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(54) Title: METHODS TO IDENTIFY FAT AND LEAN ANIMALS USING CLASS PREDICTORS

(57) **Abrégé/Abstract:**

A combination comprising two or more polynucleotides that are differentially expressed in fat animals compared to lean animals or two or more proteins produced by the expression of such polynucleotides is disclosed. The combination and probes based upon the combination are used for formulating a prognosis that an animal is likely to become fat, developing a diagnosis that an animal is fat, screening substances to determine if they are useful for modulating the amount of adipose tissue on an animal, and detecting the differential expression of one or more genes differentially expressed in fat animals compared to lean animals in a sample. Methods for using class predictor gene profiles to identify fat and lean animals are also disclosed.



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(54) Title: METHODS TO IDENTIFY FAT AND LEAN ANIMALS USING CLASS PREDICTORS

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METHODS TO IDENTIFY FAT AND LEAN ANIMALS USING CLASS PREDICTORS

[0001] This application claims benefit of U.S. Provisional No. 60/778,567 filed March 2, 2006 and US Provisional application No. 60/824,318 filed September 1, 2006 which are both hereby incorporated by reference for all purposes.

[0002] A Sequence Listing is submitted on duplicate compact discs labeled CFR (computer readable form), Copy 1 and Copy 2. The contents of the CFR, Copy 1, and Copy 2 compact disks are the same. The Sequence Listing information on the CFR, Copy 1, and Copy 2 compact disks are identical. The Sequence Listing is in a file named "8123.txt." The file was created on February 24, 2006 at 3:13 PM and contains 188 KB of data. The file was created using an IBM PC compatible computer running the Windows 2002 operating system. The Sequence Listing in 8123.txt is incorporated herein by reference in its entirety.

BACKGROUND OF THE INVENTION

Field of the Invention

[0003] The present invention relates generally to genes differentially expressed in animals and particularly to genes differentially expressed in fat animals compared to lean animals.

Description of the Related Art

[0004] 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 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 protein.

[0005] Gene expression in fat animals compared to lean animals has not been thoroughly investigated. Therefore, a need exists to identify genes and proteins encoded by genes that are differentially expressed in fat animals compared to lean animals. Such genes, proteins, and their fragments would be useful for formulating a prognosis that an animal is likely to become fat, developing a diagnosis that an animal is fat, screening substances to determine if they are likely to be useful for modulating the amount of adipose tissue on an animal, and using such substances to modulate the amount of adipose tissue on an animal.

[0006] Fat animals can be defined as those animals having an excess of body adipose tissue. Generally, animals such as humans, canines, and felines weighing more than 15% of their ideal body weight are considered fat. The most common cause of an animal being fat is an over consumption of food that results in an excess intake of calories. However, there are other factors that can increase an animal's chances for being fat, e.g., lifestyle, health, eating habits, breed, spaying, and neutering. Also, the incidence of animals becoming fat generally increases with age due to a general decrease in metabolic rate and in physical activity. Surveys estimate that 25% of dogs in the United States that visit veterinary clinics are fat to the point of being obese. Studies have shown that fat animals are significantly more at risk for diseases such as arthritis, heart disease, respiratory disease, diabetes, bladder cancer, hypothyroidism, and pancreatitis.

[0007] Modulating the amount of adipose tissue on an animal, including preventing an animal from becoming fat or treating a fat animal to reduce the amount of adipose tissue on the animal or treating a lean animal to increase the amount of adipose tissue in the animal, is difficult. Increasing the amount of adipose tissue on an animal usually involved increasing the amount of food consumed. The most effective and easiest way to prevent an animal from becoming fat or to reduce the amount of fat on an animal is with dietary restriction and exercise. However, it is often difficult to ensure compliance with diet and exercise programs. Other methods involve the use of drugs such as phentermine, fenfluramine, sibutramine, orlistat, and phenylpropanolamine. Unfortunately, side effects occur with these drugs. For example, the administration of fenfluramine and phentermine for the treatment of human obesity can result in cardiac valve damage in humans. Sibutramine can increase blood pressure and orlistat may have unpleasant gastrointestinal side effects.

[0008] Given the problems with current methods for dealing with adipose tissue on an animal, there is a continuing need for new methods and compositions useful for formulating a prognosis that an animal is likely to become fat, developing a diagnosis that an animal is fat, screening substances to determine if they are likely to be useful for modulating the amount of adipose tissue on an animal, and using such substances to modulate the amount of adipose tissue on an animal.

SUMMARY OF THE INVENTION

[0009] It is, therefore, an object of the present invention to provide one or more genes or gene segments that are differentially expressed in fat animals compared to lean animals.

[0010] It is another object of the present invention to provide combinations of two or more polynucleotides or polypeptides that are differentially expressed in fat animals compared to lean animals.

[0011] It is another object of the present invention to provide compositions of two or more polynucleotide or polypeptide probes suitable for detecting the expression of genes differentially expressed in fat animals compared to lean animals and devices such as substrate arrays containing the probes.

[0012] It is a further object of the present invention to provide methods and compositions for detecting the differential expression of one or more genes differentially expressed in fat animals compared to lean animals in a sample.

[0013] It is another object of the present invention to provide a method for measuring the effect of a test substance on the expression profile of one or more genes differentially expressed in fat animals compared to lean animals as a method for screening a test substance to determine if it is likely to be useful for modulating the amount of adipose tissue on an animal.

[0014] It is another object of the invention to provide methods for formulating a prognosis that an animal is likely to become fat or developing a diagnosis that an animal is fat.

[0015] It is another object of the invention to provide methods and compositions for modulating the expression of one or more genes differentially expressed in fat animals compared to lean animals or for modulating the amount of adipose tissue on an animal.

[0016] One or more of these other objects are achieved using novel combinations of 295 polynucleotide probes representing 254 genes and gene segments that are differentially expressed in fat animals compared to lean animals. The polynucleotides are used to produce compositions, probes, devices based on the probes, and methods for determining the status of polynucleotides differentially expressed in fat animals compared to lean animals useful for achieving the above-identified objects, e.g., prognosing and diagnosing conditions relating to animal adipose tissue and for screening substances to determine if they are likely to be useful for modulating the amount of adipose tissue on an animal. Such substances, once identified, may be used to modulate the amount of adipose tissue on an animal. Various kits comprising combinations of probes, devices utilizing the probes, and substances are also provided.

[0017] It is also an object of this invention to provide methods for using "class predictor" gene profiles to differentiate between fat and lean animals. Class predictor technology can be used to facilitate the clinical diagnosis of an animal's body type, e.g., class prediction can be used in a

blood-based test to make a positive determination as to whether an animal is fat or lean or has the propensity to become fat or lean. This and other objects disclosed herein may be achieved using novel combinations of 65 polynucleotide probes identified herein that can act as class predictors for fat and lean animals using blood samples taken from fat and lean animals. These class predictor genes can be used e.g., to develop blood-based test kits to predict if an animal is fat or has the propensity to become fat or they can be used to predict if a lean animal can maintain its leanness. Class predictors can also be used to define the body condition score of an animal and as such may have various useful applications in veterinary clinics.

[0018] It is also a further object of this invention to provide methods for using class predictor gene profiles to accurately identify fat animals and follow their progression at the biochemical level and indicate whether their gene expression profiles are consistent with being fat or lean.

[0019] It is also an object of this invention to provide methods to modulate the amount of adipose tissue in an animal in vivo by administration of one or more active ingredients that are shown in vitro to modulate the expression of genes involved in fat metabolism.

[0020] Further objects of the invention include use of the polynucleotides, probes, active ingredients and class predictor data disclosed herein in the manufacture of compositions, devices and kits as described herein, e.g., for modulating the expression of one or more genes differentially expressed in fat animals compared to lean animals or for modulating the amount of adipose tissue on an animal, for detecting the expression of genes differentially expressed in fat animals compared to lean animals and for predicting or diagnosing the body condition score of an animal, including the identification of fat animals from lean animals, and in methods for detecting the expression of genes differentially expressed in fat animals compared to lean animals, for modulating the expression of one or more genes differentially expressed in fat animals compared to lean animals, for measuring the effect of a test substance on the expression profile of one or more genes differentially expressed in fat animals compared to lean animals, for screening a test substance to determine if it is likely to be useful for modulating the amount of adipose tissue on an animal, for formulating a prognosis that an animal is likely to become fat or developing a diagnosis that an animal is fat or for modulating the amount of adipose tissue on an animal.

[0021] Other and further objects, features, and advantages of the present invention will be readily apparent to those skilled in the art.

DETAILED DESCRIPTION OF THE INVENTION

Definitions

[0022] The term "animal" means a human or other animal, including avian, bovine, canine, equine, feline, hircine, murine, ovine, and porcine animals, that has adipose tissue. When the term is

used in the context of comparing fat to lean animals, the animals that are compared are animals of the same species and possibly of the same race or breed. In preferred embodiments, the animal is a canine or feline, most preferably a canine.

[0023] 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.

[0024] 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.

[0025] The term “body condition score” (BCS) means a method for body composition analysis based upon an animal’s body size and shape. Several methods are known to skilled artisans, e.g., methods disclosed in US. Patent No. 6,691,639 and in the reference entitled “Small Animal Clinical Nutrition”, 4th Edition, in Chapter 13 (ISBN 0-945837-05-4).

[0026] The term “Body Mass Index” (BMI) means an animal’s weight (in kilograms) divided by its height (in meters) squared.

[0027] The term “Class Predictor” as used herein refers to a genomic, proteomic or metabolomic profile that is generated using supervised learning methods employing algorithms such as, but not limited to, Weighted Voting, Class Neighbors, K-Nearest Neighbors and Support Vector Machines from a group of pre-defined samples (“the training set”) to establish a prediction rule that then can be applied to classify new samples (“the test set”).

[0028] The term “DEXA” means body composition analysis dual-energy X-ray absorptiometry.

[0029] 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 change in the amount of transcribed messenger RNA or translated protein in a sample.

[0030] The term “fat” as applied to an animal means any animal that is determined to have an excess amount of body adipose tissue or an animal that is prone to developing an excess amount of body adipose tissue using techniques and methods known to health care providers and other skilled artisans. An animal is prone to becoming fat if the animal has an inclination or a higher likelihood of developing excess adipose tissue when compared to an average animal in the general population. Generally, without limiting the definition, an animal is considered fat if (1) the animal has a BMI of 25 or more (a number considered to include “overweight” and “obese” in some methods of

characterizing animal conditions), (2) the animal's weight is 15% or more than its "ideal" body weight as defined by health care professionals or related skilled artisans, (3) an animal's percent body fat is 27% or more as determined by DEXA, or (4) an animal has a body condition score of more than 3 as determined by skilled artisans using the method disclosed in "Small Animal Clinical Nutrition", 4th Edition, in Chapter 13 (ISBN 0-945837-05-4) or its equivalent using other BCS methods.

[0031] The term "fat-associated genes" means all or a subset of the genes identified by SEQ ID NOs:1-295, particularly the 254 genes identified herein as differentially expressed in fat animals compared to lean animals.

[0032] 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., a fat animals compared to a lean 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.

[0033] 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.

[0034] 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.

[0035] The term "genes differentially expressed in fat animals" means genes from which the amount of mRNA expressed or the amount of gene product translated from the mRNA is detectably different, either more or less, in tissue from fat animals as compared to lean animals.

[0036] 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 identified by SEQ ID NOs:1-295 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 identified by

SEQ ID NOs:1-295 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 identified by SEQ ID NOs:1-295 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 identified by SEQ ID NOs:1-295. 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://www.ncbi.nlm.nih.gov>.

[0037] 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 complementarity and the use of nucleotide analogs affect the efficiency and stringency of hybridization reactions.

[0038] 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.

[0039] The term “lean” as applied to an animal means any animal that is determined not to be fat using techniques and methods known to health care providers and other skilled artisans. Generally, without limiting the definition, an animal is considered lean if (1) the animal has a BMI of less than 25 or (2) the animal's weight is less than 15% more than its “ideal” body weight as defined by health care professionals or related skilled artisans, (3) an animal's percent body fat is less than 27% as determined by DEXA, or (4) an animal has a body condition score of 3 or less as determined by skilled artisans using the method disclosed in “Small Animal Clinical Nutrition”, 4th Edition, in Chapter 13 (ISBN 0-945837-05-4) or it equivalent using other BCS methods.

[0040] The term “modulating the amount of adipose tissue on an animal” means causing the animal to lose adipose tissue, causing the animal to gain adipose tissue, or causing the animal to maintain the amount of adipose tissue on the animal if the animal is prone to gaining or losing adipose tissue. Thus, modulating the amount of adipose tissue on an animal encompasses preventing a lean animal from becoming fat and treating a fat animal to reduce the amount of adipose tissue on the animal, as well as treating a lean animal to add adipose tissue in appropriate circumstances, e.g., when treating a lean animal that is determined by skilled artisans to be so underweight that the addition of adipose tissue is desirable. Conventional methods may be used to assess the amount of adipose tissue on an animal, as well as to determine the animal’s lean muscle mass and /or bone mineral content, information which may be of relevance in such an assessment.

[0041] 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 sequence, 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.”

[0042] 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.

[0043] 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.

[0044] 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 adipose, 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.

[0045] 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.

[0046] 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.

[0047] 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.

[0048] The term “standard” means (1) a control sample that contains tissue from a lean animal if a fat animal is being tested or tissue from a fat animal if a lean animal is being tested or (2) a control sample that contains tissue from a lean or fat test animal that has not been exposed to a test substance being examined in the corresponding lean or fat animal to determine if the test substance causes differential gene expression, as appropriate for the context of its use.

[0049] 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% Na₂SO₄ at 50°C or similar procedures employing similar low ionic strength and high temperature washing agents and similar denaturing agents.

[0050] 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 amount of adipose tissue on animals, including any drug, chemical entity, or biologic entity.

[0051] 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.

[0052] 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.

[0053] 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.

[0054] 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.

[0055] 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.

[0056] 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.

[0057] 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.

[0058] In one aspect, the present invention provides one or more genes or gene segments ("genes" as defined herein) that are differentially expressed in fat animals compared to lean animals. The invention is based upon the discovery of 295 polynucleotides representing 254 genes that are differentially expressed in fat animals compared to lean animals. The genes were identified by comparing the expression of genes in adipose tissue from animals diagnosed as fat with genes in adipose tissue from animals diagnosed as lean using Affymetrix GeneChip® technology. The polynucleotides are shown in the Sequence Listing and referenced in Table 1 as SEQ ID NOs:1-295. Table 1 also shows the Affymetrix Probe Identification Number (herein "APIN") in Column 2, fold expression (fat/lean) in Column 3, Accession Number of Highest BLAST Hit in Column 4, and Accession Number of Highest BLAST Hit for a Human Sequence in Column 5 (column descriptions are also relevant for Tables 2 and 3). A description of the putative or actual gene function can be obtained from the BLAST database using methods known to skilled artisans. Generally, the putative or actual gene function is determined by (1) identifying the APIN for each gene that had 2 fold or greater gene expression in fat animals compared to lean animals, (2) determining the nucleotide sequence of each such gene by inputting the APIN into the publicly available Affymetrix database that correlates APIN numbers with sequences, and (3) inputting the nucleotide sequence into the BLAST database provided by the National Institutes of Health and determining the putative or actual gene function from the resulting sequence matches to homologous sequences in the database. Table 4 shows the gene description obtained for the highest blast hit accession number for the corresponding SEQ ID NO and Table 5 shows the gene description for the highest blast hit for a human sequence accession number for the corresponding SEQ ID NO.

[0059] The polynucleotides are divided into groups based upon several criteria. First, the polynucleotides are divided into three groups based upon a an analysis of expression that determines the amount of or fold differential gene expression between fat and lean animals. Group 1 corresponds to the polynucleotides identified by SEQ ID NOs:1-295. These polynucleotides are differentially expressed in fat animals compared to lean animals by at least 2 fold. Group 2 corresponds to the polynucleotides identified by SEQ ID NOs:1-70. These polynucleotides are differentially expressed in fat animals compared to lean animals by at least 2.5 fold. Group 3 corresponds to the polynucleotides identified by SEQ ID NOs:1-25. These polynucleotides are differentially expressed in fat animals compared to lean animals by at least 3 fold. Second, the polynucleotides are divided into a group based upon their function. Group 4 corresponds to the polynucleotides identified in Table 2. These polynucleotides are associated with lipid and glucose

metabolism pathways in animals. Third, the polynucleotides are divided into a group based upon their relevance. Group 5 corresponds to the polynucleotides identified in Table 3. These polynucleotides were identified as particularly relevant to fat animals compared to lean animals because they were identified by more than one probe when the differential expression analysis was conducted.

[0060] The polynucleotides and genes are identified by measuring differences in gene expression from adipose tissue from canines diagnosed as fat with gene expression in adipose tissue from canines diagnosed as lean. 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.

[0061] Generally, differential gene expression in fat animals compared to lean 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.

[0062] The polynucleotides, genes, proteins encoded by the polynucleotides and genes, and the complements, homologs, variants, or fragments based upon the sequences are useful in a variety of prognostic and diagnostic assays relating to the amount of adipose tissue on an animal and are useful for screening test substances to determine if the substances are useful for modulating the amount of adipose tissue on an animal. Other uses will be apparent from the description of the invention contained herein.

[0063] In another aspect, the invention provides a combination comprising two or more polynucleotides that are differentially expressed in fat animals compared to lean animals or two or more proteins produced by the expression of two or more polynucleotides that are differentially

expressed in fat animals compared to lean animals. In one embodiment, the combination comprises two or more polynucleotides or proteins expressed from polynucleotides selected from SEQ ID NOs:1-295. In another, the combination comprises two or more polynucleotides or proteins expressed from polynucleotides selected from SEQ ID NOs:1-70. In another, the combination comprises two or more polynucleotides or proteins expressed from polynucleotides selected from SEQ ID NOs:1-25. In another, the combination comprises two or more polynucleotides or proteins expressed from polynucleotides selected from the SEQ ID NOs identified in Table 2. In a further, the combination comprises two or more polynucleotides or proteins expressed from polynucleotides selected from the SEQ ID NOs identified in Table 3. In another, the combination comprises useful variations of such polynucleotides. Preferably, the combination comprises a plurality of polynucleotides or proteins expressed from polynucleotides, generally about 10, 20, 50, 100, 200, or more polynucleotides or proteins, as appropriate for a particular Group and use. When the combination comprises one or more fragments, the fragments can be of any size that retains the properties and function of the original polynucleotide or protein, preferably from about 30%, 60%, or 90% of the original. The polynucleotides and proteins can be from any animal, preferably canines and felines, most preferable canines.

[0064] In another aspect, the invention provides a composition comprising two or more oligonucleotide or polynucleotide probes suitable for detecting the expression of genes differentially expressed in fat animals compared to lean animals. In one embodiment, the probes comprise polynucleotides selected from SEQ ID NOs:1-295. In another, the probes comprise polynucleotides selected from SEQ ID NOs:1-70. In a further, the probes comprise polynucleotides selected from SEQ ID NOs:1-25. In another, the probes comprise polynucleotides selected from the SEQ ID NOs identified in Table 2. In another, the probes comprise polynucleotides selected from the SEQ ID NOs identified in Table 3. In another, the probes comprise useful variations of such polynucleotides. The probes contain a sufficient number of nucleotides to specifically hybridize substantially exclusively with appropriate complementary polynucleotides. Preferably, the probes comprise at least about 10, 15, 20, 25, or 30 nucleotides. In some embodiments, the probes contain more nucleotides and comprise at least about 30, 50, 70, 90 or 100 nucleotides, or more. The probes may comprise full length functional genes of the present invention. Preferably, the composition comprises a plurality of polynucleotide probes suitable for detecting genes differentially expressed in fat animals compared to lean animals, generally about 10, 50, 200, 500, 1000, or 2000, or more probes. The polynucleotide probes are made or obtained using methods known to skilled artisans, e.g., in vitro synthesis from nucleotides, isolation and purification from natural sources, or enzymatic cleavage of the genes of the present invention.

[0065] In another aspect, the invention provides a device suitable for detecting the expression of a plurality of genes differentially expressed in fat animals compared to lean 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.

[0066] In another aspect, the invention provides a composition comprising two or more peptide or polypeptide probes suitable for detecting the expression of genes differentially expressed in fat animals compared to lean animals. In one embodiment, the probes comprise peptides or polypeptides that specifically bind to proteins produced by the expression of one or more polynucleotides comprising sequences selected from SEQ ID NOs:1-295. In another, the probes comprise peptides or polypeptides that specifically bind to proteins produced by expression of one or more polynucleotides comprising sequences selected from SEQ ID NOs:1-70. In another, the probes comprise peptides or polypeptides that specifically bind to proteins produced by expression of one or more polynucleotides selected from SEQ ID NOs:1-25. In a further, the probes comprise peptides or polypeptides that specifically bind to proteins produced by expression of one or more polynucleotides selected from the SEQ ID NOs identified in Table 2. In another, the probes comprise peptides or polypeptides that specifically bind to proteins produced by expression of one or more polynucleotides selected from the SEQ ID NOs identified in Table 3. In another, the probes comprise peptides or polypeptides that specifically bind to proteins produced by expression of one or more useful variations of such polypeptides. The probes contain a sufficient number of amino acids to specifically bind to the appropriate polypeptides. Preferably, the probes comprise at least about 4, 10, 20, 40, or 80 amino acids. In some embodiments, the probes contain more amino acids and comprise at least about 100 or more amino acids. The probes may comprise full length functional proteins derived from the expression of full length functional genes identified by the

present invention. Preferably, the invention provides a plurality of polypeptide probes suitable for detecting genes differentially expressed in fat animals compared to lean animals, more preferably a collection of about 10, 50, 100, 500, or 1000 or more of such probes. In one embodiment, the probes are antibodies, preferably monoclonal antibodies.

[0067] 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.

[0068] In another aspect, the invention provides a device suitable for detecting the expression of a plurality of genes differentially expressed in fat animals compared to lean 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. Either 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.

[0069] 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.

[0070] 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.

[0071] In some embodiments, expression patterns or profiles of a plurality of genes differentially expressed in fat animals compared to lean 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.

[0072] 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. 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 fat animals compared to lean animals.

[0073] In a further aspect, the invention provides a method for detecting the differential expression of one or more genes differentially expressed in fat animals compared to lean animals in a sample. The method comprises (a) hybridizing a combination comprising a plurality of polynucleotide probes that are differentially expressed in fat animals compared to lean 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 fat animals compared to lean 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 fat animals compared to lean animals in the sample. In various embodiments, the plurality of polynucleotide probes are selected from SEQ ID NOs:1-295 with difference of 2 fold or more, SEQ ID NOs:1-70 with difference of 2.5 fold or more, SEQ ID NOs:1-25 with difference of 3 fold or more, polynucleotides identified in Table 2 with difference of 2 fold or more, polynucleotides identified in Table 3 with difference of 2 fold or more, and useful variations of such polynucleotides with the appropriate fold for the Group. These polynucleotides are used to prepare probes that hybridize with sample polynucleotides to form hybridization complexes that are detected and compared with those of the standard. In some embodiments, the sample polynucleotides are amplified prior to hybridization. In some embodiments, the probes are bound to a substrate, preferably in an array.

[0074] 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.

[0075] 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 fat animals compared to lean 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.

[0076] 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 fat animals compared to lean animals, particularly fat-associated genes, in the sample.

[0077] In another aspect, the invention provides a method for detecting the differential expression of genes differentially expressed in fat animals compared to lean 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 fat animal compared to a lean 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 fat animal compared to a lean 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 fat animals compared to lean animals in the sample.

[0078] In various embodiments, the plurality of polypeptide probes are probes that specifically bind to proteins produced by expression of one or more polynucleotides selected from SEQ ID NOs:1-295 with difference of 2 fold or more, SEQ ID NOs:1-70 with difference of 2.5 fold or more, SEQ ID NOs:1-25 with difference of 3 fold or more, polynucleotides identified in Table 2 with difference of 2 fold or more, polynucleotides identified in Table 3 with difference of 2 fold or more, and useful variations of such polynucleotides with the appropriate fold for the Group. These polynucleotides are used to prepare probes that specifically bind to proteins that are detected and compared with those of the standard. In some embodiments, the probes are bound to a substrate, preferably in an array. In one embodiment, the probes are antibodies.

[0079] 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.

[0080] 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 fat animals compared to lean animals, particularly fat-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.

[0081] 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 fat animals compared to lean animals, particularly fat-associated genes, in the sample.

[0082] In another aspect, the method for detecting the expression of genes differentially expressed in fat animals compared to lean animals in a sample is used to monitor an animal's progress when attempting to modulate the amount of adipose tissue on the animal in response to an adipose 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 fat animals compared to lean animals, particularly fat-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. For example, an adipose tissue modulation program designed to reduce the amount of adipose tissue on an animal could be monitored and shown to be effective if the amount of gene expression for genes differentially expressed in fat animals compared to lean animals, particularly fat-associated genes, declines over time in response to the stimulus in the program. Similarly, a program to increase adipose tissue in a lean or overly lean animal should increase the expression profile for such genes. The modulation program can be any plan to modulate the amount of adipose tissue on the animal such as a diet, exercise, drug, or other similar program.

[0083] In a further aspect, the invention provides a method for measuring the effect of a test substance on the expression profile of one or more genes differentially expressed in fat animals compared to lean animals and a method for screening a test substance to determine if it is likely to be useful for modulating the amount of adipose tissue on an animal. The methods comprise (a) determining a first expression profile by measuring the transcription or translation products of two or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof in a test system in the absence of the test substance; (b) determining a second expression profile by

measuring the transcription or translation products of two or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof in a test system in the presence of the test substance; and (c) comparing the first expression profile to the second expression profile.

[0084] A change in the second expression profile compared to the first expression profile of 2 fold or more indicates that the test substance effects the expression of genes differentially expressed in fat animals compared to lean animals and that the test substance is likely to be useful for modulating the amount of adipose tissue on an animal. In a preferred embodiment, the genes differentially expressed in fat animals compared to lean animals are fat-associated genes and the change is a 2 fold or more change in expression of at least two genes between the first expression profile to the second expression profile. The invention also provides the substances identified using the method.

[0085] In one embodiment, the polynucleotides are selected from SEQ ID NOs:1-70 or useful variations thereof and the change is 2.5 fold or higher. In another, the polynucleotides are selected from SEQ ID NOs:1-25 or useful variations thereof and the change is 3 fold or higher. In a further, the polynucleotides are identified in Table 2 or Table 3, or useful variations thereof, and the change is 2 fold or higher.

[0086] In one embodiment, the test system is an in vitro test system such as a tissue culture, cell extract, or cell line. In another, the test system is an in vivo test system, i.e., an animal such as a canine. In other embodiments, the test system is an ex vivo tissue system or an in silico system.

[0087] Test substances can be any substance that may have an effect on polynucleotides or genes differentially expressed in fat animals compared to lean animals, particularly fat-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 lycopanthin; 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.

[0088] In a preferred embodiment, the substances useful for affecting the expression of genes differentially expressed in fat animals compared to lean animals, particularly fat-associated genes, may be identified using methods disclosed 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.

[0089] In a further aspect, the invention provides a method for formulating a prognosis that an animal is likely to become fat or developing a diagnosis that an animal is fat. The method comprises determining if one or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof or one or more polypeptides that specifically bind to proteins produced by expression of one or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof are differentially expressed in the animal compared to one or more lean animals. The animal is determined to be likely to become fat or determined to be fat if the comparison indicates that the polynucleotides are differentially expressed in the animal compared to the lean animals by a fold of 2 or more.

[0090] In various embodiments, the prognosis or diagnosis is based upon the polynucleotides selected from SEQ ID NOs:1-70, SEQ ID NOs:1-25, the sequences identified in Table 2, the sequences identified in Table 3, or useful variations of such polypeptides.

[0091] The expression profile for lean animals used in the comparison can be obtained from one or more lean animals contemporaneously with the expression profile for the animal being tested or from a database of lean animal expression profiles. Preferably, a database of expression profiles for lean animals accumulated over time is available for use as a reference.

[0092] 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.

[0093] In another aspect, the invention provides a method for manipulating the genome or the expression of the genome of an animal, particularly a non-human animal. The method comprises disrupting the expression of one or more genes differentially expressed in fat animals compared to lean animals, preferably using oligonucleotides or polynucleotides constructed using polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof.

[0094] Methods of manipulating the genome are known to those of skill in the art. Such methods include the production of transgenic and knockout animals and the disruption of transcription or translation. In one embodiment, one or more polynucleotides selected from SEQ ID

NOs:1-295 or useful variations thereof are used to prepare a construct useful to disrupt or “knock out” the corresponding endogenous gene in an animal. This method produces an animal having a null mutation for that gene locus. In other embodiments, the animals exhibit a reduction or complete elimination of the expression of one or more genes differentially expressed in fat animals compared to lean animals, particularly fat-associated genes. The invention also provides an animal produced using the method. In various embodiments, the genome is manipulated using the one or more polynucleotides selected from SEQ ID NOs:1-70, SEQ ID NOs:1-25, the sequences identified in Table 2, the sequences identified in Table 3, or useful variations of such sequences. The transgenic animals are preferably mammals, e.g., rodents such as mice and rats, but may be other mammal such as felines and canines.

[0095] Methods of manipulating the expression of genome are known to those of skilled in the art. Such methods include the use of antisense or siRNA molecules and using such molecules to disrupt the translation or transcription of the genome. In one embodiment, one or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof are used to prepare antisense and similar DNA binding molecules that are useful for disrupting transcription or to prepare short (small) interfering RNAs (siRNA) useful for functionally disrupting translation. Briefly, gene expression is inhibited by antisense molecules through binding to DNA and preventing transcription and a siRNA through RNA interference (RNAi) or post-transcriptional gene silencing (PTGS). siRNA molecules target homologous mRNA molecules for destruction by cleaving the mRNA molecule within the region spanned by the siRNA molecule. Accordingly, siRNAs capable of targeting and cleaving a mRNA transcribed from a fat-associated gene is used to decrease or eliminate expression of one or more of such genes. In other embodiments, antisense molecules capable of binding to DNA and siRNAs capable of targeting and cleaving mRNA transcribed from one or more polynucleotides or genes selected from Group 2, Group 3, Group 4, or Group 5 polynucleotides or genes may be used to decrease or eliminate expression of one or more of these genes. In preferred embodiments, siRNAs are constructed from the transcripts of polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof.

[0096] 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 fat animals compared to lean animals, particularly fat-associated genes. Preferably, substances comprise oligonucleotides or polynucleotides that bind to one or more of the genes or their transcription products and interferes with their replication, transcription, or translation, most preferably oligonucleotides or polynucleotides constructed using polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof. In various embodiments, the substances comprise antisense molecules or siRNAs.

[0097] In another aspect, the invention provides a method for modulating the expression of one or more genes differentially expressed in fat animals compared to lean animals, particularly fat-associated genes, or modulating the amount of adipose tissue on an animal comprising administering to the animal a gene expression or tissue modulating amount of a composition comprising one or more of DHA, EPA, EPA and DHA, ALA, LA, ARA, and SA. 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 adipose tissue on an animal. The drugs or substances include, but are not limited to, substances that suppress appetite, increase metabolism, or interfere with the absorption of specific nutrients, particularly from food. Examples include, but are not limited to, orlistat (blocks fat breakdown and absorption), anorexigenics such as dexedrine (suppresses appetite), anorectics such as fenfluramine and phentermine, and sibutramine, and phenylpropanolamine.

[0098] In another aspect, the invention provides a composition suitable for modulating the expression of one or more genes differentially expressed in fat animals compared to lean animals, particularly fat-associated genes, or modulating the amount of adipose tissue on 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 are useful for modulating the amount of adipose tissue on 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 adipose tissue on an animal.

[0099] In another aspect, the invention provides a method for selecting an animal for inclusion in one or more groups or subgroups. The method comprises determining the expression profile of the animal for (a) polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof or (b) polypeptides each of which specifically binds to proteins produced by expression of one or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof and assigning the animal to a group based upon the expression profile. The groups can be any useful groups, preferably those involved in a research experiment, trial, clinical trial, or other similar category. For example, the groups can be groups involved in a research experiment or clinical trial that requires a one or more control groups and one or more treatment groups. In one embodiment, the control group comprises lean animals and the treatment group comprises fat animals, or vice versa in another. The expression profile for a plurality of animals can be determined and the animals assigned to the control group or treatment group based upon the results of the profile, i.e., animals with a differential expression of 2 fold or more compared to a standard are assigned to the fat group and animals with a differential expression of 2 fold or less compared to a standard are assigned to the lean group. The method is particularly useful for assigning animals to a clinical trial when testing potential drugs or other substances for their ability to reduce the amount of adipose tissue on the animal.

[00100] In another aspect, the invention provides a computer system suitable for manipulating data relating to one or more genes differentially expressed in fat animals compared to lean animals, particularly fat-associated genes. The system comprises a database containing information identifying the expression level of one or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof and/or polypeptides that specifically bind to proteins produced by the expression of one or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof in lean animals and/or fat animals and a user interface to interact with the database, particularly to input, manipulate, and review the information for different animals or categories or animals, e.g., lean or fat animals. In one embodiment, the database further contains information identifying the activity level of one or more polypeptides encoded by one or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof. In another, the database further comprises sequence information for one or more of the polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof. In other embodiments, the database contains additional

information describing the putative description of the genes in one or more animal species. The computer system is any electronic device capable of containing and manipulating the data and interacting with a user., e.g., a typical computer or an analytical instrument designed to facilitate using the present invention and outputting the results relating to the status of an animal.

[00101] In another aspect, the invention provides a method for using a computer system or the present invention to present information identifying the expression profile of one or more genes differentially expressed in fat animals compared to lean animals, particularly fat-associated genes. The method comprises comparing the expression level of two or more polynucleotides or proteins expressed from polynucleotides selected from SEQ ID NOs:1-295 from a sample to the expression profile of the polynucleotides or proteins in the computer system.

[00102] In a further aspect, the present invention provides kits suitable for determining the differential expression of one or more genes differentially expressed in fat animals compared to lean animals, particularly fat-associated genes, in a test system. The kits comprise in separate containers in a single package or in separate containers in a virtual package, as appropriate for the use and kit component, two or more probes suitable for detecting the expression of genes differentially expressed in fat animals compared to lean animals, the probes comprising (a) polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof or (b) polypeptides that specifically bind to proteins produced by the expression of one or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof and at least one of (1) instructions for how to use the probes of the present invention; (2) reagents and equipment necessary to use the probes; (3) a composition suitable for modulating the expression of one or more genes differentially expressed in fat animals compared to lean animals; (4) a composition suitable for disrupting the expression of one or more genes differentially expressed in fat animals compared to lean animals; (5) a food composition suitable for modulating the amount of adipose tissue on an animal; and (6) one or more drugs or other substances that modulate the amount of adipose tissue on an animal. In one preferred embodiment, the probes are bound to a substrate, preferably in an array.

[00103] When the kit comprises a virtual package, the kit is limited to instructions in a virtual environment in combination with one or more physical kit components. In one embodiment, the kit contains probes and/or other physical components and the instructions for using the probes and other components are available via the internet. The kit may contain additional items such as a device for mixing samples, probes, and reagents and device for using the kit, e.g., test tubes or mixing utensils.

[00104] In another aspect, the present invention provides a means for communicating information about or instructions for one or more of (1) using the polynucleotides of the present invention for detecting the expression of genes differentially expressed in fat animals compared to lean animals in a sample, (2) using the polynucleotides of the present invention for measuring the effect of a test substance on the expression of one or more genes differentially expressed in fat animals compared

to lean animals, (3) using the polynucleotides of the present invention for screening a test substance to determine if it is likely to be useful for modulating the amount of adipose tissue on an animal, (4) using the polynucleotides of the present invention for formulating a prognosis that an animal is likely to become fat or developing a diagnosis that an animal is fat, (5) using the polynucleotides of the present invention for manipulating the genome of a non-human animal or the expression of the genome of an animal, (6) using the polynucleotides of the present invention for modulating the expression of one or more genes differentially expressed in fat animals compared to lean animals, particularly fat-associated genes, or modulating the amount of adipose tissue on an animal, (7) using the polynucleotides of the present invention for selecting an animal for inclusion in one or more groups, (8) using the polynucleotides of the present invention for using computer system to manipulate data relating to genes differentially expressed in fat animals compared to lean animals, particularly fat-associated genes, (9) administering substances of the present invention to an animal, alone or in combination with the other elements of the present invention, (10) using the substances of the present invention for modulating the amount of adipose tissue on an animal, (11) using the computer system of the present invention, (12) using the kits of the present invention, and (13) instructions for using the methods and compositions of the present invention with one or more drugs or other substances that that modulate the amount of adipose tissue on an animal. The means comprises a document, digital storage media, optical storage media, audio presentation, or visual display containing the information or instructions. In certain embodiments, the communication means is a displayed web site, visual display, kiosk, brochure, product label, package insert, advertisement, handout, public announcement, audiotape, videotape, DVD, CD-ROM, computer readable chip, computer readable card, computer readable disk, computer memory, or combination thereof containing such information or instructions. Useful information includes one or more of (1) methods for promoting the health and wellness of animals and (2) contact information for the animal's caregivers to use if they have a question about the invention and its use. Useful instructions include techniques for using the probes, instructions for performing a gene expression assay, and administration amounts and frequency for the substances. The communication means is useful for instructing on the benefits of using the present invention.

[00105] Disclosed herein are typical preferred embodiments of the invention and, although specific terms are employed, they are used in a generic and descriptive sense only and not for purposes of limitation as many modifications and variation of the invention are possible in light of the teachings contained herein. The invention can be further illustrated by the following examples, although it will be understood that these examples are included merely for purposes of illustration and are not intended to limit the scope of the invention unless otherwise specifically indicated.

EXAMPLES

Materials and Methods

Isolation of Ribonucleic Acid (RNA) from Tissue

[00106] Tissue samples that have been collected, frozen in liquid nitrogen, and thawed are homogenized and processed using a TRIzol® RNA extraction method to produce good quality RNA which is then subjected to further genomic analysis.

[00107] 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.

[00108] 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.

[00109] Preparations: Prepare 50mL polypropylene tubes with 4mL TRIzol® (one tube for each tissue selected for RNA isolation).

[00110] 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.

[00111] 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 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.

[00112] 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.

[00113] 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.

[00114] Reagents: 10X PBS, deionized H₂O, absolute ethanol, RNA Storage Solution, β-Mercaptoethanol, RNase Zap®, Buffer RLT, and Buffer RW1 and Buffer RPE (provided in the RNeasy Mini Kit)

[00115] 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.

[00116] 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.

[00117] 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.

[00118] 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

[00119] Using the Agilent 2100 Bioanalyzer and the RNA 6000 Nano Assay, analyze RNA isolated from cultured mammalian cells, lymphocytes or tissues for quality.

[00120] 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.

[00121] 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.

[00122] 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.

Affymetrix Genechip Expression Analysis

[00123] Gene expression is analyzed using Affymetrix Canine 1 and Canine 2 GeneChip® Arrays are available commercially 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.

[00124] 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.

[00125] 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.

[00126] 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 BioAnalyser 2100. Use 100 Format (Midi Array) for the canine genechip.

Example 1

Determining Differential Gene Expression between Adipose Tissue Samples from Fat and Lean Animals

[00127] Adipose tissue samples are obtained from 16 (3 lean and 13 fat) canine animals diagnosed as either “fat” or “lean” using conventional methods. The “fatness” or “leanness” of an animal is determined based on measurements by DEXA using conventional methods or based on a 5 point body condition scoring system. For example, an animal is considered lean if it has a body condition score of 2 or 2.5 and/or a DEXA total body fat percentage of 27% or less. An animal is considered to be fat if it has a body condition score of 4 or higher and a total body fat percentage of 30% or higher. All tissue samples are snap frozen in liquid nitrogen immediately after removal from the animal.

[00128] The tissues are analyzed using Affymetrix “Canine-2” canine gene chip according to conventional methods in order to determine which genes, if any, are differentially expressed in fat animals compared to lean animals. Data from the fat and lean samples are compared and analyzed using the GeneSpring and R-Bioconductor software. For any given gene to be assigned a “present” call, it had to exhibit a 2-fold change in expression level to be considered for further scrutiny. Furthermore, genes that are present in only one condition and are either “absent” or “marginal” in the other group are also selected for further scrutiny. Results are provided in the tables below:

**Table 1: Genes Differentially Expressed at least 2 fold
in Adipose Tissue in Fat Animals compared to Lean Animals**

Column	1	2	3	4	5
1	Cfa.6562.1.A1_at	6.48	XM_516142	BC065271	
2	CfaAffx.26065.1.S1_at	3.94	XM_547914	AF111167	
3	CfaAffx.2782.1.S1_s_at	3.78	XM_538649	AJ243425	
4	CfaAffx.2790.1.S1_s_at	3.66	XM_538649	BC073983	
5	Cfa.18367.1.S1_at	3.19	NM_001032284	AC013418	
6	Cfa.9039.1.A1_at	3.07	XM_547914	BX647104	
7	CfaAffx.7975.1.S1_at	3.06	NM_182490	NM_182490	
8	CfaAffx.24964.1.S1_at	3.05	XM_543892	NM_032803	
9	Cfa.3011.1.A1_a_at	0.33	XM_782177	AC005227	
10	CfaAffx.14652.1.S1_at	0.33	XM_848392	BT020098	
11	Cfa.15689.1.A1_at	0.33	XM_844220	AC020550	
12	CfaAffx.2909.1.S1_at	0.33	XM_538880	NM_004117	
13	CfaAffx.4844.1.S1_s_at	0.33	XM_538481	BT019766	
14	Cfa.12840.1.A1_at	0.32	BC034770	AL157823	
15	CfaAffx.4097.1.S1_s_at	0.32	XM_539427	BC040239	
16	CfaAffx.20841.1.S1_at	0.31	XM_537163	AC107394	
17	Cfa.15420.1.A1_at	0.3	NM_077876	AC061958	
18	CfaAffx.17336.1.S1_s_at	0.28	AJ575592	NM_001093	
19	CfaAffx.4844.1.S1_at	0.26	XM_538481	BT019766	
20	Cfa.8932.1.A1_at	0.25	AB089806	AC006431	
21	Cfa.15612.1.A1_at	0.24	U09019	AC073838	
22	CfaAffx.11400.1.S1_at	0.21	XM_850381	NM_198538	
23	CfaAffx.20763.1.S1_at	0.16	XM_719217	AC090018	
24	CfaAffx.732.1.S1_x_at	0.14	NM_181756	AK095351	
25	CfaAffx.732.1.S1_at	0.12	NM_181756	NM_181756	
26	Cfa.2343.1.S1_at	2.97	XM_532944	CR617129	
27	Cfa.13082.1.A1_s_at	2.83	D38312	AC072022	
28	Cfa.9807.1.A1_at	2.77	NM_005458	AL591502	
29	CfaAffx.4729.1.S1_at	2.76	XM_532014	NM_003692	
30	Cfa.1213.1.S1_s_at	2.73	X97226	BC016147	
31	Cfa.15795.1.A1_s_at	2.66	XM_582039	X53683	
32	Cfa.14576.1.A1_at	2.65	Z73942	AK097232	
33	Cfa.3851.1.S1_s_at	2.64	NM_001003297	M28226	
34	CfaAffx.19953.1.S1_s_at	2.63	AY342349	AB023135	
35	CfaAffx.18514.1.S1_at	2.63	XM_547393	BC058922	
36	CfaAffx.17954.1.S1_at	2.6	XM_545023	NM_024090	
37	Cfa.3093.1.A1_at	2.59	AJ011893	AC018680	
38	Cfa.19016.1.S1_at	2.58	XM_843279	BC061637	

39	CfaAffx.28084.1.S1_s_at	2.58	NM_001005255	NM_005623
40	CfaAffx.19953.1.S1_at	2.53	AC150702	AL109797
41	Cfa.1980.1.S1_at	2.52	BC014339	NM_138786
42	Cfa.13370.1.A1_at	0.4	NM_001021464	AL356954
43	Cfa.15388.1.S1_at	0.4	XM_532002	AF131836
44	Cfa.7478.1.A1_s_at	0.4	BC028417	NM_001093
45	Cfa.3749.1.S1_at	0.4	NM_001003220	NM_001006624
46	CfaAffx.7949.1.S1_s_at	0.39	AK023099	NM_013380
47	CfaAffx.52.1.S1_at	0.39	AF159295	X03205
48	Cfa.4556.3.A1_x_at	0.39	L36871	BC073765
49	CfaAffx.4308.1.S1_at	0.39	XM_861344	NM_001498
50	Cfa.16772.1.A1_at	0.38	AF488410	AB060808
51	Cfa.15343.1.A1_s_at	0.38	XM_851829	NM_144583
52	CfaAffx.14437.1.S1_at	0.38	XM_865312	BC015752
53	CfaAffx.18491.1.S1_s_at	0.38	XM_546093	NM_022786
54	CfaAffx.7597.1.S1_at	0.38	XM_534118	AL136960
55	CfaAffx.9291.1.S1_s_at	0.38	AB020887	CR626508
56	CfaAffx.25065.1.S1_at	0.38	NM_001003220	NM_006474
57	CfaAffx.4309.1.S1_s_at	0.38	XM_861358	NM_001498
58	Cfa.3478.1.S1_at	0.37	AF354266	NA
59	CfaAffx.17532.1.S1_s_at	0.37	XM_843264	AY358562
60	Cfa.8843.1.A1_s_at	0.37	XM_847490	AY889090
61	CfaAffx.28117.1.S1_at	0.37	XM_892932	AC013265
62	CfaAffx.16813.1.S1_at	0.37	XM_533208	NM_001876
63	CfaAffx.7431.1.S1_at	0.37	XM_533636	BC080551
64	CfaAffx.9128.1.S1_s_at	0.36	XM_534163	NM_182848
65	CfaAffx.17376.1.S1_s_at	0.36	AJ575592	NM_001093
66	Cfa.15138.1.A1_at	0.36	NM_001093	AC007637
67	Cfa.101.1.S1_s_at	0.35	XM_533208	BC000185
68	Cfa.12375.1.A1_at	0.35	XM_538880	BC042605
69	CfaAffx.2191.1.S1_at	0.34	XM_532317	AY082381
70	CfaAffx.22979.1.S1_s_at	0.34	XM_533208	AJ420748
71	Cfa.15036.1.A1_at	2.49	AB169961	AC005331
72	Cfa.2753.1.A1_at	2.48	NM_052832	NM_052832
73	Cfa.12493.1.A1_at	2.45	XM_860169	AK168808
74	CfaAffx.26260.1.S1_at	2.45	XM_542043	NM_002229
75	Cfa.14626.3.S1_at	2.41	XM_857812	AC090341
76	Cfa.19427.1.S1_s_at	2.38	XM_537080	AB003698
77	CfaAffx.7333.1.S1_at	2.38	NM_001031692	NM_001031692
78	Cfa.15094.1.S1_a_at	2.37	XM_533973	AL136962
79	Cfa.20568.1.S1_at	2.36	NM_003105	NM_003105
80	Cfa.98.1.S1_at	2.31	AF479316	S64152
81	Cfa.16947.1.A1_at	2.31	XM_543596	AL512286
82	Cfa.5178.2.A1_at	2.26	XM_863647	AC104391
83	Cfa.719.1.S1_at	2.24	XM_863084	AB169815
84	Cfa.13618.1.A1_at	2.22	U10047	AC002546
85	Cfa.15094.2.S1_a_at	2.22	XM_847625	AC107464
86	CfaAffx.23392.1.S1_x_at	2.2	M59174	CR542241
87	Cfa.1803.1.S1_at	2.17	BK001590	BK001591
88	Cfa.9482.1.A1_at	2.17	XM_601210	AY164533
89	Cfa.7527.1.A1_at	2.17	NM_001018072	NM_001018072
90	Cfa.18826.1.S1_at	2.17	XM_853197	BC015510
91	CfaAffx.28599.1.S1_s_at	2.17	XM_584816	BC001421
92	CfaAffx.18323.1.S1_at	2.17	XM_536545	NM_003105

93	Cfa.19768.1.S1_at	2.16	XM_847004	AC117525
94	CfaAffx.11365.1.S1_at	2.16	XM_535242	AF059617
95	CfaAffx.13216.1.S1_s_at	2.15	XM_534302	AL833134
96	CfaAffx.30642.1.S1_s_at	2.15	XM_547262	NM_144620
97	Cfa.19447.1.S1_at	2.13	NM_005573	NM_005573
98	Cfa.9467.1.A1_at	2.13	XM_540392	NM_173054
99	Cfa.17456.1.S1_at	2.13	XM_542013	AK123265
100	Cfa.12527.1.A1_at	2.13	XM_586687	AL513326
101	CfaAffx.22739.1.S1_at	2.12	XM_548713	AL162272
102	CfaAffx.6614.1.S1_at	2.11	AB168572	AB168572
103	Cfa.5981.1.A1_at	2.11	XM_603519	AC100793
104	CfaAffx.822.1.S1_s_at	2.11	XM_542033	M62831
105	CfaAffx.1705.1.S1_at	2.1	XM_538592	AL008720
106	Cfa.5059.1.A1_at	2.1	NM_014656	CR618094
107	Cfa.5178.1.S1_at	2.09	XM_863647	AL050322
108	CfaAffx.27806.1.S1_x_at	2.09	XM_537720	AY766458
109	CfaAffx.9557.1.S1_x_at	2.09	BC106930	BC106930
110	Cfa.12326.1.A1_at	2.08	XM_723947	AC072022
111	Cfa.13636.1.A1_at	2.08	XM_857774	U49732
112	Cfa.825.1.S2_at	2.08	AY357941	AL606517
113	CfaAffx.13129.1.S1_at	2.07	XM_882294	AC074032
114	CfaAffx.11365.1.S1_s_at	2.07	XM_854900	NM_006622
115	Cfa.8466.1.A1_at	2.06	XM_756136	AL591004
116	Cfa.1200.1.S1_s_at	2.06	AJ560716	AK093922
117	Cfa.15627.1.A1_at	2.06	AC097712	AC097712
118	Cfa.14528.1.A1_at	2.05	Z25418	AJ420250
119	CfaAffx.28832.1.S1_at	2.05	XM_548297	AF134593
120	CfaAffx.30647.1.S1_at	2.04	XM_547263	BX641109
121	CfaAffx.30748.1.S1_at	2.04	XM_857229	BT019397
122	CfaAffx.9190.1.S1_at	2.03	XM_857374	XM_371614
123	Cfa.6729.1.A1_at	2.03	BC000671	BC000671
124	Cfa.3358.1.S1_at	2.03	NM_024090	AK027031
125	CfaAffx.18323.1.S1_s_at	2.03	XM_536545	U60975
126	Cfa.10880.1.A1_s_at	2.01	XM_535526	BC010122
127	Cfa.9325.1.A1_x_at	2.01	XM_848389	U50912
128	CfaAffx.5584.1.S1_at	0.5	XM_539037	BC045583
129	Cfa.11382.1.A1_s_at	0.5	XM_537673	BC012053
130	Cfa.13871.1.A1_at	0.5	AP001099	AP001099
131	Cfa.1794.1.S1_at	0.5	XM_532481	BC108676
132	CfaAffx.22344.1.S1_s_at	0.5	AF082505	AJ841720
133	CfaAffx.25283.1.S1_at	0.5	XM_846648	AF186379
134	CfaAffx.3950.1.S1_at	0.5	XM_531769	XM_290985
135	Cfa.11227.1.A1_at	0.5	XM_610609	AC130450
136	CfaAffx.3808.1.S1_s_at	0.5	XM_617831	NM_003558
137	Cfa.3648.1.S1_s_at	0.5	NM_001003160	NM_014475
138	Cfa.12746.1.S1_at	0.5	XM_538481	AC093840
139	Cfa.204.1.S1_s_at	0.49	U91844	U01120
140	CfaAffx.28227.1.S1_at	0.49	AF306861	BX161420
141	CfaAffx.20380.1.S1_at	0.49	XM_854986	NM_020990
142	Cfa.15430.1.A1_at	0.49	XM_516700	AK127468
143	Cfa.20429.1.S1_at	0.49	BC006523	Z98752
144	Cfa.15663.1.A1_at	0.49	BC077424	AC027237
145	Cfa.10921.1.S1_s_at	0.49	XM_544508	AF087892
146	Cfa.18524.1.S1_at	0.49	XM_546093	NM_022786

147	CfaAffx.28491.1.S1_at	0.49	NM_001003186	AL596025
148	Cfa.20844.1.S1_at	0.49	XM_582329	CR749368
149	CfaAffx.9612.1.S1_at	0.49	XM_849157	CR536549
150	CfaAffx.22561.1.S1_s_at	0.49	XM_535367	BC030153
151	Cfa.1465.1.S1_at	0.49	AF165917	NA
152	CfaAffx.25677.1.S1_s_at	0.49	XM_847754	AK122675
153	CfaAffx.9880.1.S1_at	0.49	XM_844822	NM_019095
154	Cfa.4978.1.A1_at	0.49	AF281074	AF281074
155	CfaAffx.16101.1.S1_s_at	0.49	XM_845625	AC108159
156	CfaAffx.21065.1.S1_s_at	0.49	XM_844257	NA
157	CfaAffx.14411.1.S1_at	0.49	XM_535129	BC064978
158	Cfa.12167.1.A1_at	0.49	XM_857472	CR614711
159	CfaAffx.9452.1.S1_s_at	0.49	XM_857591	U06117
160	Cfa.6037.1.S1_s_at	0.49	XM_534893	CR749334
161	CfaAffx.28621.1.S1_at	0.48	XM_537333	CR592932
162	CfaAffx.5225.1.S1_s_at	0.48	XM_532395	NM_014465
163	Cfa.21549.1.S1_s_at	0.48	XM_849503	AL356218
164	Cfa.2610.1.A1_at	0.48	AY136628	AL033519
165	CfaAffx.27146.1.S1_at	0.48	XM_537549	AK055200
166	Cfa.5002.1.A1_at	0.48	CR749631	NM_019885
167	Cfa.7057.1.A1_at	0.48	NM_017688	AC096766
168	Cfa.11035.1.A1_at	0.48	XM_240178	AC136767
169	CfaAffx.15155.1.S1_s_at	0.48	XM_534433	AL049767
170	CfaAffx.7365.1.S1_at	0.48	XM_542677	BC029656
171	CfaAffx.18625.1.S1_at	0.48	AP008207	NA
172	Cfa.349.1.A1_s_at	0.48	XM_861720	NM_015548
173	Cfa.14387.1.A1_s_at	0.48	XM_533030	CR620074
174	CfaAffx.23219.1.S1_s_at	0.48	XM_860432	BC022516
175	CfaAffx.5036.1.S1_s_at	0.48	XM_538773	AK027864
176	CfaAffx.20922.1.S1_at	0.48	XM_856200	BC026902
177	CfaAffx.3482.1.S1_s_at	0.48	XM_538691	BC068445
178	CfaAffx.20220.1.S1_at	0.48	XM_548885	NM_001001671
179	Cfa.18842.1.S1_at	0.48	XM_862359	AF268387
180	CfaAffx.24173.1.S1_s_at	0.48	BC025390	BC025390
181	Cfa.19533.1.S1_s_at	0.48	AB208922	AB208922
182	Cfa.11839.1.A1_s_at	0.48	XM_535129	BC064978
183	Cfa.12915.1.A1_at	0.48	NM_145693	AC012456
184	Cfa.4465.2.S1_s_at	0.48	XM_845215	NA
185	Cfa.4590.1.S1_s_at	0.48	XM_848228	NM_017680
186	Cfa.533.1.S1_at	0.48	NM_001034309	AY358329
187	CfaAffx.3714.1.S1_at	0.48	XM_541288	AL162390
188	CfaAffx.2004.1.S1_s_at	0.47	XM_531894	NM_001017372
189	Cfa.9853.1.A1_at	0.47	XM_656697	AC105753
190	CfaAffx.18687.1.S1_at	0.47	XM_545513	NM_199204
191	Cfa.3524.1.S2_at	0.47	AF336151	AY506357
192	Cfa.4556.3.A1_a_at	0.47	L36871	BC073765
193	Cfa.3542.1.S1_at	0.47	AB028042	AC140113
194	Cfa.16857.1.S1_at	0.47	XM_544507	BC008983
195	CfaAffx.21305.1.S1_at	0.47	XM_548543	AC099669
196	CfaAffx.12845.1.S1_at	0.47	XM_539763	NM_001009555
197	CfaAffx.18456.1.S1_s_at	0.47	XM_535819	BX648812
198	Cfa.16364.1.A1_at	0.47	AB220502	AB220502
199	CfaAffx.12483.1.S1_at	0.47	NM_175920	AL080312
200	Cfa.10092.1.A1_at	0.47	NM_000480	AC021914

201	Cfa.3491.1.S1_s_at	0.47	XM_535088	BC041784
202	Cfa.11292.1.A1_at	0.47	XM_532002	AK056752
203	Cfa.12131.1.A1_at	0.47	XM_548431	Y17448
204	CfaAffx.30657.1.S1_s_at	0.47	XM_548431	NM_004059
205	CfaAffx.3284.1.S1_at	0.47	XM_846138	NM_018965
206	CfaAffx.3283.1.S1_at	0.47	XM_874820	AY204749
207	Cfa.18689.1.S1_at	0.47	XM_534893	CR749334
208	Cfa.16744.1.S1_at	0.47	XM_873620	AL162390
209	Cfa.12462.1.A1_at	0.46	DQ113909	AC098799
210	CfaAffx.29802.1.S1_at	0.46	XM_546742	NM_020710
211	Cfa.16431.1.A1_at	0.46	CR860237	AF495544
212	CfaAffx.27879.1.S1_s_at	0.46	XM_542108	BC047591
213	CfaAffx.6394.1.S1_at	0.46	XM_844361	NM_020724
214	Cfa.12296.1.A1_at	0.46	BC046475	AC010243
215	CfaAffx.14851.1.S1_s_at	0.46	XM_535300	BC002576
216	Cfa.14057.1.A1_at	0.46	XM_536086	NM_003413
217	Cfa.5948.1.A1_at	0.46	NM_080165	AC010887
218	Cfa.12143.1.A1_at	0.46	XM_850039	AP002414
219	Cfa.9627.1.A1_at	0.46	AF526382	AF526382
220	CfaAffx.8473.1.S1_s_at	0.46	XM_852658	BC042131
221	Cfa.14620.1.A1_at	0.46	XM_532317	CR623165
222	CfaAffx.5908.1.S1_at	0.46	XM_860659	NM_001550
223	CfaAffx.13161.1.S1_s_at	0.46	XM_544819	CR620760
224	Cfa.11008.1.A1_at	0.46	BC102635	BC014225
225	Cfa.3324.1.S1_at	0.46	XM_538691	AL451123
226	Cfa.10039.1.A1_at	0.46	XM_844773	AF374726
227	Cfa.17677.1.S1_at	0.46	XM_838131	AL031676
228	CfaAffx.26949.1.S1_s_at	0.46	XM_547958	AL132642
229	CfaAffx.30657.1.S1_at	0.46	XM_548431	NM_004059
230	CfaAffx.21066.1.S1_s_at	0.46	XM_844290	NA
231	Cfa.18689.1.S1_s_at	0.46	XM_534893	BC040071
232	CfaAffx.15436.1.S1_at	0.45	XM_543027	BC019898
233	CfaAffx.12835.1.S1_at	0.45	XM_854906	NM_144668
234	Cfa.19549.1.S1_s_at	0.45	BC022526	AJ298293
235	Cfa.4555.1.S1_s_at	0.45	L36871	AY647979
236	Cfa.18258.2.S1_a_at	0.45	NM_001009867	NA
237	CfaAffx.3919.1.S1_s_at	0.45	XM_515679	AC010095
238	Cfa.19518.2.A1_s_at	0.45	XM_535260	NM_018695
239	Cfa.19549.1.S1_at	0.45	AJ298293	AJ298293
240	CfaAffx.22832.1.S1_s_at	0.45	XM_536069	NM_032726
241	Cfa.2282.1.S1_at	0.45	XM_539427	AK096428
242	CfaAffx.26949.1.S1_at	0.45	XM_547958	AL137735
243	Cfa.10854.1.S1_at	0.45	XM_532878	AL513550
244	CfaAffx.7437.1.S1_s_at	0.45	XM_533636	AB054067
245	Cfa.3664.1.S1_s_at	0.45	NM_001003173	AC004485
246	Cfa.15462.1.A1_at	0.45	NM_001003173	AL161729
247	CfaAffx.9797.1.S1_s_at	0.44	XM_534252	AL831925
248	CfaAffx.25159.1.S1_at	0.44	NM_001002838	NM_020922
249	Cfa.4556.3.A1_s_at	0.44	L36871	AY647979
250	Cfa.16500.1.S1_at	0.44	XM_531940	AB070011
251	Cfa.18258.3.S1_at	0.44	XM_844019	AB169867
252	CfaAffx.11992.1.S1_s_at	0.44	XM_535094	NM_024790
253	CfaAffx.4328.1.S1_at	0.44	XM_848235	NM_005014
254	Cfa.19653.1.A1_at	0.44	BC081135	AC112777

255	CfaAffx.27578.1.S1_at	0.44	XM_547618	NM_022751
256	CfaAffx.30551.1.S1_at	0.44	XM_546802	AF302109
257	Cfa.13268.1.A1_at	0.44	AB126596	AC026778
258	Cfa.18183.1.S1_at	0.44	XM_857210	AC008387
259	Cfa.6019.1.A1_at	0.44	XM_724777	AC147004
260	Cfa.93.1.S1_at	0.44	CR860955	AL137918
261	CfaAffx.25065.1.S1_s_at	0.44	NM_001003220	AF030428
262	Cfa.13033.1.A1_at	0.43	CR858688	NA
263	Cfa.5688.1.A1_at	0.43	NM_015336	AL158196
264	Cfa.15343.1.A1_a_at	0.43	XM_843630	NM_144583
265	CfaAffx.25467.1.S1_at	0.43	XM_537659	NM_006310
266	CfaAffx.4613.1.S1_at	0.43	XM_538986	XM_498111
267	CfaAffx.2014.1.S1_at	0.43	XM_214555	AC008591
268	Cfa.9659.1.A1_at	0.43	AB051389	AC108046
269	Cfa.1465.2.A1_at	0.43	NM_213992	AC106768
270	Cfa.11205.1.A1_at	0.43	NM_000216	S60088
271	CfaAffx.30851.1.S1_s_at	0.43	XM_537071	BC056667
272	CfaAffx.10452.1.S1_s_at	0.43	XM_590483	AC009194
273	CfaAffx.6374.1.S1_s_at	0.43	XM_851910	AB168681
274	CfaAffx.8051.1.S1_at	0.43	XM_844206	BC102460
275	CfaAffx.9808.1.S1_at	0.43	XM_534351	AL035668
276	Cfa.7153.1.A1_s_at	0.43	XM_534351	AL035668
277	Cfa.15136.1.S1_at	0.43	NM_001206	AL162390
278	Cfa.5277.1.A1_s_at	0.42	XM_532120	NM_145028
279	CfaAffx.3288.1.S1_at	0.42	XM_846150	AL138898
280	CfaAffx.14664.1.S1_s_at	0.42	XM_844773	AF374726
281	Cfa.13412.1.A1_at	0.42	XM_854906	BC028421
282	Cfa.20984.1.S1_at	0.42	XM_539525	AB169259
283	CfaAffx.8004.1.S1_s_at	0.42	XM_850120	XM_371174
284	Cfa.5715.1.S1_at	0.42	XM_532133	AL133404
285	Cfa.1286.1.A1_at	0.42	XM_583309	CR599853
286	Cfa.17433.1.S1_s_at	0.42	XM_548431	NM_004059
287	CfaAffx.11552.1.S1_s_at	0.41	XM_533773	BC017772
288	Cfa.13150.1.A1_at	0.41	NM_177737	AC044787
289	CfaAffx.11212.1.S1_s_at	0.41	XM_540544	AL832391
290	CfaAffx.1928.1.S1_at	0.41	XM_541178	NM_032532
291	Cfa.11092.1.A1_at	0.41	NM_021197	AC009123
292	CfaAffx.19304.1.S1_at	0.41	XM_846272	AC079151
293	CfaAffx.5035.1.S1_s_at	0.41	XM_858105	CR625459
294	Cfa.3648.1.S1_at	0.41	XM_517428	AC006320
295	Cfa.11104.1.S1_at	0.41	XM_535184	AC083886

Table 2: Genes associated with lipid and glucose metabolism differentially expressed in adipose tissue from fat compared to lean animals (group 4)

Column	1	2	3	4	5
55	CfaAffx.9291.1.S1_s_at	0.38	AB020887	CR626508	
60	Cfa.8843.1.A1_s_at	0.37	XM_847490	AY889090	
81	Cfa.16947.1.A1_at	2.31	XM_543596	AL512286	
112	Cfa.825.1.S2_at	2.08	AY357941	AL606517	
133	CfaAffx.25283.1.S1_at	0.5	XM_846648	AF186379	

204	Cfa.204.1.S1_s_at	0.49	U91844	U01120
188	CfaAffx.2004.1.S1_s_at	0.47	XM_531894	NM_001017372
212	CfaAffx.27879.1.S1_s_at	0.46	XM_542108	BC047591
216	Cfa.14057.1.A1_at	0.46	XM_536086	NM_003413
232	CfaAffx.15436.1.S1_at	0.45	XM_543027	BC019898
240	CfaAffx.22832.1.S1_s_at	0.45	XM_536069	NM_032726
274	CfaAffx.8051.1.S1_at	0.43	XM_844206	BC102460
295	Cfa.11104.1.S1_at	0.41	XM_535184	AC083886
11	Cfa.15689.1.A1_at	0.33	XM_844220	AC020550
241	Cfa.2282.1.S1_at	0.45	XM_539427	AK096428
15	CfaAffx.4097.1.S1_s_at	0.32	XM_539427	BC040239
44	Cfa.7478.1.A1_s_at	0.4	BC028417	NM_001093
18	CfaAffx.17336.1.S1_s_at	0.28	AJ575592	NM_001093
65	CfaAffx.17376.1.S1_s_at	0.36	AJ575592	NM_001093
66	Cfa.15138.1.A1_at	0.36	NM_001093	AC007637
124	Cfa.3358.1.S1_at	2.03	NM_024090	AK027031
36	CfaAffx.17954.1.S1_at	2.6	XM_545023	NM_024090
285	Cfa.1286.1.A1_at	0.42	XM_583309	CR599853
67	Cfa.101.1.S1_s_at	0.35	XM_533208	BC000185
62	CfaAffx.16813.1.S1_at	0.37	XM_533208	NM_001876
70	CfaAffx.22979.1.S1_s_at	0.34	XM_533208	AJ420748
182	Cfa.11839.1.A1_s_at	0.48	XM_535129	BC064978
157	CfaAffx.14411.1.S1_at	0.49	XM_535129	BC064978
183	Cfa.12915.1.A1_at	0.48	NM_145693	AC012456
243	Cfa.10854.1.S1_at	0.45	XM_532878	AL513550
273	CfaAffx.6374.1.S1_s_at	0.43	XM_851910	AB168681

Table 3: Genes identified as particularly relevant to fat**animals compared to lean animals (group 5)**

Column	1	2	3	4	5
6	Cfa.9039.1.A1_at	3.07	XM_547914	BX647104	
2	CfaAffx.26065.1.S1_at	3.94	XM_547914	AF111167	
3	CfaAffx.2782.1.S1_s_at	3.78	XM_538649	AJ243425	
4	CfaAffx.2790.1.S1_s_at	3.66	XM_538649	BC073983	
274	CfaAffx.8051.1.S1_at	0.43	XM_844206	BC102460	
295	Cfa.11104.1.S1_at	0.41	XM_535184	AC083886	
11	Cfa.15689.1.A1_at	0.33	XM_844220	AC020550	
68	Cfa.12375.1.A1_at	0.35	XM_538880	BC042605	
				NM_004117	
12	CfaAffx.2909.1.S1_at	0.33	XM_538880	7	
241	Cfa.2282.1.S1_at	0.45	XM_539427	AK096428	
15	CfaAffx.4097.1.S1_s_at	0.32	XM_539427	BC040239	
				NM_001093	
44	Cfa.7478.1.A1_s_at	0.4	BC028417	3	
				NM_001093	
18	CfaAffx.17336.1.S1_s_at	0.28	AJ575592	3	
				NM_001093	
65	CfaAffx.17376.1.S1_s_at	0.36	AJ575592	3	
66	Cfa.15138.1.A1_at	0.36	NM_001093	AC007637	

13	CfaAffx.4844.1.S1_s_at	0.33	XM_538481	BT019766
19	CfaAffx.4844.1.S1_at	0.26	XM_538481	BT019766
138	Cfa.12746.1.S1_at	0.5	XM_538481	AC093840
				NM_18175
25	CfaAffx.732.1.S1_at	0.12	NM_181756	6
24	CfaAffx.732.1.S1_x_at	0.14	NM_181756	AK095351
124	Cfa.3358.1.S1_at	2.03	NM_024090	AK027031
				NM_02409
36	CfaAffx.17954.1.S1_at	2.6	XM_545023	0
				NM_00647
56	CfaAffx.25065.1.S1_at	0.38	NM_001003220	4
				NM_00100
45	Cfa.3749.1.S1_at	0.4	NM_001003220	6624
261	CfaAffx.25065.1.S1_s_at	0.44	NM_001003220	AF030428
				NM_00149
49	CfaAffx.4308.1.S1_at	0.39	XM_861344	8
				NM_00149
57	CfaAffx.4309.1.S1_s_at	0.38	XM_861358	8
63	CfaAffx.7431.1.S1_at	0.37	XM_533636	BC080551
244	CfaAffx.7437.1.S1_s_at	0.45	XM_533636	AB054067
285	Cfa.1286.1.A1_at	0.42	XM_583309	CR599853
67	Cfa.101.1.S1_s_at	0.35	XM_533208	BC000185
				NM_00187
62	CfaAffx.16813.1.S1_at	0.37	XM_533208	6
70	CfaAffx.22979.1.S1_s_at	0.34	XM_533208	AJ420748
78	Cfa.15094.1.S1_a_at	2.37	XM_533973	AL136962
85	Cfa.15094.2.S1_a_at	2.22	XM_847625	AC107464
				NM_00310
92	CfaAffx.18323.1.S1_at	2.17	XM_536545	5
				NM_00310
79	Cfa.20568.1.S1_at	2.36	NM_003105	5
125	CfaAffx.18323.1.S1_s_at	2.03	XM_536545	U60975
94	CfaAffx.11365.1.S1_at	2.16	XM_535242	AF059617
				NM_00662
114	CfaAffx.11365.1.S1_s_at	2.07	XM_854900	2
158	Cfa.12167.1.A1_at	0.49	XM_857472	CR614711
159	CfaAffx.9452.1.S1_s_at	0.49	XM_857591	U06117
182	Cfa.11839.1.A1_s_at	0.48	XM_535129	BC064978
157	CfaAffx.14411.1.S1_at	0.49	XM_535129	BC064978
				NM_01768
185	Cfa.4590.1.S1_s_at	0.48	XM_848228	0
186	Cfa.533.1.S1_at	0.48	NM_001034309	AY358329
				NM_01896
205	CfaAffx.3284.1.S1_at	0.47	XM_846138	5
206	CfaAffx.3283.1.S1_at	0.47	XM_874820	AY204749
184	Cfa.4465.2.S1_s_at	0.48	XM_845215	NA
230	CfaAffx.21066.1.S1_s_at	0.46	XM_844290	NA
207	Cfa.18689.1.S1_at	0.47	XM_534893	CR749334
231	Cfa.18689.1.S1_s_at	0.46	XM_534893	BC040071
160	Cfa.6037.1.S1_s_at	0.49	XM_534893	CR749334
242	CfaAffx.26949.1.S1_at	0.45	XM_547958	AL137735
228	CfaAffx.26949.1.S1_s_at	0.46	XM_547958	AL132642
245	Cfa.3664.1.S1_s_at	0.45	NM_001003173	AC004485
246	Cfa.15462.1.A1_at	0.45	NM_001003173	AL161729

183	Cfa.12915.1.A1_at	0.48	NM_145693	AC012456
243	Cfa.10854.1.S1_at	0.45	XM_532878	AL513550
273	CfaAffx.6374.1.S1_s_at	0.43	XM_851910	AB168681
275	CfaAffx.9808.1.S1_at	0.43	XM_534351	AL035668
276	Cfa.7153.1.A1_s_at	0.43	XM_534351	AL035668
187	CfaAffx.3714.1.S1_at	0.48	XM_541288	AL162390
277	Cfa.15136.1.S1_at	0.43	NM_001206	AL162390
208	Cfa.16744.1.S1_at	0.47	XM_873620	AL162390
203	Cfa.12131.1.A1_at	0.47	XM_548431	Y17448
				NM_00405
229	CfaAffx.30657.1.S1_at	0.46	XM_548431	9
				NM_00405
204	CfaAffx.30657.1.S1_s_at	0.47	XM_548431	9
				NM_00405
286	Cfa.17433.1.S1_s_at	0.42	XM_548431	9

Table 4: Gene Description - Highest BLAST Hit Accession Number

SEQ ID NO Gene Description - Highest BLAST Hit Accession Number

- 1 PREDICTED: Pan troglodytes similar to hypothetical protein ARM (LOC460002), mRNA
- 2 PREDICTED: Canis familiaris similar to Proto-oncogene protein c-fos (Cellular oncogene fos) (G0/G1 switch regulatory protein 7), transcript variant 1 (LOC490792), mRNA
- 3 PREDICTED: Canis familiaris similar to Early growth response protein 1 (EGR-1) (Krox-24 protein) (ZIF268) (Nerve growth factor-induced protein A) (NGFI-A) (Transcription factor ETR103) (Zinc finger protein 225) (AT225), transcript variant 2 (LOC481528), mRNA
- 4 PREDICTED: Canis familiaris similar to Early growth response protein 1 (EGR-1) (Krox-24 protein) (ZIF268) (Nerve growth factor-induced protein A) (NGFI-A) (Transcription factor ETR103) (Zinc finger protein 225) (AT225), transcript variant 2 (LOC481528), mRNA
- 5 Homo sapiens thymopoietin (TMPO), transcript variant 3, mRNA
- 6 PREDICTED: Canis familiaris similar to Proto-oncogene protein c-fos (Cellular oncogene fos) (G0/G1 switch regulatory protein 7), transcript variant 1 (LOC490792), mRNA
- 7 Homo sapiens zinc finger protein 227 (ZNF227), mRNA
- 8 PREDICTED: Canis familiaris similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 3 (LOC486765), mRNA
- 9 PREDICTED: Strongylocentrotus purpuratus similar to CG31108-PA (LOC582217), partial mRNA
- 10 PREDICTED: Canis familiaris similar to serum/glucocorticoid regulated kinase 2 isoform beta (LOC610835), mRNA
- 11 PREDICTED: Canis familiaris similar to phytanoyl-CoA hydroxylase precursor (LOC478001), mRNA
- 12 PREDICTED: Canis familiaris similar to FK506-binding protein 5 (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (51 kDa FK506-binding protein) (FKBP-51) (54 kDa progesterone receptor-associated immunophilin) (FKBP54) (P54) (FF1 antigen) (HSP90-binding immunophilin) (... (LOC481759), mRNA
- 13 PREDICTED: Canis familiaris similar to Tumor-associated calcium signal transducer 1 precursor (Major gastrointestinal tumor-associated protein GA733-2) (Epithelial cell surface antigen) (Epithelial glycoprotein) (EGP) (Adenocarcinoma-associated antigen) (KSA) (KS 1/4 antigen)... (LOC481360), mRNA
- 14 Homo sapiens, clone IMAGE:5171802, mRNA
- 15 PREDICTED: Canis familiaris similar to [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4, mitochondrial precursor (Pyruvate dehydrogenase kinase isoform 4) (LOC482310), mRNA

- 16 PREDICTED: *Canis familiaris* similar to niban protein isoform 2 (LOC480041), mRNA
- 17 *Caenorhabditis elegans* BMP receptor Associated protein family member (*bra-1*) (*bra-1*) mRNA, complete cds
- 18 *Homo sapiens* mRNA for Acetyl-CoA carboxylase 2 (ACACB gene)
- 19 PREDICTED: *Canis familiaris* similar to Tumor-associated calcium signal transducer 1 precursor (Major gastrointestinal tumor-associated protein GA733-2) (Epithelial cell surface antigen) (Epithelial glycoprotein) (EGP) (Adenocarcinoma-associated antigen) (KSA) (KS 1/4 antigen)... (LOC481360), mRNA
- 20 *Mus musculus* Murr1 and U2af1-rs1 genes, partial and complete cds
- 21 *Campylobacter jejuni* 81-176 (*pflA*) gene, complete cds, *orf1* and *orf2*, partial cds
- 22 PREDICTED: *Canis familiaris* similar to suprabasin (LOC612650), mRNA
- 23 *Plasmodium yoelii yoelii* str. 17XNL hypothetical protein (PY04060) mRNA, partial cds
- 24 *Homo sapiens* zinc finger protein 233 (ZNF233), mRNA
- 25 *Homo sapiens* zinc finger protein 233 (ZNF233), mRNA
- 26 PREDICTED: *Canis familiaris* hypothetical LOC130733 (LOC475737), mRNA
- 27 *Homo sapiens* *bcl6* gene, 5' flanking region
- 28 *Homo sapiens* G protein-coupled receptor 51 (GPR51), mRNA
- 29 PREDICTED: *Canis familiaris* similar to transmembrane protein with EGF-like and two follistatin-like domains 1, transcript variant 1 (LOC612942), mRNA
- 30 *C.familiaris* mRNA for orphan nuclear receptor dNGFI-B protein
- 31 PREDICTED: *Bos taurus* putative MIP1-beta protein (LOC414347), mRNA
- 32 *L.japonicus* mRNA for small GTP-binding protein, RAB7C
- 33 *Canis familiaris* chemokine (C-C motif) ligand 2 (CCL2), mRNA
- 34 *Canis familiaris* inducible T-cell co-stimulator (ICOS) mRNA, complete cds
- 35 PREDICTED: *Canis familiaris* laminin beta 3 (LOC442953), mRNA
- 36 PREDICTED: *Canis familiaris* similar to ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast) (LOC487900), mRNA
- 37 *Nicotiana tabacum* mRNA for cyclin D3.1 protein (CycD3.1)
- 38 PREDICTED: *Canis familiaris* similar to Protein C14orf119 (LOC607014), mRNA
- 39 *Canis familiaris* chemokine (C-C motif) ligand 8 (CCL8), mRNA
- 40 *Oryza sativa* (*japonica* cultivar-group) chromosome 11 clone B1356E08, complete sequence
- 41 *Homo sapiens* transmembrane 4 L six family member 18, mRNA (cDNA clone MGC:23935 IMAGE:3828466), complete cds
- 42 *Schizosaccharomyces pombe* 972h- isoleucine-tRNA ligase (SPBC8D2.06), partial mRNA
- 43 PREDICTED: *Canis familiaris* similar to tropomodulin 1, transcript variant 1 (LOC474771), mRNA
- 44 *Homo sapiens* acetyl-Coenzyme A carboxylase beta, mRNA (cDNA clone IMAGE:4824130), complete cds
- 45 *Canis familiaris* podoplanin (PDPN), mRNA
- 46 *Homo sapiens* cDNA FLJ13037 fis, clone NT2RP3001268, highly similar to *Homo sapiens* zinc finger protein ZNF228 (ZNF228) mRNA
- 47 *Homo sapiens* serine/threonine protein kinase Kp78 splice variant CTAK75a mRNA, complete cds
- 48 *Canis familiaris* IgA heavy chain constant region gene, partial cds
- 49 PREDICTED: *Canis familiaris* similar to Glutamate--cysteine ligase catalytic subunit (Gamma-glutamylcysteine synthetase) (Gamma-ECS) (GCS heavy chain), transcript variant 3 (LOC609822), mRNA
- 50 *Homo sapiens* cyclin-dependent kinase inhibitor mRNA, partial cds
- 51 PREDICTED: *Canis familiaris* similar to ATPase, H⁺ transporting, lysosomal 42kDa, V1 subunit C isoform 2, transcript variant 4 (LOC475667), mRNA
- 52 PREDICTED: *Bos taurus* similar to Interferon regulatory factor 4 (IRF-4) (Lymphocyte specific interferon regulatory factor) (LSIRF) (NF-EM5) (Multiple myeloma oncogene 1), transcript variant 2 (LOC506141), mRNA

- 53 PREDICTED: *Canis familiaris* similar to ARV1 homolog, transcript variant 1 (LOC488975), mRNA
- 54 PREDICTED: *Canis familiaris* retinoblastoma 1 (RB1), mRNA
- 55 *Canis familiaris* ucp2 mRNA for uncoupling protein 2, complete cds
- 56 *Canis familiaris* podoplanin (PDPN), mRNA
- 57 PREDICTED: *Canis familiaris* similar to Glutamate--cysteine ligase catalytic subunit (Gamma-glutamylcysteine synthetase) (Gamma-ECS) (GCS heavy chain), transcript variant 4 (LOC609822), mRNA
- 58 *Canis familiaris* immunoglobulin gamma heavy chain C mRNA, complete cds
- 59 PREDICTED: *Canis familiaris* similar to X-linked neuroligin 4, transcript variant 1 (LOC607406), mRNA
- 60 PREDICTED: *Canis familiaris* similar to Apolipoprotein C-I precursor (Apo-CI) (ApoC-I), transcript variant 2 (LOC476437), mRNA
- 61 PREDICTED: *Mus musculus* hypothetical protein LOC628198 (LOC628198), mRNA
- 62 PREDICTED: *Canis familiaris* carnitine palmitoyl transferase I isoform (CPT1), mRNA
- 63 PREDICTED: *Canis familiaris* similar to hypoxia-inducible factor-3 alpha isoform a (LOC476429), mRNA
- 64 PREDICTED: *Canis familiaris* similar to claudin 10 isoform b, transcript variant 1 (LOC476963), mRNA
- 65 *Homo sapiens* mRNA for Acetyl-CoA carboxylase 2 (ACACB gene)
- 66 *Homo sapiens* acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
- 67 PREDICTED: *Canis familiaris* carnitine palmitoyl transferase I isoform (CPT1), mRNA
- 68 PREDICTED: *Canis familiaris* similar to FK506-binding protein 5 (Peptidyl-prolyl cis-trans isomerase) (PPlase) (Rotamase) (51 kDa FK506-binding protein) (FKBP-51) (54 kDa progesterone receptor-associated immunophilin) (FKBP54) (P54) (FF1 antigen) (HSP90-binding immunophilin) (... (LOC481759), mRNA
- 69 PREDICTED: *Canis familiaris* similar to NOV protein homolog precursor (NovH) (Nephroblastoma overexpressed gene protein homolog) (LOC475083), mRNA
- 70 PREDICTED: *Canis familiaris* carnitine palmitoyl transferase I isoform (CPT1), mRNA
- 71 *Nitella japonica* chromoplast atpB gene for ATP synthase beta subunit, partial cds, strain:S090
- 72 *Homo sapiens* solute carrier family 26, member 7 (SLC26A7), transcript variant 1, mRNA
- 73 PREDICTED: *Canis familiaris* similar to NHP2-like protein 1 (High mobility group-like nuclear protein 2 homolog 1) ([U4/U6.U5] tri-snRNP 15.5 kDa protein) (Sperm specific antigen 1) (Fertilization antigen 1) (FA-1), transcript variant 2 (LOC609886), mRNA
- 74 PREDICTED: *Canis familiaris* similar to Transcription factor jun-B (LOC484927), mRNA
- 75 PREDICTED: *Canis familiaris* similar to Collagen alpha 1(III) chain precursor, transcript variant 3 (LOC478835), mRNA
- 76 PREDICTED: *Canis familiaris* similar to Cell division cycle 7-related protein kinase (CDC7-related kinase) (HsCdc7) (huCdc7) (LOC479955), mRNA
- 77 *Homo sapiens* leucine rich repeat containing 17 (LRRC17), transcript variant 1, mRNA
- 78 PREDICTED: *Canis familiaris* similar to expressed in non-metastatic cells 1, protein (NM23A) (nucleoside diphosphate kinase) (LOC476767), mRNA
- 79 *Homo sapiens* sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA
- 80 *Canis familiaris* dystrophin (DMD) mRNA, 5' untranslated region, alternatively spliced
- 81 PREDICTED: *Canis familiaris* similar to cholesterol 25-hydroxylase (LOC486470), mRNA
- 82 PREDICTED: *Canis familiaris* hypothetical protein LOC612422 (LOC612422), mRNA
- 83 PREDICTED: *Canis familiaris* aldolase C, transcript variant 4 (LOC480622), mRNA
- 84 *Pisum sativum* ribosomal protein L34 homolog (RPL34) mRNA, complete cds
- 85 PREDICTED: *Canis familiaris* similar to expressed in non-metastatic cells 1, protein (NM23A) (nucleoside diphosphate kinase) (LOC609873), mRNA
- 86 *Canis familiaris* serum amyloid A protein (SAA) mRNA, partial cds
- 87 TPA: *Homo sapiens* chromosome 17 middle SMS-REP low-copy repeat, genomic sequence
- 88 PREDICTED: *Bos taurus* similar to heparin-binding EGF-like growth factor (LOC522921), mRNA

- 89 Homo sapiens BTB (POZ) domain containing 11 (BTBD11), transcript variant 3, mRNA
- 90 PREDICTED: Canis familiaris similar to Regulator of G-protein signaling 1 (RGS1) (Early response protein 1R20) (B-cell activation protein BL34), transcript variant 2 (LOC488585), mRNA
- 91 PREDICTED: Bos taurus similar to nuclear distribution gene E homolog 1 (LOC508088), mRNA
- 92 PREDICTED: Canis familiaris similar to sortilin-related receptor containing LDLR class A repeats preproprotein (LOC479408), mRNA
- 93 PREDICTED: Canis familiaris similar to ankyrin repeat domain 26 (LOC609691), mRNA
- 94 PREDICTED: Canis familiaris similar to polo-like kinase 2, transcript variant 1 (LOC478063), mRNA
- 95 PREDICTED: Canis familiaris similar to Transmembrane 4 L6 family member 1 (Tumor-associated antigen L6) (Membrane component, surface marker 1) (M3S1) (LOC477107), mRNA
- 96 PREDICTED: Canis familiaris similar to leucine rich repeat containing 39, transcript variant 1 (LOC490141), mRNA
- 97 Homo sapiens lamin B1 (LMNB1), mRNA
- 98 PREDICTED: Canis familiaris similar to reelin isoform b, transcript variant 1 (LOC483273), mRNA
- 99 PREDICTED: Canis familiaris similar to egf-like module containing, mucin-like, hormone receptor-like sequence 2 isoform d (LOC484897), mRNA
- 100 PREDICTED: Bos taurus similar to BTG2 protein (NGF-inducible protein TIS21) (LOC539364), mRNA
- 101 PREDICTED: Canis familiaris similar to ankyrin repeat domain 26 (LOC491592), mRNA
- 102 Macaca fascicularis testis cDNA clone: QtsA-13105, similar to human armadillo repeat containing 2 (ARMC2), mRNA, RefSeq: NM_032131.3
- 103 PREDICTED: Bos taurus similar to glycerophosphodiester phosphodiesterase domain containing 4 (LOC525172), mRNA
- 104 PREDICTED: Canis familiaris similar to immediate early response 2 (LOC484917), mRNA
- 105 PREDICTED: Canis familiaris similar to interferon gamma inducible protein 47 (LOC481471), mRNA
- 106 Homo sapiens KIAA0040 (KIAA0040), mRNA
- 107 PREDICTED: Canis familiaris hypothetical protein LOC612422 (LOC612422), mRNA
- 108 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
- 109 Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian), mRNA (cDNA clone MGC:126110 IMAGE:40033200), complete cds
- 110 Plasmodium yoelii yoelii str. 17XNL hypothetical protein (PY01308) mRNA, partial cds
- 111 PREDICTED: Canis familiaris similar to mitogen-activated protein kinase kinase 6 isoform 1, transcript variant 3 (LOC480454), mRNA
- 112 Homo sapiens glucose transporter 14 short isoform mRNA, complete cds; alternatively spliced
- 113 PREDICTED: Bos taurus similar to LAG1 longevity assurance homolog 5, transcript variant 2 (LOC530776), mRNA
- 114 PREDICTED: Canis familiaris similar to polo-like kinase 2, transcript variant 3 (LOC478063), mRNA
- 115 Ustilago maydis 521 hypothetical protein (UM05082.1), mRNA
- 116 Canis familiaris mRNA for putative secreted frizzled related protein 2 (sfrp2 gene)
- 117 Homo sapiens BAC clone RP11-216H12 from 4, complete sequence
- 118 C.familiaris MHC class Ib gene (DLA-79) gene, complete CDS
- 119 PREDICTED: Canis familiaris similar to Peroxisomal sarcosine oxidase (PSO) (L-pipecolate oxidase) (L-pipecolic acid oxidase) (LOC491177), mRNA

- 120 PREDICTED: Canis familiaris similar to spindle assembly abnormal protein 6 (LOC490142), mRNA
- 121 PREDICTED: Canis familiaris similar to Neutrophil gelatinase-associated lipocalin precursor (NGAL) (P25) (25 kDa alpha-2-microglobulin-related subunit of MMP-9) (Lipocalin 2) (Oncogene 24p3), transcript variant 2 (LOC491320), mRNA
- 122 PREDICTED: Canis familiaris similar to myeloid/lymphoid or mixed-lineage leukemia 5, transcript variant 11 (LOC476542), mRNA
- 123 Homo sapiens claudin 4, mRNA (cDNA clone MGC:1778 IMAGE:3349211), complete cds
- 124 Homo sapiens ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast) (ELOVL6), mRNA
- 125 PREDICTED: Canis familiaris similar to sortilin-related receptor containing LDLR class A repeats preproprotein (LOC479408), mRNA
- 126 PREDICTED: Canis familiaris similar to fem-1 homolog b (LOC478352), mRNA
- 127 PREDICTED: Canis familiaris similar to FXYD domain-containing ion transport regulator 6 (LOC610831), mRNA
- 128 PREDICTED: Canis familiaris hypothetical LOC481916 (LOC481916), mRNA
- 129 PREDICTED: Canis familiaris similar to F46E10.1a (LOC480551), mRNA
- 130 Homo sapiens genomic DNA, chromosome 18 clone:RP11-883A18, complete sequence
- 131 PREDICTED: Canis familiaris similar to BE10.2 (LOC475247), mRNA
- 132 Canis familiaris T cell receptor beta chain hcvb3 (hcvb3) mRNA, partial cds
- 133 PREDICTED: Canis familiaris similar to peroxisome proliferative activated receptor, gamma, coactivator 1 alpha, transcript variant 1 (LOC479127), mRNA
- 134 PREDICTED: Canis familiaris similar to LIM and senescent cell antigen-like domains 1, transcript variant 1 (LOC474540), mRNA
- 135 PREDICTED: Bos taurus similar to heparan sulfate D-glucosaminyl 3-O-sulfotransferase 2 (LOC532099), partial mRNA
- 136 PREDICTED: Bos taurus similar to phosphatidylinositol-4-phosphate 5-kinase, type I, beta isoform 2, transcript variant 1 (LOC537654), mRNA
- 137 Canis familiaris dihydrodiol dehydrogenase (dimeric) (DHDH), mRNA
- 138 PREDICTED: Canis familiaris similar to Tumor-associated calcium signal transducer 1 precursor (Major gastrointestinal tumor-associated protein GA733-2) (Epithelial cell surface antigen) (Epithelial glycoprotein) (EGP) (Adenocarcinoma-associated antigen) (KSA) (KS 1/4 antigen)... (LOC481360), mRNA
- 139 Canis familiaris glucose-6-phosphatase mRNA, complete cds
- 140 Tursiops truncatus IgM heavy chain mRNA, complete cds
- 141 PREDICTED: Canis familiaris similar to creatine kinase, mitochondrial 1B precursor, transcript variant 3 (LOC478277), mRNA
- 142 PREDICTED: Pan troglodytes kinase related protein, telokin (LOC460640), mRNA
- 143 Homo sapiens serum/glucocorticoid regulated kinase 2, mRNA (cDNA clone IMAGE:2988475), containing frame-shift errors
- 144 Xenopus laevis ubiquitously transcribed tetratricopeptide repeat gene, Y-linked, mRNA (cDNA clone MGC:82191 IMAGE:3401210), complete cds
- 145 PREDICTED: Canis familiaris similar to complement component 1, q subcomponent, gamma polypeptide (LOC487382), mRNA
- 146 PREDICTED: Canis familiaris similar to ARV1 homolog, transcript variant 1 (LOC488975), mRNA
- 147 Canis familiaris nitric oxide synthase 2A (inducible, hepatocytes) (NOS2A), mRNA
- 148 PREDICTED: Bos taurus similar to F-box protein 44 isoform 1 (LOC505957), mRNA
- 149 PREDICTED: Canis familiaris similar to PRKC, apoptosis, WT1, regulator (LOC611487), mRNA
- 150 PREDICTED: Canis familiaris similar to Complement C1q subcomponent, A chain precursor (LOC478194), mRNA
- 151 Canis familiaris triadin isoform 3 mRNA, complete cds

- 152 PREDICTED: *Canis familiaris* similar to CG13624-PC, isoform C, transcript variant 2 (LOC612888), mRNA
- 153 PREDICTED: *Canis familiaris* similar to CG4774-PA, isoform A, transcript variant 2 (LOC607530), mRNA
- 154 *Homo sapiens* neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
- 155 PREDICTED: *Canis familiaris* similar to Tetraspanin-5 (Tspan-5) (Transmembrane 4 superfamily member 9) (Tetraspan NET-4), transcript variant 2 (LOC478486), mRNA
- 156 PREDICTED: *Canis familiaris* similar to Ig lambda chain C regions (LOC607541), mRNA
- 157 PREDICTED: *Canis familiaris* similar to pyruvate dehydrogenase phosphatase precursor (LOC477941), mRNA
- 158 PREDICTED: *Canis familiaris* similar to Xanthine dehydrogenase/oxidase, transcript variant 3 (LOC483028), mRNA
- 159 PREDICTED: *Canis familiaris* similar to Xanthine dehydrogenase/oxidase, transcript variant 8 (LOC483028), mRNA
- 160 PREDICTED: *Canis familiaris* similar to Alpha-2-macroglobulin precursor (Alpha-2-M) (LOC477699), mRNA
- 161 PREDICTED: *Canis familiaris* hypothetical LOC480209 (LOC480209), mRNA
- 162 PREDICTED: *Canis familiaris* sulfotransferase family, cytosolic, 1B, member 1 (SULT1B1), mRNA
- 163 PREDICTED: *Canis familiaris* similar to Aquaporin 3 (LOC611792), mRNA
- 164 *Petunia integrifolia* subsp. *inflata* S2 self-incompatibility ribonuclease (S2-RNase) and S2-locus F-box protein (SLF2) genes, complete cds
- 165 PREDICTED: *Canis familiaris* similar to Protein C14orf103 homolog (LOC480428), mRNA
- 166 *Homo sapiens* mRNA; cDNA DKFZp686G0638 (from clone DKFZp686G0638)
- 167 *Homo sapiens* B-box and SPRY domain containing (BSPRY), mRNA
- 168 PREDICTED: *Rattus norvegicus* apoptotic chromatin condensation inducer 1 (predicted) (Acin1_predicted), mRNA
- 169 PREDICTED: *Canis familiaris* similar to Elafin precursor (Elastase-specific inhibitor) (ESI) (Skin-derived antileukoprotease) (SKALP) (WAP four-disulfide core domain protein 14) (Protease inhibitor WAP3) (LOC477241), mRNA
- 170 PREDICTED: *Canis familiaris* similar to cystatin 9-like precursor (LOC485559), mRNA
- 171 *Oryza sativa* (japonica cultivar-group) genomic DNA, chromosome 1, complete sequence
- 172 PREDICTED: *Canis familiaris* dystonin, transcript variant 16 (DST), mRNA
- 173 PREDICTED: *Canis familiaris* similar to acid phosphatase 6, lysophosphatidic (LOC475822), mRNA
- 174 PREDICTED: *Canis familiaris* similar to arrestin domain containing 2 isoform 2, transcript variant 3 (LOC609489), mRNA
- 175 PREDICTED: *Canis familiaris* similar to ATP-binding cassette, sub-family A member 1 (LOC481651), mRNA
- 176 PREDICTED: *Canis familiaris* similar to promyelocytic leukemia zinc finger protein, transcript variant 3 (LOC489398), mRNA
- 177 PREDICTED: *Canis familiaris* similar to Protein C9orf72 homolog, transcript variant 1 (LOC481569), mRNA
- 178 PREDICTED: *Canis familiaris* similar to mitogen-activated protein kinase kinase kinase 5 (LOC491765), mRNA
- 179 PREDICTED: *Canis familiaris* similar to zinc finger protein 403, transcript variant 4 (LOC480594), mRNA
- 180 *Homo sapiens* tetratricopeptide repeat domain 25, mRNA (cDNA clone IMAGE:4831078), complete cds
- 181 *Homo sapiens* mRNA for laminin alpha 2 subunit precursor variant protein
- 182 PREDICTED: *Canis familiaris* similar to pyruvate dehydrogenase phosphatase precursor (LOC477941), mRNA
- 183 *Homo sapiens* lipin 1 (LPIN1), mRNA

- 184 PREDICTED: *Canis familiaris* similar to Immunoglobulin lambda-like polypeptide 1 precursor (Immunoglobulin-related 14.1 protein) (Immunoglobulin omega polypeptide) (Lambda 5) (CD179b antigen) (LOC608248), mRNA
- 185 PREDICTED: *Canis familiaris* similar to Asporin precursor (LOC610685), mRNA
- 186 *Bos taurus* similar to Asporin precursor (Periodontal ligament associated protein 1) (PLAP-1) (MGC128677), mRNA
- 187 PREDICTED: *Canis familiaris* similar to Transcription factor BTEB1 (Basic transcription element binding protein 1) (BTE-binding protein 1) (GC box binding protein 1) (Krueppel-like factor 9) (LOC484172), mRNA
- 188 PREDICTED: *Canis familiaris* similar to solute carrier family 27 (fatty acid transporter), member 6 (LOC474666), mRNA
- 189 *Aspergillus nidulans* FGSC A4 hypothetical protein (AN4185.2), mRNA
- 190 PREDICTED: *Canis familiaris* similar to NADP-dependent retinol dehydrogenase/reductase (LOC488391), mRNA
- 191 *Sus scrofa* epidermal growth factor precursor (EGF) mRNA, complete cds
- 192 *Canis familiaris* IgA heavy chain constant region gene, partial cds
- 193 *Canis familiaris* mRNA for metallothionein-II, complete cds
- 194 PREDICTED: *Canis familiaris* similar to complement component 1, q subcomponent, beta polypeptide precursor (LOC487381), mRNA
- 195 PREDICTED: *Canis familiaris* similar to zinc finger protein 660 (LOC491422), mRNA
- 196 PREDICTED: *Canis familiaris* similar to SH3 domain protein D19, transcript variant 1 (LOC482645), mRNA
- 197 PREDICTED: *Canis familiaris* similar to DRE1 protein (LOC478647), mRNA
- 198 *Macaca fascicularis* mRNA, clone QnpA-12979: similar to *Homo sapiens* neuroepithelial cell transforming gene 1 (NET1), mRNA, NM_005863.2
- 199 *Homo sapiens* leucyl/cystinyl aminopeptidase (LNPEP), transcript variant 2, mRNA
- 200 *Homo sapiens* adenosine monophosphate deaminase (isoform E) (AMPD3), transcript variant 1, mRNA
- 201 PREDICTED: *Canis familiaris* tocopherol (alpha) transfer protein (TTPA), mRNA
- 202 PREDICTED: *Canis familiaris* similar to tropomodulin 1, transcript variant 1 (LOC474771), mRNA
- 203 PREDICTED: *Canis familiaris* similar to Kynurenine--oxoglutarate, transaminase I (Kynurenine aminotransferase I) (KATI) (Glutamine--phenylpyruvate transaminase) (Glutamine transaminase K) (GTK) (Cysteine-S-conjugate beta-lyase) (LOC491310), mRNA
- 204 PREDICTED: *Canis familiaris* similar to Kynurenine--oxoglutarate transaminase I (Kynurenine aminotransferase I) (KATI) (Glutamine--phenylpyruvate transaminase) (Glutamine transaminase K) (GTK) (Cysteine-S-conjugate beta-lyase) (LOC491310), mRNA
- 205 PREDICTED: *Canis familiaris* similar to Triggering receptor expressed on myeloid cells 2 precursor (Triggering receptor expressed on monocytes 2) (TREM-2) (LOC608965), mRNA
- 206 PREDICTED: *Bos taurus* similar to Triggering receptor expressed on myeloid cells 2 precursor (Triggering receptor expressed on monocytes 2) (TREM-2), transcript variant 2 (LOC506467), mRNA
- 207 PREDICTED: *Canis familiaris* similar to Alpha-2-macroglobulin precursor (Alpha-2-M) (LOC477699), mRNA
- 208 PREDICTED: *Bos taurus* similar to Transcription factor BTEB1 (Basic transcription element binding protein 1) (BTE-binding protein 1) (GC box binding protein 1) (Krueppel-like factor 9), transcript variant 3 (LOC539139), mRNA
- 209 *Hordeum vulgare* subsp. *vulgare* cultivar Morex inducer of CBF expression 2 (ICE2) gene, partial cds
- 210 PREDICTED: *Canis familiaris* similar to Y54E10A.6 (LOC489622), mRNA
- 211 *Pongo pygmaeus* mRNA; cDNA DKFZp469L0319 (from clone DKFZp469L0319)
- 212 PREDICTED: *Canis familiaris* similar to Insulin receptor precursor (IR) (CD220 antigen) (LOC484990), mRNA
- 213 PREDICTED: *Canis familiaris* similar to ring finger protein 150 (LOC607611), mRNA

- 214 Homo sapiens cDNA clone MGC:51010 IMAGE:5270267, complete cds
- 215 PREDICTED: Canis familiaris matrix metalloproteinase-2 (MMP-2), mRNA
- 216 PREDICTED: Canis familiaris similar to acyl-CoA synthetase long-chain family member 3, transcript variant 1 (LOC478927), mRNA
- 217 Drosophila melanogaster CG18211-PA (betaTry) mRNA, complete cds
- 218 PREDICTED: Canis familiaris similar to retinoic acid receptor responder (tazarotene induced) 1 isoform 1 (LOC612298), mRNA
- 219 Homo sapiens protein upregulated in metastatic prostate cancer mRNA, complete cds
- 220 PREDICTED: Canis familiaris similar to Krueppel-like factor 5 (Intestinal-enriched krueppel-like factor) (Colon krueppel-like factor) (Transcription factor BTEB2) (Basic transcription element binding protein 2) (BTE-binding protein 2) (GC box binding protein 2)..., transcript variant 3 (LOC612788), mRNA
- 221 PREDICTED: Canis familiaris similar to NOV protein homolog precursor (NovH) (Nephroblastoma overexpressed gene protein homolog) (LOC475083), mRNA
- 222 PREDICTED: Canis familiaris similar to interferon-related developmental regulator 1, transcript variant 2 (LOC482408), mRNA
- 223 PREDICTED: Canis familiaris similar to BTG3 protein (Tob5 protein) (Abundant in neuroepithelium area protein), transcript variant 2 (LOC487695), mRNA
- 224 Bos taurus homeodomain only protein, mRNA (cDNA clone MGC:127764 IMAGE:7963031), complete cds
- 225 PREDICTED: Canis familiaris similar to Protein C9orf72 homolog, transcript variant 1 (LOC481569), mRNA
- 226 PREDICTED: Canis familiaris similar to Proteinase activated receptor 3 precursor (PAR-3) (Thrombin receptor-like 2) (Coagulation factor II receptor-like 2) (LOC607963), mRNA
- 227 Leishmania major strain Friedlin hypothetical protein (LMJ_1048) mRNA, partial cds
- 228 PREDICTED: Canis familiaris similar to ankyrin repeat and SOCS box-containing protein 2 (predicted), transcript variant 1 (LOC490836), mRNA
- 229 PREDICTED: Canis familiaris similar to Kynurenine--oxoglutarate transaminase I (Kynurenine aminotransferase I) (KATI) (Glutamine--phenylpyruvate transaminase) (Glutamine transaminase K) (GTK) (Cysteine-S-conjugate beta-lyase) (LOC491310), mRNA
- 230 PREDICTED: Canis familiaris similar to Immunoglobulin lambda-like polypeptide 1 precursor (Immunoglobulin-related 14.1 protein) (Immunoglobulin omega polypeptide) (Lambda 5) (CD179b antigen) (LOC607558), mRNA
- 231 PREDICTED: Canis familiaris similar to Alpha-2-macroglobulin precursor (Alpha-2-M) (LOC477699), mRNA
- 232 PREDICTED: Canis familiaris similar to Phospholipid transfer protein precursor (Lipid transfer protein II) (LOC485903), mRNA
- 233 PREDICTED: Canis familiaris similar to WD repeat domain 66, transcript variant 2 (LOC477466), mRNA
- 234 Homo sapiens alanine-glyoxylate aminotransferase 2-like 1, mRNA (cDNA clone MGC:26665 IMAGE:4797767), complete cds
- 235 Canis familiaris IgA heavy chain constant region gene, partial cds
- 236 Felis catus CD8 antigen, beta polypeptide (CD8B), mRNA
- 237 PREDICTED: Pan troglodytes RAN binding protein 2 (LOC459477), mRNA
- 238 PREDICTED: Canis familiaris similar to ERBB2 interacting protein isoform 7 (LOC478082), mRNA
- 239 Homo sapiens mRNA for alanine:glyoxylate aminotransferase 2 homolog 1, splice form 1 (AGXT2L1 gene)
- 240 PREDICTED: Canis familiaris similar to phospholipase C, delta 4 (LOC478910), mRNA
- 241 PREDICTED: Canis familiaris similar to [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4, mitochondrial precursor (Pyruvate dehydrogenase kinase isoform 4) (LOC482310), mRNA
- 242 PREDICTED: Canis familiaris similar to ankyrin repeat and SOCS box-containing protein 2 (predicted), transcript variant 1 (LOC490836), mRNA

- 243 PREDICTED: *Canis familiaris* similar to lipin 1, transcript variant 1 (LOC475670), mRNA
- 244 PREDICTED: *Canis familiaris* similar to hypoxia-inducible factor-3 alpha isoform a (LOC476429), mRNA
- 245 *Canis familiaris* metallothionein 1X (MT1X), mRNA
- 246 *Canis familiaris* metallothionein 1X (MT1X), mRNA
- 247 PREDICTED: *Canis familiaris* similar to UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl galactosaminyltransferase-like 2 (LOC477056), mRNA
- 248 *Homo sapiens* WNK lysine deficient protein kinase 3 (WNK3), transcript variant 2, mRNA
- 249 *Canis familiaris* IgA heavy chain constant region gene, partial cds
- 250 PREDICTED: *Canis familiaris* similar to Myosin-3 (Myosin heavy chain A) (MHC A) (LOC474713), mRNA
- 251 PREDICTED: *Canis familiaris* similar to downregulated in renal cell carcinoma (LOC607380), mRNA
- 252 PREDICTED: *Canis familiaris* similar to centrosome spindle pole associated protein (LOC477902), mRNA
- 253 PREDICTED: *Canis familiaris* similar to Osteomodulin precursor (Osteoadherin) (OSAD) (Keratan sulfate proteoglycan osteomodulin) (KSPG osteomodulin) (LOC610693), mRNA
- 254 *Xenopus laevis* MGC83953 protein, mRNA (cDNA clone MGC:83953 IMAGE:6862234), complete cds
- 255 PREDICTED: *Canis familiaris* hypothetical LOC490496 (LOC490496), mRNA
- 256 PREDICTED: *Canis familiaris* similar to WAP four-disulfide core domain 1 precursor (LOC489682), mRNA
- 257 *Pongo pygmaeus* C6 gene for complement component 6, partial cds
- 258 PREDICTED: *Canis familiaris* similar to ankyrin repeat, family A (RFXANK-like), 2, transcript variant 3 (LOC478097), mRNA
- 259 *Plasmodium yoelii yoelii* str. 17XNL hypothetical protein (PY02022) mRNA, partial cds
- 260 *Pongo pygmaeus* mRNA; cDNA DKFZp470P1633 (from clone DKFZp470P1633)
- 261 *Canis familiaris* podoplanin (PDPN), mRNA
- 262 *Pongo pygmaeus* mRNA; cDNA DKFZp468I0813 (from clone DKFZp468I0813)
- 263 *Homo sapiens* zinc finger, DHHC-type containing 17 (ZDHHC17), mRNA
- 264 PREDICTED: *Canis familiaris* similar to ATPase, H⁺ transporting, lysosomal 42kDa, V1 subunit C isoform 2, transcript variant 3 (LOC475667), mRNA
- 265 PREDICTED: *Canis familiaris* similar to aminopeptidase puromycin sensitive (LOC480538), mRNA
- 266 PREDICTED: *Canis familiaris* similar to CG7245-PA (LOC481865), mRNA
- 267 PREDICTED: *Rattus norvegicus* similar to DD1 (predicted) (LOC291580), mRNA
- 268 *Bos taurus* mRNA for VSGP/F-spondin, complete cds
- 269 *Sus scrofa* estrogen sulfotransferase (STE), mRNA
- 270 *Homo sapiens* Kallmann syndrome 1 sequence (KAL1), mRNA
- 271 PREDICTED: *Canis familiaris* similar to sarcoma antigen NY-SAR-41 (LOC479946), mRNA
- 272 PREDICTED: *Bos taurus* similar to zinc finger protein 420 (LOC512882), mRNA
- 273 PREDICTED: *Canis familiaris* similar to lipin 1, transcript variant 4 (LOC475670), mRNA
- 274 PREDICTED: *Canis familiaris* similar to phytanoyl-CoA hydroxylase precursor (LOC607509), mRNA
- 275 PREDICTED: *Canis familiaris* similar to Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A), transcript variant 1 (LOC477162), mRNA
- 276 PREDICTED: *Canis familiaris* similar to Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A), transcript variant 1 (LOC477162), mRNA
- 277 *Homo sapiens* Kruppel-like factor 9 (KLF9), mRNA
- 278 PREDICTED: *Canis familiaris* hypothetical LOC474886, transcript variant 2 (LOC474886), mRNA
- 279 PREDICTED: *Canis familiaris* similar to triggering receptor expressed on myeloid cells-like 4 (LOC608975), mRNA

- 280 PREDICTED: Canis familiaris similar to Proteinase activated receptor 3 precursor (PAR-3) (Thrombin receptor-like 2) (Coagulation factor II receptor-like 2) (LOC607963), mRNA
- 281 PREDICTED: Canis familiaris similar to WD repeat domain 66, transcript variant 2 (LOC477466), mRNA
- 282 PREDICTED: Canis familiaris similar to interferon-related developmental regulator 1, transcript variant 1 (LOC482408), mRNA
- 283 PREDICTED: Canis familiaris similar to Zinc finger protein 283 (LOC613011), mRNA
- 284 PREDICTED: Canis familiaris similar to triggering receptor expressed on myeloid cells-like 1 (LOC474898), mRNA
- 285 PREDICTED: Bos taurus similar to Carnitine O-palmitoyltransferase I, mitochondrial liver isoform (CPT I) (CPTI-L) (Carnitine palmitoyltransferase 1A) (LOC506812), partial mRNA
- 286 PREDICTED: Canis familiaris similar to Kynurenine--oxoglutarate transaminase I (Kynurenine aminotransferase I) (KATI) (Glutamine--phenylpyruvate transaminase) (Glutamine transaminase K) (GTK) (Cysteine-S-conjugate beta-lyase) (LOC491310), mRNA
- 287 PREDICTED: Canis familiaris hypothetical LOC476569 (LOC476569), mRNA
- 288 Mus musculus expressed sequence AI854703 (AI854703), mRNA
- 289 PREDICTED: Canis familiaris similar to regeneration associated muscle protease isoform b (LOC483426), mRNA
- 290 PREDICTED: Canis familiaris similar to fibronectin type III domain containing 1 (LOC484061), mRNA
- 291 Homo sapiens WAP four-disulfide core domain 1 (WFDC1), mRNA
- 292 PREDICTED: Canis familiaris similar to CG1530-PA (LOC609071), mRNA
- 293 PREDICTED: Canis familiaris similar to glycoprotein (transmembrane) nmb isoform b precursor, transcript variant 3 (LOC482355), mRNA
- 294 PREDICTED: Pan troglodytes similar to sprouty homolog 1, antagonist of FGF signaling; sprouty, Drosophila, homolog of, 1 (antagonist of FGF signaling); sprouty (Drosophila) homolog 1 (antagonist of FGF signaling) (LOC461476), mRNA
- 295 PREDICTED: Canis familiaris similar to phytanoyl-CoA hydroxylase precursor (LOC478000), mRNA

**Table 5: Gene Description - Highest BLAST Hit
for a Human Sequence Accession Number**

<u>SEQ ID NO</u>	<u>Gene Description - Highest BLAST Hit for a Human Sequence Accession Number</u>
1	Homo sapiens armadillo repeat containing 9, mRNA (cDNA clone MGC:74894 IMAGE:6165433), complete cds
2	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3	Homo sapiens EGR1 gene for early growth response protein 1
4	Homo sapiens early growth response 1, mRNA (cDNA clone MGC:88036 IMAGE:6188360), complete cds
5	Homo sapiens 12 BAC RP11-181C3 (Roswell Park Cancer Institute Human BAC Library) complete sequence
6	Homo sapiens mRNA; cDNA DKFZp686J04124 (from clone DKFZp686J04124)
7	Homo sapiens zinc finger protein 227 (ZNF227), mRNA
8	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 3 (SLC7A3), mRNA
9	Homo sapiens PAC clone RP5-1003N18 from 14q24.3, complete sequence
10	Homo sapiens serum/glucocorticoid regulated kinase 2 mRNA, complete cds
11	Homo sapiens BAC clone RP11-198M19 from 2, complete sequence
12	Homo sapiens FK506 binding protein 5 (FKBP5), mRNA
13	Synthetic construct Homo sapiens tumor-associated calcium signal transducer 1 mRNA, partial cds

- 14 Human DNA sequence from clone RP3-510O8 on chromosome 6 Contains the 5' end of the FKBP5 gene for FK506 binding protein 5 (FKBP51), four novel genes (including FLJ25390), a UMP-CMP (uridine monophosphate - cytidine monophosphate) kinase pseudogene, the CLPS gene for pancreatic colipase, the 5' end of a novel gene and two CpG islands, complete sequence
- 15 Homo sapiens pyruvate dehydrogenase kinase, isozyme 4, mRNA (cDNA clone MGC:5281 IMAGE:3047987), complete cds
- 16 Homo sapiens BAC clone RP11-617I14 from 4, complete sequence
- 17 Homo sapiens chromosome 3 clone RP11-6B7, complete sequence
- 18 Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
- 19 Synthetic construct Homo sapiens tumor-associated calcium signal transducer 1 mRNA, partial cds
- 20 Homo sapiens 12 BAC RP11-451H11 (Roswell Park Cancer Institute Human BAC Library) complete sequence
- 21 Homo sapiens BAC clone RP11-398G12 from 2, complete sequence
- 22 Homo sapiens suprabasin (SBSN), mRNA
- 23 Homo sapiens 3 BAC RP11-1D19 (Roswell Park Cancer Institute Human BAC Library) complete sequence
- 24 Homo sapiens cDNA FLJ38032 fis, clone CTONG2013352, moderately similar to ZINC FINGER PROTEIN 228
- 25 Homo sapiens zinc finger protein 233 (ZNF233), mRNA
- 26 full-length cDNA clone CS0DI004YK24 of Placenta Cot 25-normalized of Homo sapiens (human)
- 27 Homo sapiens 3 BAC RP11-211G3 (Roswell Park Cancer Institute Human BAC Library) complete sequence
- 28 Human DNA sequence from clone RP11-199C17 on chromosome 9 Contains the 5' end of the TBC1D2 gene for TBC1 domain family, member 2 (PARIS1, PARIS-1, DKFZP761D1823, DKFZp761D1823), the 3' end of the GPR51 gene for G protein-coupled receptor 51 (HG20, GABBR2, GPRC3B, GABABR2) and a CpG island, complete sequence
- 29 Homo sapiens transmembrane protein with EGF-like and two follistatin-like domains 1 (TMEFF1), mRNA
- 30 Homo sapiens nuclear receptor subfamily 4, group A, member 1, transcript variant 1, mRNA (cDNA clone MGC:9485 IMAGE:3921259), complete cds
- 31 Human LAG-1 mRNA
- 32 Homo sapiens cDNA FLJ39913 fis, clone SPLEN2018643, highly similar to PROBABLE G PROTEIN-COUPLED RECEPTOR API
- 33 Human JE gene encoding a monocyte secretory protein mRNA, complete cds
- 34 Homo sapiens mRNA for activation-inducible lymphocyte immunomediatory molecule AILIM, complete cds
- 35 Homo sapiens cDNA clone IMAGE:5175186, containing frame-shift errors
- 36 Homo sapiens ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast) (ELOVL6), mRNA
- 37 Homo sapiens BAC clone RP11-384E2 from 4, complete sequence
- 38 Homo sapiens chromosome 14 open reading frame 119, mRNA (cDNA clone MGC:74723 IMAGE:5532778), complete cds
- 39 Homo sapiens chemokine (C-C motif) ligand 8 (CCL8), mRNA
- 40 Human DNA sequence from clone RP5-1172N10 on chromosome Xp11.3-11.4 Contains the 3' end of the USP9X gene for X chromosome ubiquitin specific protease 9 (fat facets-like Drosophila), a novel gene and a CpG island, complete sequence
- 41 Homo sapiens transmembrane 4 L six family member 18 (TM4SF18), mRNA
- 42 Human DNA sequence from clone RP11-520F24 on chromosome 13 Contains an HNRPA1 (heterogenous nuclear ribonucleoprotein A1) pseudogene, an ELL-related RNA polymerase II, elongation factor (ELL2) pseudogene and a ribosomal protein L37 (RPL37) pseudogene, complete sequence

- 43 Homo sapiens clone 25081 tropomodulin mRNA sequence
- 44 Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
- 45 Homo sapiens podoplanin (PDPN), transcript variant 3, mRNA
- 46 Homo sapiens zinc finger protein 228 (ZNF228), mRNA
- 47 Human 18S ribosomal RNA
- 48 Homo sapiens cDNA clone MGC:88772 IMAGE:4765168, complete cds
- 49 Homo sapiens glutamate-cysteine ligase, catalytic subunit (GCLC), mRNA
- 50 Homo sapiens gene for p16/CDKN2A, complete cds
- 51 Homo sapiens ATPase, H⁺ transporting, lysosomal 42kDa, V1 subunit C isoform 2 (ATP6V1C2), mRNA
- 52 Homo sapiens interferon regulatory factor 4, mRNA (cDNA clone MGC:23069 IMAGE:4861223), complete cds
- 53 Homo sapiens ARV1 homolog (yeast) (ARV1), mRNA
- 54 Human DNA sequence from clone RP11-174I10 on chromosome 13 Contains the 3' end of the RB1 gene for retinoblastoma 1 (including osteosarcoma) and the 5' end of a novel gene, complete sequence
- 55 full-length cDNA clone CS0DJ010YA15 of T cells (Jurkat cell line) Cot 10-normalized of Homo sapiens (human)
- 56 Homo sapiens podoplanin (PDPN), transcript variant 1, mRNA
- 57 Homo sapiens glutamate-cysteine ligase, catalytic subunit (GCLC), mRNA
- 58 NA
- 59 Homo sapiens clone DNA44205 NLGN4 (UNQ365) mRNA, complete cds
- 60 Synthetic construct Homo sapiens clone FLH025847.01X apolipoprotein C-I (APOC1) mRNA, complete cds
- 61 Homo sapiens BAC clone RP11-197H3 from 2, complete sequence
- 62 Homo sapiens carnitine palmitoyltransferase 1A (liver) (CPT1A), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA
- 63 Homo sapiens hypoxia inducible factor 3, alpha subunit, mRNA (cDNA clone MGC:99497 IMAGE:6250259), complete cds
- 64 Homo sapiens claudin 10 (CLDN10), transcript variant 1, mRNA
- 65 Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
- 66 Homo sapiens 12q24 BAC RCPI11-443D10 (Roswell Park Cancer Institute Human BAC Library) complete sequence
- 67 Homo sapiens carnitine palmitoyltransferase 1A (liver), transcript variant 2, mRNA (cDNA clone MGC:1772 IMAGE:3352642), complete cds
- 68 Homo sapiens FK506 binding protein 5, mRNA (cDNA clone MGC:34489 IMAGE:4539929), complete cds
- 69 Homo sapiens NOVH protein mRNA, complete cds
- 70 Homo sapiens partial CPT1A gene for carnitine O-palmitoyltransferase 1, promoter region, CDS and splice variants a and b
- 71 Homo sapiens chromosome 19, cosmid R31341, complete sequence
- 72 Homo sapiens solute carrier family 26, member 7 (SLC26A7), transcript variant 1, mRNA
- 73 Mus musculus 17 days embryo stomach cDNA, RIKEN full-length enriched library, clone:I920056H18 product:NHP2-like protein 1 (High mobility group-like nuclear protein 2 homolog 1) ([U4/U6.U5] tri-snRNP 15.5 kDa protein) (OTK27) homolog [Homo sapiens], full insert sequence
- 74 Homo sapiens jun B proto-oncogene (JUNB), mRNA
- 75 Homo sapiens chromosome 8, clone RP11-734H6, complete sequence
- 76 Homo sapiens mRNA for Cdc7-related kinase, complete cds
- 77 Homo sapiens leucine rich repeat containing 17 (LRRC17), transcript variant 1, mRNA
- 78 Human DNA sequence from clone RP11-273F15 on chromosome 13 Contains a pseudogene similar to part of NADH dehydrogenase 3 (NADH dehydrogenase, subunit 3 (complex I)) (MTND3) and a non-metastatic cells 1, protein (NM23A) expressed in (NME1)(NM23, NM23-H1) pseudogene, complete sequence

- 79 Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA
- 80 dystrophin {5' region, alternatively spliced} [human, cerebellar Purkinje neurons, mRNA Partial, 320 nt]
- 81 Human DNA sequence from clone RP11-45J1 on chromosome X Contains a prefoldin 4 (PFDN4) pseudogene, the 5' end of a novel gene and a CpG island, complete sequence
- 82 Homo sapiens chromosome 8, clone CTD-3071K10, complete sequence
- 83 Macaca fascicularis brain cDNA, clone: QccE-21970, similar to human aldolase C, fructose-bisphosphate (ALDOC), mRNA, RefSeq: NM_005165.1
- 84 Homo sapiens chromosome 17, clone 193h18, complete sequence
- 85 Homo sapiens BAC clone RP11-1191J2 from 4, complete sequence
- 86 Homo sapiens full open reading frame cDNA clone RZPDo834A0126D for gene SAA1, serum amyloid A1; complete cds, without stopcodon
- 87 TPA: Homo sapiens chromosome 17 proximal SMS-REP low-copy repeat, genomic sequence
- 88 Homo sapiens diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) (DTR) gene, complete cds
- 89 Homo sapiens BTB (POZ) domain containing 11 (BTBD11), transcript variant 3, mRNA
- 90 Homo sapiens regulator of G-protein signalling 1, mRNA (cDNA clone MGC:9198 IMAGE:3916789), complete cds
- 91 Homo sapiens nudE nuclear distribution gene E homolog 1 (A. nidulans), mRNA (cDNA clone MGC:1075 IMAGE:3140369), complete cds
- 92 Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA
- 93 Homo sapiens chromosome 5 clone RP11-1152B5, complete sequence
- 94 Homo sapiens serum-inducible kinase mRNA, complete cds
- 95 Homo sapiens mRNA; cDNA DKFZp313N1532 (from clone DKFZp313N1532)
- 96 Homo sapiens leucine rich repeat containing 39 (LRRC39), mRNA
- 97 Homo sapiens lamin B1 (LMNB1), mRNA
- 98 Homo sapiens reelin (RELN), transcript variant 2, mRNA
- 99 Homo sapiens cDNA FLJ41271 fis, clone BRAMY2036396
- 100 Human DNA sequence from clone RP11-134P9 on chromosome 1 Contains the 3' end of a novel gene, a novel gene, the BTG2 gene for BTG family, member 2 and a CpG island, complete sequence
- 101 Human DNA sequence from clone RP11-145E8 on chromosome 10 Contains a novel gene (KIAA1074), the 3' end of the YME1L1 gene for YME1-like 1 (S. cerevisiae) and a CpG island, complete sequence
- 102 Macaca fascicularis testis cDNA clone: QtsA-13105, similar to human armadillo repeat containing 2 (ARMC2), mRNA, RefSeq: NM_032131.3
- 103 Homo sapiens chromosome 17, clone CTD-3193K9, complete sequence
- 104 Human transcription factor ETR101 mRNA, complete cds
- 105 Human DNA sequence from clone CTA-343C1 on chromosome 22, complete sequence
- 106 full-length cDNA clone CS0DI069YJ22 of Placenta Cot 25-normalized of Homo sapiens (human)
- 107 Human DNA sequence from clone RP4-727I10 on chromosome 20 Contains a novel gene, ESTs, STSs and GSSs, complete sequence
- 108 Homo sapiens CC chemokine ligand 4L2f (CCL4L) mRNA, CCL4L-2 allele, complete cds, alternatively spliced
- 109 Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian), mRNA (cDNA clone MGC:126110 IMAGE:40033200), complete cds
- 110 Homo sapiens 3 BAC RP11-211G3 (Roswell Park Cancer Institute Human BAC Library) complete sequence
- 111 Human MAP kinase kinase MEK6 (MEK6) mRNA, complete cds
- 112 Human DNA sequence from clone RP11-182I10 on chromosome 1 Contains the 5' end of the JAK1 gene for anus kinase 1 (a protein tyrosine kinase), a NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4 9kDa (NDUFA4) pseudogene, a SIPL protein (SIPL)

- pseudogene, part of a novel gene, a solute carrier family 2 (facilitated glucose transporter) member 14 (SLC2A14) pseudogene and a CpG island, complete sequence
- 113 Homo sapiens 12 BAC RP4-605O3 (Roswell Park Cancer Institute Human BAC Library) complete sequence
- 114 Homo sapiens polo-like kinase 2 (Drosophila) (PLK2), mRNA
- 115 Human DNA sequence from clone RP11-497F24 on chromosome 6, complete sequence
- 116 Homo sapiens cDNA FLJ36603 fis, clone TRACH2015180, highly similar to Frizzled protein-2
- 117 Homo sapiens BAC clone RP11-216H12 from 4, complete sequence
- 118 Homo sapiens HLA-C gene for MHC class I antigen, CW*15021 allele, exons 1-8
- 119 Homo sapiens L-pipecolic acid oxidase (LPIPOX) mRNA, complete cds
- 120 Homo sapiens mRNA; cDNA DKFZp686C24224 (from clone DKFZp686C24224)
- 121 Synthetic construct Homo sapiens lipocalin 2 (oncogene 24p3) mRNA, partial cds
- 122 PREDICTED: Homo sapiens hypothetical protein FLJ10707 (FLJ10707), mRNA
- 123 Homo sapiens claudin 4, mRNA (cDNA clone MGC:1778 IMAGE:3349211), complete cds
- 124 Homo sapiens cDNA: FLJ23378 fis, clone HEP16248
- 125 Homo sapiens gp250 precursor, mRNA, complete cds
- 126 Homo sapiens fem-1 homolog b (C. elegans), mRNA (cDNA clone MGC:19792 IMAGE:3840453), complete cds
- 127 Human XIST gene, poly purine-pyrimidine repeat region
- 128 Homo sapiens aminoacylase 1-like 2, mRNA (cDNA clone IMAGE:5262663), partial cds
- 129 Homo sapiens hypothetical protein FLJ20920, mRNA (cDNA clone MGC:19867 IMAGE:4577089), complete cds
- 130 Homo sapiens genomic DNA, chromosome 18 clone:RP11-883A18, complete sequence
- 131 Homo sapiens hypothetical protein LOC392636, mRNA (cDNA clone MGC:131748 IMAGE:6152531), complete cds
- 132 Homo sapiens partial BV03S1J2.2 gene for T-cell receptor beta, variable region
- 133 Homo sapiens ligand effect modulator-6 (LEM6) mRNA, complete cds
- 134 PREDICTED: Homo sapiens similar to LIM and senescent cell antigen-like domains 1 (LOC440895), mRNA
- 135 Homo sapiens chromosome 16 clone CTA-237H1, complete sequence
- 136 Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type I, beta (PIP5K1B), transcript variant 2, mRNA
- 137 Homo sapiens dihydrodiol dehydrogenase (dimeric) (DHDH), mRNA
- 138 Homo sapiens BAC clone RP11-433O3 from 4, complete sequence
- 139 Human glucose-6-phosphatase mRNA, complete cds
- 140 human full-length cDNA clone CS0DD006YL02 of Neuroblastoma of Homo sapiens (human)
- 141 Homo sapiens creatine kinase, mitochondrial 1B (CKMT1B), nuclear gene encoding mitochondrial protein, mRNA
- 142 Homo sapiens cDNA FLJ45560 fis, clone BRTHA3003417
- 143 Human DNA sequence from clone RP11-138B7 on chromosome 20q13.12 Contains the 3' end of the L3MBTL gene for l(3)mbt-like (Drosophila), the SGK2 gene for serum/glucocorticoid regulated kinase 2, the 5' end of the C20orf9 gene (NGD5, CGI-53), an HSPC194 pseudogene and a CpG island, complete sequence
- 144 Homo sapiens chromosome 15, clone RP11-253M7, complete sequence
- 145 Homo sapiens C1q-C mRNA, complete cds
- 146 Homo sapiens ARV1 homolog (yeast) (ARV1), mRNA
- 147 Mouse DNA sequence from clone RP23-215H18 on chromosome 11 Contains a novel gene and the 3' end of a gene that is a possible ortholog of human dynein axonemal heavy polypeptide 9 (DNAH9), complete sequence
- 148 Homo sapiens mRNA; cDNA DKFZp781J0852 (from clone DKFZp781J0852)
- 149 Homo sapiens full open reading frame cDNA clone RZPDo834F0920D for gene PAWR, PRKC, apoptosis, WT1, regulator; complete cds, incl. stopcodon

- 150 Homo sapiens complement component 1, q subcomponent, alpha polypeptide, mRNA (cDNA clone MGC:29490 IMAGE:4850418), complete cds
- 151 NA
- 152 Homo sapiens cDNA FLJ16122 fis, clone BLADE2008995
- 153 Homo sapiens chromosome 20 open reading frame 155 (C20orf155), mRNA
- 154 Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
- 155 Homo sapiens chromosome 4 clone RP11-603B8, complete sequence
- 156 NA
- 157 Homo sapiens protein phosphatase 2C, magnesium-dependent, catalytic subunit, mRNA (cDNA clone IMAGE:6158636), partial cds
- 158 full-length cDNA clone CS0DI070YL04 of Placenta Cot 25-normalized of Homo sapiens (human)
- 159 Human xanthine dehydrogenase (XDH) mRNA, complete cds
- 160 Homo sapiens mRNA; cDNA DKFZp779B086 (from clone DKFZp779B086)
- 161 full-length cDNA clone CS0DI068YG02 of Placenta Cot 25-normalized of Homo sapiens (human)
- 162 Homo sapiens sulfotransferase family, cytosolic, 1B, member 1 (SULT1B1), mRNA
- 163 Human DNA sequence from clone RP11-311H10 on chromosome 9 Contains the 3' end of the NFX1 gene for X-box binding nuclear transcription factor 1, the AQP7 and AQP3 genes for aquaporin 7 and 3, a novel gene, the gene for nucleolar RNA-associated protein alpha, beta and gamma and a CpG island, complete sequence
- 164 Human DNA sequence from clone RP3-340B19 on chromosome 6p21.2-21.3 Contains the TULP1 gene for tubby like protein 1, a novel gene, ribosomal protein S15A (RPS15A) and L36 (RPL36) pseudogenes, the 3' end of the FKBP5 gene for FK506 binding protein 5 (FKBP51) and two CpG islands, complete sequence
- 165 Homo sapiens cDNA FLJ30638 fis, clone CTONG2002721, weakly similar to VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13
- 166 Homo sapiens cytochrome P450, family 26, subfamily B, polypeptide 1 (CYP26B1), mRNA
- 167 Homo sapiens BAC clone RP11-678H22 from 4, complete sequence
- 168 Homo sapiens chromosome 11, clone RP13-25N22, complete sequence
- 169 Human DNA sequence from clone RP1-172H20 on chromosome 20q12-13.12 Contains the PI3 gene for skin-derived protease inhibitor 3 (SKALP) the SEMG1 gene for semenogelin I, the SEMG2 gene for semenogelin II, complete sequence
- 170 Homo sapiens cystatin 9-like (mouse), mRNA (cDNA clone MGC:34724 IMAGE:5163974), complete cds
- 171 NA
- 172 Homo sapiens dystonin (DST), transcript variant 1eA, mRNA
- 173 full-length cDNA clone CS0DL009YM20 of B cells (Ramos cell line) Cot 25-normalized of Homo sapiens (human)
- 174 Homo sapiens arrestin domain containing 2, transcript variant 1, mRNA (cDNA clone MGC:26574 IMAGE:4817429), complete cds
- 175 Homo sapiens cDNA FLJ14958 fis, clone PLACE4000052, highly similar to Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA
- 176 Homo sapiens zinc finger and BTB domain containing 16, transcript variant 2, mRNA (cDNA clone MGC:24908 IMAGE:4944546), complete cds
- 177 Homo sapiens chromosome 9 open reading frame 72, mRNA (cDNA clone MGC:86985 IMAGE:5298741), complete cds
- 178 Homo sapiens mitogen-activated protein kinase kinase kinase 15 (MAP3K15), mRNA
- 179 Homo sapiens laryngeal carcinoma related protein 1 mRNA, complete cds
- 180 Homo sapiens tetratricopeptide repeat domain 25, mRNA (cDNA clone IMAGE:4831078), complete cds
- 181 Homo sapiens mRNA for laminin alpha 2 subunit precursor variant protein
- 182 Homo sapiens protein phosphatase 2C, magnesium-dependent, catalytic subunit, mRNA (cDNA clone IMAGE:6158636), partial cds

- 183 Homo sapiens BAC clone RP11-484O9 from 2, complete sequence
- 184 NA
- 185 Homo sapiens asporin (LRR class 1) (ASPN), mRNA
- 186 Homo sapiens clone DNA34392 ASPN (UNQ215) mRNA, complete cds
- 187 Human DNA sequence from clone RP11-386J22 on chromosome 9 Contains the SMC5L1 gene for SMC5 structural maintenance of chromosomes 5-like 1 (yeast) (SMC5, KIAA0594), the BTEB1 gene for basic transcription element binding protein 1 (BTEB, KLF9) and three CpG islands, complete sequence
- 188 Homo sapiens solute carrier family 27 (fatty acid transporter), member 6 (SLC27A6), transcript variant 2, mRNA
- 189 Homo sapiens chromosome 3 clone RP11-189A1, complete sequence
- 190 Homo sapiens dehydrogenase/reductase (SDR family) member 9 (DHRS9), transcript variant 2, mRNA
- 191 Homo sapiens truncated epidermal growth factor (beta-urogastrone) (EGF) gene, complete cds
- 192 Homo sapiens cDNA clone MGC:88772 IMAGE:4765168, complete cds
- 193 Homo sapiens PAC clone RP1-85D24 from Y, complete sequence
- 194 Homo sapiens complement component 1, q subcomponent, beta polypeptide, mRNA (cDNA clone MGC:17227 IMAGE:4212848), complete cds
- 195 Homo sapiens chromosome 3 clone RP11-944L7, complete sequence
- 196 Homo sapiens SH3 domain protein D19 (SH3D19), mRNA
- 197 Homo sapiens mRNA; cDNA DKFZp686E15208 (from clone DKFZp686E15208)
- 198 Macaca fascicularis mRNA, clone QnpA-12979: similar to Homo sapiens neuroepithelial cell transforming gene 1 (NET1), mRNA, NM_005863.2
- 199 Human DNA sequence from clone RP5-1025A1 on chromosome 20p11.21-11.23 Contains the 5' part of the ACAS2L gene for acetyl-Coenzyme A synthetase (AMP forming)-like, the VSX1 gene for visual system homeobox 1 (zebrafish) homolog (CHX10-like), variants L1 and S1 and four CpG islands, complete sequence
- 200 Homo sapiens chromosome 11, clone RP11-68C8, complete sequence
- 201 Homo sapiens tocopherol (alpha) transfer protein (ataxia (Friedreich-like) with vitamin E deficiency), mRNA (cDNA clone IMAGE:4593015), partial cds
- 202 Homo sapiens cDNA FLJ32190 fis, clone PLACE6002102
- 203 Homo sapiens CCBL1 gene, last two exons
- 204 Homo sapiens cysteine conjugate-beta lyase; cytoplasmic (glutamine transaminase K, kyneurenine aminotransferase) (CCBL1), mRNA
- 205 Homo sapiens triggering receptor expressed on myeloid cells 2 (TREM2), mRNA
- 206 Homo sapiens chromosome 21 open reading frame 24 isoform 7 (C21orf24) mRNA, complete cds
- 207 Homo sapiens mRNA; cDNA DKFZp779B086 (from clone DKFZp779B086)
- 208 Human DNA sequence from clone RP11-386J22 on chromosome 9 Contains the SMC5L1 gene for SMC5 structural maintenance of chromosomes 5-like 1 (yeast) (SMC5, KIAA0594), the BTEB1 gene for basic transcription element binding protein 1 (BTEB, KLF9) and three CpG islands, complete sequence
- 209 Homo sapiens BAC clone RP11-642E20 from 4, complete sequence
- 210 Homo sapiens leucine rich repeat containing 47 (LRRC47), mRNA
- 211 Homo sapiens translation initiation factor 2 (MTIF2) gene, exons 6 through 9; nuclear genes for mitochondrial products
- 212 Homo sapiens insulin receptor, mRNA (cDNA clone IMAGE:4823710), partial cds
- 213 Homo sapiens ring finger protein 150 (RNF150), mRNA
- 214 Homo sapiens chromosome 5 clone CTC-361G14, complete sequence
- 215 Homo sapiens matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase), mRNA (cDNA clone MGC:2313 IMAGE:3161383), complete cds
- 216 Homo sapiens Zic family member 3 heterotaxy 1 (odd-paired homolog, Drosophila) (ZIC3), mRNA
- 217 Homo sapiens BAC clone RP11-395A12 from 2, complete sequence

- 218 Homo sapiens genomic DNA, chromosome 18 clone:RP11-815J4, complete sequence
- 219 Homo sapiens protein upregulated in metastatic prostate cancer mRNA, complete cds
- 220 Homo sapiens Kruppel-like factor 5 (intestinal), mRNA (cDNA clone MGC:52153 IMAGE:5454169), complete cds
- 221 full-length cDNA clone CS0DK004YO15 of HeLa cells Cot 25-normalized of Homo sapiens (human)
- 222 Homo sapiens interferon-related developmental regulator 1 (IFRD1), transcript variant 1, mRNA
- 223 full-length cDNA clone CS0DK010YA19 of HeLa cells Cot 25-normalized of Homo sapiens (human)
- 224 Homo sapiens homeodomain-only protein, mRNA (cDNA clone MGC:20820 IMAGE:4335211), complete cds
- 225 Human DNA sequence from clone RP11-27J8 on chromosome 9 Contains the gene for interferon kappa precursor (IFNK), the 5' UTR of a novel gene (FLJ13204), a novel gene, includes FLJ25077 and FLJ11109 (MGC23980) and 2 CpG islands, complete sequence
- 226 Homo sapiens coagulation factor II receptor-like 2 (F2RL2) gene, complete cds
- 227 Human DNA sequence from clone RP4-753D4 on chromosome 20q12 Contains part of the PTPRT gene for protein tyrosine phosphatase receptor type T and a novel gene, complete sequence
- 228 Human chromosome 14 DNA sequence BAC R-131H24 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence
- 229 Homo sapiens cysteine conjugate-beta lyase; cytoplasmic (glutamine transaminase K, kyneurenine aminotransferase) (CCBL1), mRNA
- 230 NA
- 231 Homo sapiens alpha-2-macroglobulin, mRNA (cDNA clone MGC:47683 IMAGE:6056126), complete cds
- 232 Homo sapiens phospholipid transfer protein, transcript variant 1, mRNA (cDNA clone MGC:30183 IMAGE:4992839), complete cds
- 233 Homo sapiens WD repeat domain 66 (WDR66), mRNA
- 234 Homo sapiens mRNA for alanine:glyoxylate aminotransferase 2 homolog 1, splice form 1 (AGXT2L1 gene)
- 235 Homo sapiens immunoglobulin alpha 2m(1) heavy chain constant region gene, partial cds
- 236 NA
- 237 Homo sapiens BAC clone RP11-348G16 from 2, complete sequence
- 238 Homo sapiens erbb2 interacting protein (ERBB2IP), transcript variant 2, mRNA
- 239 Homo sapiens mRNA for alanine:glyoxylate aminotransferase 2 homolog 1, splice form 1 (AGXT2L1 gene)
- 240 Homo sapiens phospholipase C, delta 4 (PLCD4), mRNA
- 241 Homo sapiens cDNA FLJ39109 fis, clone NTONG2005137, highly similar to [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 4, MITOCHONDRIAL PRECURSOR (EC 2.7.1.99)
- 242 Homo sapiens mRNA; cDNA DKFZp586M2121 (from clone DKFZp586M2121)
- 243 Human DNA sequence from clone RP11-98I9 on chromosome 6 Contains the gene for hexaprenyldihydroxybenzoate methyltransferase, mitochondrial precursor (COQ3), the gene for SR rich protein (FLJ14992), the USP45 gene for ubiquitin specific protease 45, the 3' end of the gene for a novel protein similar to ubiquitin carboxyl-terminal hydrolase 16 (EC 3.1.2.15) and 2 CpG islands, complete sequence
- 244 Homo sapiens HIF-3A mRNA for hypoxia-inducible factor-3 alpha, complete cds
- 245 Homo sapiens BAC clone CTB-118E13 from 7, complete sequence
- 246 Human DNA sequence from clone RP11-435O5 on chromosome 9q22.1-22.33 Contains the PTCH gene for patched homolog, a novel gene, the gene for a novel protein similar to a metallothionein protein (MT1) and three CpG islands, complete sequence
- 247 Homo sapiens mRNA; cDNA DKFZp313I2220 (from clone DKFZp313I2220); complete cds
- 248 Homo sapiens WNK lysine deficient protein kinase 3 (WNK3), transcript variant 1, mRNA

- 249 Homo sapiens immunoglobulin alpha 2m(1) heavy chain constant region gene, partial cds
- 250 Macaca fascicularis testis cDNA clone: QtsA-11169, similar to human hypothetical protein C9orf93, mRNA, NM_173550.1
- 251 Macaca fascicularis brain cDNA, clone: QflA-10289, similar to human TU3A protein (TU3A), mRNA, RefSeq: NM_007177.1
- 252 Homo sapiens centrosome and spindle pole associated protein 1 (CSPP1), mRNA
- 253 Homo sapiens osteomodulin (OMD), mRNA
- 254 Homo sapiens 12 BAC RP11-424C20 (Roswell Park Cancer Institute Human BAC Library) complete sequence
- 255 Homo sapiens family with sequence similarity 59, member A (FAM59A), mRNA
- 256 Homo sapiens ps20 WAP-type four-disulfide core domain protein mRNA, complete cds
- 257 Homo sapiens chromosome 5 clone CTC-428I11, complete sequence
- 258 Homo sapiens chromosome 5 clone CTC-229P9, complete sequence
- 259 Homo sapiens chromosome 8, clone RP13-895A16, complete sequence
- 260 Human chromosome 14 DNA sequence BAC R-442G21 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence
- 261 Homo sapiens lung type-I cell membrane-associated protein hT1a-2 (hT1a-2) mRNA, complete cds
- 262 NA
- 263 Human DNA sequence from clone RP11-90M2 on chromosome 13 Contains gene FLJ10956, the gene for HSPC126 protein (DRIP36), a novel gene similar to polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa (POLR2K), a novel gene and two CpG islands, complete sequence
- 264 Homo sapiens ATPase, H⁺ transporting, lysosomal 42kDa, V1 subunit C isoform 2 (ATP6V1C2), mRNA
- 265 Homo sapiens aminopeptidase puromycin sensitive (NPEPPS), mRNA
- 266 PREDICTED: Homo sapiens similar to dJ22I17.2 (novel protein with EGF-like and laminin G domains) (LOC442228), mRNA
- 267 Homo sapiens chromosome 5 clone CTC-575N7, complete sequence
- 268 Homo sapiens BAC clone RP11-308K2 from 4, complete sequence
- 269 Homo sapiens chromosome 5 clone RP11-270H9, complete sequence
- 270 ADMLX=putative adhesion molecule [human, mRNA, 4121 nt, segment 2 of 2]
- 271 Homo sapiens coiled-coil domain containing 18, mRNA (cDNA clone IMAGE:4686590), partial cds
- 272 Homo sapiens, clone RP11-44B13, complete sequence
- 273 Macaca fascicularis testis cDNA clone: QtsA-14119, similar to human lipin 1 (LPIN1), mRNA, RefSeq: NM_145693.1
- 274 Bos taurus phytanoyl-CoA hydroxylase [human : Refsum disease], mRNA (cDNA clone MGC:127428 IMAGE:7949271), complete cds
- 275 Human DNA sequence from clone RP5-859D4 on chromosome 20p12.1-13 Contains the BMP2 gene for bone morphogenetic protein 2, a novel gene and a CpG island, complete sequence
- 276 Human DNA sequence from clone RP5-859D4 on chromosome 20p12.1-13 Contains the BMP2 gene for bone morphogenetic protein 2, a novel gene and a CpG island, complete sequence
- 277 Human DNA sequence from clone RP11-386J22 on chromosome 9 Contains the SMC5L1 gene for SMC5 structural maintenance of chromosomes 5-like 1 (yeast) (SMC5, KIAA0594), the BTEB1 gene for basic transcription element binding protein 1 (BTEB, KLF9) and three CpG islands, complete sequence
- 278 Homo sapiens chromosome 6 open reading frame 81 (C6orf81), mRNA
- 279 Human DNA sequence from clone RP11-401F24 on chromosome 10 Contains gene FLJ20909, the gene for a novel protein (MGC35403), a novel gene (LOC219731), the 3' end of the UPF2 gene for UPF2 regulator of nonsense transcripts homolog (yeast) (FLJ38872) and four CpG islands, complete sequence

- 280 Homo sapiens coagulation factor II receptor-like 2 (F2RL2) gene, complete cds
- 281 Homo sapiens WD repeat domain 66, mRNA (cDNA clone MGC:33630 IMAGE:4826893), complete cds
- 282 Macaca fascicularis testis cDNA, clone: QtsA-18294, similar to human interferon-related developmental regulator 1 (IFRD1), mRNA, RefSeq: NM_001550.1
- 283 PREDICTED: Homo sapiens zinc finger protein 283 (ZNF283), mRNA
- 284 Human DNA sequence from clone RP1-238O23 on chromosome 6 Contains part of the a novel gene, the gene for triggering receptor expressed on myeloid cells 2 (TREM2), a novel gene, part of a novel gene, a pseudogene similar to soluble adenylyl cyclase (SAC),, complete sequence
- 285 full-length cDNA clone CS0DK009YI05 of HeLa cells Cot 25-normalized of Homo sapiens (human)
- 286 Homo sapiens cysteine conjugate-beta lyase; cytoplasmic (glutamine transaminase K, kyneurenine aminotransferase) (CCBL1), mRNA
- 287 Homo sapiens chromosome 3 open reading frame 14, mRNA (cDNA clone MGC:22227 IMAGE:4307022), complete cds
- 288 Homo sapiens chromosome 15 clone CTD-2270N23 map 15q21, complete sequence
- 289 Homo sapiens mRNA; cDNA DKFZp667H2312 (from clone DKFZp667H2312)
- 290 Homo sapiens fibronectin type III domain containing 1 (FNDC1), mRNA
- 291 Homo sapiens chromosome 16 clone RP11-486L19, complete sequence
- 292 Homo sapiens BAC clone RP11-178D14 from 2, complete sequence
- 293 full-length cDNA clone CS0DN005YJ09 of Adult brain of Homo sapiens (human)
- 294 Homo sapiens PAC clone RP5-839O24 from 7, complete sequence
- 295 Homo sapiens 3 BAC RP11-364F11 (Roswell Park Cancer Institute Human BAC Library) complete sequence

Example 2

Determining the Effect of Various Substances or Ingredients on Gene Expression in Canine Cell Lines

[00129] Affymetrix canine gene chips Canine-1 and Canine-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 6. 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.

[00130] 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.

[00131] 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.

[00132] 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 7. Table 7 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.

[00133] Based upon the physiological condition of the canines (a diagnosis as fat) and a comparison of the information from the Tables 1-7, i.e, noting genes that are influenced by a test substance or ingredient and are also differentially expressed in fat canines compared to lean canines, a nutritional formula useful for selecting and preparing a food composition for fat 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 fat animals compared to lean animals. Such regulation will cause the modulation of the amount of adipose tissue on the animal and, therefore, in one embodiment, promote a shift to a desirable or normal (more lean) status and promote better health and wellness of the animal.

Table 6: 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	0.015 mg/ml EPA & 0.010	0.030 mg/ml EPA & 0.02	ETOH
Combo 1.5:1	mg/ml DHA (total is 0.025	mg/ml DHA (total is 0.050	
ratio (like in fish	mg/ml)	mg/ml)	
oil)			
Alpha linolenic	0.05 mg/ml (50 micro g/ml)	0.1 mg/ml (100 micro g/ml)	ETOH
acid			
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	0.02 mg/ml (20 micro g/ml)	0.1 mg/ml (100 micro g/ml)	MEOH
Linoleic acid			

**Table 7: Expression Profiling Results From Canine Cell Lines
in the Presence of Listed Ingredients**

Column	1	2	3	4	5
	DHA	1582387_at	DOW	Canis familiaris type I iodothyronine	AC027016
			N	deiodinase (dio 1) mRNA, complete cds	
	DHA	1582824_at	UP	PREDICTED: Canis familiaris carnitine	BC000185
				palmitoyl transferase I isoform (CPT1),	
				mRNA	
	DHA	1584133_at	UP	PREDICTED: Canis familiaris similar to	BC038344
				dynein, cytoplasmic, heavy polypeptide	
				2 (LOC479461), mRNA	
	DHA	1584742_at	UP	Human DNA sequence from clone	AL591206
				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)	
	DHA	1584951_at	UP	PREDICTED: Canis familiaris similar to	CR605429
				Adipophilin (Adipose differentiation-	
				related protein) (ADRP) (LOC474720),	
				mRNA	
	DHA	1585355_at	UP	PREDICTED: Canis familiaris similar to	CR597463
				Adipophilin (Adipose differentiation-	
				related protein) (ADRP) (LOC474720),	
				mRNA	

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
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
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	AB208911

			IMAGE:4861744), complete cds	
DHA	1593831_at	DOW N	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	DOW N	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	DOW N	Homo sapiens hypothetical protein LOC92558 (LOC92558), mRNA	NM_207311
DHA	1598607_at	DOW N	PREDICTED: Canis familiaris similar to Thioredoxin domain containing protein 6 (Thioredoxin-like protein 2) (Txl-2) (LOC485685), mRNA	AC099518
DHA	1598932_at	DOW N	PREDICTED: Canis familiaris similar to SAP90/PSD-95 associated protein 2 (LOC488556), mRNA	AL354836
DHA	1599339_at	DOW N	Canis familiaris clone RP81-117B1, complete sequence	NA
DHA	1599453_at	DOW N	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	DOW N	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	DOW N	Zebrafish DNA sequence from clone DKEYP-75A7 in linkage group 21, complete sequence	AL590621
DHA	1603771_at	DOW N	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	DOW N	Homo sapiens, Similar to secreted frizzled-related protein 4, clone IMAGE:4828181, mRNA	AC018634
EPA	1583403_at	UP	Sus scrofa carnitine palmitoyltransferase	AK172798

EPA	1584742_at	UP	I mRNA, nuclear gene encoding mitochondrial protein, complete cds 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
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
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	DOW N	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	DOW N	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	DOW N	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 abundant protein	AC113382
EPA	1596553_s_at	DOW N	Homo sapiens chromosome 16 open reading frame 55 (C16orf55), mRNA	AK056168
EPA	1597390_at	DOW N	PREDICTED: Canis familiaris similar to Ataxin-10 (Spinocerebellar ataxia type 10 protein) (Brain protein E46 homolog) (LOC474467), mRNA	AY400068
EPA	1597801_at	DOW N	Homo sapiens, clone IMAGE:4822875, mRNA	AL442128
EPA	1597802_at	DOW N	Mus musculus BAC clone RP23-451111 from 12, complete sequence	AL078583
EPA	1598585_at	DOW N	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds	AC011306
EPA	1599557_at	DOW N	PREDICTED: Canis familiaris similar to hypothetical protein MGC12103 (LOC481489), mRNA	AY414168
EPA	1599565_at	DOW N	Human DNA sequence from clone RP4-615P17 on chromosome 1p13-14.3, complete sequence	AL139175
EPA	1599601_s_at	DOW N	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	DOW N	PREDICTED: Canis familiaris LOC479025 (LOC479025), mRNA	XM_372592
EPA	1602471_at	DOW N	Homo sapiens cDNA clone IMAGE:4797645, partial cds	AC073120
EPA	1603225_at	UP	Haemonchus contortus microsatellite Hcms51 sequence	AC008429
EPA	1603875_at	DOW N	Homo sapiens cDNA FLJ33460 fis, clone BRAMY2000653, highly similar to Homo sapiens tousled-like kinase 1 (TLK1) mRNA	AC010092
EPA	1604439_at	DOW	Homo sapiens mRNA; cDNA	AL137346

		N	DKFZp761M0111 (from clone DKFZp761M0111)	
EPA	1604600_at	DOW N	Homo sapiens mRNA; cDNA DKFZp686K122 (from clone DKFZp686K122)	AC010733
EPA	1605028_at	DOW N	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	DOW N	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 protein, complete cds	AK172798
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	DOW N	PREDICTED: Canis familiaris similar to KIAA2025 protein (LOC480065), mRNA	AL121983
DHA/ EPA	1585339_at	DOW N	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	DOW N	Homo sapiens chromosome 11, clone RP11-348A11, complete sequence	AC131263
DHA/ EPA	1586287_at	DOW N	Bos taurus mRNA for transcription factor COUP-TFI (COUP-TFI gene)	AC106818
DHA/ EPA	1586614_at	DOW	PREDICTED: Canis familiaris similar to	BC037320

EPA		N	F-box protein SEL10 (LOC475465), mRNA	
DHA/ EPA	1586695_at	DOW N	Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), transcript variant 2, mRNA	BX161515
DHA/ EPA	1587254_at	DOW N	PREDICTED: Canis familiaris janus kinase 1 (JAK1), mRNA	AC008785
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	DOW N	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	DOW N	Homo sapiens solute carrier family 34 (sodium phosphate), member 1, mRNA (cDNA clone IMAGE:5182821), with apparent retained intron	AC145098
DHA/ EPA	1590942_at	DOW N	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	DOW N	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	DOW N	PREDICTED: Canis familiaris similar to vimentin (LOC477991), mRNA	AY891766
DHA/ EPA	1592160_at	DOW N	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 1.1 (KLF11), mRNA	BC063286
DHA/ EPA	1593855_at	DOW N	Felis catus clone RP86-117J4, complete sequence	AL353710
DHA/ EPA	1593993_at	DOW N	Pan troglodytes BAC clone RP43-75I2 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	DOW N	PREDICTED: Canis familiaris similar to methylcrotonoyl-Coenzyme A	BC014897

			carboxylase 2 (beta) (LOC478091), mRNA	
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 RP11-813L8, complete sequence	AC090133
DHA/ EPA	1595083_at	DOW N	PREDICTED: Canis familiaris similar to hypothetical protein MGC18257 (LOC474943), mRNA	AK055530
DHA/ EPA	1595280_at	DOW N	Homo sapiens mRNA; cDNA DKFZp686N1929 (from clone DKFZp686N1929)	AL355298
DHA/ EPA	1595481_at	DOW N	PREDICTED: Canis familiaris LOC478639 (LOC478639), mRNA	NM_002492
DHA/ EPA	1595587_at	DOW N	PREDICTED: Canis familiaris similar to copine VIII (LOC477646), mRNA	BC048260
DHA/ EPA	1595673_at	DOW N	PREDICTED: Canis familiaris similar to SDA1 domain containing 1 (LOC478431), mRNA	BC048351
DHA/ EPA	1596041_at	DOW N	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	DOW N	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	DOW N	PREDICTED: Canis familiaris similar to ORF2 (LOC475183), mRNA	NA
DHA/ EPA	1599950_at	DOW N	PREDICTED: Canis familiaris similar to male-enhanced antigen - bovine (LOC474906), mRNA	AL136304
DHA/ EPA	1600310_at	DOW N	PREDICTED: Canis familiaris similar to piggyBac transposable element derived 1 (LOC488322), mRNA	AK223446

DHA/ EPA	1600683_at	DOW N	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	DOW N	Homo sapiens lactamase, beta 2, mRNA (cDNA clone IMAGE:3452575)	AC022731
DHA/ EPA	1602033_at	DOW N	PREDICTED: Bos taurus similar to G protein-coupled receptor 23 (LOC539738), mRNA	AL445467
DHA/ EPA	1602162_at	DOW N	Homo sapiens BAC clone RP11-489P15 from 2, complete sequence	AC093850
DHA/ EPA	1603521_at	DOW N	Homo sapiens cDNA FLJ33134 fis, clone UMVEN2000453, weakly similar to Mus musculus fetal globin inducing factor mRNA	BC017798
DHA/ EPA	1603534_at	DOW N	PREDICTED: Canis familiaris similar to protein tyrosine phosphatase, receptor type, Q isoform 1 precursor (LOC482581), mRNA	AL592064
DHA/ EPA	1603559_s_ at	DOW N	PREDICTED: Canis familiaris similar to neural activity-related ring finger protein (LOC475470), mRNA	AY413985
DHA/ EPA	1603658_s_ at	UP	Homo sapiens mRNA; cDNA DKFZp451E012 (from clone DKFZp451E012); complete cds	AL834247
DHA/ EPA	1603674_at	DOW N	Homo sapiens cDNA FLJ13648 fis, clone PLACE1011340, weakly similar to Homo sapiens IDN3-B mRNA	AK023710
DHA/ EPA	1605317_at	DOW N	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	DOW N	Homo sapiens mRNA; cDNA DKFZp451J152 (from clone DKFZp451J152); complete cds	AK097112
DHA/ EPA	1605935_at	DOW N	Mus musculus mRNA for NFI-B protein, complete cds	AK024964
ALA	1582455_at	DOW N	Canis familiaris type I collagen pre-pro- alpha1(I) chain (COL1A1) mRNA, complete cds	AB209597
ALA	1584508_at	DOW N	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	CR605429

			Adipophilin (Adipose differentiation-related protein) (ADRP) (LOC474720), mRNA	
ALA	1585266_at	DOW	PREDICTED: Canis familiaris similar to	BC005053
		N	FLJ20859 protein (LOC475396), mRNA	
ALA	1585355_at	UP	PREDICTED: Canis familiaris similar to	CR597463
			Adipophilin (Adipose differentiation-related protein) (ADRP) (LOC474720), mRNA	
ALA	1585515_at	UP	PREDICTED: Canis familiaris	AF303134
			LOC476210 (LOC476210), mRNA	
ALA	1585553_at	DOW	PREDICTED: Canis familiaris similar to	BC032361
		N	tenascin-N (LOC490335), mRNA	
ALA	1586185_at	UP	PREDICTED: Canis familiaris similar to	AC093611
			hypothetical protein LOC90637 (LOC480809), mRNA	
ALA	1587312_at	UP	PREDICTED: Canis familiaris	AC124862
			LOC491404 (LOC491404), mRNA	
ALA	1587413_at	UP	Hirudo medicinalis intermediate	AC005996
			filament gliarin mRNA, complete cds	
ALA	1587838_at	DOW	Homo sapiens fibroblast growth factor	AL031386
		N	13 (FGF13), transcript variant 1B, mRNA	
ALA	1588093_at	DOW	Homo sapiens hypothetical protein	BC039892
		N	FLJ20507, mRNA (cDNA clone MGC:47628 IMAGE:5725347), complete cds	
ALA	1588502_at	DOW	Homo sapiens mRNA for cAMP	AB209262
		N	responsive element binding protein 5 isoform beta variant protein	
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	AC025842
			ATP/GTP binding protein 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	AL139243
			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	
ALA	1593224_at	UP	PREDICTED: Canis familiaris similar to	AL138842
			hemojuvelin isoform a (LOC475830),	

			mRNA	
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-kinase	AL355315
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
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 (FLJ1	AL713895
ALA	1605187_at	UP	Human DNA sequence from clone RP11-8N6 on chromosome 9 Contains the 3' end of the MELK gene for	AL442063

ALA	1605429_at	DOWN	maternal embryonic leucine zipper kinase (KIAA0175), complete sequence 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)	AL358073
ALA	1605486_at	UP	pseudogene, the VPS45A gene for 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 calyntenin 2, mRNA (cDNA clone IMAGE:4130487), partial cds	BC007943
LA	1584677_at	DOWN	PREDICTED: Pan troglodytes similar to cystatin T (LOC469901), mRNA	BC024006
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 monooxygenase, 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) pseudogene	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	BC027860

		N	cancer 1, mRNA (cDNA clone MGC:34368 IMAGE:5228947), complete cds	
LA	1588088_at	UP	Homo sapiens hypoxia-inducible protein 2, mRNA (cDNA clone MGC:17005 IMAGE:4182067), complete cds	BC008573
LA	1589569_at	DOW N	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	DOW N	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	DOW N	Bos taurus mRNA for sodium chloride cotransporter, partial	NM_000339
LA	1595753_at	DOW N	Homo sapiens CrkRS mRNA, complete cds	CR954985
LA	1596117_at	DOW N	Mus musculus piccolo (presynaptic cytomatrix protein) (Pclo), mRNA	AP001266
LA	1600646_at	DOW N	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	DOW N	PREDICTED: Canis familiaris similar to family with sequence similarity 20, member A (LOC480458), mRNA	AC026358
LA	1603578_at	DOW N	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	DOW N	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	DOW N	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
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 phosphatase 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
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), mRNA	AC025467
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
ARA	1603093_at	UP	Homo sapiens genomic DNA,	AP003083

			chromosome 11q clone:RP11-179B7, complete sequence	
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_	DOW	Homo sapiens cDNA clone	AC006211
	at	N	IMAGE:4611044, partial cds	
ARA	1603454_at	UP	Bos taurus mRNA for similar to cytochrome c oxidase subunit VIb, partial cds, clone: ORCS10538	AL158068
ARA	1603839_at	DOW	PREDICTED: Rattus norvegicus transcription factor EB (predicted) (Tcfef_predicted), mRNA	BX284687
		N		
ARA	1604372_at	UP	PREDICTED: Canis familiaris LOC475665 (LOC475665), mRNA	AY411810
ARA	1604969_at	DOW	Homo sapiens chromosome 17, clone hRPK.147_L_13, complete sequence	AC005332
		N		
ARA	1605486_at	UP	Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence	AK096428
SA	Cfa.10737.1	DOW	PREDICTED: Canis familiaris similar to HP1-BP74, transcript variant 4 (LOC478203), mRNA	AL663074
	.A1_at	N		
SA	Cfa.10872.1	UP	Homo sapiens Kruppel-like factor 11, mRNA (cDNA clone MGC:71570 IMAGE:30343877), complete cds	CR591795
	.A1_at			
SA	Cfa.12323.1	UP	PREDICTED: Canis familiaris similar to angiopoietin-like 4 protein (LOC476724), mRNA	AC010323
	.A1_at			
SA	Cfa.12533.1	UP	PREDICTED: Bos taurus similar to insulin induced gene 1 isoform 1 (LOC511899), mRNA	AC144438
	.A1_at			
SA	Cfa.12594.1	UP	Homo sapiens G protein-coupled receptor 17, mRNA (cDNA clone MGC:35264 IMAGE:5174146), complete cds	AC096920
	.A1_at			
SA	Cfa.12839.1	DOW	PREDICTED: Canis familiaris similar to nexilin isoform s (LOC490202), mRNA	AC103591
	.A1_at	N		
SA	Cfa.17.1.S1	UP	Canis familiaris organic anion transporting polypeptide A (OATPA) mRNA, partial cds	NM_134431
	_s_at			
SA	Cfa.17302.1	DOW	PREDICTED: Canis familiaris similar to pleckstrin homology domain containing, family G, member 3 (LOC611460), mRNA	NM_015549
	.S1_s_at	N		
SA	Cfa.17415.1	DOW	PREDICTED: Canis familiaris similar to regucalcin gene promotor region related protein (LOC607434), mRNA	XM_088459
	.S1_s_at	N		
SA	Cfa.17931.1	DOW	PREDICTED: Canis familiaris similar to von Willebrand factor A domain-related protein isoform 1 (LOC607112), mRNA	NM_022834
	.S1_s_at	N		
SA	Cfa.1854.1.	UP	Homo sapiens fatty acid desaturase 1	AP002380

	A1_at		(FADS1), mRNA	
SA	Cfa.18958.1 .S1_at	DOW N	PREDICTED: Canis familiaris similar to OCIA domain containing 1, transcript variant 3 (LOC475140), mRNA	BC003409
SA	Cfa.19447.1 .S1_at	DOW N	Homo sapiens lamin B1 (LMNB1), mRNA	NM_005573
SA	Cfa.19635.1 .S1_at	DOW N	Lotus corniculatus var. japonicus gene for hypothetical proteins, complete and partial cds, clone:BAC259.12D-1	AF165140
SA	Cfa.19704.1 .S1_at	DOW N	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.A l_x_at	UP	PREDICTED: Canis familiaris similar to 60S ribosomal protein L23a (LOC478212), mRNA	NM_000984
SA	Cfa.431.1.A l_at	UP	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP), transcript variant 4 (LOC474720), mRNA	AL591206
SA	Cfa.431.2.A l_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	DOW N	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 (LOC474720), mRNA	NM_001122
SA	Cfa.6361.1. A1_at	DOW N	PREDICTED: Canis familiaris similar to 60S ribosomal protein L17 (L23), transcript variant 4 (LOC480221), mRNA	BX679664
SA	Cfa.6482.1. A1_at	DOW N	PREDICTED: Canis familiaris hypothetical protein LOC612422 (LOC612422), mRNA	AL162191
SA	Cfa.6915.1. A1_at	DOW N	Homo sapiens 12 BAC RP11-1105G2 (Roswell Park Cancer Institute Human BAC Library) complete sequence	AC073655
SA	Cfa.7119.1.	DOW	PREDICTED: Canis familiaris similar to	AC109357

	A1_s_at	N	coilin (LOC480564), mRNA	
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	DOW N	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	DOW N	Mus musculus SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae), mRNA (cDNA clone IMAGE:5372918)	AC091133
SA	Cfa.9506.1.A1_at	UP	Homo sapiens hypoxia-inducible protein 2 (HIG2) mRNA, complete cds	AF144755
SA	Cfa.9531.1.A1_at	DOW N	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	DOW N	Plasmodium yoelii yoelii str. 17XNL hypothetical protein (PY00634) mRNA, partial cds	AL359317
SA	CfaAffx.1102.1.S1_at	DOW N	PREDICTED: Canis familiaris similar to RAB5B, member RAS oncogene family, transcript variant 3 (LOC474394), mRNA	BC065298
SA	CfaAffx.12967.1.S1_at	DOW N	Canis familiaris isolate cOR5D23 olfactory receptor family 5 subfamily D gene, partial cds	AF399364
SA	CfaAffx.13599.1.S1_at	DOW N	Nicotiana benthamiana clone 6-272 unknown mRNA	NA
SA	CfaAffx.14479.1.S1_at	DOW N	PREDICTED: Canis familiaris similar to Protein KIAA0652 (LOC483632), mRNA	AK223603
SA	CfaAffx.14595.1.S1_s_a_t	DOW N	PREDICTED: Canis familiaris similar to diacylglycerol kinase zeta (LOC611321), mRNA	NM_201532
SA	CfaAffx.15202.1.S1_s_a_t	DOW N	PREDICTED: Canis familiaris similar to Syndecan-4 precursor (Amphiglycan) (SYND4) (Ryudocan core protein) (LOC485893), mRNA	AK222695
SA	CfaAffx.16302.1.S1_x_a_t	DOW N	PREDICTED: Canis familiaris similar to zinc finger protein 25 (LOC611218), mRNA	AB169501
SA	CfaAffx.16493.1.S1_at	DOW N	PREDICTED: Bos taurus similar to Phosphatidylinositol 4-kinase beta (PtdIns 4-kinase) (PI4Kbeta) (PI4K-	AL079340

			beta) (NPIK) (PI4K92) (LOC613348), mRNA	
SA	CfaAffx.191	UP	Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) (ALS2), mRNA	NM_020919
SA	CfaAffx.192	DOW	Ipomoea nil Magenta gene for flavonoid 3'-hydroxylase, complete cds	BX647478
SA	CfaAffx.197	DOW	PREDICTED: Canis familiaris bZIP protein, transcript variant 1 (LCR-F1), mRNA	NM_003204
SA	CfaAffx.205	UP	PREDICTED: Canis familiaris similar to protein tyrosine phosphatase, non-receptor type 23 (LOC609220), mRNA	AL110210
SA	CfaAffx.211	DOW	PREDICTED: Canis familiaris similar to CG4699-PA, isoform A, transcript variant 4 (LOC480489), mRNA	BC098376
SA	CfaAffx.212	DOW	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.220	DOW	PREDICTED: Canis familiaris similar to zinc finger CCCH type containing 12A (LOC489416), mRNA	XM_370654
SA	CfaAffx.225	DOW	PREDICTED: Canis familiaris similar to Cullin-5 (CUL-5) (Vasopressin-activated calcium-mobilizing receptor) (VACM-1) (LOC489422), mRNA	BC063306
SA	CfaAffx.233	DOW	PREDICTED: Canis familiaris similar to RAD52B (LOC480794), mRNA	BC032114
SA	CfaAffx.237	DOW	PREDICTED: Canis familiaris similar to aldehyde dehydrogenase 4A1 precursor (LOC612452), mRNA	BC023600
SA	CfaAffx.238	UP	PREDICTED: Canis familiaris similar to cleavage stimulation factor, 3 pre-RNA subunit 2, tau (LOC486459), mRNA	AL136747
SA	CfaAffx.240	UP	PREDICTED: Canis familiaris similar to serine/threonine kinase 11 interacting protein (LOC488541), mRNA	NA
SA	CfaAffx.258	UP	PREDICTED: Canis familiaris hypothetical LOC22889, transcript variant 1 (LOC612936), mRNA	AK170490
SA	CfaAffx.283	UP	PREDICTED: Canis familiaris similar to angiopoietin-like 4 protein (LOC476724), mRNA	AK222489
SA	CfaAffx.289	DOW	PREDICTED: Canis familiaris similar to Mitogen-activated protein kinase kinase 7 interacting protein 1 (TAK1-binding protein 1), transcript variant 1 (LOC481245), mRNA	NM_006116
SA	CfaAffx.298	UP	PREDICTED: Canis familiaris similar to melanoma ubiquitous mutated protein (LOC612320), mRNA	BC110874
SA	CfaAffx.331	UP	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-	NM_001122

			related protein) (ADRP), transcript variant 4 (LOC474720), mRNA	
SA	CfaAffx.442	UP	PREDICTED: Canis familiaris similar to zinc finger protein 329 (LOC484234), mRNA	NM_024620
	5.1.S1_at			
SA	CfaAffx.443	UP	PREDICTED: Canis familiaris similar to FERM and PDZ domain containing 1 (LOC481614), mRNA	AB023184
	8.1.S1_at			
SA	CfaAffx.536	DOW	PREDICTED: Canis familiaris similar to claudin 6 (LOC490048), mRNA	CR614114
	7.1.S1_at	N		
SA	CfaAffx.654	UP	PREDICTED: Homo sapiens similar to ribosomal protein S27 (LOC442598), mRNA	XM_499342
	.1.S1_at			
SA	CfaAffx.668	DOW	Homo sapiens Kazal type serine protease inhibitor 5-like 2 (SPINK5L2), mRNA	NM_001001325
	.1.S1_at	N		
SA	CfaAffx.670	DOW	PREDICTED: Canis familiaris similar to pumilio homolog 2, transcript variant 6 (LOC607618), mRNA	AK093847
	3.1.S1_at	N		
SA	CfaAffx.782	DOW	PREDICTED: Canis familiaris similar to FYVE-finger-containing Rab5 effector protein rabenosyn-5 (LOC484642), mRNA	BC106940
	2.1.S1_s_at	N		
SA	CfaAffx.784	UP	Homo sapiens mRNA for TSC-22 protein	AJ222700
	5.1.S1_s_at			
SA	CfaAffx.886	UP	Homo sapiens hypothetical LOC387790 (LOC387790), mRNA	AK095089
	1.1.S1_at			
SA	CfaAffx.908	UP	PREDICTED: Canis familiaris similar to FLJ20859 protein isoform 2 (LOC475396), mRNA	AK155096
	3.1.S1_at			
SA	CfaAffx.935	DOW	PREDICTED: Canis familiaris similar to chromatin-specific transcription elongation factor large subunit, transcript variant 1 (LOC612874), mRNA	NM_007192
	3.1.S1_s_at	N		
SA	CfaAffx.984	UP	PREDICTED: Canis familiaris similar to leucine rich repeat containing 45 (LOC483375), mRNA	NM_144999
	5.1.S1_s_at			
CLA	Cfa.10478.1	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
	.A1_at			
CLA	Cfa.11267.1	DOW	Homo sapiens cDNA clone IMAGE:4456146, partial cds	BC024645
	.A1_at	N		
CLA	Cfa.11358.1	UP	Homo sapiens solute carrier family 20 (phosphate transporter), member 2 (SLC20A2), mRNA	AF170802
	.A1_at			
CLA	Cfa.11413.1	DOW	Homo sapiens BAC clone RP11-17N4 from 2, complete sequence	AC016673
	.A1_at	N		
CLA	Cfa.11483.1	DOW	Danio rerio POU domain, class 4, transcription factor 1, mRNA (cDNA clone MGC:77341 IMAGE:6967996), complete cds	AL138810
	.A1_at	N		

CLA	Cfa.11868.1 .A1_at	DOW N	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	DOW N	PREDICTED: Canis familiaris similar to Sodium- and chloride-dependent transporter XTRP2 (Solute carrier family 6 member 18) (LOC478631), mRNA	AK074468
CLA	Cfa.13707.1 .A1_at	DOW N	PREDICTED: Bos taurus similar to Ssu72 RNA polymerase II CTD phosphatase homolog, transcript variant 2 (LOC614837), mRNA	BC008070
CLA	Cfa.13930.1 .A1_at	DOW N	Aspergillus nidulans FGSC A4 hypothetical protein (AN0430.2), mRNA	AL031779
CLA	Cfa.14103.1 .A1_at	DOW N	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	DOW N	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) (Piwi4), mRNA	AC108065
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	DOW N	Mus musculus nephrin NPHS1 (Nphs1) gene, partial cds	AC024166
CLA	Cfa.5394.1. A1_at	DOW N	Xenopus laevis MGC80410 protein, mRNA (cDNA clone MGC:80410 IMAGE:5155047), complete cds	AC012618
CLA	Cfa.5400.1. A1_at	DOW N	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	DOW N	Human mRNA for KIAA0297 gene, partial cds	AL589763
CLA	Cfa.7584.1. A1_at	DOW N	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
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.108 53.1.S1_at	UP	PREDICTED: Canis familiaris cOR2AG1 olfactory receptor family 2 subfamily AG-like (cOR2AG1), mRNA	AC090440
CLA	CfaAffx.122 8.1.S1_at	DOW N	Homo sapiens gene for LIM-homeodomain protein Lhx8, partial cds	AP002762
CLA	CfaAffx.132 10.1.S1_s_a t	UP	Homo sapiens olfactory receptor, family 6, subfamily C, member 6 (OR6C6), mRNA	NM_001005493
CLA	CfaAffx.135 99.1.S1_at	DOW N	Nicotiana benthamiana clone 6-272 unknown mRNA	NA
CLA	CfaAffx.137 93.1.S1_at	DOW N	PREDICTED: Strongylocentrotus purpuratus similar to apurinic/apyrimidinic endonuclease (44.7 kD) (apn-1) (LOC592745), mRNA	AL391114
CLA	CfaAffx.170 03.1.S1_s_a t	UP	PREDICTED: Canis familiaris similar to actinin, alpha 2, transcript variant 11 (LOC479191), mRNA	CR593118
CLA	CfaAffx.182 14.1.S1_s_a t	UP	PREDICTED: Canis familiaris complement component receptor 2 (CR2), mRNA	AK223627

CLA	CfaAffx.184 14.1.S1_at	DOW N	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
CLA	CfaAffx.189 22.1.S1_at	DOW N	PREDICTED: Canis familiaris similar to dystonia 2, torsion (autosomal recessive) (LOC488341), mRNA	U18799
CLA	CfaAffx.241 69.1.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.246 75.1.S1_x_a t	UP	PREDICTED: Canis familiaris similar to expressed in non-metastatic cells 1, protein (NM23A) (nucleoside diphosphate kinase) (LOC611984), mRNA	BC000293
CLA	CfaAffx.248 8.1.S1_at	UP	PREDICTED: Canis familiaris hypothetical protein LOC612694 (LOC612694), mRNA	AL583806
CLA	CfaAffx.297 68.1.S1_s_a t	UP	PREDICTED: Canis familiaris similar to tripartite motif protein 32 (predicted) (LOC491233), mRNA	BX255925
CLA	CfaAffx.443 8.1.S1_at	UP	PREDICTED: Canis familiaris similar to FERM and PDZ domain containing 1 (LOC481614), mRNA	AB023184
CLA	CfaAffx.667 0.1.S1_at	UP	PREDICTED: Canis familiaris similar to microtubule associated monooxygenase, calponin and LIM domain containing 1 (LOC481958), mRNA	BC009972
CLA	CfaAffx.732 6.1.S1_s_at	DOW N	PREDICTED: Canis familiaris similar to F-box and leucine-rich repeat protein 13 (LOC609997), mRNA	NM_145032

Example 3

Genes differentially expressed in the blood of fat and lean animals that can be used as class predictors for fat and lean animals.

In order to simplify clinical and scientific analyses and eliminate the need for using solid tissue samples that have to be biopsied from live animals, blood samples from fat and lean dogs may be obtained and used to develop a "class predictor" that can be used to differentiate between fat and lean animals. Class prediction is a form of pattern recognition that involves the use of supervised learning algorithms familiar to one of skill in the art (e.g., Weighted Voting, Class Neighbors, K-Nearest Neighbors and Support Vector Machines) to define a group of genes or gene products that

can recognize and differentiate between two groups or classes of animals. Developing class predictors generally involves the following steps:

A training step:

In this step two unambiguously defined groups or classes of animals (for example fat and lean animals) are used to train an algorithm to recognize and differentiate between them.

This step results in the generation of a “class predictor” set of genes. Once a “class predictor” group of genes and or gene products is established and validated it can be used to classify new and unknown samples as they become available.

A validation or testing step:

The ability of the class predictor to make the distinction between the two groups is then tested by using new samples that are different from those used in the training step and allowing the algorithm to use what it had learned in the training step to predict the class to which each new sample belongs.

In our studies with fat and lean animals, Affymetrix Canine-2 GeneChips are used according to methods provided hereinabove to measure the gene expression levels in blood samples taken from animals that are conventionally identified as clinically fat (28 animals with a body condition score of 4 or 5) or lean (12 animals with a body condition score of 2 or 2.5). The GeneChip data is then used to train an algorithm (Support Vector Machines) that is included in the software program GeneSpring (version 7.2 ,Agilent Technologies) to generate the class predictor. Accordingly, data indicate 65 probes that exhibit differential expression levels between the fat and lean samples with a “p” value of 0.01 (after the application of a false discovery rate correction) (see Table 8). RMA normalized data provided in Table 9 indicates the intensity of the fold change in expression in a fat animal versus lean animal such that a value greater than one indicates that the gene is upregulated in a fat animal, a value of one indicates no change in expression in a fat versus lean animal and a value of less than one indicates that the expression of the gene is greater in a lean animal than a fat animal. Thus, it is contemplated herein that these probes and the genes and gene products that they represent can potentially be used as class predictors to identify fat and lean animals using blood samples without the need to use adipose tissue samples.

Table 8: Affymetrix probes representing genes that can be used as class predictors for fat and lean animals using blood samples instead of adipose tissue samples

	Affymetrix probe id	top-annotation based on BLAST sequence similarity
1	Cfa.10128.1.A1_at	PREDICTED: Canis familiaris similar to alpha-synuclein isoform NACP140; transcript variant 3 (LOC478478); mRNA PREDICTED: Canis familiaris similar to ADP-ribosylation factor GTPase activating protein 3; transcript variant 5 (LOC474477); mRNA
2	Cfa.10772.1.A1_at	

3	Cfa.11444.1.A1_at	Homo sapiens elk1 oncogene; complete cds
4	Cfa.1152.1.A1_s_at	PREDICTED: Canis familiaris similar to ubiquitin C-terminal hydrolase UCH37 (LOC478958); mRNA
5	Cfa.11624.1.A1_at	PREDICTED: Canis familiaris similar to retinaldehyde binding protein 1 (LOC479039); mRNA PREDICTED: Canis familiaris similar to Coiled-coil-helix-coiled-coil-helix domain containing protein 3; transcript variant 5 (LOC607574); mRNA
6	Cfa.13515.1.S1_at	No available annotation
7	Cfa.13669.1.A1_at	Pongo pygmaeus mRNA; cDNA DKFZp468H0312 (from clone DKFZp468H0312)
8	Cfa.15521.1.A1_at	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 11; 14.7kDa; transcript variant 1 (LOC476735); mRNA
9	Cfa.16699.1.S1_s_at	PREDICTED: Canis familiaris similar to ADP-ribosylation factor GTPase activating protein 3; transcript variant 2 (LOC474477); mRNA
10	Cfa.17093.1.S1_at	PREDICTED: Canis familiaris similar to MAK31-like protein (LOC479488); mRNA
11	Cfa.18024.1.S1_s_at	No available annotation
12	Cfa.1945.1.A1_at	PREDICTED: Rattus norvegicus similar to hypothetical protein FLJ25439 (LOC502510); mRNA
13	Cfa.19577.1.S1_at	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8; transcript variant 1 (LOC477798); mRNA
14	Cfa.273.3.A1_s_at	Canis familiaris angiotensin II type 2 receptor mRNA; partial cds
15	Cfa.3698.1.A1_at	Canis familiaris Sec61 beta subunit (Sec61b); mRNA
16	Cfa.3895.1.A1_s_at	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) Fe-S protein 6; 13kDa (NADH-coenzyme Q reductase) (LOC478629); mRNA
17	Cfa.4245.1.S1_s_at	PREDICTED: Bos taurus similar to mal; T-cell differentiation protein-like (LOC512289); mRNA
18	Cfa.4779.1.A1_at	Magnaporthe grisea 70-15 hypothetical protein (MG04641.4) partial mRNA
19	Cfa.5440.1.A1_at	PREDICTED: Canis familiaris similar to growth differentiation factor 3 precursor (LOC477702); mRNA
20	Cfa.5628.1.A1_s_at	PREDICTED: Canis familiaris similar to glyceraldehyde-3-phosphate dehydrogenase (LOC481027); mRNA
21	Cfa.5672.1.A1_s_at	Homo sapiens mRNA; cDNA DKFZp761M0111 (from clone DKFZp761M0111)
22	Cfa.583.1.S1_at	PREDICTED: Canis familiaris similar to presenilin enhancer 2 (LOC476479); mRNA
23	Cfa.6307.1.A1_s_at	PREDICTED: Canis familiaris similar to presenilin enhancer 2 (LOC476479); mRNA
24	Cfa.6307.1.A1_x_at	PREDICTED: Canis familiaris similar to adiponectin receptor 2; transcript variant 2 (LOC477732); mRNA
25	Cfa.7730.1.A1_at	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
26	Cfa.8497.1.A1_at	PREDICTED: Canis familiaris similar to MADS box transcription enhancer factor 2; polypeptide C (myocyte enhancer factor 2C); transcript variant 30 (LOC479155); mRNA
27	Cfa.9073.1.A1_s_at	full-length cDNA clone CS0DF038YH13 of Fetal brain of Homo sapiens (human)
28	Cfa.9519.1.A1_at	

29	CfaAffx.11304.1.S1_ at	PREDICTED: Canis familiaris similar to solute carrier family 5 (iodide transporter); member 8 (LOC482626); mRNA
30	CfaAffx.12600.1.S1_ s_at	C.familiaris mRNA for TRAM-protein
31	CfaAffx.12899.1.S1_ at	PREDICTED: Bos taurus similar to olfactory receptor Olr535 (LOC510433); mRNA
32	CfaAffx.13068.1.S1_ s_at	Canis familiaris carboxypeptidase B1 (tissue) (CPB1); mRNA
33	CfaAffx.13084.1.S1_ at	Mus musculus olfactory receptor MOR232-2 gene; complete cds
34	CfaAffx.13369.1.S1_ s_at	PREDICTED: Canis familiaris similar to selenoprotein T (LOC612992); mRNA
35	CfaAffx.13927.1.S1_ at	PREDICTED: Canis familiaris similar to CG10510-PA (LOC477622); mRNA
36	CfaAffx.13999.1.S1_ s_at	PREDICTED: Canis familiaris similar to Transmembrane 9 superfamily protein member 3 precursor; transcript variant 5 (LOC612786); mRNA
37	CfaAffx.14593.1.S1_ s_at	PREDICTED: Canis familiaris similar to chromodomain helicase DNA binding protein 6; transcript variant 1 (LOC477230); mRNA
38	CfaAffx.16220.1.S1_ s_at	PREDICTED: Canis familiaris similar to membrane-spanning 4-domains; subfamily A; member 6A isoform 2 (LOC612553); mRNA
39	CfaAffx.16368.1.S1_ s_at	Canine mRNA for signal recognition particle receptor
40	CfaAffx.17233.1.S1_ s_at	PREDICTED: Canis familiaris similar to ubiquitin-conjugating enzyme E2G 2 (LOC611581); mRNA
41	CfaAffx.18688.1.S1_ at	PREDICTED: Canis familiaris hypothetical protein LOC609372 (LOC609372); mRNA
42	CfaAffx.19132.1.S1_ s_at	PREDICTED: Canis familiaris similar to uroplakin 2 (LOC610673); mRNA
43	CfaAffx.19769.1.S1_ at	PREDICTED: Canis familiaris similar to YTH domain protein 1 (Dermatomyositis associated with cancer putative autoantigen-1 homolog) (DACA-1 homolog) (LOC485968); mRNA
44	CfaAffx.20665.1.S1_ at	PREDICTED: Canis familiaris similar to patched domain containing 1; transcript variant 1 (LOC491775); mRNA
45	CfaAffx.20740.1.S1_ s_at	PREDICTED: Canis familiaris similar to a disintegrin and metalloproteinase domain 23 preproprotein; transcript variant 2 (LOC607871); mRNA
46	CfaAffx.21676.1.S1_ at	PREDICTED: Canis familiaris similar to Ferritin light chain (Ferritin L subunit) (LOC491829); mRNA
47	CfaAffx.2327.1.S1_s _at	PREDICTED: Canis familiaris similar to ADP-ribosylation factor GTPase activating protein 3; transcript variant 5 (LOC474477); mRNA
48	CfaAffx.23835.1.S1_ at	Homo sapiens protocadherin 15 (PCDH15); mRNA
49	CfaAffx.24356.1.S1_ s_at	PREDICTED: Canis familiaris similar to Growth hormone inducible transmembrane protein (Dermal papilla derived protein 2); transcript variant 3 (LOC479266); mRNA
50	CfaAffx.24849.1.S1_ at	PREDICTED: Canis familiaris similar to Olfactory receptor 7A5 (Olfactory receptor TPCR92) (LOC610545); mRNA
51	CfaAffx.25142.1.S1_ s_at	PREDICTED: Canis familiaris similar to Renal sodium-dependent phosphate transport protein 2 (Sodium/phosphate cotransporter 2) (Na(+)/Pi cotransporter 2) (Renal sodium-phosphate transport protein 2) (Renal Na(+)-dependent

		phosphate cotransporter 2); t
52	CfaAffx.25751.1.S1_at	Macaca fascicularis brain cDNA; clone:QfIA-12135; similar to human progesterin and adipoQ receptor family member VI (PAQR6); mRNA; NM_024897.2
53	CfaAffx.26483.1.S1_s_at	Canis familiaris non-metastatic cells 2; protein (NM23B) expressed in (NME2); mRNA
54	CfaAffx.28078.1.S1_s_at	PREDICTED: Canis familiaris similar to CD27-binding (Siva) protein isoform 1 (LOC612693); mRNA
55	CfaAffx.28164.1.S1_at	PREDICTED: Canis familiaris similar to Ubiquitin-conjugating enzyme E2 A (Ubiquitin-protein ligase A) (Ubiquitin carrier protein A) (HR6A) (mHR6A) (LOC492095); mRNA
56	CfaAffx.2860.1.S1_s_at	PREDICTED: Canis familiaris similar to Coiled-coil-helix-coiled-coil-helix domain containing protein 3; transcript variant 2 (LOC607574); mRNA
57	CfaAffx.28798.1.S1_at	PREDICTED: Canis familiaris similar to seizure related gene 6 (LOC491175); mRNA
58	CfaAffx.29250.1.S1_s_at	PREDICTED: Canis familiaris similar to CG4646-PA (LOC479563); mRNA
59	CfaAffx.32063.1.S1_at	No available annotation
60	CfaAffx.360.1.S1_s_at	PREDICTED: Canis familiaris similar to ADAM DEC1 precursor (A disintegrin and metalloproteinase domain-like protein decysin 1) (ADAM-like protein decysin 1) (LOC608742); mRNA
61	CfaAffx.3860.1.S1_s_at	Homo sapiens mRNA for KIAA1045 protein; partial cds
62	CfaAffx.604.1.S1_at	PREDICTED: Canis familiaris similar to zinc finger protein 91 (HPF7; HTF10) (LOC484590); mRNA
63	CfaAffx.6669.1.S1_at	PREDICTED: Canis familiaris similar to progesterone membrane binding protein (LOC476084); mRNA
64	CfaAffx.7079.1.S1_at	PREDICTED: Canis familiaris TATA-box binding protein (LOC475040); mRNA
65	CfaAffx.9326.1.S1_s_at	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L48 isoform 1 (LOC476812); mRNA

Table 9 Class Predictor Gene Set Expression Values Fat vrs Lean

Gene	Fold Change Fat vrs Lean
Cfa.10128.1.A1_at	1.178
Cfa.10772.1.A1_at	0.673
Cfa.11444.1.A1_at	1.167
Cfa.1152.1.A1_s_at	0.682
Cfa.11624.1.A1_at	1.128
Cfa.13515.1.S1_at	0.702
Cfa.13669.1.A1_at	1.123
Cfa.15521.1.A1_at	1.103
Cfa.16699.1.S1_s_at	0.806
Cfa.17093.1.S1_at	0.688
Cfa.18024.1.S1_s_at	0.667
Cfa.1945.1.A1_at	1.141
Cfa.19577.1.S1_at	1.167
Cfa.273.3.A1_s_at	0.708

Cfa.3698.1.A1_at	1.129
Cfa.3895.1.A1_s_at	0.718
Cfa.4245.1.S1_s_at	0.696
Cfa.4779.1.A1_at	1.206
Cfa.5440.1.A1_at	1.101
Cfa.5628.1.A1_s_at	1.156
Cfa.5672.1.A1_s_at	1.105
Cfa.583.1.S1_at	0.556
Cfa.6307.1.A1_s_at	0.755
Cfa.6307.1.A1_x_at	0.837
Cfa.7730.1.A1_at	1.208
Cfa.8497.1.A1_at	1.116
Cfa.9073.1.A1_s_at	0.718
Cfa.9519.1.A1_at	0.64
CfaAffx.11304.1.S1_at	1.187
CfaAffx.12600.1.S1_s_at	0.74
CfaAffx.12899.1.S1_at	1.32
CfaAffx.13068.1.S1_s_at	1.298
CfaAffx.13084.1.S1_at	1.209
CfaAffx.13369.1.S1_s_at	0.757
CfaAffx.13927.1.S1_at	1.137
CfaAffx.13999.1.S1_s_at	0.781
CfaAffx.14593.1.S1_s_at	1.258
CfaAffx.16220.1.S1_s_at	1.132
CfaAffx.16368.1.S1_s_at	0.809
CfaAffx.17233.1.S1_s_at	0.811
CfaAffx.18688.1.S1_at	1.193
CfaAffx.19132.1.S1_s_at	1.164
CfaAffx.19769.1.S1_at	0.849
CfaAffx.20665.1.S1_at	1.205
CfaAffx.20740.1.S1_s_at	1.184
CfaAffx.21676.1.S1_at	1.156
CfaAffx.2327.1.S1_s_at	0.657
CfaAffx.23835.1.S1_at	1.116
CfaAffx.24356.1.S1_s_at	0.729
CfaAffx.24849.1.S1_at	1.126
CfaAffx.25142.1.S1_s_at	1.184
CfaAffx.25751.1.S1_at	1.102
CfaAffx.26483.1.S1_s_at	0.807
CfaAffx.28078.1.S1_s_at	0.883
CfaAffx.28164.1.S1_at	0.752
CfaAffx.2860.1.S1_s_at	0.646
CfaAffx.28798.1.S1_at	1.066
CfaAffx.29250.1.S1_s_at	0.789
CfaAffx.32063.1.S1_at	1.16
CfaAffx.360.1.S1_s_at	1.141
CfaAffx.3860.1.S1_s_at	1.163
CfaAffx.604.1.S1_at	1.154
CfaAffx.6669.1.S1_at	0.816
CfaAffx.7079.1.S1_at	0.709
CfaAffx.9326.1.S1_s_at	0.794

Example 4

Diets containing higher amounts of long chain fatty acids promote weight loss and can be used to re-program the gene expression of the animal so that it reflects a propensity to become lean and potentially maintain leanness

The data obtained from *in vitro* ingredient screens discussed above indicate that some ingredients that are high in long chain fatty acids (see Table 7) may have the potential to affect the expression of genes involved in fat metabolism in a way that would promote leanness of the animal as a whole. This is determined by analyzing data obtained from adipose tissue and from the ingredient assays discussed above using conventional computer algorithm analyses. Code for algorithms useful in this regard are familiar to one of skill in the art and may be developed without undue experimentation. An example of such code is provided below:

```
SELECT A.PROBE, TO_CHAR ( AVG(DECODE(A.EXPTDAY, 'D0', GENE_NORM_INT,
null))/AVG(DECODE(A.EXPTDAY, 'D14', GENE_NORM_INT, null)), '99999.99999' )
FATLEAN_FC, STATS_T_TEST_INDEPU( A.EXPTDAY, GENE_NORM_INT) P_VALUE,
B.TOP_HIT_DEF,

COUNT(DISTINCT C.INGREDIENT),

COUNT(DISTINCT D.INGREDIENT)

FROM GERIATRICS_RNRM2 A, TOP_PROBE_ANNOT_2_3 B,
FILT_INDIV_CELLS_2 C, FILT_ACROSS_4_CELLS_2 D

WHERE A.PROBE=B.PROBE AND A.PROBE=C.PROBE (+) AND
A.PROBE=D.PROBE (+) AND
UPPER(A.PROBE) NOT LIKE 'AFFX%'

GROUP BY A.PROBE, B.TOP_HIT_DEF

HAVING STATS_T_TEST_INDEPU( A.EXPTDAY, GENE_NORM_INT) <= .01 AND
AVG(DECODE(A.EXPTDAY, 'D0', GENE_NORM_INT, null))/AVG(DECODE(A.EXPTDAY,
'D14', GENE_NORM_INT, null)) >= 5 AND
SUM(DECODE(PAMCALL, 'P', 1, 0)) = 40 ORDER BY PROBE
```

To confirm that the inclusion of linolenic acid or EPA/DHA (1.5:1) in diets fed to dogs does affect weight loss in dogs, three high protein diets containing either no added long chain fatty acids (Diet A) or added linolenic acid (approximately 1% based on 100% dry matter basis, Diet B) or EPA/DHA (1.5:1, approximately 0.30%: 0.20 %) (Diet C) were developed for comparison to a high fiber diet that is known to induce weight loss in dogs. In the study, 45 clinically fat dogs are all first fed a nutritionally complete control diet for 30 days prior to the start of the test. After the initial 30 days, the dogs are randomized into 4 groups. Three of the four groups receive one of the test diets and one group is given the high fiber diet as a control for a set period of time, e.g., 4 months.. Results indicate that the three experimental foods (Diets A, B and C) have substantially higher digestibility than the higher fiber food. Results also indicate that approximately 38% of the dogs consuming the food containing EPA/DHA reach their weight loss goal at 90 days. Interestingly, dogs consuming the EPA/DHA food also maintain lean muscle mass and bone mineral content. The results also indicate that, at least at the clinical level, diets containing EPA/DHA may be as effective as high fiber diets in affecting weight loss.

In order to validate the class predictor probe set and to test its ability to predict fatness or leanness in animals, the class predictor probe set (described in Example 3 above) is applied to gene expression data obtained from the 45 animals participating in the experiment above (expression data not shown). The class predictor analysis confirms that 41 of the 45 animals (approximately 90%) designated "fat" at the beginning of the test are in fact fat (the discrepancy may be due to the subjective nature of the conventional body condition scoring system that is currently used in the clinic). Interestingly, after 14 days of feeding the four diets described above, the class predictor analysis indicates that all animals, regardless of diet, display a "lean" gene expression profile. At the end of the study, it appears that all the animals on the control high fiber diet reflect a "fat" gene expression profile, approximately 25% of the animals on test Diets A and B reflect a biochemically

“lean” gene expression profile and approximately 40% of the animals fed on Diet C containing EPA/DHA exhibit a biochemically “lean” gene expression profile (see Table 10).

**Table 10: Approximate Percentage of Lean Animals
as Predicted by the 65-probe Class Predictor**

	Diet Day 0	Diet Day 14	Diet Day 120
Diet A (n = 12)	9%	33%	25%
Diet B (n = 10)	10%	40%	25%
Diet C (n = 14)	7%	29%	40%
High Fiber Diet (n = 9)	11%	30%	0%

Example 5

Possible Weight Loss Maintenance Experiment

Based on the results of the weight loss experiment discussed above, it is hypothesized that animals fed a diet containing EPA/DHA will not only lose weight but also will maintain the loss for a longer period of time compared to animals fed the other test and control high fiber diets.

In order to characterize the effects of Diets A, B, and C and the high fiber diet on weight loss maintenance, one could perform, for example, the following type of experiment:

Fat animals may be fed the four different diets (as described in Example 4) until they reach an optimum level of “leanness”. They may then be randomized and divided into subgroups that either continue to be fed the same test diet that they were fed previously or are switched to a maintenance diet that is nutritionally balanced but is not designed to induce or maintain weight loss and does not include appreciable amounts of linolenic acid or EPA/DHA, for example.

The animals may then be observed for a set period of time, e.g., up to 3 months, with their weights recorded daily, their body condition scores determined weekly and their percentage body fat determined on a monthly basis using conventional DEXA technologies.

What is claimed is:

1. A combination comprising (a) two or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof or (b) two or more proteins produced by the expression of two or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof.
2. The combination of claim 1 wherein the polynucleotides are selected from SEQ ID NOs:1-70 or useful variations thereof.
3. The combination of claim 1 wherein the polynucleotides are selected from SEQ ID NOs:1-25 or useful variations thereof.
4. The combination of claim 1 wherein the polynucleotides are selected from SEQ ID NOs identified in Table 2 or useful variations thereof.
5. The combination of claim 1 wherein the polynucleotides are selected from SEQ ID NOs identified in Table 3 or useful variations thereof.
6. The combination of claim 1 wherein the polynucleotides are canine polynucleotides.
7. A composition comprising two or more probes suitable for detecting the expression of genes differentially expressed in fat animals compared to lean animals, the probes comprising:
 - (a) polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof; or
 - (b) polypeptides that specifically bind to proteins produced by the expression of one or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof.
8. The composition of claim 7 wherein the polynucleotides are selected from SEQ ID NOs:1-70 or useful variations thereof.
9. The composition of claim 7 wherein the polynucleotides are selected from SEQ ID NOs:1-25 or useful variations thereof.
10. The composition of claim 7 wherein the polynucleotides are selected from SEQ ID NOs identified in Table 2 or useful variations thereof.
11. The composition of claim 7 wherein the polynucleotides are selected from SEQ ID NOs identified in Table 3 or useful variations thereof.
12. The composition of claim 7 wherein the polynucleotides are canine polynucleotides.
13. A device suitable for detecting the expression of a plurality of genes differentially expressed in fat animals compared to lean animals comprising a substrate having a plurality of probes affixed to the substrate at known locations, the probes comprising:
 - (a) polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof; or
 - (b) polypeptides each of which specifically binds to proteins produced by expression of one or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof.
14. The device of claim 13 wherein the polynucleotides are selected from SEQ ID NOs:1-70 or useful variations thereof.

15. The device of claim 13 wherein the polynucleotides are selected from SEQ ID NOs:1-25 or useful variations thereof.
16. The device of claim 13 wherein the polynucleotides are selected from SEQ ID NOs identified in Table 2 or useful variations thereof.
17. The device of claim 13 wherein the polynucleotides are selected from SEQ ID NOs identified in Table 3 or useful variations thereof.
18. The device of claim 13 wherein the polynucleotides are canine polynucleotides.
19. The device of claim 13 wherein the probes are arranged in an array.
20. The device of claim 13 wherein the polypeptide probes are antibodies.
21. The device of claim 20 wherein the antibodies are monoclonal antibodies.
22. A method for detecting the differential expression of one or more genes differentially expressed in fat animals compared to lean animals in a sample comprising:
 - (a) hybridizing a combination comprising a plurality of polynucleotide probes selected from SEQ ID NOs:1-295 or useful variations thereof with polynucleotides in the sample to form one or more hybridization complexes;
 - (b) optionally, hybridizing a combination comprising a plurality of polynucleotide probes selected from SEQ ID NOs:1-295 or useful variations thereof 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 of 2 fold or more indicate differential expression of genes differentially expressed in fat animals compared to lean animals in the sample.
23. The method of claim 22 wherein the probes are selected from SEQ ID NOs:1-70 or useful variations thereof and the fold difference is 2.5 or more.
24. The method of claim 22 wherein the probes are selected from SEQ ID NOs:1-25 or useful variations thereof and the fold difference is 3 or more.
25. The method of claim 22 wherein the probes are selected from SEQ ID NOs identified in Table 2 or useful variations thereof and the fold difference is 2 or more.
26. The method of claim 22 wherein the probes are selected from SEQ ID NOs identified in Table 3 or useful variations thereof and the fold difference is 2 or more.
27. The method of claim 22 wherein the probes are bound to a substrate.
28. The method of claim 27 wherein the probes are in an array.

29. The method of claim 22 wherein the detecting is performed at intervals for an animal and used to monitor the animal's progress when attempting to modulate the amount of adipose tissue on the animal in response to an adipose tissue modulation program.
30. The method of claim 22 wherein the probes are canine polynucleotides.
31. The method of claim 22 further comprising exposing the sample to a test substance before hybridization, wherein comparison to a standard is indicative of whether the test substance altered the expression of genes differentially expressed in fat animals compared to lean animals in the sample.
32. A method for detecting the differential expression of genes differentially expressed in fat animals compared to lean animals in a sample comprising:
 - (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 produced by expression of one or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof;
 - (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 produced by expression of one or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof;
 - (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 a difference between the specific binding in the standard and the sample of 2 fold or more indicates differential expression of genes differentially expressed in fat animals compared to lean animals in the sample.
33. The method of claim 32 wherein the probes are selected from SEQ ID NOs:1-70 or useful variations thereof and the fold difference is 2.5 or more.
34. The method of claim 32 wherein the probes are selected from SEQ ID NOs:1-25 or useful variations thereof and the fold difference is 3 or more.
35. The method of claim 32 wherein the probes are selected from SEQ ID NOs identified in Table 2 or useful variations thereof and the fold difference is 2 or more.
36. The method of claim 32 wherein the probes are selected from SEQ ID NOs identified in Table 3 or useful variations thereof and the fold difference is 2 or more.
37. The method of claim 32 wherein the probes are bound to a substrate.
38. The method of claim 37 wherein the probes are in an array.
39. The method of claim 32 further comprising detecting the differential expression of genes differentially expressed in fat animals compared to lean animals for an animal at intervals

during an adipose tissue modulation program and determining the effectiveness of the program by observing changes in the expression of the genes.

40. The method of claim 39 wherein a decrease in gene expression indicates a reduction in adipose tissue on the animal.
41. The method of claim 32 wherein the probes are canine polypeptides.
42. The method of claim 32 further comprising exposing the sample to a test substance before reacting the polypeptides with the proteins, wherein comparison to a standard is indicative of whether the test substance altered the expression of genes differentially expressed in fat animals compared to lean animals in the sample.
43. A method for measuring the effect of a test substance on the expression of one or more genes differentially expressed in fat animals compared to lean animals and a method for screening a test substance to determine if it is likely to be useful for modulating the amount of adipose tissue on an animal comprising:
 - (a) determining a first expression profile by measuring the transcription or translation products of one or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof in a test system in the absence of the test substance;
 - (b) determining a second expression profile by measuring the transcription or translation products of one or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof in a test system in the presence of the test substance; and
 - (c) comparing the first expression profile to the second expression profile, wherein a change in the second expression profile compared to the first expression profile of 2 fold or more indicates that the test substance effects the expression of polynucleotides differentially expressed in fat animals compared to lean animals and that the test substance is likely to be useful for modulating the amount of adipose tissue on an animal.
44. The method of claim 43 wherein the polynucleotides are selected from SEQ ID NOs:1-70 or useful variations thereof and the fold difference is 2.5 or more.
45. The method of claim 43 wherein the polynucleotides are selected from SEQ ID NOs:1-25 or useful variations thereof and the fold difference is 3 or more.
46. The method of claim 43 wherein the polynucleotides are selected from SEQ ID NOs identified in Table 2 or useful variations thereof and the fold difference is 2 or more.
47. The method of claim 43 wherein the polynucleotides are selected from SEQ ID NOs identified in Table 3 or useful variations thereof and the fold difference is 2 or more.
48. The method of claim 43 wherein determining an expression profile utilizes a plurality of polynucleotides.
49. The method of claim 48 wherein the polynucleotides are bound to a substrate.
50. The method of claim 49 wherein the probes are in an array.

51. The method of claim 43 wherein the standard and test samples are obtained from a canine.
52. A substance identified by the method of claim 42.
53. A method for formulating a prognosis that an animal is likely to become fat or developing a diagnosis that an animal is fat comprising determining if one or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof or one or more polypeptides that specifically bind to proteins produced by expression of one or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof are differentially expressed in the animal compared to one or more lean animals, wherein the animal is determined to be likely to become fat or determined to be fat if the comparison indicates that the polynucleotides or polypeptides are differentially expressed in the animal compared to the lean animals by a fold of 2 or more.
54. The method of claim 53 wherein the polynucleotides are selected from SEQ ID NOs:1-70 or useful variations thereof and the fold difference is 2.5 or more.
55. The method of claim 53 wherein the polynucleotides are selected from SEQ ID NOs:1-25 or useful variations thereof and the fold difference is 3 or more.
56. The method of claim 53 wherein the polynucleotides are selected from SEQ ID NOs identified in Table 2 or useful variations thereof and the fold difference is 2 or more.
57. The method of claim 53 wherein the polynucleotides are selected from SEQ ID NOs identified in Table 3 or useful variations thereof and the fold difference is 2 or more.
58. A method for manipulating the genome of a non-human animal or the expression of the genome of an animal comprising disrupting the expression of one or more genes differentially expressed in fat animals compared to lean animals.
59. The method of claim 58 wherein expression is disrupted by "knocking out" endogenous genes in the animal.
60. The method of claim 58 wherein expression is disrupted by interfering with transcription or translation.
61. The method of claim 58 wherein expression is disrupted using polynucleotides constructed using polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof.
62. A transgenic animal produced using the method of claim 58.
63. A composition suitable for manipulating the genome of an animal comprising one or more substances that interfere with the expression of one or more genes differentially expressed in fat animals compared to lean animals.
64. The composition of claim 63 wherein the substances are antisense molecules or siRNAs.
65. The composition of claim 63 wherein the substances are polynucleotides constructed using polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof.
66. A method for modulating the expression of one or more genes differentially expressed in fat animals compared to lean animals or modulating the amount of adipose tissue on an animal

- comprising administering to the animal a gene expression or tissue modulating amount of a composition comprising one or more of DHA, EPA, EPA and DHA, ALA, LA, ARA, and SA.
67. The method of claim 66 wherein DHA is administered in amounts of from about 1 to about 30; EPA is administered in amounts of from about 1 to about 30; EPA/DHA Combo (1.5:1 ratio) are administered in amounts of from about 4/2 to about 30/45; ALA is administered in amounts of from about 10 to about 100; LA is administered in amounts of from about 30 to about 600; ARA is administered in amounts of from about 5 to about 50; and SA is administered in amounts of from about 3 to about 60, all in mg/kg/day.
68. The method of claim 66 further comprising administering to the animal one or more drugs or other substances that modulate the amount of adipose tissue on an animal.
69. A composition suitable for modulating the expression of one or more genes differentially expressed in fat animals compared to lean animals or modulating the amount of adipose tissue on an animal comprising a gene expression or tissue modulating amount of one or more of DHA, EPA, EPA and DHA, ALA, LA, ARA, and SA.
70. The composition of claim 69 comprising 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; and SA in amounts sufficient to administer to an animal from about 3 to about 60, all in mg/kg/day.
71. The composition of claim 69 further comprising one or more drugs or other substances that modulate the amount of adipose tissue on an animal.
72. A method for selecting an animal for inclusion in one or more groups comprising determining the expression profile of the animal for (a) polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof or (b) polypeptides each of which specifically binds to proteins produced by expression of one or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof and assigning the animal to a group based upon the expression profile.
73. The method of claim 72 wherein the groups are lean and fat groups and animals are assigned to the fat group based upon a differential expression of 2 fold or more and animals are assigned to the lean group based upon a differential expression of less than 2 fold compared to a standard.
74. A computer system suitable for manipulating data relating to one or more genes differentially expressed in fat animals compared to lean animals comprising a database containing information identifying the expression level of one or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof and/or polypeptides that specifically bind to proteins produced by the expression of one or more polynucleotides selected from SEQ ID NOs:1-295

or useful variations thereof in lean animals and/or fat animals and a user interface to interact with the database.

75. A method for producing an antibody suitable for use in detecting one or more genes differentially expressed in fat animals compared to lean animals comprising:
- (a) immunizing an animal with polypeptides produced by expression of one or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof under conditions that elicit an antibody response;
 - (b) isolating animal antibodies; and
 - (c) screening the isolated antibodies with the polypeptide, thereby identifying an antibody that specifically binds the polypeptide.
76. An isolated and purified antibody produced using the method of claim 75.
77. A kit suitable for determining the differential expression of one or more genes differentially expressed in fat animals compared to lean animals in a test system comprising in separate containers in a single package or in separate containers in a virtual package, as appropriate for the use and kit component, two or more probes suitable for detecting the expression of genes differentially expressed in fat animals compared to lean animals, the probes comprising:
- (a) polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof; or
 - (b) polypeptides that specifically bind to proteins produced by the expression of one or more polynucleotides selected from SEQ ID NOs:1-295 or useful variations thereof; and
- at least one of (1) instructions for how to use the probes of the present invention; (2) reagents and equipment necessary to use the probes; (3) a composition suitable for modulating the expression of one or more genes differentially expressed in fat animals compared to lean animals; (4) a composition suitable for disrupting the expression of one or more genes differentially expressed in fat animals compared to lean animals; (5) a food composition suitable for modulating the amount of adipose tissue on an animal; and (6) one or more drugs or other substances that modulate the amount of adipose tissue on an animal.
78. The kit of claim 77 wherein the probes are bound to a substrate.
79. The kit of claim 78 wherein the probes are in an array.
80. The kit of claim 77 wherein the compositions comprise one or more of DHA, EPA, EPA and DHA, ALA, LA, ARA, and SA.
81. A means for communicating information about or instructions for one or more of (1) using the polynucleotides of the present invention for detecting the expression of genes differentially expressed in fat animals compared to lean animals in a sample, (2) using the polynucleotides of the present invention for measuring the effect of a test substance on the expression of one or more genes differentially expressed in fat animals compared to lean animals, (3) using the polynucleotides of the present invention for screening a test substance to determine if it is likely

to be useful for modulating the amount of adipose tissue on an animal, (4) using the polynucleotides of the present invention for formulating a prognosis that an animal is likely to become fat or developing a diagnosis that an animal is fat, (5) using the polynucleotides of the present invention for manipulating the genome of a non-human animal or the expression of the genome of an animal, (6) using the polynucleotides of the present invention for modulating the expression of one or more genes differentially expressed in fat animals compared to lean animals or modulating the amount of adipose tissue on an animal, (7) using the polynucleotides of the present invention for selecting an animal for inclusion in one or more groups, (8) using the polynucleotides of the present invention for using computer system to manipulate data relating to genes differentially expressed in fat animals compared to lean animals, (9) administering substances of the present invention to an animal, alone or in combination with the other elements of the present invention, (10) using the substances of the present invention for modulating the amount of adipose tissue on an animal, (11) using the computer system of the present invention, (12) using the kits of the present invention, and (13) using the methods and compositions of the present invention with one or more drugs or other substances that modulate the amount of adipose tissue on an animal comprising a document, digital storage media, optical storage media, audio presentation, or visual display containing the information or instructions.

82. The means of claim 81 selected from the group consisting of a displayed web site, visual display, kiosk, brochure, product label, package insert, advertisement, handout, public announcement, audiotape, videotape, DVD, CD-ROM, computer readable chip, computer readable card, computer readable disk, computer memory, or combination thereof.
83. Use of the polynucleotide data of Table 1 in the manufacture of a composition for modulating the expression of one or more genes differentially expressed in fat animals compared to lean animals.
84. Use of the class predictor data of Table 8 and Table 9 in the manufacture of a composition for modulating the expression of one or more genes differentially expressed in fat animals compared to lean animals.
85. Use of the polynucleotide data of Table 1 in the manufacture of a kit for diagnosing the body condition score of an animal.
86. Use of the class predictor data of Table 8 and Table 9 in the manufacture of a kit for diagnosing the body condition score of an animal.