	PSMA2	proteasome (prosome, macropain) subunit, alpha type, 2
CfaAffx.624.1.S1_at	6.273460E-04	5.125131E-02	1.18	.85	PREDICTED: Bos taurus similar to seven transmembrane helix receptor (LOC790274); partial mRNA	88.6	NM_001004058	XM_001256791	LOC790274	similar to olfactory receptor, family 8, subfamily K, member 5
CfaAffx.628.1.S1_x_at	1.153020E-05	4.771175E-03	1.19	.84	PREDICTED: Canis familiaris olfactory receptor (OR08D07); mRNA	100.0	NULL	XM_542007	OR08D07	olfactory receptor
CfaAffx.629.1.S1_x_at	6.840240E-03	1.767452E-01	1.11	.90	PREDICTED: Canis familiaris similar to olfactory receptor Olr1347 (LOC608416); mRNA	96.0	NULL	XM_534623	LOC608416	similar to olfactory receptor Olr1347
CfaAffx.6301.1.S1_s_at	3.219690E-03	1.219713E-01	1.12	.90	PREDICTED: Canis familiaris similar to GREB1 protein isoform a (LOC610007); mRNA	100.0	AB385351	XM_847384	LOC610007	similar to GREB1 protein isoform a
CfaAffx.631.1.S1_x_at	4.419420E-03	1.424642E-01	1.2	.83	PREDICTED: Canis familiaris similar to olfactory receptor Olr1347 (LOC486190); mRNA	92.2	NULL	XM_543315	LOC486190	similar to olfactory receptor Olr1347

CfaAffx.6315.1.S1_s_at	5.061050E-04	4.604700E-02	1.13	.89	PREDICTED: Equus caballus similar to EAA4 (LOC100066235); mRNA	97.7	NM_021956	XM_001503914	GRIK5	glutamate receptor, ionotropic, kainate 5
CfaAffx.6330.1.S1_s_at	1.999400E-02	2.922407E-01	0.87	1.15	PREDICTED: Canis familiaris similar to zinc finger protein 262; transcript variant 2 (LOC482484); mRNA	100.0	NM_005095	XM_844369	ZMYM4	zinc finger, MYM-type 4
CfaAffx.634.1.S1_at	6.227830E-03	1.695222E-01	1.11	.90	PREDICTED: Canis familiaris similar to olfactory receptor Olr758 (LOC487459); mRNA	100.0	AC005603	XM_843713	LOC487459	similar to olfactory receptor Olr758
CfaAffx.6363.1.S1_at	1.154600E-02	2.272224E-01	1.11	.90	Homo sapiens GRB2-associated binding protein 1 (GAB1) gene; complete cds	54.1	DQ021880	DQ021880		
CfaAffx.6380.1.S1_s_at	1.468930E-02	2.548942E-01	0.86	1.16	PREDICTED: Canis familiaris interleukin 15 (IL15); mRNA	100.0	NULL	XM_844053	IL15	interleukin 15
CfaAffx.6418.1.S1_s_at	3.568290E-03	1.277456E-01	1.11	.90	PREDICTED: Canis familiaris similar to NM23-H8 (LOC609441); mRNA	100.0	AB169010	XM_846701	TXNDC3	thioredoxin domain containing 3 (spermatozoa)
CfaAffx.642.1.S1_s_at	2.385000E-03	1.047144E-01	1.14	.88	PREDICTED: Canis familiaris olfactory receptor family 1 subfamily E (LOC491216); mRNA	100.0	NULL	XM_548336	LOC491216	olfactory receptor family 1 subfamily E
CfaAffx.6421.1.S1_at	5.204950E-08	1.866625E-04	1.23	.82	PREDICTED: Equus caballus similar to odorant receptor ORZ6; transcript variant 1 (LOC100050381); mRNA	86.1	BK004391	XM_001491416	LOC100050381	similar to rCG27846
CfaAffx.6435.1.S1_s_at	1.789280E-02	2.786886E-01	0.89	1.12	PREDICTED: Canis familiaris similar to neuroblastoma-amplified protein (LOC482975); mRNA	100.0	AK097726	XM_540088	LOC482975	similar to neuroblastoma-amplified protein
CfaAffx.6454.1.S1_at	8.588410E-06	4.061563E-03	1.19	.84	Aplysia californica translation initiation factor eIF4E mRNA; complete cds	19.6	CU691993	AF085810		
CfaAffx.6478.1.S1_s_at	1.816670E-03	9.210656E-02	0.89	1.12	PREDICTED: Canis familiaris similar to suppressor of G2 allele of SKP1 (LOC477951); mRNA	98.7	AY889273	XM_535139	LOC477951	similar to suppressor of G2 allele of SKP1
CfaAffx.6517.1.S1_s_at	8.114670E-03	1.916905E-01	0.88	1.13	PREDICTED: Canis familiaris similar to zyg-11 homolog B (C. elegans)-like (LOC482495); mRNA	99.6	AK095643	XM_539612	ZYG11B	zyg-11 homolog B (C. elegans)

CfaAffx.6524.1.S1_at	1.244940E-03	7.481848E-02	1.11	.90	PREDICTED: Canis familiaris similar to solute carrier family 6; member 20 isoform 2 (LOC476416); mRNA	56.4	NULL	XM_533622	LOC476416	similar to solute carrier family 6, member 20 isoform 2
CfaAffx.654.1.S1_at	1.168950E-02	2.289748E-01	1.18	.85	PREDICTED: Macaca mulatta similar to ribosomal protein S27 (LOC696068); mRNA	69.4	XM_001723889	XM_001084710	LOC696068	similar to ribosomal protein S27
CfaAffx.6559.1.S1_at	6.398080E-05	1.336609E-02	1.21	.83	Homo sapiens neuronal cell adhesion molecule short isoform (NRCAM) mRNA; complete cds; alternatively spliced	80.0	NM_001037133	AY528240	NRCAM	neuronal cell adhesion molecule
CfaAffx.656.1.S1_x_at	1.922170E-02	2.882250E-01	1.14	.88	PREDICTED: Canis familiaris similar to 40S ribosomal protein S27-like protein (LOC490449); mRNA	93.5	AC005912	XM_547571	RPS27	ribosomal protein S27 (metallopanstimulin 1)
CfaAffx.6574.1.S1_s_at	9.905910E-03	2.116687E-01	0.9	1.11	PREDICTED: Canis familiaris similar to Translocation protein SEC63 homolog (LOC475016); mRNA	100.0	AK125856	XM_532252	SEC63	SEC63 homolog (S. cerevisiae)
CfaAffx.6591.1.S1_s_at	8.321730E-03	1.945649E-01	0.86	1.16	PREDICTED: Canis familiaris similar to arginyl-tRNA synthetase; transcript variant 4 (LOC609803); mRNA	97.7	AB171354	XM_861845	RARS	arginyl-tRNA synthetase
CfaAffx.6603.1.S1_at	2.241090E-03	1.015214E-01	0.84	1.18	PREDICTED: Canis familiaris similar to lactation elevated 1 (LOC481952); mRNA	44.2	AF520418	XM_539073	LACE1	lactation elevated 1
CfaAffx.6609.1.S1_at	7.634670E-06	3.799443E-03	1.2	.83	Arabidopsis thaliana EMB1611/MEE22 (EMBRYO DEFECTIVE 1611; maternal effect embryo arrest 22) (EMB1611/MEE22) mRNA; complete cds	23.8	AL353700	NM_179906	EMB1611/MEE22	EMB1611/MEE22 (EMBRYO DEFECTIVE 1611); binding
CfaAffx.6637.1.S1_at	3.610500E-04	3.800811E-02	0.77	1.30	PREDICTED: Canis familiaris similar to sodium channel associated protein 1 (LOC483829); mRNA	98.3	NM_144643	XM_540949	SCLT1	sodium channel and clathrin linker 1
CfaAffx.6650.1.S1_at	1.365550E-02	2.450662E-01	0.9	1.11	PREDICTED: Canis familiaris similar to WD repeat domain 35 (LOC475677); mRNA	100.0	NULL	XM_532884	WDR35	WD repeat domain 35
CfaAffx.6670.1.S1_at	1.060770E-02	2.175082E-01	0.9	1.11	PREDICTED: Canis familiaris similar to microtubule associated monoxygenase; calponin and LIM domain containing 1 (LOC481958); mRNA	69.8	NULL	XM_539079	MICAL1	microtubule associated monoxygenase, calponin and LIM domain containing 1

CfaAffx.6674.1.S1_at	3.972840E-06	2.555108E-03	1.28	.78	Physcomitrella patens subsp. patens predicted protein (PHYPADRAFT_132416) mRNA; complete cds	14.6	AP003086	XM_001767693	PHYPADRAFT_132416	hypothetical protein
CfaAffx.6723.1.S1_at	1.362120E-03	7.900112E-02	1.14	.87	Canis familiaris DNA for bitter taste receptor; complete cds; clone: Cafa-T2R38	100.0	BC104937	AB249694		
CfaAffx.6742.1.S1_s_at	2.169890E-03	1.003052E-01	0.84	1.20	Canis lupus familiaris BCL2-associated X protein (BAX); mRNA >gi|27372189|dbj|AB080230.1| Canis familiaris mRNA for Bax; complete cds	100.0	CU680816	NM_001003011	BAX	BCL2-associated X protein
CfaAffx.6745.1.S1_at	1.289340E-03	7.615957E-02	1.22	.82	Paramecium tetraurelia hypothetical protein (GSPATT00034643001) partial mRNA	28.2	AL162377	XM_001432525	GSPATT00034643001	hypothetical protein
CfaAffx.6764.1.S1_at	2.042190E-02	2.949586E-01	1.14	.88	Canis familiaris DNA for bitter taste receptor; complete cds; clone: Cafa-T2R5	62.8	CU686869	AB249688		
CfaAffx.6768.1.S1_at	1.474150E-03	8.251919E-02	0.85	1.18	PREDICTED: Canis familiaris similar to single-stranded DNA binding protein 1 isoform 1; transcript variant 1 (LOC475524); mRNA	100.0	AK311200	XM_532747	LOC475524	similar to single-stranded DNA binding protein 1 isoform 1
CfaAffx.6780.1.S1_s_at	8.498880E-03	1.971650E-01	1.12	.89	PREDICTED: Canis familiaris similar to solute carrier family 22; member 16 (LOC475027); mRNA	100.0	BC037247	XM_532263	SLC22A16	solute carrier family 22 (organic cation/carnitine transporter), member 16
CfaAffx.6789.1.S1_s_at	2.166740E-03	1.003052E-01	1.21	.83	PREDICTED: Canis familiaris similar to pendrin (LOC483263); mRNA	100.0	BC153002	XM_540382	SLC26A4	solute carrier family 26, member 4
CfaAffx.6795.1.S1_at	6.976960E-03	1.787223E-01	1.15	.87	Oryza sativa (japonica cultivar-group) Os06g0680900 (Os06g0680900) mRNA; complete cds	15.3	AL049843	NM_001064909	Os06g0680900	Os06g0680900
CfaAffx.6818.1.S1_s_at	4.225580E-03	1.394031E-01	1.2	.83	PREDICTED: Canis familiaris similar to palmitoylated membrane protein 7 (LOC487080); mRNA	100.0	BC038105	XM_544208	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)
CfaAffx.6823.1.S1_s_at	1.258650E-02	2.363264E-01	1.11	.90	PREDICTED: Canis familiaris similar to KIAA1919 protein (LOC481962); mRNA	99.8	AK315016	XM_539083	LOC481962	similar to KIAA1919 protein
CfaAffx.683.1.S1_s_at	8.176360E-	5.906785E-	0.79	1.26	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) 1 beta	100.0	AF047181	XM_535812	LOC478639	similar to NADH dehydrogenase

	04	02			subcomplex; 5 (LOC478639); mRNA					(ubiquinone) 1 beta subcomplex, 5
CfaAffx.6832.1.S1_at	2.730250E-03	1.121148E-01	1.13	.88	Homo sapiens cDNA clone IMAGE:30369327; partial cds	76.5	BC065735	BC065735		
CfaAffx.6835.1.S1_at	6.507870E-03	1.732327E-01	1.11	.90	PREDICTED: Equus caballus similar to TSP-EAR protein (LOC100063327); mRNA	95.0	AK094826	XM_001494593		
CfaAffx.6838.1.S1_at	1.037460E-02	2.153015E-01	1.16	.86	PREDICTED: Monodelphis domestica hypothetical protein LOC100026801 (LOC100026801); mRNA	45.2	AL392173	XM_001377256	LOC100026801	hypothetical protein LOC100026801
CfaAffx.6843.1.S1_at	1.389720E-02	2.472369E-01	1.15	.87	PREDICTED: Canis familiaris similar to PDZ domain containing 6; transcript variant 2 (LOC607233); mRNA	97.1	AK291481	XM_843557	INTU	inturned planar cell polarity effector homolog (Drosophila)
CfaAffx.687.1.S1_at	7.830600E-03	1.881574E-01	1.14	.88	PREDICTED: Canis familiaris similar to olfactory receptor Olr818 (LOC609983); mRNA	99.6	NULL	XM_847349	LOC609983	similar to olfactory receptor Olr818
CfaAffx.688.1.S1_at	5.238830E-04	4.677449E-02	1.15	.87	PREDICTED: Canis familiaris similar to Olfactory receptor 4C6 (LOC491531); mRNA	99.0	BK004330	XM_848499	LOC491531	similar to Olfactory receptor 4C6
CfaAffx.6921.1.S1_at	8.968710E-04	6.245444E-02	1.12	.89	PREDICTED: Canis familiaris similar to CG17941-PA (LOC475891); mRNA	85.9	BC111738	XM_533098	LOC475891	similar to CG17941-PA
CfaAffx.700.1.S1_s_at	3.925400E-04	4.031732E-02	1.23	.81	PREDICTED: Canis familiaris similar to olfactory receptor Olr621 (LOC610430); mRNA	100.0	NULL	XM_847938	LOC610430	similar to olfactory receptor Olr621
CfaAffx.7064.1.S1_s_at	2.114090E-02	2.989080E-01	1.1	.91	PREDICTED: Canis familiaris similar to cytochrome P450; family 4; subfamily B; polypeptide 1; transcript variant 2 (LOC608452); mRNA	100.0	NULL	XM_845151	LOC608452	similar to cytochrome P450, family 4, subfamily B, polypeptide 1
CfaAffx.7073.1.S1_s_at	1.582060E-02	2.636643E-01	1.12	.89	PREDICTED: Canis familiaris similar to cytochrome P450; family 4; subfamily X; polypeptide 1 (LOC482505); mRNA	100.0	CU688399	XM_539622	LOC482505	similar to cytochrome P450, family 4, subfamily X, polypeptide 1
CfaAffx.7076.1.S1_at	1.316430E-02	2.408697E-01	1.13	.89	Homo sapiens cytochrome P450; family 4; subfamily B; polypeptide 1 (CYP4B1) gene; complete cds	43.0	DQ518907	DQ518907		

CfaAffx.7077.1.S1_at	1.013670E-02	2.133766E-01	0.85	1.18	PREDICTED: Equus caballus hypothetical protein LOC100055892 (LOC100055892); mRNA	86.7	AF378757	XM_001496595	LOC100055892	hypothetical protein LOC100055892
CfaAffx.708.1.S1_at	8.714630E-03	2.001249E-01	1.18	.85	Macaca fascicularis testis cDNA; clone: QtsA-19889; similar to human chromosome 11 open reading frame 1 (C11orf1); mRNA; RefSeq: NM_022761.1	87.6	AB169412	AB169412		
CfaAffx.7110.1.S1_at	5.072830E-05	1.167429E-02	1.18	.85	PREDICTED: Canis familiaris similar to Nebulette (Actin-binding Z-disk protein); transcript variant 3 (LOC477974); mRNA	59.3	AL157398	XM_844454	NEBL	nebulette
CfaAffx.7153.1.S1_at	1.361890E-04	2.162691E-02	1.21	.82	Physcomitrella patens subsp. patens predicted protein (PHYPADRAFT_165630) mRNA; complete cds	28.6	AC016961	XM_001767299	PHYPADRAFT_165630	hypothetical protein
CfaAffx.7234.1.S1_s_at	6.414390E-03	1.720925E-01	0.86	1.16	PREDICTED: Canis familiaris similar to Methionine-R-sulfoxide reductase B (LOC608357); mRNA	99.1	BC130380	XM_845365	MSRB2	methionine sulfoxide reductase B2
CfaAffx.7342.1.S1_at	7.479650E-09	6.437735E-05	1.35	.74	PREDICTED: Canis familiaris similar to O-linked mannose beta1;2-N-acetylglucosaminyltransferase; transcript variant 2 (LOC482511); mRNA	95.9	CR612816	XM_845273	POMGNT1	protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase
CfaAffx.7346.1.S1_s_at	4.002280E-06	2.555108E-03	1.31	.76	PREDICTED: Canis familiaris similar to ATPase; H+ transporting; lysosomal V0 subunit a isoform 4; transcript variant 9 (LOC482779); mRNA	100.0	AF245517	XM_854136	ATP6V0A4	ATPase, H+ transporting, lysosomal V0 subunit a4
CfaAffx.7347.1.S1_at	4.309560E-03	1.409285E-01	1.16	.86	Homo sapiens mRNA for KIAA1393 protein; partial cds	12.5	NM_020810	AB037814	TRMT5	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)
CfaAffx.735.1.S1_at	5.760350E-03	1.628197E-01	1.1	.91	PREDICTED: Bos taurus similar to olfactory receptor MOR230-6 (LOC788089); mRNA	82.1	NULL	XM_001255253	LOC788089	similar to olfactory receptor 1183
CfaAffx.738.1.S1_x_at	1.217950E-02	2.337430E-01	0.86	1.16	PREDICTED: Canis familiaris similar to DNA replication complex GINS protein PSF1; transcript variant 2 (LOC477005); mRNA	98.3	AB383787	XM_843559	GINS1	GINS complex subunit 1 (Psf1 homolog)
CfaAffx.7411.1.S1_at	3.189990E-07	5.227780E-04	1.36	.74	NULL	null	AF128525	NULL		

CfaAffx.7411.1.S1_s_at	1.049860E-02	2.162123E-01	1.15	.87	PREDICTED: Canis familiaris similar to tripartite motif protein 17 (LOC485140); mRNA	98.8	XR_019359	XM_542258	LOC485140	similar to tripartite motif protein 17
CfaAffx.7418.1.S1_s_at	1.788180E-02	2.786886E-01	1.11	.90	Mus musculus 0 day neonate skin cDNA; RIKEN full-length enriched library; clone:4631422L12 product:hypothetical CDP-alcohol phosphatidyltransferase containing protein; full insert sequence	90.2	AB051511	AK014530	D5Wsu178e	DNA segment, Chr 5, Wayne State University 178, expressed
CfaAffx.7508.1.S1_at	1.028010E-03	6.728568E-02	1.18	.85	null	null	null	null		
CfaAffx.7541.1.S1_s_at	8.942720E-03	2.017033E-01	0.89	1.12	PREDICTED: Canis familiaris similar to CG14025-PB; isoform B (LOC477006); mRNA	58.1	AB023197	XM_534204	LOC477006	similar to CG14025-PB, isoform B
CfaAffx.7547.1.S1_at	3.563550E-03	1.277456E-01	0.83	1.20	PREDICTED: Canis familiaris similar to Microtubule-associated serine/threonine-protein kinase 2 (LOC482513); mRNA	100.0	NM_015112	XM_539630	MAST2	microtubule associated serine/threonine kinase 2
CfaAffx.7575.1.S1_at	7.502610E-03	1.841842E-01	0.87	1.14	PREDICTED: Canis familiaris similar to CG13295-PA; transcript variant 2 (LOC485567); mRNA	100.0	AK292756	XM_851711	LOC485567	similar to CG13295-PA
CfaAffx.7581.1.S1_at	9.126940E-03	2.028678E-01	0.89	1.12	PREDICTED: Canis familiaris similar to Ssu72 RNA polymerase II CTD phosphatase homolog (LOC608299); mRNA	100.0	AK019168	XM_845279	LOC608299	similar to Ssu72 RNA polymerase II CTD phosphatase homolog
CfaAffx.760.1.S1_s_at	1.873550E-03	9.342784E-02	0.82	1.21	PREDICTED: Canis familiaris similar to small nuclear ribonucleoprotein polypeptide G (LOC612653); mRNA	99.4	BC066302	XM_850384	LOC612653	similar to small nuclear ribonucleoprotein polypeptide G
CfaAffx.7630.1.S1_at	7.040290E-03	1.795988E-01	0.88	1.13	PREDICTED: Canis familiaris similar to CGI58 protein; transcript variant 2 (LOC485570); mRNA	100.0	CU692423	XM_851834	ABHD5	abhydrolase domain containing 5
CfaAffx.7688.1.S1_at	7.522710E-07	9.249709E-04	1.36	.74	Entamoeba dispar SAW760 trichohyalin; putative EDI_024060 mRNA; complete cds	42.6	AC079269	XM_001737560	EDI_024060	trichohyalin, putative
CfaAffx.7702.1.S1_at	1.025490E-02	2.148586E-01	0.87	1.15	PREDICTED: Canis familiaris similar to lung cancer-related protein 8 (LOC610011); mRNA	100.0	CU678855	XM_847390	LOC610011	similar to lung cancer-related protein 8

CfaAffx.7704.1.S1_s_at	3.899500E-03	1.341447E-01	0.85	1.17	PREDICTED: Canis familiaris similar to lung cancer-related protein 8 (LOC610011); mRNA	100.0	CU678855	XM_847390	LOC610011	similar to lung cancer-related protein 8
CfaAffx.7740.1.S1_at	1.092340E-03	6.984971E-02	1.24	.81	PREDICTED: Canis familiaris similar to Mitogen-activated protein kinase kinase kinase 2 (MAPK/ERK kinase kinase 2) (MEK kinase 2) (MEKK 2) (LOC612902); mRNA	100.0	AF111105	XM_847181	MAP3K2	mitogen-activated protein kinase kinase kinase 2
CfaAffx.7749.1.S1_at	2.098540E-02	2.978695E-01	0.9	1.12	PREDICTED: Canis familiaris similar to Dynein intermediate chain 2; axonemal (Axonemal dynein intermediate chain 2) (LOC483284); mRNA	100.0	NM_023036	XM_540403	DNAI2	dynein, axonemal, intermediate chain 2
CfaAffx.7761.1.S1_at	7.476000E-03	1.839506E-01	1.12	.90	PREDICTED: Canis familiaris similar to nucleophosmin 1; transcript variant 1 (LOC475722); mRNA	52.7	NULL	XM_532930	LOC475722	similar to nucleophosmin 1
CfaAffx.7792.1.S1_at	2.559780E-04	3.134647E-02	1.2	.83	NULL	null	AC008278	NULL		
CfaAffx.7799.1.S1_s_at	5.556170E-03	1.592432E-01	0.85	1.17	Candida glabrata CBS138; CAGL0H01463g partial mRNA	17.6	AP006305	XM_446862	CAGL0H01463g	hypothetical protein
CfaAffx.7802.1.S1_at	1.857820E-02	2.823561E-01	1.13	.89	Mus musculus CLM2 mRNA; complete cds	30.5	NULL	AY457048	Cd300e	CD300e antigen
CfaAffx.7809.1.S1_s_at	5.354220E-03	1.560046E-01	1.1	.91	PREDICTED: Canis familiaris similar to GTPase; IMAP family member 8 (LOC482794); mRNA	100.0	NULL	XM_848456	GIMAP8	GTPase, IMAP family member 8
CfaAffx.7826.1.S1_at	6.686020E-03	1.752332E-01	1.15	.87	PREDICTED: Canis familiaris similar to Ras-related protein Rab-37 (LOC483298); mRNA	100.0	BC016615	XM_540417	RAB37	RAB37, member RAS oncogene family
CfaAffx.7832.1.S1_s_at	8.934500E-03	2.017033E-01	1.17	.86	PREDICTED: Canis familiaris similar to Ras suppressor protein 1 (LOC477993); mRNA	100.0	NULL	XM_535177	RSU1	Ras suppressor protein 1
CfaAffx.7858.1.S1_at	6.138760E-03	1.686566E-01	0.9	1.11	PREDICTED: Canis familiaris similar to cleft lip and palate associated transmembrane protein 1; transcript variant 2 (LOC484455); mRNA	100.0	CU680307	XM_847485	CLPTM1	cleft lip and palate associated transmembrane protein 1

CfaAffx.789.1.S1_at	1.322800E-03	7.738874E-02	0.8	1.25	PREDICTED: Canis familiaris similar to CG7818-PA (LOC487920); mRNA	100.0	AB173603	XM_545043	LOC487920	similar to CG7818-PA
CfaAffx.7929.1.S1_s_at	1.532970E-03	8.414715E-02	1.11	.90	PREDICTED: Canis familiaris similar to otopetrin 2 (LOC483303); mRNA	60.1	NULL	XM_540422	OTOP2	otopetrin 2
CfaAffx.7934.1.S1_at	1.605690E-03	8.670122E-02	1.12	.89	PREDICTED: Canis familiaris similar to Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF)... (LOC609418); mRNA	92.7	NM_033012	XM_846672	TNFSF11	tumor necrosis factor (ligand) superfamily, member 11
CfaAffx.7968.1.S1_at	2.739140E-03	1.123689E-01	1.13	.89	PREDICTED: Equus caballus similar to sONE (LOC100064027); mRNA	89.7	BK004019	XM_001495054	LOC100064027	similar to sONE
CfaAffx.7970.1.S1_at	1.951700E-05	6.884542E-03	1.26	.79	Homo sapiens endothelin converting enzyme 1 (ECE1) gene; complete cds	44.7	AC104537	AY953519		
CfaAffx.7990.1.S1_x_at	1.492800E-03	8.310821E-02	0.83	1.21	PREDICTED: Canis familiaris similar to Zinc finger protein 208 (LOC484461); mRNA	67.8	EU446734	XM_541576	LOC484461	similar to Zinc finger protein 208
CfaAffx.7992.1.S1_at	7.022040E-04	5.444928E-02	0.86	1.16	PREDICTED: Canis familiaris similar to Zinc finger protein 208 (LOC484461); mRNA	69.5	AF246126	XM_541576	LOC484461	similar to Zinc finger protein 208
CfaAffx.8022.1.S1_at	1.969350E-08	9.416775E-05	1.48	.68	Homo sapiens myosin VC (MYO5C); mRNA	48.7	AL163973	NM_018728	MYO5C	myosin VC
CfaAffx.8034.1.S1_at	1.987610E-02	2.916359E-01	0.89	1.12	PREDICTED: Canis familiaris hypothetical protein LOC611184; transcript variant 2 (LOC611184); mRNA	22.4	BC015950	XM_861043	ZNF428	zinc finger protein 428
CfaAffx.8064.1.S1_s_at	2.017400E-02	2.930098E-01	1.1	.91	PREDICTED: Canis familiaris similar to cyclic AMP-regulated phosphoprotein; 21 kD isoform 1; transcript variant 16 (LOC477016); mRNA	100.0	NULL	XM_853990	LOC477016	similar to cyclic AMP-regulated phosphoprotein, 21 kD isoform 1
CfaAffx.8069.1.S1_at	6.101960E-04	5.075435E-02	1.2	.83	Mus musculus 0 day neonate head cDNA; RIKEN full-length enriched library; clone:4833441O04 product:protein phosphatase 1; regulatory (inhibitor)	30.6	AC016943	AK029467	Arpp21	cyclic AMP-regulated phosphoprotein, 21

					subunit 1C; full insert sequence					
CfaAffx.8085.1.S1_at	4.461360E-03	1.428212E-01	1.13	.88	null	null	null	null		
CfaAffx.8085.1.S1_s_at	2.859140E-05	8.604412E-03	1.18	.85	PREDICTED: Canis familiaris similar to Stac protein (SRC homology 3 and cysteine-rich domain protein) (LOC477017); mRNA	100.0	AK313493	XM_534217	STAC	SH3 and cysteine rich domain
CfaAffx.8158.1.S1_at	4.525440E-04	4.366644E-02	1.14	.88	PREDICTED: Canis familiaris similar to Golgi autoantigen; golgin subfamily A member 4 (Trans-Golgi p230) (256 kDa golgin) (Golgin-245) (72.1 protein) (LOC477020); mRNA	29.4	AC097359	XM_846110	LOC477020	similar to Golgi autoantigen, golgin subfamily A member 4 (Trans-Golgi p230) (256 kDa golgin) (Golgin-245) (72.1 protein)
CfaAffx.8249.1.S1_s_at	5.179970E-03	1.530867E-01	0.89	1.12	PREDICTED: Canis familiaris similar to SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily d; member 3 isoform 1; transcript variant 3 (LOC475541); mRNA	100.0	AY892091	XM_845234	SMARCD3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3
CfaAffx.834.1.S1_s_at	1.842430E-02	2.818510E-01	1.15	.87	PREDICTED: Canis familiaris similar to F26E4.12; transcript variant 1 (LOC478059); mRNA	100.0	CU688647	XM_535237	LOC478059	similar to F26E4.12
CfaAffx.8357.1.S1_at	1.313680E-06	1.429676E-03	1.27	.79	PREDICTED: Canis familiaris similar to T-complex protein 1 (LOC482811); mRNA	100.0	AL022394	XM_539926	LOC482811	similar to T-complex protein 1
CfaAffx.8369.1.S1_at	2.201900E-04	2.897822E-02	1.21	.82	Canis lupus familiaris ATP-binding cassette; sub-family G (WHITE); member 2 (ABCG2); mRNA >gi|77812224|gb|DQ222459.1| Canis familiaris breast cancer resistance protein (BCRP) mRNA; complete cds	29.7	NULL	NM_001048021	ABCG2	ATP-binding cassette, sub-family G (WHITE), member 2
CfaAffx.8373.1.S1_at	6.595220E-06	3.548256E-03	1.21	.82	PREDICTED: Pan troglodytes kelch-like 1 protein (KLHL1); mRNA	88.8	AK291435	XM_509677	KLHL1	kelch-like 1 (Drosophila)
CfaAffx.8423.1.S1_at	1.523070E-02	2.601005E-01	1.11	.90	PREDICTED: Canis familiaris similar to Nck-associated protein 5 (LOC483893); mRNA	100.0	NM_207481	XM_541013	LOC483893	similar to Nck-associated protein 5
CfaAffx.8444.1.S1_at	1.148350E-02	2.266411E-01	0.9	1.11	PREDICTED: Canis familiaris similar to CG7810-PA (LOC484489); mRNA	48.4	AL833726	XM_541603	CCDC97	coiled-coil domain containing 97

CfaAffx.846.1.S1_at	4.461720E-04	4.328827E-02	1.2	.83	Mus musculus olfactory receptor 810; mRNA (cDNA clone MGC:155988 IMAGE:40129674); complete cds	80.9	NULL	BC120751	Olfr810	olfactory receptor 810
CfaAffx.846.1.S1_s_at	2.279940E-04	2.963465E-02	1.25	.80	Rattus norvegicus olfactory receptor 1002 (predicted) (Olr1002_predicted); mRNA	85.1	NULL	NM_001001371	Olr1002	olfactory receptor 1002
CfaAffx.8470.1.S1_at	1.177730E-02	2.294862E-01	0.79	1.26	PREDICTED: Canis familiaris similar to chromosome 13 open reading frame 24 (LOC476945); mRNA	100.0	NM_006346	XM_534145	PIBF1	progesterone immunomodulatory binding factor 1
CfaAffx.855.1.S1_at	1.595790E-03	8.649547E-02	1.15	.87	PREDICTED: Bos taurus similar to olfactory receptor Olfr594 (LOC786121); mRNA	49.5	AC113331	XM_001253904		
CfaAffx.8607.1.S1_s_at	2.979680E-03	1.178589E-01	1.1	.91	PREDICTED: Canis familiaris similar to cystatin 11 isoform 1 precursor (LOC606832); mRNA	99.5	BC121080	XM_843270	CST11	cystatin 11
CfaAffx.861.1.S1_at	1.181600E-02	2.296042E-01	1.14	.87	PREDICTED: Canis familiaris hypothetical protein LOC611413 (LOC611413); mRNA	98.3	BC130306	XM_849082	TMEM182	transmembrane protein 182
CfaAffx.8613.1.S1_at	6.095330E-03	1.681491E-01	1.11	.90	NULL	null	AL022719	NULL		
CfaAffx.8618.1.S1_s_at	3.759670E-03	1.319718E-01	1.17	.85	PREDICTED: Canis familiaris similar to lactase-phlorizin hydrolase preproprotein (LOC483898); mRNA	100.0	AY191611	XM_541018	LCT	lactase
CfaAffx.864.1.S1_at	5.530500E-03	1.592432E-01	1.21	.83	PREDICTED: Canis familiaris cOR8B15 olfactory receptor family 8 subfamily B-like (cOR8B15); mRNA	87.9	NULL	XM_847337	cOR8B15	cOR8B15 olfactory receptor family 8 subfamily B-like
CfaAffx.8653.1.S1_s_at	6.308500E-03	1.708536E-01	1.17	.86	PREDICTED: Canis familiaris similar to limb region 1 protein (LOC482819); mRNA	100.0	AK291037	XM_539934	LMBR1	limb region 1 homolog (mouse)
CfaAffx.8694.1.S1_at	1.199680E-03	7.311141E-02	1.12	.90	PREDICTED: Equus caballus similar to Thrombospondin type-1 domain-containing protein 7B; transcript variant 1 (LOC100051048); mRNA	95.1	NM_001080427	XM_001490246	LOC100051048	similar to Thrombospondin type-1 domain-containing protein 7B
CfaAffx.8715.1.S1_s_at	7.770970E-03	1.874380E-01	0.7	1.42	PREDICTED: Canis familiaris similar to Histamine N-methyltransferase (HMT)	100.0	D16224	XM_533340	HNMT	histamine N-methyltransferase

					(LOC476133); mRNA					
CfaAffx.8720.1.S1_at	1.308850E-02	2.403652E-01	0.84	1.19	Paramecium tetraurelia hypothetical protein (GSPATT00007927001) partial mRNA	40.8	AL133335	XM_001438152	GSPATT00007927001	hypothetical protein
CfaAffx.8732.1.S1_at	4.234290E-04	4.208376E-02	0.89	1.12	PREDICTED: Canis familiaris similar to beta-1;3-N-acetylglucosaminyltransferase protein (LOC485176); mRNA	82.6	AK313682	XM_542294	B3GNT1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1
CfaAffx.874.1.S1_at	1.068950E-02	2.176197E-01	0.87	1.15	Homo sapiens cDNA; FLJ92145	36.0	AC213270	AK311879	COX7B	cytochrome c oxidase subunit VIIb
CfaAffx.8748.1.S1_at	1.414040E-03	8.049367E-02	1.22	.82	PREDICTED: Pan troglodytes ADAM metallopeptidase domain 22; transcript variant 3 (ADAM22); mRNA	21.9	AL160395	XM_001164160	ADAM22	ADAM metallopeptidase domain 22
CfaAffx.875.1.S1_s_at	1.062220E-04	1.829779E-02	0.79	1.26	PREDICTED: Canis familiaris similar to LSM5 homolog; U6 small nuclear RNA associated (LOC611686); mRNA	100.0	CU675199	XM_849384	LSM5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)
CfaAffx.879.1.S1_at	9.096960E-03	2.025064E-01	1.12	.89	PREDICTED: Equus caballus similar to olfactory receptor 1039 (LOC100065500); mRNA	86.8	AP002512	XM_001496063	LOC100065500	similar to olfactory receptor 1039
CfaAffx.880.1.S1_at	3.743190E-03	1.315364E-01	1.1	.91	Canis familiaris DNA for bitter taste receptor; complete cds; clone: Cafa-T2R1	100.0	AC026787	AB249684		
CfaAffx.8836.1.S1_s_at	1.822140E-02	2.803568E-01	0.88	1.14	PREDICTED: Canis familiaris similar to WD-repeat protein 43 (LOC475713); mRNA	100.0	AB383703	XM_532920	WDR43	WD repeat domain 43
CfaAffx.8903.1.S1_s_at	1.376310E-02	2.460894E-01	0.9	1.11	PREDICTED: Canis familiaris similar to tubulin tyrosine ligase-like family; member 3 isoform 1 (LOC484664); mRNA	100.0	AK127786	XM_541779	TTLL3	tubulin tyrosine ligase-like family, member 3
CfaAffx.8920.1.S1_s_at	4.533650E-03	1.440957E-01	0.86	1.17	PREDICTED: Canis familiaris similar to ubiquitin-conjugating enzyme E2E 1 isoform 2 (LOC475563); mRNA	100.0	NM_182666	XM_532783	LOC475563	similar to ubiquitin-conjugating enzyme E2E 1 isoform 2
CfaAffx.8921.1.S1_at	7.660140E-04	5.666965E-02	1.11	.90	PREDICTED: Canis familiaris similar to tyrosinase-related protein-2 (LOC485520); mRNA	100.0	CU688451	XM_542639	DCT	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)

CfaAffx.8962.1.S1_s_at	3.607790E-03	1.285275E-01	1.13	.89	PREDICTED: Canis familiaris olfactory receptor (OR03E02); mRNA	99.8	NULL	XM_539657	OR03E02	olfactory receptor
CfaAffx.8963.1.S1_at	5.927720E-03	1.652817E-01	1.11	.90	PREDICTED: Equus caballus similar to olfactory receptor; family 11; subfamily H; member 1; transcript variant 2 (LOC100058174); mRNA	89.7	NM_001013354	XM_001504632	LOC100058174	similar to olfactory receptor, family 11, subfamily H, member 1
CfaAffx.8965.1.S1_at	3.152390E-05	9.216261E-03	1.18	.85	PREDICTED: Canis familiaris similar to olfactory receptor 745 (LOC482541); mRNA	100.0	NULL	XM_539658	LOC482541	similar to olfactory receptor 745
CfaAffx.8967.1.S1_at	9.732570E-03	2.098850E-01	1.11	.90	PREDICTED: Equus caballus similar to Olfr736 protein (LOC100072499); mRNA	90.4	NULL	XM_001502449	LOC100072499	similar to Olfr736 protein
CfaAffx.897.1.S1_at	1.009540E-02	2.131774E-01	1.15	.87	PREDICTED: Canis familiaris similar to olfactory receptor 437; transcript variant 1 (LOC482722); mRNA	100.0	NULL	XM_843425	LOC482722	similar to olfactory receptor 437
CfaAffx.8978.1.S1_x_at	1.667160E-03	8.901517E-02	0.84	1.19	PREDICTED: Canis familiaris similar to ribosomal protein L31; transcript variant 3 (LOC607190); mRNA	83.6	NULL	XM_851697	LOC607190	similar to ribosomal protein L31
CfaAffx.8983.1.S1_at	1.339280E-05	5.192425E-03	1.19	.84	PREDICTED: Pan troglodytes similar to olfactory receptor (LOC473318); mRNA	65.8	AF546300	XM_528689	LOC473318	similar to olfactory receptor
CfaAffx.8993.1.S1_at	8.836480E-03	2.009348E-01	1.14	.88	Homo sapiens monoacylglycerol O-acyltransferase 2; mRNA (cDNA clone MGC:119185 IMAGE:40004283); complete cds	62.8	BC103878	BC103878	MOGAT2	monoacylglycerol O-acyltransferase 2
CfaAffx.9012.1.S1_at	3.522780E-03	1.277456E-01	1.17	.85	PREDICTED: Canis familiaris hypothetical LOC148014 (LOC484503); mRNA	92.0	AK289550	XM_541617	TTC9B	tetratricopeptide repeat domain 9B
CfaAffx.9044.1.S1_at	8.832990E-08	2.521270E-04	1.24	.80	Human metapneumovirus isolate JPS02-76 nucleoprotein (N); phosphoprotein (P); matrix protein (M); fusion protein (F); matrix protein 2-1 (M2-1); matrix protein 2-2 (M2-2); small hydrophobic protein (SH); and attachment glycoprotein (G) genes; complete cds	21.3	AL391361	AY530089		
CfaAffx.9060.1.S1_at	9.221970E-05	1.706465E-02	1.19	.84	Homo sapiens arrestin; beta 1 (ARRB1) gene; complete cds	79.6	DQ314865	DQ314865		

CfaAffx.9069.1.S1_at	1.290280E-02	2.397547E-01	1.1	.91	PREDICTED: Canis familiaris similar to olfactory receptor; family 6; subfamily S; member 1; transcript variant 1 (LOC482561); mRNA	100.0	NM_001001968	XM_539678	LOC482561	similar to olfactory receptor, family 6, subfamily S, member 1
CfaAffx.9072.1.S1_at	1.386470E-03	7.987515E-02	0.87	1.14	PREDICTED: Canis familiaris similar to Protein C20orf12 (LOC607837); mRNA	100.0	AB052150	XM_844660	LOC607837	similar to Protein C20orf12
CfaAffx.911.1.S1_at	7.604760E-04	5.662125E-02	1.18	.85	PREDICTED: Canis familiaris similar to Olfactory receptor 2D3 (LOC485359); mRNA	99.4	NULL	XM_542477	LOC485359	similar to Olfactory receptor 2D3
CfaAffx.9125.1.S1_at	1.565870E-02	2.623091E-01	1.21	.83	Trichomonas vaginalis G3 hypothetical protein (TVAG_327060) partial mRNA	46.9	AP001992	XM_001304626	TVAG_327060	hypothetical protein
CfaAffx.9128.1.S1_s_at	5.054240E-04	4.604700E-02	1.16	.86	PREDICTED: Canis familiaris similar to claudin 10 isoform b; transcript variant 1 (LOC476963); mRNA	100.0	AK315737	XM_534163	CLDN10	claudin 10
CfaAffx.9131.1.S1_s_at	5.360520E-03	1.560410E-01	1.11	.90	PREDICTED: Canis familiaris similar to Neuronal acetylcholine receptor protein; beta-3 subunit precursor (LOC482837); mRNA	100.0	NM_000749	XM_539952	CHRNB3	cholinergic receptor, nicotinic, beta 3
CfaAffx.915.1.S1_x_at	3.079410E-03	1.189972E-01	1.17	.85	PREDICTED: Canis familiaris similar to hypoxia induced gene 1; transcript variant 1 (LOC477037); mRNA	90.8	NULL	XM_534235	HIGD1A	HIG1 domain family, member 1A
CfaAffx.916.1.S1_x_at	1.374110E-04	2.166111E-02	0.84	1.19	PREDICTED: Canis familiaris similar to ribosomal protein L31 (LOC610973); mRNA	97.8	NULL	XM_534036	LOC610973	similar to ribosomal protein L31
CfaAffx.9232.1.S1_s_at	1.135650E-04	1.931727E-02	0.81	1.23	PREDICTED: Canis familiaris similar to U2 small nuclear ribonucleoprotein B; transcript variant 1 (LOC477148); mRNA	62.1	NULL	XM_534338	LOC477148	similar to U2 small nuclear ribonucleoprotein B
CfaAffx.925.1.S1_at	9.956690E-03	2.124374E-01	1.17	.85	PREDICTED: Equus caballus similar to olfactory receptor MOR114-11 (LOC100055352); mRNA	86.5	NULL	XM_001489573	LOC100055352	similar to olfactory receptor MOR114-11
CfaAffx.9251.1.S1_at	1.563710E-02	2.621012E-01	0.88	1.13	PREDICTED: Canis familiaris similar to methyl-CpG binding domain protein 5; transcript variant 3 (LOC483910); mRNA	70.4	NM_018328	XM_852451	MBD5	methyl-CpG binding domain protein 5

CfaAffx.9277.1.S1_at	9.035020E-04	6.271324E-02	1.13	.88	PREDICTED: Equus caballus hypothetical protein LOC100065345 (LOC100065345); mRNA	89.5	BC035599	XM_001495955	C2CD3	C2 calcium-dependent domain containing 3
CfaAffx.931.1.S1_x_at	2.453960E-03	1.058821E-01	1.1	.91	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 3; 9kDa (LOC608498); mRNA	100.0	NULL	XM_845540	LOC608498	similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa
CfaAffx.9328.1.S1_s_at	1.534410E-02	2.602160E-01	1.13	.89	PREDICTED: Equus caballus similar to nucleolar protein family 6 (RNA-associated); (LOC100052696); mRNA	93.1	U92458	XM_001496002	GRM7	glutamate receptor, metabotropic 7
CfaAffx.9343.1.S1_s_at	1.730330E-02	2.744615E-01	1.15	.87	NULL	null	AC105424	NULL		
CfaAffx.9392.1.S1_s_at	1.990330E-02	2.919354E-01	1.2	.83	PREDICTED: Canis familiaris similar to solute carrier family 4; sodium bicarbonate cotransporter; member 7 (LOC485637); mRNA	100.0	BC156213	XM_542756	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7
CfaAffx.952.1.S1_at	3.505410E-04	3.758122E-02	1.13	.88	PREDICTED: Equus caballus similar to pheromone receptor (LOC100064743); mRNA	69.5	NULL	XM_001495561	LOC100064743	similar to pheromone receptor
CfaAffx.9534.1.S1_at	3.551970E-03	1.277456E-01	1.18	.85	Homo sapiens nebulin (NEB) gene; exon 187 and partial cds	26.1	AF117675	AF117675		
CfaAffx.954.1.S1_at	2.670680E-03	1.107252E-01	0.81	1.23	PREDICTED: Canis familiaris similar to G protein-coupled receptor 162 isoform 2; transcript variant 3 (LOC486719); mRNA	54.3	BC080585	XM_862365	LEPREL2	leprecan-like 2
CfaAffx.9549.1.S1_at	1.610010E-02	2.655683E-01	1.19	.84	PREDICTED: Canis familiaris similar to Retinoic acid receptor beta (RAR-beta); transcript variant 9 (LOC477045); mRNA	97.7	NULL	XM_857350	RARB	retinoic acid receptor, beta
CfaAffx.955.1.S1_s_at	9.293830E-03	2.047325E-01	0.87	1.15	Canis lupus familiaris selenoprotein K (SELK); mRNA	100.0	AK289594	NM_001114878	SELK	selenoprotein K
CfaAffx.9558.1.S1_s_at	9.542280E-03	2.077548E-01	0.88	1.13	PREDICTED: Canis familiaris similar to prefoldin 1 (LOC490658); mRNA	100.0	CR603344	XM_547780	LOC490658	similar to prefoldin 1
CfaAffx.9590.1.S1_s_at	2.110300E-	9.882128E-	0.85	1.18	Sus scrofa clone ramn3517b_a24.y1.abd;	92.0	EU176472	AY610225		

	03	02			mRNA sequence					
CfaAffx.9620.1.S1_s_at	6.063190E-03	1.676924E-01	1.15	.87	PREDICTED: Canis familiaris similar to ADAM 18 precursor (A disintegrin and metalloproteinase domain 18) (Transmembrane metalloproteinase-like; disintegrin-like; and cysteine-rich protein III) (tMDC III) (LOC607708); mRNA	87.4	AK313961	XM_844491	ADAM18	ADAM metallopeptidase domain 18
CfaAffx.9641.1.S1_at	1.463370E-03	8.221427E-02	1.16	.87	Mus musculus KRIT1; ankyrin repeat containing; mRNA (cDNA clone IMAGE:4036903); **** WARNING: chimeric clone ****	21.5	NULL	BC044820	Krit1	KRIT1, ankyrin repeat containing
CfaAffx.9675.1.S1_at	1.147510E-03	7.155705E-02	1.2	.83	Equus caballus myogenic factor 5 gene; partial cds	92.5	AC025568	AF411602		
CfaAffx.968.1.S1_s_at	8.348870E-03	1.949504E-01	1.19	.84	Canis lupus familiaris cOR8V11 olfactory receptor family 8 subfamily V-like (cOR8V11); mRNA	100.0	NULL	NM_001017532	cOR8V11	cOR8V11 olfactory receptor family 8 subfamily V-like
CfaAffx.969.1.S1_at	3.600400E-03	1.283705E-01	1.13	.88	PREDICTED: Equus caballus similar to olfactory receptor MOR185-2 (LOC100052898); mRNA	85.5	AB065841	XM_001488496	LOC100052898	similar to olfactory receptor MOR185-2
CfaAffx.9698.1.S1_s_at	4.320770E-03	1.411878E-01	1.15	.87	PREDICTED: Canis familiaris similar to a disintegrin and metalloprotease domain 3 (cyritestin) (LOC607729); mRNA	78.9	BC042979	XM_844512	LOC607729	similar to a disintegrin and metalloprotease domain 3 (cyritestin)
CfaAffx.9700.1.S1_at	2.485220E-03	1.062080E-01	1.39	.72	PREDICTED: Canis familiaris similar to phospholipase C beta 4 isoform a; transcript variant 1 (LOC477160); mRNA	100.0	NULL	XM_534349	PLCB4	phospholipase C, beta 4
CfaAffx.9723.1.S1_at	1.981220E-05	6.931854E-03	1.28	.78	PREDICTED: Canis familiaris similar to phospholipase C beta 4 isoform a; transcript variant 4 (LOC477160); mRNA	57.4	AL031652	XM_854564	PLCB4	phospholipase C, beta 4
CfaAffx.9725.1.S1_s_at	1.487800E-02	2.560075E-01	0.88	1.13	PREDICTED: Canis familiaris similar to ring finger protein 121 isoform 1; transcript variant 7 (LOC476819); mRNA	78.3	AB172331	XM_856549	RNF121	ring finger protein 121
CfaAffx.9740.1.S1_at	1.945620E-02	2.895647E-01	1.12	.89	PREDICTED: Canis familiaris similar to TBC1 domain family member 5 (LOC485651);	94.2	AB168705	XM_542771	TBC1D5	TBC1 domain family, member 5

					mRNA					
CfaAffx.9746.1.S1_s_at	1.587820E-02	2.641811E-01	0.86	1.17	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 2; 8kDa (LOC478032); mRNA	100.0	AB169602	XM_535211	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa
CfaAffx.9763.1.S1_s_at	8.790860E-04	6.175431E-02	0.84	1.18	PREDICTED: Canis familiaris similar to Rho GDP dissociation inhibitor (GDI) alpha (LOC475924); mRNA	100.0	CU677553	XM_844840	ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha
CfaAffx.9807.1.S1_s_at	1.111760E-02	2.225096E-01	0.89	1.13	PREDICTED: Bos taurus similar to Ryanodine receptor 1 (Skeletal muscle-type ryanodine receptor) (RyR1) (RYR-1) (Skeletal muscle calcium release channel) (LOC505697); mRNA	93.9	NULL	XR_028565		
CfaAffx.9807.1.S1_x_at	1.396380E-02	2.478071E-01	0.86	1.17	Equus caballus ryanodine receptor 1 mRNA; exons 101 and 102 and partial cds	95.4	J05200	AY375486	LOC100034036	ryanodine receptor 1
CfaAffx.9811.1.S1_at	9.061150E-03	2.021287E-01	1.13	.89	Homo sapiens lunatic fringe (LFNG) gene; exon 1 and partial cds	12.3	AY124582	AY124582		
CfaAffx.9824.1.S1_at	1.199050E-03	7.311141E-02	0.86	1.16	PREDICTED: Canis familiaris similar to zinc finger; matrin type 2; transcript variant 2 (LOC607047); mRNA	100.0	BC056668	XM_852454	ZMAT2	zinc finger, matrin type 2
CfaAffx.9880.1.S1_at	1.607600E-02	2.654304E-01	1.16	.86	PREDICTED: Canis familiaris similar to CG4774-PA; isoform A; transcript variant 5 (LOC607530); mRNA	94.9	BC015333	XM_855150	CRLS1	cardiolipin synthase 1
CfaAffx.9886.1.S1_at	1.265480E-02	2.370916E-01	0.89	1.12	PREDICTED: Canis familiaris hypothetical LOC484530 (LOC484530); mRNA	100.0	AK310460	XM_541644	LOC484530	hypothetical LOC484530
CfaAffx.9891.1.S1_at	1.821530E-03	9.222299E-02	1.11	.90	PREDICTED: Canis familiaris similar to Potassium channel subfamily K member 6 (Inward rectifying potassium channel protein TWIK-2) (TWIK-originated similarity sequence) (LOC484531); mRNA	100.0	CU678689	XM_541645	KCNK6	potassium channel, subfamily K, member 6
CfaAffx.9894.1.S1_at	9.742100E-05	1.755740E-02	1.17	.85	PREDICTED: Canis familiaris similar to TPTE and PTEN homologous inositol lipid phosphatase isoform gamma (LOC606856); mRNA	98.8	XR_042296	XM_843320	LOC606856	similar to TPTE and PTEN homologous inositol lipid phosphatase isoform gamma

CfaAffx.9898.1.S1_at	1.636940E-04	2.420815E-02	1.21	.83	PREDICTED: Canis familiaris bikunin-like protein; transcript variant 1 (BIKUNIN); mRNA	59.3	AF195953	XM_549494	SPINT2	serine peptidase inhibitor, Kunitz type, 2
CfaAffx.9904.1.S1_at	2.089960E-02	2.975679E-01	1.14	.88	PREDICTED: Canis familiaris similar to SET domain and mariner transposase fusion gene (LOC476549); mRNA	86.5	AK307537	XM_533755	SETMAR	SET domain and mariner transposase fusion gene
CfaAffx.9910.1.S1_at	3.839750E-03	1.336757E-01	1.1	.91	Physcomitrella patens subsp. patens predicted protein (PHYPADRAFT_143981) mRNA; complete cds	17.2	NULL	XM_001776717	PHYPADRAFT_143981	hypothetical protein
CfaAffx.9912.1.S1_s_at	1.583050E-04	2.365505E-02	1.19	.84	Pongo pygmaeus mRNA; cDNA DKFZp459H1725 (from clone DKFZp459H1725)	85.4	AB385054	CR859467	SLC6A15	solute carrier family 6, member 15
CfaAffx.9919.1.S1_s_at	1.918360E-03	9.462382E-02	1.12	.89	PREDICTED: Canis familiaris similar to Orphan sodium- and chloride-dependent neurotransmitter transporter NTT73 (Orphan transporter v7-3) (Solute carrier family 6 member 15); transcript variant 5 (LOC475416); mRNA	98.3	BC022253	XM_860143	SLC6A15	solute carrier family 6, member 15
CfaAffx.992.1.S1_at	2.705840E-08	1.164458E-04	1.38	.73	PREDICTED: Canis familiaris similar to ATPas; class II; type 9B; transcript variant 7 (LOC483926); mRNA	100.0	CR600473	XM_850875	ATP9B	ATPase, class II, type 9B
CfaAffx.9944.1.S1_at	4.354380E-03	1.415338E-01	1.12	.89	PREDICTED: Canis familiaris hypothetical LOC484536 (LOC484536); mRNA	98.7	XM_940478	XM_541650	WDR87	WD repeat domain 87
CfaAffx.9945.1.S1_at	3.579450E-03	1.278354E-01	1.2	.84	PREDICTED: Canis familiaris hypothetical protein LOC612600 (LOC612600); mRNA	71.7	XM_001717392	XM_850333	LOC612600	hypothetical protein LOC612600
CfaAffx.9959.1.S1_at	5.242600E-03	1.537963E-01	0.82	1.23	PREDICTED: Canis familiaris similar to component of oligomeric golgi complex 6 (LOC477296); mRNA	100.0	NM_020751	XM_534488	COG6	component of oligomeric golgi complex 6
CfaAffx.9979.1.S1_at	3.083990E-05	9.216261E-03	1.16	.86	PREDICTED: Equus caballus similar to olfactory receptor MOR31-4 (LOC100066712); mRNA	65.3	NULL	XM_001496909	LOC100066712	similar to olfactory receptor MOR31-4
CfaAffx.9983.1.S1_s_at	2.995740E-03	1.183056E-01	1.1	.91	PREDICTED: Canis familiaris similar to *Protocadherin alpha C2 precursor* (PCDH-alpha-C2); transcript variant 1	100.0	NULL	XM_535216	PCDHAC2	protocadherin alpha subfamily C, 2

					(LOC478037); mRNA					
CfaAffx.9992.1.S1_at	1.793480E-02	2.788662E-01	1.1	.91	PREDICTED: Canis familiaris similar to Fras1 related extracellular matrix protein 2 (LOC486002); mRNA	100.0	NM_207361	XM_543127	FREM2	FRAS1 related extracellular matrix protein 2
RPTR-Cfa-AF292559-1_at	6.314180E-03	1.708998E-01	1.11	.90	null	null	null	null		
RPTR-Cfa-AF292560-1_s_at	1.550360E-04	2.324730E-02	1.12	.89	Synthetic construct dsRed1/N-WASP/Cdc42/ECFP fusion protein gene; complete cds	82.5	NULL	EU438752		
RPTR-Cfa-AJ002682-1_s_at	3.764890E-04	3.923052E-02	1.15	.87	null	null	null	null		
RPTR-Cfa-M62653-1_at	8.313460E-04	5.946195E-02	1.2	.83	Aequorea victoria green-fluorescent protein mRNA; complete cds	100.0	NULL	M62653		
RPTR-Cfa-NC_001669-2_at	3.652800E-04	3.834104E-02	1.15	.87	null	null	null	null		

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A composition comprising,

   a) at least one omega-3 fatty acid,

   b) at least one glysosaminoglycan,

   c) at least one amino sugar,

   d) at least one antioxidant, and

   e) carnitine or acetylcarnitine.

2. The composition of claim 1, wherein the omega-3 fatty acid is selected from the group consisting of alpha-linoleic acid (ALA), docosahexanoic acid (DHA) and eicosapentaenoic acid (EPA).

3. The composition of claim 1 or claim 2, wherein the glysosaminoglycan is selected from the group consisting of chondroitin sulfate, dermatan sulfate, keratan sulfate, heparin, heparan sulfate and hyaluronan.

4. The composition of any one of claims 1 to 3, wherein the amino sugar is selected from the group consisting of galactosamine, glucosamine, sialic acid and N-acetylglucosamine.

5. The composition of any one of claims 1 to 4, wherein the antioxidant is selected from the group consisting of vitamin C, tocopherols, tocotrienols, glutathione, lipoic acid, melatonin, and beta-carotene.

6. The composition of any one of claims 1-5 further comprising at least one dietary mineral.

7. The composition of claim 6, wherein the dietary mineral is selected from the group consisting of Calcium, Chloride, Magnesium, Phosphorus, Potassium, Sodium, Cobalt, Copper, Fluorine, Iodine, Iron, Manganese, Molybdenum, Nickel, Selenium, Sulfur, Zinc and Vanadium.

8. The composition of any one of claims 1 to 7, further comprising at least one essential amino acid.

9. A method of treating an abnormal joint condition in a subject, the method comprising administering the composition of any one of claims 1 to 8 to a subject in need thereof.

10. The method of claim 9, wherein the abnormal joint condition is osteoarthritis, rheumatoid arthritis and/or local joint inflammation.

11. A method of delaying the onset of an abnormal joint condition in a subject, the method comprising administering the composition of any one of claims 1 to 8 to a subject in need thereof.

12. The method of claim 11, wherein the abnormal joint condition is osteoarthritis, rheumatoid arthritis and/or local joint inflammation.

13. A method of reducing the risk in a subject of acquiring an abnormal joint condition in a subject, the method comprising administering the composition of any one of claims 1 to 8 to a subject in need thereof.

14. The method of claim 13, wherein the abnormal joint condition is osteoarthritis, rheumatoid arthritis and/or local joint inflammation.

15. A method of altering the expression of one or more genes in a subject, the method comprising administering to the subject the composition of any one of claims 1 to 8, the one or more genes being selected from the group consisting of Annexin A1, Cathepsin D, Cathepsin F, Cathepsin S, RELA, HMGB1, IL- 1β, TNFα, TNFβ, TLR-2, TLR-4, p38 MAPK, TIMP-1, TIMP-2, MMP-1, MMP-2, MMP- 13, IL- 15 and IL- 17 receptor.

16. Use of the composition of any one of claims 1 to 8 in the preparation of a medicament for the treatment of an abnormal joint condition in a subject in need thereof.

17. A composition comprising,

a) at least one omega-3 fatty acid,

b) at least one glysosaminoglycan,

c) at least one amino sugar,

d) at least one antioxidant, and

e) carnitine or acetylcarnitine, substantially as hereinbefore described with reference to the Examples or Drawings, excluding comparative Examples.

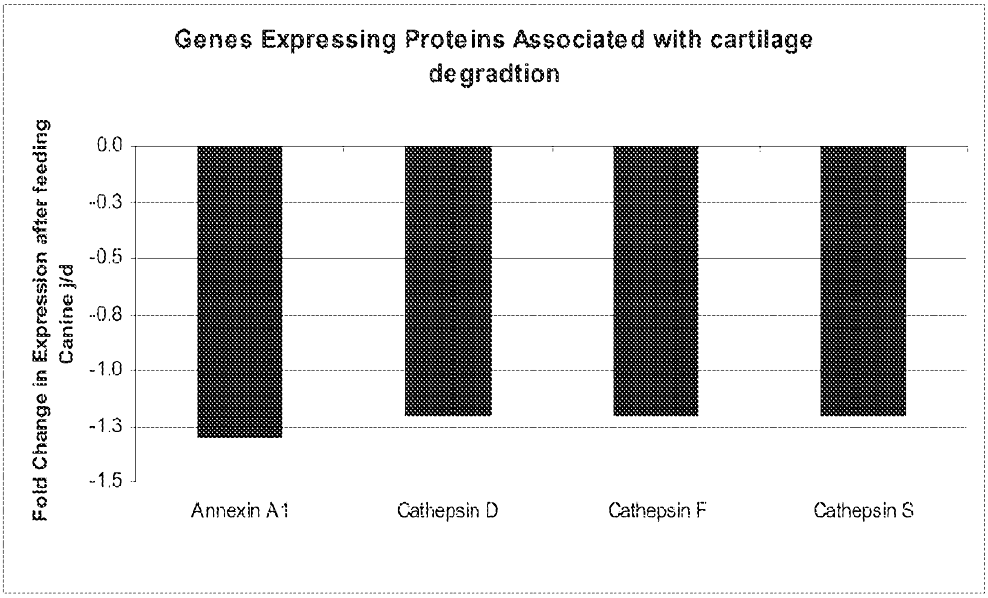
Genes Expressing Proteins Associated with cartilage degradtion
Fold Change in Expression after feeding Canine j/d
0.0
-0.3
-0.5
-0.8
-1.0
-1.3
-1.5
Annexin A1
Cathepsin D
Cathepsin F
Cathepsin S

Figure 1

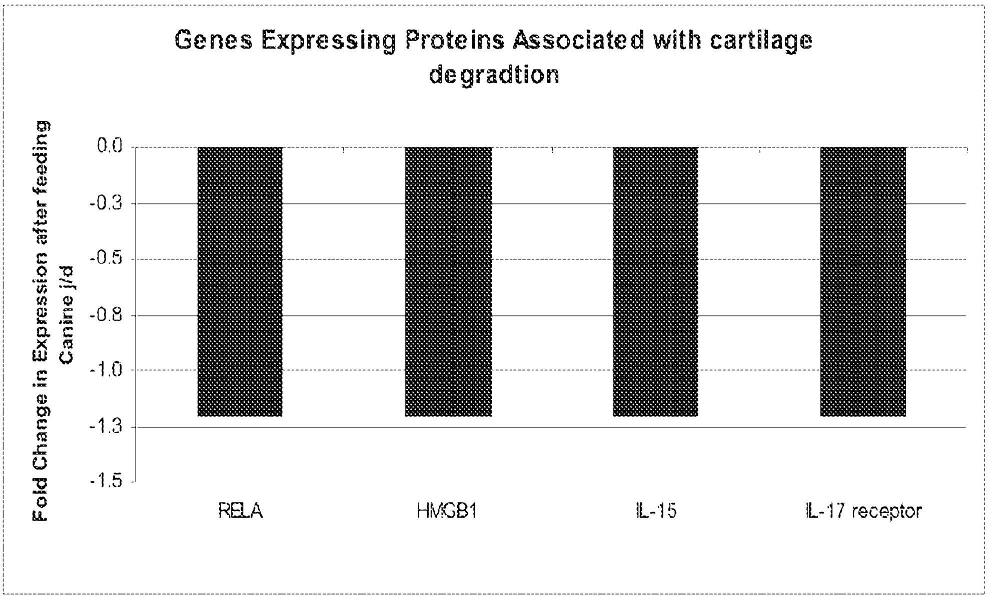
Genes Expressing Proteins Associated with cartilage degradtion
Fold Change in Expression after feeding Canine j/d
0.0
-0.3
-0.5
-0.8
-1.0
-1.3
-1.5
RELA
HMGB1
IL-15
IL-17 receptor

Figure 2

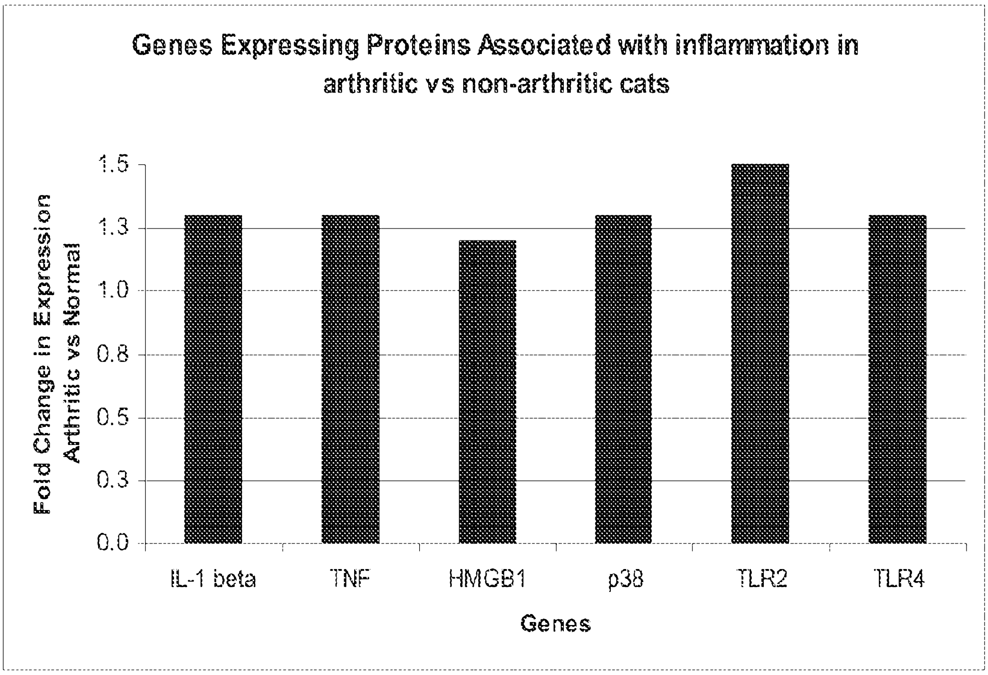
Genes Expressing Proteins Associated with inflammation in arthritic vs non-arthritic cats
Fold Change in Expression Arthritic vs Normal
1.5
1.3
1.0
0.8
0.5
0.3
0.0
IL-1 beta
TNF
HMGB1
p38
TLR2
TLR4
Genes

Figure 3

Nutrient	Nutrient Guarantee %	As Fed %	Dry Matter %	As Fed, Caloric Basis g/100 kcal
Protein	17.0 Minimum	18.5	20.1	5.1
Fat	11.0 Minimum	14.4	15.7	4.0
Carbohydrate (NFE)		46.9	51.0	13.0
Crude Fiber	12.0 Maximum	8.0	8.7	2.2
				mg/100 kcal^3
Calcium	0.45 Minimum	0.64	0.70	177
Phosphorus	0.30 Minimum	0.50	0.54	138
Sodium		0.16	0.17	44
Potassium		0.76	0.83	210
Magnesium		0.128	0.139	35
Carnitine	200 ppm Minimum	323 ppm	351 ppm	9
Omega-3 Fatty Acids Total	2.00 Minimum	3.49	3.79	965
Omega-6:Omega-3 Fatty Acid Ratio		0.7 : 1		
Omega-6 Fatty Acids Total		2.46	2.67	680.50
Alpha-Linolenic Acid (ALA)		2.55	2.77	705.4

Figure 4

Canine data

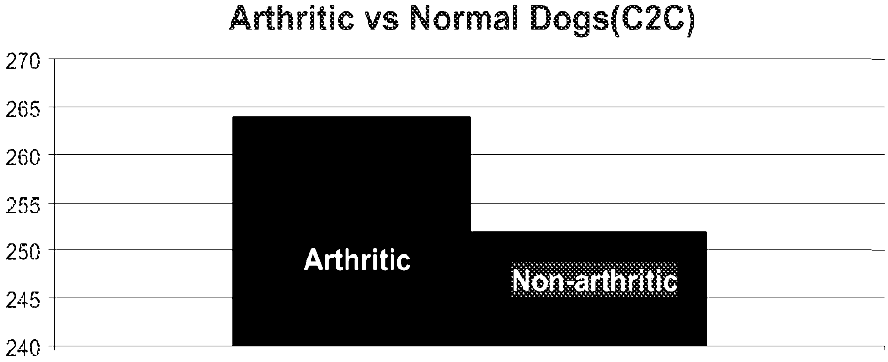

Figure 5

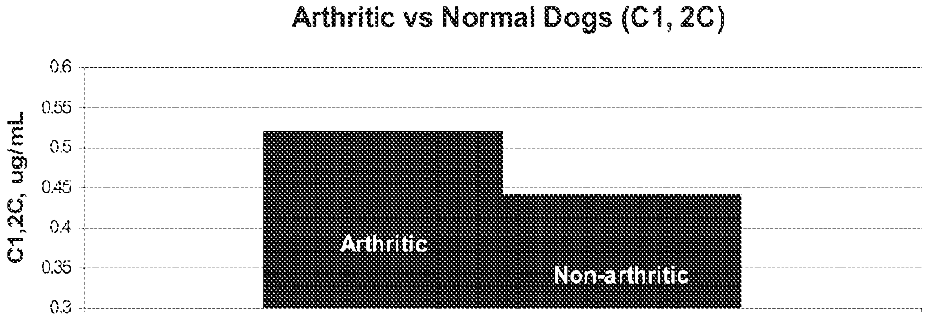
Arthritic vs Normal Dogs (C1, 2C)
C1,2C, ug/mL
0.6
0.55
0.5
0.45
0.4
0.35
0.3
Arthritic
Non-arthritic

Figure 6

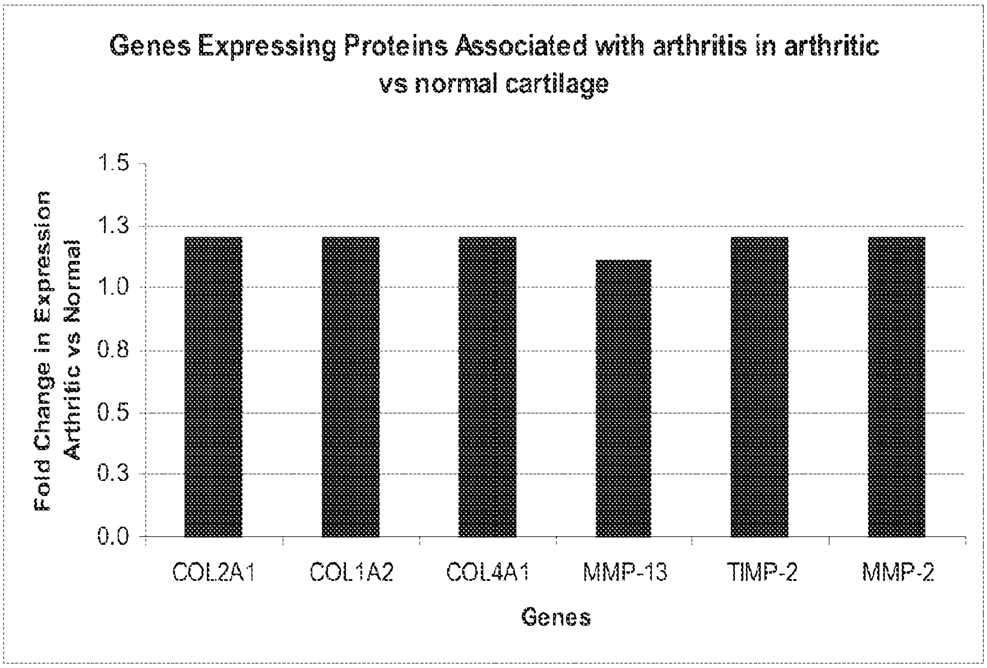
Genes Expressing Proteins Associated with arthritis in arthritic vs normal cartilage
Fold Change in Expression Arthritic vs Normal
1.5
1.3
1.0
0.8
0.5
0.3
0.0
COL2A1
COL1A2
COL4A1
MMP-13
TIMP-2
MMP-2
Genes

Figure 7

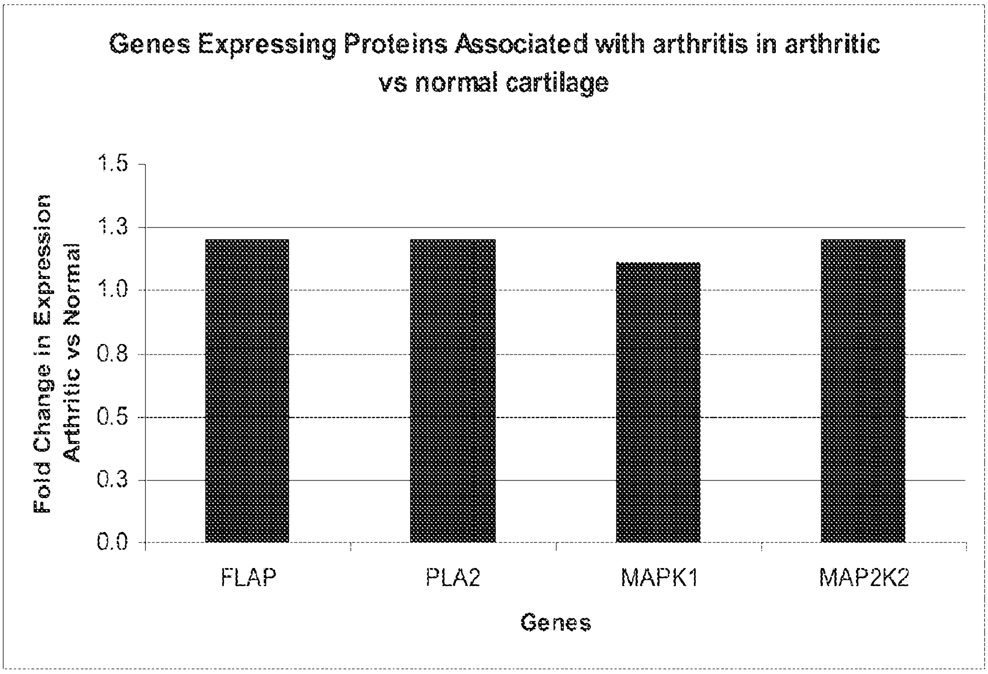
Genes Expressing Proteins Associated with arthritis in arthritic vs normal cartilage
Fold Change in Expression Arthritic vs Normal
1.5
1.3
1.0
0.8
0.5
0.3
0.0
FLAP
PLA2
MAPK1
MAP2K2
Genes

Figure 8

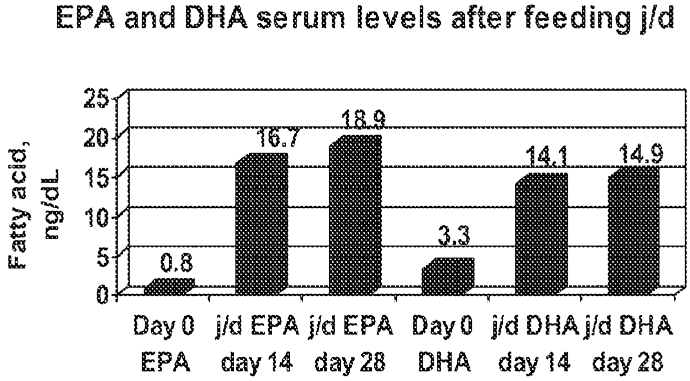
EPA and DHA serum levels after feeding j/d
Fatty acid, ng/dL
25
20
15
10
5
0
0.8
16.7
18.9
3.3
14.1
14.9
Day 0 EPA
j/d EPA day 14
j/d EPA day 28
Day 0 DHA
j/d DHA day 14
j/d DHA day 28

Figure 9

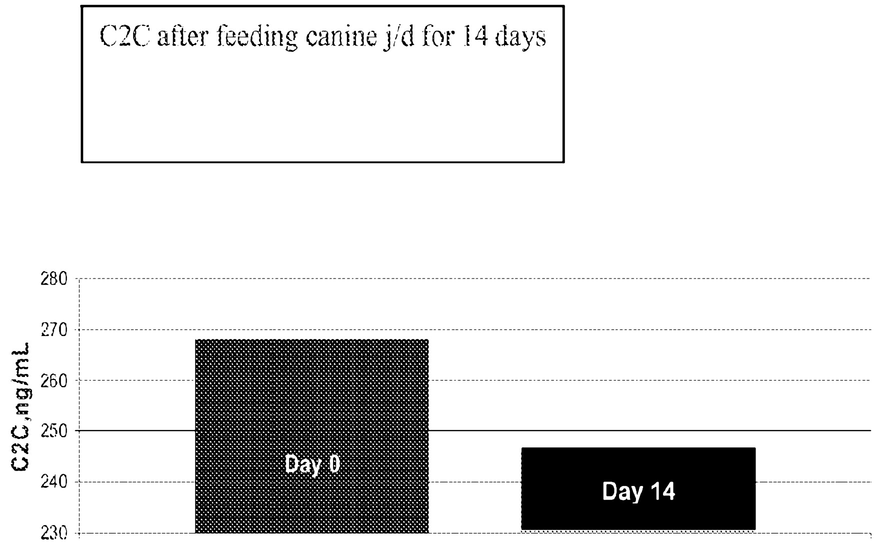
C2C after feeding canine j/d for 14 days
280
270
260
250
240
230
C2C,ng/mL
Day 0
Day 14

Figure 10

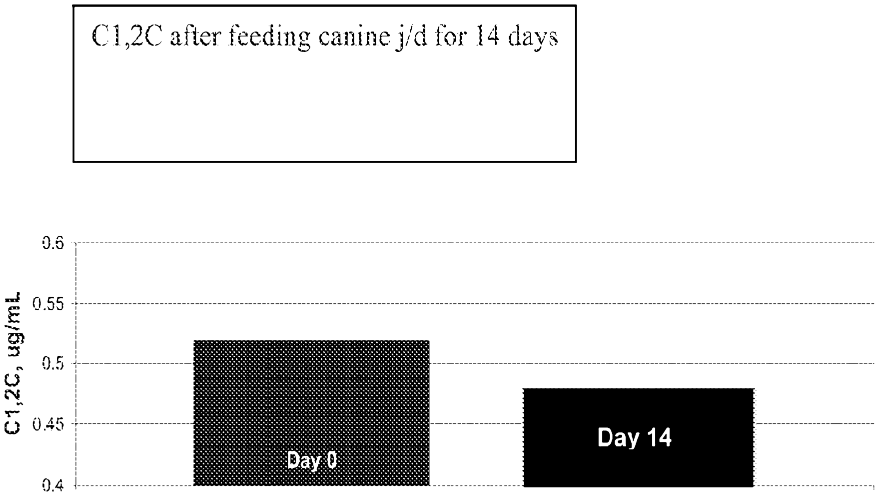
C1,2C after feeding canine j/d for 14 days
C1,2C, ug/mL
0.6
0.55
0.5
0.45
0.4
Day 0
Day 14

Figure 11

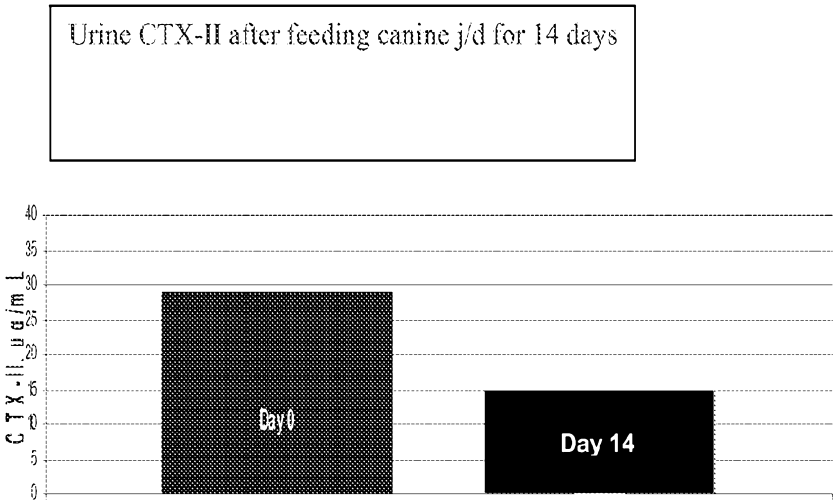
Urine CTX-II after feeding canine j/d for 14 days
CTX-II, µg/mL
40
35
30
25
20
15
10
5
0
Day 0
Day 14

Figure 12

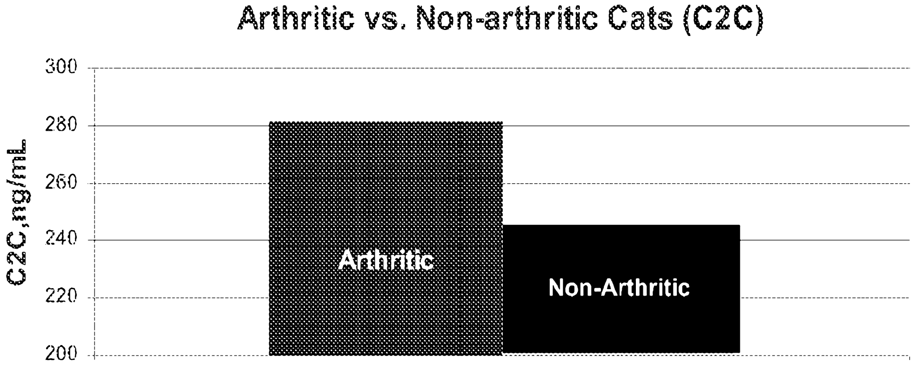
Arthritic vs. Non-arthritic Cats (C2C)
C2C,ng/mL
300
280
260
240
220
200
Arthritic
Non-Arthritic

Figure 13

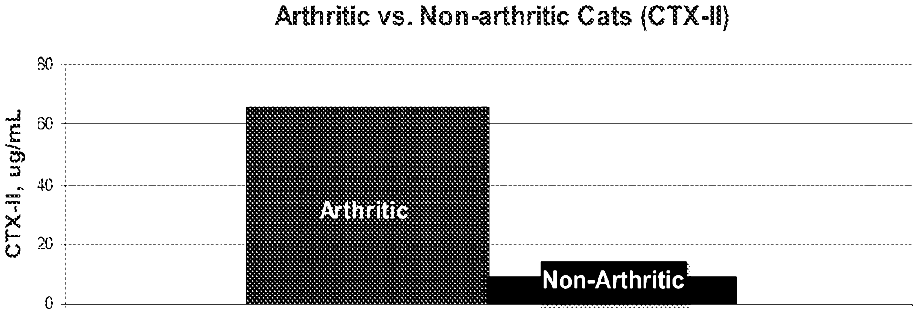
Arthritic vs. Non-arthritic Cats (CTX-II)
CTX-II, ug/mL
80
60
40
20
0
Arthritic
Non-Arthritic

Figure 14

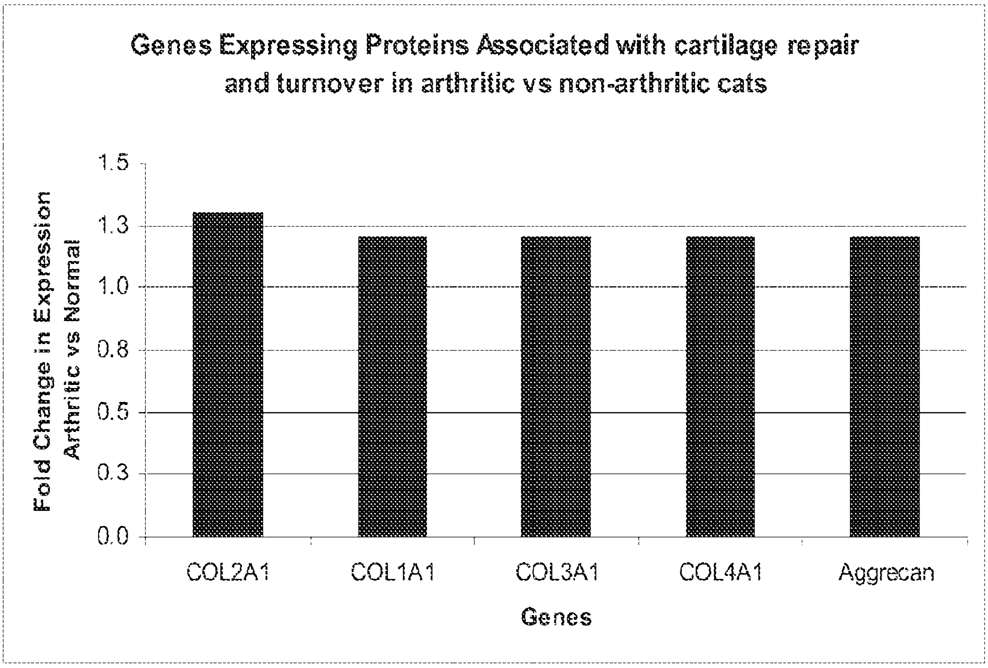
Genes Expressing Proteins Associated with cartilage repair and turnover in arthritic vs non-arthritic cats
Fold Change in Expression Arthritic vs Normal
1.5
1.3
1.0
0.8
0.5
0.3
0.0
COL2A1
COL1A1
COL3A1
COL4A1
Aggrecan
Genes

Figure 15

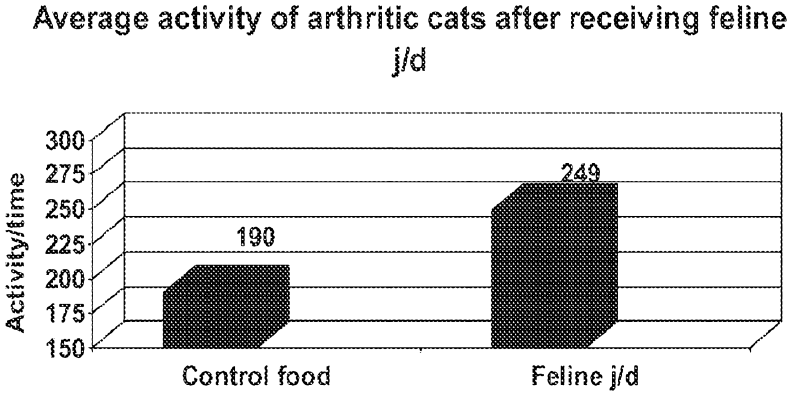
Average activity of arthritic cats after receiving feline j/d
Activity/time
300
275
250
225
200
175
150
190
249
Control food
Feline j/d

Figure 16

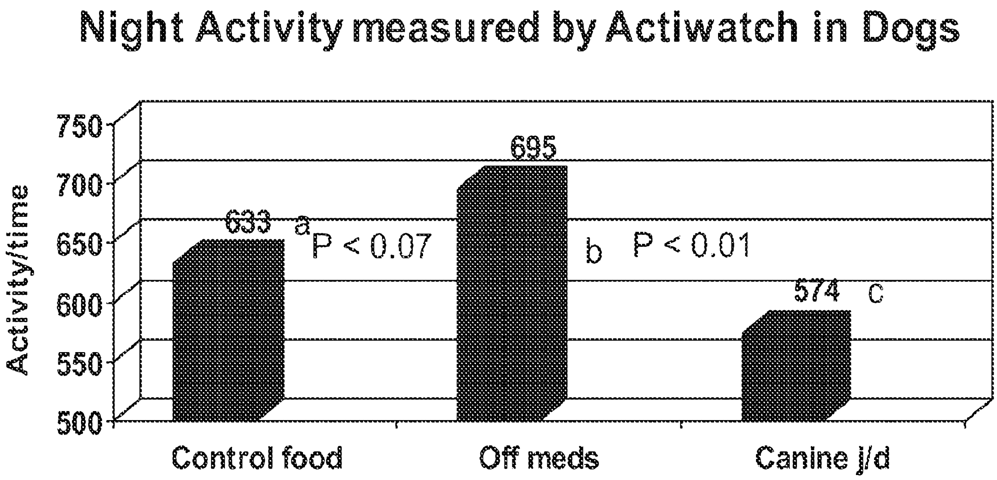
Night Activity measured by Actiwatch in Dogs
Activity/time
750
700
650
600
550
500
633 a
P < 0.07
695
b P < 0.01
574 c
Control food
Off meds
Canine j/d

Figure 17