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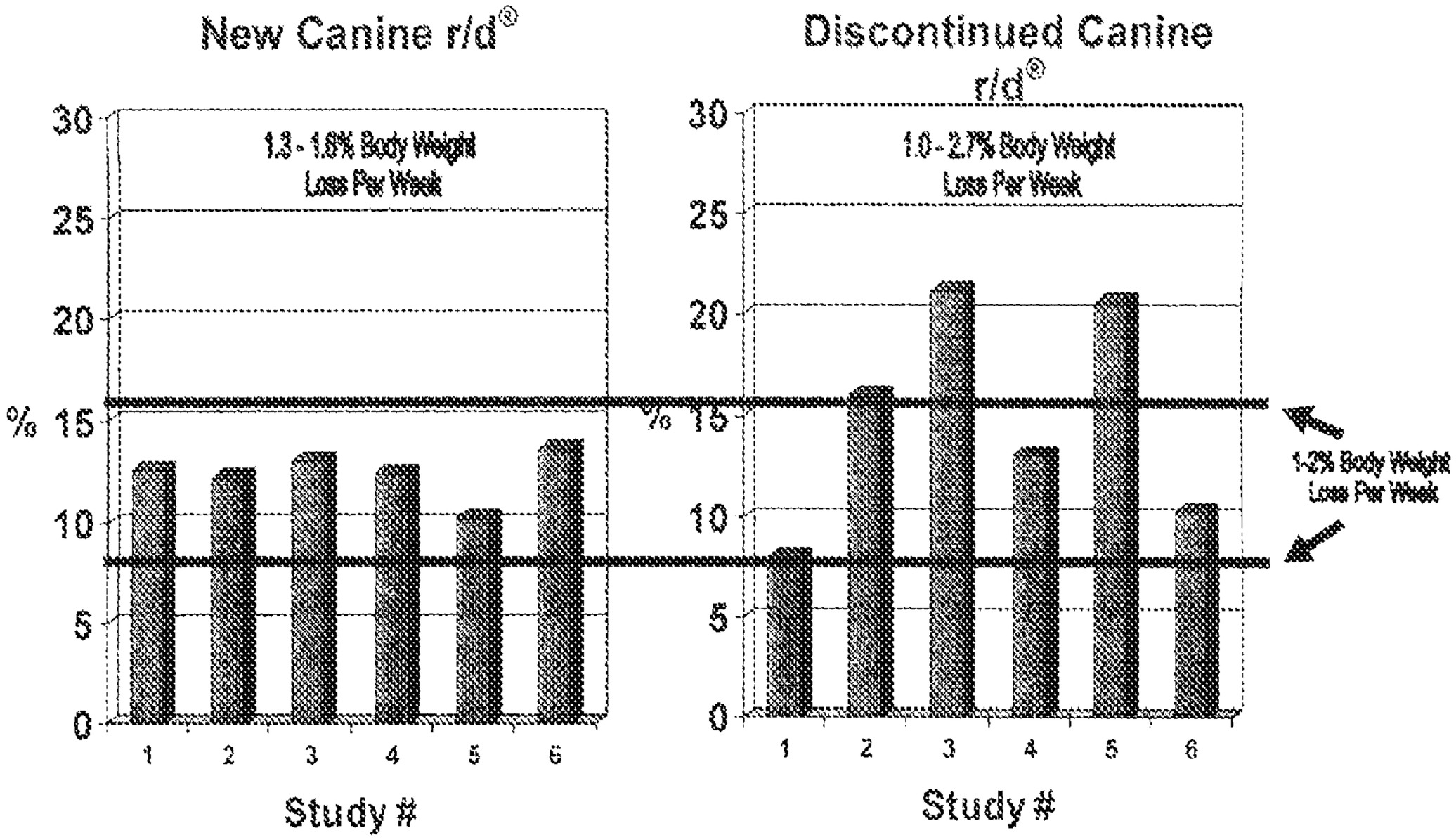
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(54) Title: COMPOSITIONS AND METHODS FOR TREATING DISORDERS ASSOCIATED WITH OVERWEIGHT ANIMALS



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The invention encompasses compositions and methods for treating disorders and diseases associated with overweight. The application also encompasses genes differentially expressed in animals and particularly to genes differentially expressed in overweight animals compared to lean animals.

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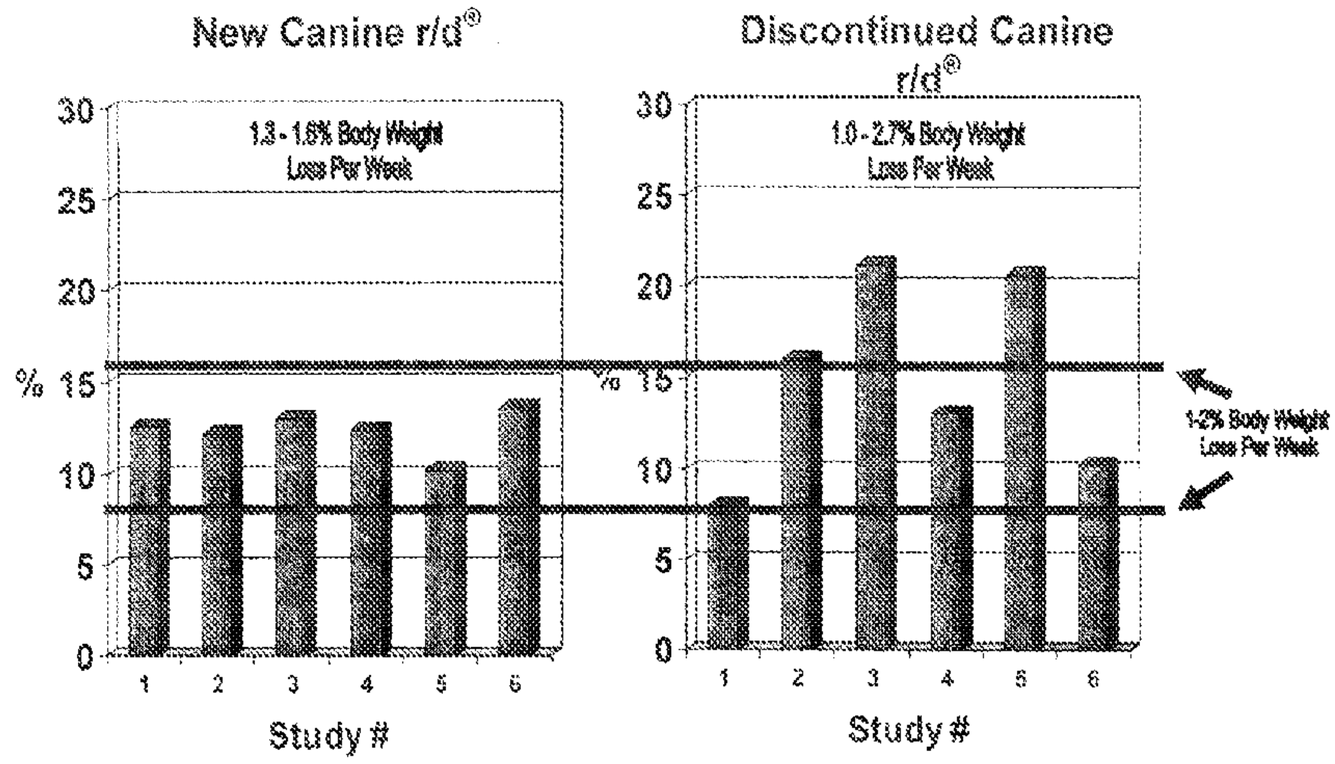
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(54) Title: COMPOSITIONS AND METHODS FOR TREATING DISORDERS ASSOCIATED WITH OVERWEIGHT ANIMALS

FIGURE 1



(57) Abstract: The invention encompasses compositions and methods for treating disorders and diseases associated with overweight. The application also encompasses genes differentially expressed in animals and particularly to genes differentially expressed in overweight animals compared to lean animals.

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CECI EST LE TOME 1 DE 2
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COMPOSITIONS AND METHODS FOR TREATING DISORDERS ASSOCIATED WITH OVERWEIGHT ANIMALS

FIELD OF THE INVENTION

[0001] The invention encompasses compositions and methods for treating disorders and diseases associated with obesity. The application also encompasses genes differentially expressed in animals and particularly to genes differentially expressed in obese animals compared to lean animals. The invention also encompasses compositions and methods for modulating the amount of fat in animals with targeted nutrition that is designed to affect, among others, key genes involved in fat metabolism. The invention further identifies bioactive dietary components that individually or together can affect the expression and activity of key genes involved in fat metabolism.

BACKGROUND OF THE INVENTION

[0002] It is generally accepted in the scientific community 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 Sequence Tags (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, Reverse Phase protein array and arrays.

[0003] Gene expression in overweight animals compared to lean animals has not been thoroughly investigated. Therefore, a need exists to identify genes and proteins that are differentially expressed in overweight 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.

[0004] Overweight 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 overweight 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 overweight animals are significantly more at risk for diseases such as arthritis, heart disease, respiratory disease, diabetes, bladder cancer, hypothyroidism, and pancreatitis.

[0005] Modulating the amount of adipose tissue on an animal, including preventing an animal from becoming overweight or treating a overweight 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 involves increasing the amount of food consumed. The most effective and easiest way to prevent an animal from becoming overweight 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.

[0006] Given the problems with current methods for dealing with adipose tissue on an animal, the inventors have developed methods and compositions useful for treating diseases and disorders in animals and in 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

[0007] The invention encompasses compositions and methods useful in treating disorders in companion animals in need thereof.

[0008] In one embodiment, the invention encompasses a canine pet food composition comprising an effective amount of one or more ingredients that interfere with the expression of one or more genes differentially expressed in overweight animals compared to lean animals, wherein said one or more ingredients that interfere with the expression of one or more genes comprise 26 wt. % to 35 wt. % of crude protein on a dry matter basis, 7.5 wt. % to 8.5 wt. % of crude fat on a dry matter basis, 20 wt. % to 30 wt. % of total dietary fiber on a dry matter basis, and 10 wt. % to 20 wt. % of crude fiber on a dry matter basis.

[0009] In another embodiment, the invention encompasses a feline pet food composition comprising an effective amount of one or more ingredients that interfere with the expression of one or more genes differentially expressed in overweight animals compared to lean animals, wherein said one or more ingredients that interfere with the expression of one or more genes comprise: 30 wt. % to 37 wt. % of crude protein on a dry matter basis, 7.5 wt. % to 9 wt. % of crude fat on a dry matter basis, 30 wt. % to 35 wt. % of total dietary fiber on a dry matter basis, and 20 wt. % to 25 wt. % of crude fiber on a dry matter basis.

[0010] Another embodiment encompasses a method of treating or preventing insulin resistance in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0011] Another embodiment encompasses a method of treating or preventing pancreatitis in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0012] Another embodiment encompasses a method of treating or preventing hypothyroidism in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0013] Another embodiment encompasses a method of treating or preventing osteoarthritis in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0014] Another embodiment encompasses a method of treating or preventing dyslipidemia in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0015] Another embodiment encompasses a method of treating or preventing hypertension in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0016] Another embodiment encompasses a method of treating or preventing ocular disorders in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0017] Another embodiment encompasses a method of treating or preventing altered kidney function in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0018] Another embodiment encompasses a method of treating or preventing respiratory in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0019] Another embodiment encompasses a method of treating or preventing artherosclerosis in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0020] Another embodiment encompasses a method of treating or preventing diabetes mellitus in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0021] Another embodiment encompasses a method of treating or preventing urinary tract disease in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0022] Another embodiment encompasses a method of treating or preventing hepatic lipidosis in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0023] Another embodiment encompasses a method of treating or preventing hepatic dyslipidemia in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0024] Another embodiment encompasses a method of treating or preventing hepatic lipidosis in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0025] Another embodiment encompasses a method of treating or preventing neoplasia in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0026] Another embodiment encompasses a method of treating or preventing oral/dental disease in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0027] Another embodiment encompasses a method of treating or preventing dermatopathy in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0028] Another embodiment encompasses a method of treating or preventing lameness in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0029] Another embodiment encompasses a method of treating or preventing hyperlipidemia in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0030] Another embodiment encompasses a method of treating or preventing glucose metabolism disorders in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0031] Another embodiment encompasses a method of treating or preventing coronary disease in a companion animal in need thereof, for example, a canine or feline, with a composition of the invention.

[0032] Another embodiment of the invention encompasses one or more genes or gene segments that are differentially expressed in overweight animals compared to lean animals.

[0033] Another embodiment of the invention encompasses combinations of two or more polynucleotides or polypeptides that are differentially expressed in overweight animals compared to lean animals.

[0034] Another embodiment of the invention encompasses compositions of two or more polynucleotide or polypeptide probes suitable for detecting the expression

of genes differentially expressed in overweight animals compared to lean animals and devices such as substrate arrays containing the probes.

[0035] Another embodiment of the invention encompasses methods and compositions for detecting the differential expression of one or more genes differentially expressed in overweight animals compared to lean animals in a sample.

[0036] Another embodiment of the invention encompasses methods for measuring the effect of a test substance on the expression profile of one or more genes differentially expressed in overweight 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.

[0037] Another embodiment of the invention encompasses methods for formulating a prognosis that an animal is likely to become overweight or developing a diagnosis that an animal is fat.

[0038] Another embodiment of the invention encompasses methods and compositions for modulating the expression of one or more genes differentially expressed in overweight animals compared to lean animals or for modulating the amount of adipose tissue on an animal.

[0039] One or more of these embodiments are achieved using novel combinations of 433 polynucleotide probes representing genes and gene segments that are differentially expressed in the adipose tissue of overweight animals compared to the adipose tissue of lean animals (Table 1). In addition, one or more of these embodiments are achieved using novel combinations of 1703 polynucleotide probes representing genes and gene segments that are differentially expressed in lymphocytes taken from overweight animals compared to lymphocytes taken from lean animals (Table 2). Furthermore, one or more of these embodiments are achieved using novel combinations of the polynucleotide probes representing the genes and gene segments that are differentially expressed in overweight and lean dogs and are considered to be key genes for fatty acid metabolism (Table 3). The polynucleotides are used to produce compositions, probes, devices based on the probes, and methods for determining the status of polynucleotides differentially expressed in overweight 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.

[0040] It is also an embodiment of this invention to encompass methods to modulate the amount of adipose tissue in an animal *in vivo* by administration of composition of the invention that is shown to modulate the expression of genes involved in fat metabolism.

[0041] It is also an embodiment of the invention to modulate various canine biomarkers related to obesity by administering a composition of the invention to an animal in need thereof in an amount effective to modulate the biomarker. Examples of biomarkers related to obesity that can be modulated include, but are not limited to, glucose, insulin, GLP-1, IGF-1, cholesterol, triglycerides, LDL, chylomicrons, alkaline phosphatase, type-2 cartilage synthesis, leptin, ghrelin, and combinations thereof.

[0042] Other and further objects, features, and advantages of the present invention will be readily apparent to those skilled in the art.

BRIEF DESCRIPTION OF THE FIGURES

[0043] FIGURE 1 shows the result for weight loss of dogs fed the formula of the present invention as compared to a control weight loss formula.

[0044] Figure 2 shows the shift in gene profile in dogs fed the formula of the present invention as compared to lean dogs, obese

DETAILED DESCRIPTION OF THE INVENTION

Definitions

[0045] The term "animal" means a human or other animal, including avian, bovine, canine, equine, feline, hicrine, murine, ovine, and porcine animals, that has adipose tissue. When the term is used in the context of comparing overweight 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.

[0046] 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.

[0047] 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 two or more probes (there are arrays, chips and other platforms now that go over 40,000) 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.

[0048] 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).

The term "Body Mass Index" (BMI) means an animal's weight (in kilograms) divided by its height (in meters) squared.

[0049] The term "DEXA" means body composition analysis dual-energy X-ray absorptiometry.

[0050] The term "differential expression" or "differentially expressed" means increased or upregulated gene expression or means decreased or downregulated gene expression as detected by the absence, presence, or at least a 1.3-fold change in the amount of transcribed messenger RNA or translated protein in a sample.

[0051] 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 overweight 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 overweight 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.

[0052] The term "fat-associated genes" means all or a subset of the genes identified in tables 1 and 2, particularly the genes represented by the 433 probe sequences that are differentially expressed between adipose tissue taken from overweight animals and adipose tissue taken from lean animals as well as the genes represented by the 1703 probe sequences that are differentially expressed between the lymphocytes taken from overweight animals and the lymphocytes taken from lean animals.

[0053] The term "key genes" means all or a subset of genes identified in table 3

[0054] 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 overweight 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 the gene is said to be up-regulated. On the other hand 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 and is said to be down-regulated.

[0055] 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 10, 50, 100, or 1000 nucleotides and polypeptide fragments contain at least 4, 10, 20, or 50 consecutive amino acids from the complete sequence. The term encompasses polynucleotides and polypeptides variants of the fragments.

[0056] 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.

[0057] The term "genes differentially expressed in overweight 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 overweight animals as compared to lean animals.

[0058] 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 in tables 1, 2, 3 and 5 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 in tables 1, 2, 3 and 5 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 in tables 1, 2, 3 and 5 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 in tables 1, 2, 3 and 5. Sequence similarity of two polypeptide sequences or of two polynucleotide sequences is determined using methods known to skilled artisans, e.g., the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 87:2264-2268 (1990)). Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al. (J. Mol. Biol. 215:403-410 (1990)). To obtain gapped alignments for comparison purposes, Gapped Blast can

be utilized as described in Altschul et al. (Nucl. Acids Res. 25: 3389-3402 (1997)). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) are used. See http://ww.ncbi.nlm.nih.gov.

[0059] The term "hybridization complex" means a complex that is formed between sample polynucleotides when the purines of one polynucleotide hydrogen bond with the pyrimidines of the complementary polynucleotide, e.g., 5'-A-G-T-C-3' base pairs with 3'-T-C-A-G-5'. The degree of complementarily and the use of nucleotide analogs affect the efficiency and stringency of hybridization reactions.

[0060] 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 the same time or periodically. "Periodically" means that the substance is administered on a dosage schedule acceptable for a specific substance. "the same time" generally means that the substance (food or drug) is administered at the same time or within 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.

[0061] The term "lean" as applied to an animal means any animal that is determined not to be overweight 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.

[0062] 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 overweight and treating a overweight 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.

[0063] The term "polynucleotide" or "oligonucleotide" means a polymer of nucleotides. The term encompasses DNA and RNA (including cDNA and mRNA) molecules, either single or double stranded and, if single stranded, its complementary sequence in either linear or circular form. The term also encompasses fragments, variants, homologs, and alleles, as appropriate for the sequences that have the same or substantially the same properties and perform the same or substantially the same function as the original sequence. The sequences may be fully complementary (no mismatches) when aligned or may have up to a 30% sequence mismatch. Preferably, for polynucleotides, the chain contains from 50 to 10,000 nucleotides, more preferably from 150 to 3,500 nucleotides. Preferably, for oligonucleotides, the chain contains from 2 to 100 nucleotides, more preferably from 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."

[0064] 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 2 to 1000 amino acids, more preferably from 5 to 500 amino acids. The term includes

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

[0065] 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 10 to 100, 15 to 50, or 15 to 25 nucleotides. In certain diagnostic applications, a polynucleotide probe contains 100-1000, 300-600, nucleotides, preferably 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.

[0066] 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.

[0067] 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.

[0068] 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.

[0069] 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.

[0070] The term "standard" means (1) a control sample that contains tissue from a lean animal if a overweight animal is being tested or tissue from a overweight animal if a lean animal is being tested or (2) a control sample that contains tissue from a lean or overweight test animal that has not been exposed to a test substance being examined in the corresponding lean or overweight animal to determine if the test substance causes differential gene expression, as appropriate for the context of its use.

[0071] The term "stringent conditions" means (1) hybridization in 50% (vol/vol) formamide with 0.1% bovine serum albumin, 0.1% Ficoll, 0.1% polyvinylpyrrolidone, 50 mM sodium phosphate buffer at pH 6.5 with 750 mM

NaCl, 75 mM sodium citrate at 42°C, (2) hybridization in 50% formamide, 5x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C; with washes at 42°C in 0.2x SSC and 0.1% SDS or washes with 0.015 M NaCl, 0.0015 M sodium citrate, 0.1% Na_2SO_4 at 50°C or similar procedures employing similar low ionic strength and high temperature washing agents and similar denaturing agents.

[0072] 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.

[0073] 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 15-50 nucleotides and the double stranded siRNA contains 15-50 base pairs, preferably 20-30 nucleotides and base pairs.

[0074] 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.

[0075] 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.

[0076] 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.

[0077] 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.

[0078] 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.

[0079] 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.

Modulation of Gene Protein Expression

[0080] In one embodiment, the present invention encompasses one or more genes or gene segments ("genes" as defined herein) that are differentially expressed in the adipose tissue and/or lymphocytes of overweight animals compared to the adipose tissue and/or lymphocytes of lean animals. The invention is based upon the discovery of diffenrentially expressed genes that are represented by 445 polynucleotides in the adipose tissue of overweight animals compared to the adipose tissue of lean animals and 1767 polynucleotides in the lymphocytes taken from overweight animals compared to lymphocytes taken from lean animals. The invention is further based upon the identification of 7 key genes involved in fatty acid metabolism that are diffenretially expressed between overweight and lean animals and are listed in table 3. These key genes represent members of the pyruvate dehydrogenase kinase family, the carnitine palmitoyltransferase family and solute carrier family 27 (fatty acid transporters) and genes associated with the elongation of long chain fatty acids, with the pyruvate dehedrogenase kinase family and the carnitine palmitoyltransferase family being the most important and in some instances rate limiting enzymes. The genes were identified by comparing the expression of genes in adipose tissue and lymphocytes taken from animals diagnosed as overweight with genes in adipose tissue and lymphocytes from animals diagnosed as lean using Affymetrix GeneChip® technology. The polynucleotides are shown in Table 1, 2 and 3. The tables contain information the Affymetrix Probe Identification Number (herein "APIN"), the p-value, the q-value, fold expression (fat/lean), the top BLAST annotation of the probe in question, the

Accession Number of Highest BLAST Hit, the gene symbol and finally the gene description is given in the last column. A description of the putative or actual gene can be in some instances 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 1.3 fold or greater gene expression in overweight 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 AIPN 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.

[0081] The polynucleotides and genes are identified by measuring differences in gene expression from adipose tissue and the lymphocytes from canines diagnosed as overweight with gene expression in adipose tissue and the lymphocytes 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 methods including but not limited to 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 or complimentary DNA (cDNA). Protein or polypeptide expression is determined using various colormetric, flourescense and spectroscopic assays and methods including but not limited to Western Blotting, ELISA, Multiple Reaction Monitoring, Reverse Phase and Antibody Arrays. In a preferred method, changes in gene expression are determined using Affymetrix Canine-1 and Canine-2 GeneChip® available for purchase from Affymetrix, Inc. and the instructions for using such chips to determine gene expression.

[0082] Generally, differential gene expression in overweight 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.

[0083] 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.

[0084] In another aspect, the invention provides a combination comprising two or more polynucleotides that are differentially expressed in overweight animals compared to lean animals or two or more proteins produced by the expression of two or more polynucleotides that are differentially expressed in overweight animals compared to lean animals. In one embodiment, the combination comprises two or more polynucleotides or proteins expressed from polynucleotides selected from Tables 1 and 2 and preferably from table 3. Preferably, the combination comprises a plurality of polynucleotides or proteins expressed from polynucleotides identified in tables 1 and 2 and preferably from table 3, generally 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 30%, 60%, or 90% of the original. The polynucleotides and proteins can be from any animal, preferably canines and felines, most preferable canines.

[0085] 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 overweight animals compared to lean animals. In one embodiment, the probes comprise polynucleotides selected from tables 1 and 2 and preferably from 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. In certain embodiments, the probes comprise at least 10, 15, 20, 25, or 30 nucleotides. In some embodiments, the probes contain more nucleotides and comprise at least 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 overweight animals compared to lean animals, generally 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.

[0086] In another aspect, the invention provides a device suitable for detecting the expression of a plurality of genes differentially expressed in overweight 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.

[0087] 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 overweight 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 tables 1 and 2. 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 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 4, 10, 20, 40, or 80 amino acids. In some embodiments, the probes contain more amino acids and comprise at least 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 overweight animals compared to lean animals, more preferably a collection of 10, 50, 100, 500, or 1000 or more of such probes. In one embodiment, the probes are antibodies, preferably monoclonal antibodies.

[0088] 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.

[0089] In another aspect, the invention provides a device suitable for detecting the expression of a plurality of genes differentially expressed in overweight 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. In certain embodiments, the probes, the sample proteins, or both, are labeled and detected, typically with a fluorophore or other agent known to skilled artisans. Generally, the same methods and instrumentation used for reading polynucleotide microarrays is applicable to protein arrays. Preferably, the probes are immobilized on a substrate suitable for forming an array.

[0090] 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.

[0091] 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.

[0092] In some embodiments, expression patterns or profiles of a plurality of genes differentially expressed in overweight 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.

[0093] 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 overweight animals compared to lean animals.

[0094] In a further aspect, the invention provides a method for detecting the differential expression of one or more genes differentially expressed in overweight 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 overweight 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 overweight 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 overweight animals compared to lean animals in the sample. In various embodiments, the plurality of polynucleotide probes are selected from Tables 1 and 2 and preferably from table 3. 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.

[0095] 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.

[0096] 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 overweight 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.

[0097] 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 overweight animals compared to lean animals, particularly fat-associated genes, in the sample.

[0098] In another aspect, the invention provides a method for detecting the differential expression of genes differentially expressed in overweight 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 overweight 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 overweight 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 overweight animals compared to lean animals in the sample.

[0099] 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 Tables 1 and 2 and preferably from table 3 and useful variations of such polynucleotides. 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.

[00100] 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.

[00101] 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 overweight 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.

[00102] 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 overweight animals compared to lean animals, particularly fat-associated genes, in the sample.

[00103] In another aspect, the method for detecting the expression of genes differentially expressed in overweight 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 overweight 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 overweight 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.

[00104] 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 overweight 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 Tables 1 and 2 and preferably from table 3 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 Tables 1 and 2 and preferably from table 3 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.

[00105] A change in the second expression profile compared to the first expression profile of 1.3 fold or more indicates that the test substance effects the expression of genes differentially expressed in overweight 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 overweight animals compared to lean animals are key genes associated with fatty acid metabolism and the change is a 1.3 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.

[00106] In one embodiment, the polynucleotides are selected from Table 3 or useful variations thereof and the change is 1.3 fold or higher.

[00107] 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.

[00108] Test substances can be any substance that may have an effect on polynucleotides or genes differentially expressed in overweight 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, MA, 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 D_2 (ergocalciferol) and vitamin D_3 (cholecalciferol), vitamin E sources such as tocopherols (*e.g.*, α-tocopherol) and tocotrienols, and vitamin K sources such as vitamin K_1 (phylloquinone) and vitamin K_2 (menadione); water-soluble vitamins including B vitamins such as riboflavin, niacin (including nicotinamide and nicotinic acid), pyridoxine, pantothenic acid, folic acid, biotin and cobalamin; and vitamin C (ascorbic acid); antioxidants, including some of the vitamins listed above, especially vitamins E and C; also bioflavonoids such as catechin, quercetin and theaflavin; quinones such as ubiquinone; carotenoids such as lycopene and lycoxanthin; resveratrol; and α-lipoic acid; L-carnitine; D-limonene; glucosamine; S-adenosylmethionine; and chitosan. In a preferred embodiment, test substances are nutrients that may be added to food or consumed as a supplement. Examples include, but are not limited to, fatty acids such as omega-3 fatty acids (e.g., DHA and EPA) and omega-6 fatty acids (e.g., ARA), carnitine, methionine, vitamin C, vitamin E, and vitamin D.

[00109] In a preferred embodiment, the substances useful for affecting the expression of genes differentially expressed in overweight animals compared to lean animals, particularly fat-associated genes, may be identified using methods discloses in co-pending US Provisional Patent Application No. 60/657980, filed March 2, 2005, and any subsequent US or foreign patent application that claims priority thereto.

[00110] In a further embodiment, the invention encompasses a method for formulating a prognosis that an animal is likely to become overweight or developing a diagnosis that an animal is fat. The method comprises determining if one or more polynucleotides selected from tables 1 and 2 or useful variations thereof or one or more polypeptides that specifically bind to proteins produced by expression of one or more polynucleotides selected from tables 1, 2 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 overweight or determined to be overweight if the comparison indicates that the polynucleotides are differentially expressed in the animal compared to the lean animals by a fold of 1.3 or more.

[00111] In various embodiments, the prognosis or diagnosis is based upon the polynucleotides selected from Table 3, or useful variations of such polypeptides.

[00112] 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 of 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.

[00113] 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.

[00114] 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 overweight animals compared to lean animals, preferably using oligonucleotides or polynucleotides constructed using

polynucleotides selected from tables 1 and 2 and preferably from table 3 or useful variations thereof.

[00115] Methods of manipulating the genome are known to those of skilled 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 tables 1 and 2 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 overweight 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 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.

[00116] 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 tables 1 and 2 and preferably from table 3 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 tables 1 and 2 and preferably from table 3 or useful variations thereof.

[00117] 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 overweight 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 tables 1 and 2 and preferably from table 3 or useful variations thereof. In various embodiments, the substances comprise antisense molecules or siRNAs.

[00118] In another embodiment, the invention encompasses a method for modulating the expression of one or more genes differentially expressed in overweight 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, SA and MA. In preferred embodiments the composition comprises, in milligrams per kilogram of body weight per day (mg/kg/day), DHA in amounts of from 1 to 30, preferably from 3 to 15; EPA in amounts of from 1 to 30, preferably from 3 to 15; EPA/DHA Combo (1.5:1 ratio) in amounts of from 4/2 to 30/45, preferably from 9/6 to 18/12; ALA in amounts of from 10 to 100, preferably from 30 to 60; LA in amounts of from 30 to 600, preferably from 60 to 300; ARA in amounts of from 5 to 50, preferably from 15 to 30; SA in amounts of from 3 to 60, preferably from 6 to 30; MA in amounts of from 3 to 60, preferably from 6 to 30; and CLA (as a control) in amounts of from 6 to 120, preferably from 12 to 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.

[00119] In another aspect, the invention provides a composition suitable for modulating the expression of one or more genes differentially expressed in overweight 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, SA, MA. In various embodiments, the composition comprises, in mg/kg/day, DHA in amounts sufficient to administer to an animal from 1 to 30; EPA in amounts sufficient to administer to an animal from 1 to 30; EPA/DHA Combo (1.5:1 ratio) in amounts sufficient to administer to an animal from 4/2 to 30/45; ALA in amounts sufficient to administer to an animal from 10 to 100; LA in amounts sufficient to administer to an animal from 30 to 600; ARA in amounts sufficient to administer to an animal from 5 to 50; SA in amounts sufficient to administer to an animal from 3 to 60; MA in amounts sufficient to administer to an animal from 3 to 60 and CLA (as a control) in amounts sufficient to administer to an animal from 6 to 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.

[00120] In another embodiment, the invention encompasses methods 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 tables 1 and 2 and preferably from table 3 or useful variations thereof or (b) polypeptides each of which specifically binds to proteins produced by expression of one or more polynucleotides selected from tables 1 and 2 and preferably from table

3 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 overweight 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 1.3 fold or more compared to a standard are assigned to the overweight group and animals with a differential expression of 1.3 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.

[00121] In another aspect, the invention provides a computer system suitable for manipulating data relating to one or more genes differentially expressed in overweight 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 tables 1 and 2 and preferably from table 3 or useful variations thereof and/or polypeptides that specifically bind to proteins produced by the expression of one or more polynucleotides selected from tables 1 and 2 and preferably from table 3 or useful variations thereof in lean animals and/or overweight 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 overweight 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 tables 1 and 2 and preferably from table 3 or useful variations thereof. In another, the database further comprises sequence information for one or more of the polynucleotides selected from tables 1 and 2 and preferably from table 3 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.

[00122] 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 overweight 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 tables 1 and 2 and preferably from table 3 form a sample to the expression profile of the polynucleotides or proteins in the computer system.

[00123] In a further aspect, the present invention provides kits suitable for determining the differential expression of one or more genes differentially expressed in overweight 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 overweight animals compared to lean animals, the probes comprising (a) polynucleotides selected from tables 1 and 2 and preferably from table 3 or useful variations thereof or (b) polypeptides that specifically bind to proteins produced by the expression of one or more polynucleotides selected from tables 1 and 2 and preferably from table 3 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 overweight animals compared to lean animals; (4) a composition suitable for disrupting the expression of one or more genes differentially expressed in overweight 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 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.

Compositions of the Invention

[00124] The invention encompasses canine food compositions including 26 wt. % to 35 wt. % of crude protein on a dry matter basis, 7.5 wt. % to 8.5 wt. % of crude fat on a dry matter basis, 20 wt. % to 30 wt. % of total dietary fiber on a dry matter basis, and 10 wt. % to 20 wt. % of crude fiber on a dry matter basis.

[00125] The invention also encompasses feline food compositions including 30 wt. % to 37 wt. % of crude protein on a dry matter basis, 7.5 wt. % to 9 wt. % of crude fat on a dry matter basis, 30 wt. % to 35 wt. % of total dietary fiber on a dry matter basis, and 20 wt. % to 25 wt. % of crude fiber on a dry matter basis.

[00126] In certain embodiments, the compositions of the invention can include an omega-3 polyunsaturated fatty acid content of at least 0.02% (or 0.05 % to 10%, or 0.1% to 6%) by weight on a dry matter basis. In some embodiments, the omega-3 polyunsaturated fatty acid is DHA. In other embodiments, the omega-3 polyunsaturated fatty acid is EPA. In still other embodiments, the omega-3 polyunsaturated fatty acid comprises a mixture of DHA and EPA.

[00127] In other embodiments, the composition including the omega-3 polyunsaturated fatty acid is a food. Although both liquid and solid foods are provided, solid foods are typically advantageous. Foods include both dry foods and wet foods. Some of the non-polyunsaturated fatty acid components of the food, and useful proportions, include those listed below.

Canine Food Compositions

Component	**Proportion of the composition (% of dry weight of composition or parts per million)**
Protein	26 wt. % to 35 wt. % of crude protein on a dry matter basis or 28 wt. % to 33 wt.%, or 30 wt. % to 31 wt. %; or 26 wt. %, 26.5 wt. %, 27 wt. %, 27.5 wt. %, 28 wt. %, 28.5 wt. %, 29 wt. %, 29.5 wt. %, 30 wt. %, 30.5 wt. %, 31 wt. %, 31.5 wt. %, 32 wt. %, 32.5 wt. %, 33 wt. %, 33.5 wt. %, 34 wt. %, 34.5 wt. %, 35 wt. %,
Crude Fat	7.5 wt. % to 8.5 wt. % of crude fat on a dry matter basis, or 7.6 wt. %, 7.7 wt. %, 7.8 wt. %, 7.9 wt. %, 8.0 wt. %, 8.1 wt. %, 8.2 wt. %, 8.3 wt. %, 8.4 wt. %
Total	20 wt. % to 30 wt. % of total dietary fiber on a dry matter basis

Dietary Fiber	or 22 wt. % to 28 wt. %, or 24 wt. % to 26 %; or 20 wt. %, 20.5 wt. %, 21 wt. %, 21.5 wt. %, 22 wt. %, 22.5 wt. %, 23 wt. %, 23.5 wt. %, 24 wt. %, 24.5 wt. %, 25 wt. %, 25.5 wt. %, 26 wt. %, 26.5 wt. %, 27 wt. %, 27.5 wt. %, 28 wt. %, 28.5 wt. %, 29 wt. %, 29.5 wt. %
Crude Fiber	10 wt. % to 20 wt. % of crude fiber on a dry matter basis, or 12 wt. % to 18 wt. %, or 14 wt. % to 16 %; or 10 wt. %, 10.5 wt. %, 11 wt. %, 11.5 wt. %, 12 wt. %, 12.5 wt. %, 13 wt. %, 13.5 wt. %, 14 wt. %, 14.5 wt. %, 15 wt. %, 15.5 wt. %, 16 wt. %, 16.5 wt. %, 17 wt. %, 17.5 wt. %, 18 wt. %, 18.5 wt. %, 19 wt. %, 19.5 wt. %

Feline Food Compositions

Component	Proportion of the composition (% of dry weight of composition or parts per million)
Protein	30 wt. % to 37 wt. % of crude protein on a dry matter basis or 31 wt. % to 36 wt. %, or 33% to 35%; or 30 wt. %, 30.5 wt. %, 31 wt. %, 31.5 wt. %, 32 wt. %, 32.5 wt. %, 33 wt. %, 33.5 wt. %, 34 wt. %, 34.5 wt. %, 35 wt. %, 35.5 wt. %, 36 wt. %, 36.5 wt. %, 36 wt. %
Crude Fat	7.5 wt. % to 9 wt. % of crude fat on a dry matter basis or 7.6 wt. %, 7.7 wt. %, 7.8 wt. %, 7.9 wt. %, 8.0 wt. %, 8.1 wt. %, 8.2 wt. %, 8.3 wt. %, 8.4 wt. %, 8.5 wt. %, 8.6 wt. %, 8.7 wt. %, 8.8 wt. %, 8.9 wt. %, 9.0
Total Dietary Fiber	30 wt. % to 35 wt. % of total dietary fiber on a dry matter basis or 31 wt. % to 34 wt. %, or 32 wt. % to 33 %; or 30 wt. %, 30.5 wt. %, 31 wt. %, 31.5 wt. %, 32 wt. %, 32.5 wt. %, 33 wt. %, 33.5 wt. %, 34 wt. %, 34.5 wt. %, 35 wt. %
Crude Fiber	20 wt. % to 25 wt. % of crude fiber on a dry matter basis, or 21 wt. % to 24 wt. %, or 22 wt. % to 23 %; or 20 wt. %, 20.5 wt. %, 21 wt. %, 21.5 wt. %, 22 wt. %, 22.5 wt. %, 23 wt. %, 23.5 wt.

Component	Proportion of the composition (% of dry weight of composition or parts per million)
	%, 24 wt. %, 24.5 wt. %, 25 wt. %

[00128] In one embodiment, the canine compositions of this invention include ingredients in an amount effective to enhance the animal's quality of life. Such compositions generally comprise:

[00129] (a) 26 wt. % to 35 wt. % of crude protein on a dry matter basis,

[00130] (b) 7.5 wt. % to 8.5 wt. % of crude fat on a dry matter basis,

[00131] (c) 20 wt. % to 30 wt. % of total dietary fiber on a dry matter basis, and

[00132] (d) 10 wt. % to 20 wt. % of crude fiber on a dry matter basis.

[00133] In another embodiment, the invention encompasses feline compositions that generally comprise:

[00134] (a) 30 wt. % to 37 wt. % of crude protein on a dry matter basis,

[00135] (b) 7.5 wt. % to 9 wt. % of crude fat on a dry matter basis,

[00136] (c) 30 wt. % to 35 wt. % of total dietary fiber on a dry matter basis, and

[00137] (d) 20 wt. % to 25 wt. % of crude fiber on a dry matter basis.

[00138] In another embodiment, the compositions generally comprise:

[00139] (a) at least one of the following:

[00140] (i) at least 0.05% (or 0.05% to 0.30%, or 0.1% to 0.30%, or 0.1% to 0.2%) DHA, and

[00141] (ii) at least 0.1% (or 0.1% to 0.5%, or 0.2% to 0.5%, or 0.2% to 0.3%) EPA,

[00142] (b) at least 15% (or 15% to 55%, or 30% to 55%, or 33% to 36%) protein,

[00143] (c) at least 9% (or 9% to 35%, or 18% to 35%, or 18% to 24%) fat, and

[00144] (d) at least one of the following:

[00145] (i) at least 250 IU/kg (or 250 IU/kg to 1500 IU/kg, or 500 IU/kg to 1500 IU/kg, or 500 IU/kg to 1100 IU/kg) vitamin E ,

[00146] (xii) at least 50 ppm (or 50 ppm to 300 ppm, or 100 ppm to 300 ppm, or 100 ppm to 200 ppm) vitamin C,

[00147] (xiii)at least 1100 ppm (or 1100 ppm to 3500 ppm, or 2300 ppm to 3500 ppm, or 2300 ppm to 2350 ppm) taurine, and

[00148] (xiv)at least 200 ppm (or 200 to 750 ppm, or 400 ppm to 750 ppm, or 400 to 525 ppm) carnitine, and

[00149] (xv) at least 0.05% (or 0.05% to 0.6%, or 0.1% to 0.6%, or 0.1% to 0.4%) cystine.

[00150] In another embodiment, the compositions generally comprise:

[00151] (a) 0.02% (or 0.05 % to 10%, or 0.1% to 6%) at least one omega-3 polyunsaturated fatty acid, and

[00152] (b) at least one of the following:

[00153] (xvi)10% to 55% (or 18% to 30%, or 33% to 55% or 18% to 20% or 33% to 36%) protein,

[00154] (xvii) 7% to 35% (or 18% to 35%, or 7% to 24%, or 14% to 24%, or 14% to 16% or 18% to 24%) fat,

[00155] (xviii) at least .05 (or 0.05 ppm to 7500 ppm, or 250 to 3600, or 250 ppm to 1650 ppm, or 5 ppm to 225 ppm, or 0.05 ppm to 2.4 ppm) antioxidant, and

[00156] (xix)at least 1000 ppm (or 1000 ppm to 5000 ppm, 3300 ppm to 5000 ppm, or 2000 ppm to 3000 ppm, or 3000 ppm to 4000 ppm) choline.

[00157] In another embodiment, the compositions generally comprise:

[00158] (a) at least one of the following:

[00159] (i) at least 0.02% (or 0.02% to 0.3%, or 0.05% to 0.3%, or 0.05% to 0.2%) DHA, and (ii) at least 0.1% (or 0.1% to 0.5%, or 0.2% to 0.5%, or 0.2% to 0.3%) EPA,

[00160] (b) at least 9% (or 9% to 30%, or 18% to 30%, or 18% to 20%) protein,

[00161] (c) at least 7% (or 7% to 24%, or 14% to 24%, or 14% to 16%) fat,

[00162] (d) at least one of the following:

[00163] (i) at least 250 IU/kg (or 250 IU/kg to 1500 IU/kg, or 500 IU/kg to 1500 IU/kg, or 500 IU/kg to 1000 IU/kg) vitamin E ,

[00164] (xx) at least 50 ppm (or 50 ppm to 500 ppm, or 100 ppm to 500 ppm, or 100 ppm to 301 ppm) vitamin C,

[00165] (xxi)at least 600 ppm (or 600 ppm to 2400 ppm, or 1260 ppm to 2400 ppm, or 1260 ppm to 1545 ppm) taurine, and

[00166] (xxii) at least 50 ppm (or 50 ppm to 200 ppm, or 100 to 160, or 100 to 155) lipoic acid, and

[00167] (xxiii) at least 50 ppm (or 50 ppm to 500 ppm, or 200 ppm to 500 ppm, or 200 ppm to 350 ppm) carnitine,

[00168] (e) at least 1000 ppm (or 1000 ppm to 3200 ppm, or 2000 ppm to 3200 ppm, or 2000 ppm to 2500 ppm) choline,

[00169] (f) at least 50 ppm (or 50 ppm to 150 ppm, or 100 ppm to 150 ppm, or 100 ppm to 110 ppm) manganese, and

[00170] (g) at least 0.4% (or 0.4% to 2%, or 0.9% to 2%, or 0.9% to 1.2%) lysine, and

[00171] (h) at least 0.4% to 1.5% methionine.

[00172] In another embodiment, the compositions generally comprise:

[00173] (a) at least one of the following:

[00174] (i) at least 0.02% (or 0.02% to 0.3%, or 0.05% to 0.3%, or 0.05% to 0.2%) DHA, and

[00175] (ii) at least 0.1% (or 0.1% to 0.5%, or 0.2% to 0.5%, or 0.2% to 0.3%) EPA,

[00176] (b) at least 9% (or 9% to 30%, or 18% to 30%, or 18% to 20%) protein,

[00177] (c) at least 7% (or 7% to 24%, or 14% to 24%, or 14% to 16%) fat,

[00178] (d) at least one of the following:

[00179] (i) at least 250 IU/kg (or 250 IU/kg to 1500 IU/kg, or 500 IU/kg to 1500 IU/kg, or 500 IU/kg to 1000 IU/kg) vitamin E ,

[00180] (xxiv) at least 50 ppm (or 50 ppm to 500 ppm, or 100 ppm to 500 ppm, or 100 ppm to 301 ppm) vitamin C,

[00181] (xxv) at least 600 ppm (or 600 ppm to 2400 ppm, or 1260 ppm to 2400 ppm, or 1260 ppm to 1575 ppm) taurine, and

[00182] (xxvi) at least 50 ppm (or 50 ppm to 200 ppm, or 100 to 160, or 100 to 155) lipoic acid, and

[00183] (xxvii) at least 50 ppm (or 50 ppm to 500 ppm, or 200 ppm to 500 ppm, or 200 ppm to 350 ppm) carnitine,

[00184] (e) at least 1000 ppm (or 1000 ppm to 3200 ppm, or 2000 ppm to 3200 ppm, or 2000 ppm to 2500 ppm) choline,

[00185] (f) at least 50 ppm (or 50 ppm to 150 ppm, or 100 ppm to 150 ppm, or 100 ppm to 110 ppm) manganese, and

[00186] (g) at least 0.4% (or 0.4% to 2%, or 0.9% to 2%, or 0.9% to 1.2%) lysine, and

[00187] (h) at least 0.4% to 1.5% methionine.

[00188] In another embodiment, the compositions generally comprise:

[00189] (a) at least one of the following:

[00190] (i) at least 0.05% (or 0.05% to 0.30%, or 0.1% to 0.30%, or 0.1% to 0.2%) DHA, and

[00191] (ii) at least 0.1% (or 0.1% to 0.5%, or 0.2% to 0.5%, or 0.2% to 0.3%) EPA,

[00192] (b) at least 15% (or 15% to 55%, or 30% to 55%, or 33% to 36%) protein,

[00193] (c) at least 9% (or 9% to 35%, or 18% to 35%, or 18% to 24%) fat,

[00194] (d) at least one of the following:

[00195] (i) at least 250 IU/kg (or 250 IU/kg to 1500 IU/kg, or 500 IU/kg to 1500 IU/kg, or 500 IU/kg to 1100 IU/kg) vitamin E ,

[00196] (xxviii) at least 50 ppm (or 50 ppm to 300 ppm, or 100 ppm to 300 ppm, or 100 ppm to 200 ppm) vitamin C,

[00197] (xxix) at least 1100 ppm (or 1100 ppm to 3500 ppm, or 2300 ppm to 3500 ppm, or 2300 ppm to 2350 ppm) taurine, and

[00198] (xxx) at least 200 ppm (or 200 to 750 ppm, or 400 ppm to 750 ppm, or 400 to 525 ppm) carnitine, and

[00199] (xxxi) at least 0.05% (or 0.05% to 0.6%, or 0.1% to 0.6%, or 0.1% to 0.4%) cystine,

[00200] (e) at least 1600 ppm (or 1600 ppm to 5000 ppm, or 3300 ppm to 5000 ppm, or 3300 ppm to 3400 ppm) choline,

[00201] (f) at least 50 ppm (or 50 ppm to 150 ppm, or 100 ppm to 150 ppm, or 100 ppm to 110 ppm) manganese, and

[00202] (g) at least 0.7% (or 0.7% to 3%, or 1.4% to 3%, or 1.4% to 1.7%) lysine, and

[00203] (h) at least 0.4% to 1.5% methionine.

Methods Of Treating Or Preventing Diseases And Disorders

[00204] The invention encompasses methods for treating or preventing diseases and disorders, including the administration of the compositions of the invention that are effective in modulating the expression and/or activity of proteins associated with obesity in animals both *in vitro* and *in vivo*. The inventors have surprisingly found that the compositions of the invention are effective in modulating proteins associated with obesity in animals. Without being limited by theory, it is believed that modulation of protein expression and/or activity associated with obesity in animals is useful in treating or preventing a disorder associated with abnormal blood glucose levels, weight gain, or fat depot levels. The invention further encompasses compositions and formulations that are useful in modulating protein activity in overweight and/or obese animals. The invention also encompasses methods of modulating protein or gene activity including administering subject, preferably to a companion mammal in need of said treatment or prevention a therapeutically or prophylactically effective amount of a composition to modulate the activity of the protein or gene associate with obesity in the subject. In an illustrative embodiment, the agent for modulating lyn kinase activity is a compound of the invention.

[00205] In one embodiment, a composition of the invention is administered to a mammal, preferably a companion animal, with a cardiovascular disease, a dyslipidemia, a dyslipoproteinemia, a disorder of glucose metabolism, metabolic syndrome (*i.e.*, Syndrome X), a PPAR-associated disorder, septicemia, a thrombotic disorder, type II diabetes, obesity, pancreatitis, hypertension, a renal disease, or inflammation.

[00206] In one embodiment, "treatment" or "treating" refers to an amelioration of a disease or disorder, or at least one discernible symptom thereof, preferably associated with obesity. In another embodiment, "treatment" or "treating" refers to an amelioration of at least one measurable physical parameter, not necessarily discernible by the animal. In yet another embodiment, "treatment" or "treating" refers to inhibiting the progression of a disease or disorder, either physically, e.g., stabilization of a discernible symptom, physiologically, e.g., stabilization of a physical parameter, or both. In yet another embodiment, "treatment" or "treating" refers to delaying the onset of a disease or disorder.

[00207] In certain embodiments, the compositions of the invention are administered to a patient, preferably a companion animal, as a preventative measure against such diseases. As used herein, "prevention" or "preventing" refers to a reduction of the risk of acquiring a given disease or disorder. In a preferred mode of the embodiment, the compositions of the present invention are administered as a preventative measure to a patient, preferably a companion animal having a genetic predisposition to a cardiovascular disease, a dyslipidemia, a dyslipoproteinemia, a disorder of glucose metabolism, metabolic syndrome (*i.e.*, Syndrome X), a PPAR-associated disorder, septicemia, a thrombotic disorder, type II diabetes, obesity, pancreatitis, hypertension, a renal disease, or inflammation.

[00208] In another illustrative mode of the embodiment, the compositions of the invention are administered as a preventative measure to a companion animal having a predisposition to a cardiovascular disease, a dyslipidemia, a dyslipoproteinemia, a disorder of glucose metabolism, metabolic syndrome (*i.e.*, Syndrome X), a PPAR-associated disorder, septicemia, a thrombotic disorder, type II diabetes, obesity, pancreatitis, hypertension, a renal disease, or inflammation. Accordingly, the compositions of the invention may be used for the prevention of one disease or disorder and concurrently treating another (*e.g.*, prevention of obesity while treating diabetes; prevention of inflammation while treating a cardiovascular disease).

Cardiovascular Diseases for Treatment or Prevention

[00209] The invention provides methods for the treatment or prevention of a cardiovascular disease, comprising administering to a companion animal a therapeutically effective amount of a composition of the invention and a pharmaceutically acceptable vehicle. In some embodiments, the cardiovascular disease is associated with abnormal/altered protein expression. As used herein, the term "cardiovascular diseases" refers to diseases of the heart and circulatory system. These diseases are often associated with dyslipoproteinemias and/or dyslipidemias. Cardiovascular diseases, which the compositions of the invention are useful for preventing or treating include, but are not limited to, arteriosclerosis; atherosclerosis; stroke; ischemia; endothelium dysfunctions, in particular those dysfunctions affecting blood vessel elasticity; peripheral vascular disease; coronary heart disease; myocardial infarction; cerebral infarction and restenosis.

Dyslipidemias for Treatment or Prevention

[00210] The present invention provides methods for the treatment or prevention of a dyslipidemia comprising administering to a companion animal a therapeutically effective amount of a composition of the invention and a pharmaceutically acceptable vehicle. In some embodiments, the dyslipidemia is associated with abnormal/altered lyn kinase activity and/or expression. As used herein, the term "dyslipidemias" refers to disorders that lead to or are manifested by aberrant levels of circulating lipids. To the extent that levels of lipids in the blood are too high, the compositions of the invention are administered to a companion animal to restore normal levels. Normal levels of lipids are reported in medical treatises known to those of skill in the art. For example, recommended blood levels of LDL, HDL, free triglycerides and others parameters relating to lipid metabolism can be found at the web site of the American Heart Association and that of the National Cholesterol Education Program of the National Heart, Lung and Blood Institute. At the present time, the recommended level of HDL cholesterol in the blood is above 35 mg/dL; the recommended level of LDL cholesterol in the blood is below 130 mg/dL; the recommended LDL:HDL cholesterol ratio in the blood is below 5:1, ideally 3.5:1; and the recommended level of free triglycerides in the blood is less than 200 mg/dL.

[00211] Dyslipidemias which the compositions of the invention are useful for preventing or treating include but are not limited to hyperlipidemia and low blood levels of high density lipoprotein (HDL) cholesterol. In certain embodiments, the hyperlipidemia for prevention or treatment by the compounds of the present invention is familial hypercholesterolemia; familial combined hyperlipidemia; reduced or deficient lipoprotein lipase levels or activity, including reductions or deficiencies resulting from lipoprotein lipase mutations; hypertriglyceridemia; hypercholesterolemia; high blood levels of ketone bodies (*e.g.*, β-OH butyric acid); high blood levels of Lp(a) cholesterol; high blood levels of low density lipoprotein (LDL) cholesterol; high blood levels of very low density lipoprotein (VLDL) cholesterol and high blood levels of non-esterified fatty acids.

[00212] The present invention further provides methods for altering lipid metabolism in a patient, for example, reducing LDL in the blood of a companion

animal, reducing free triglycerides in the blood of a patient, increasing the ratio of HDL to LDL in the blood of a patient, and inhibiting saponified and/or non-saponified fatty acid synthesis, said methods comprising administering to the patient a composition comprising a compound of the invention in an amount effective alter lipid metabolism.

Dyslipoproteinemias for Treatment or Prevention

[00213] The invention provides methods for the treatment or prevention of a dyslipoproteinemia comprising administering to a companion animal a therapeutically effective amount of a composition of the invention and a pharmaceutically acceptable vehicle. As used herein, the term "dyslipoproteinemias" refers to disorders that lead to or are manifested by aberrant levels of circulating lipoproteins. To the extent that levels of lipoproteins in the blood are too high, the compositions of the invention are administered to a patient to restore normal levels. Conversely, to the extent that levels of lipoproteins in the blood are too low, the compositions of the invention are administered to a patient to restore normal levels. Normal levels of lipoproteins are reported in medical treatises known to those of skill in the art.

[00214] Dyslipoproteinemias, which the compositions of the present invention are useful for preventing or treating include, but are not limited to, high blood levels of LDL; high blood levels of apolipoprotein B (apo B); high blood levels of Lp(a); high blood levels of apo(a); high blood levels of VLDL; low blood levels of HDL; reduced or deficient lipoprotein lipase levels or activity, including reductions or deficiencies resulting from lipoprotein lipase mutations; hypoalphalipoproteinemia; lipoprotein abnormalities associated with diabetes; lipoprotein abnormalities associated with type II diabetes, obesity; lipoprotein abnormalities associated with Alzheimer's Disease; and familial combined hyperlipidemia.

Glucose Metabolism Disorders for Treatment or Prevention

[00215] The invention provides methods for the treatment or prevention of a glucose metabolism disorder, comprising administering to a companion animal a therapeutically effective amount of a composition of the invention and a pharmaceutically acceptable vehicle. As used herein, the term "glucose

metabolism disorders" refers to disorders that lead to or are manifested by aberrant glucose storage and/or utilization. To the extent that indicia of glucose metabolism (*i.e.*, blood insulin, blood glucose) are too high, the compositions of the invention are administered to a patient to restore normal levels. Conversely, to the extent that indicia of glucose metabolism are too low, the compositions of the invention are administered to a patient to restore normal levels. Normal indicia of glucose metabolism are reported in medical treatises known to those of skill in the art. In some embodiments, the glucose metabolism disorder is associated with abnormal/altered lyn kinase activity and/or expression.

[00216] Glucose metabolism disorders which the compositions of the present invention are useful for preventing or treating include but are not limited to impaired glucose tolerance; insulin resistance; insulin resistance related breast, colon or prostate cancer; diabetes, including but not limited to non-insulin dependent diabetes mellitus (NIDDM), insulin dependent diabetes mellitus (IDDM), gestational diabetes mellitus (GDM), and maturity onset diabetes of the young (MODY); pancreatitis; hypertension; polycystic ovarian disease; and high levels of blood insulin and/or glucose.

[00217] The invention further provides methods for altering glucose metabolism in a patient, for example to increase insulin sensitivity and/or oxygen consumption of a companion animal, said methods comprising administering to the companion animal a composition comprising a compound of the invention in an amount effective to alter glucose metabolism.

Treatment or Prevention of Metabolic Syndrome

[00218] As used herein, "treatment or prevention of Syndrome X or Metabolic Syndrome" encompasses treatment or prevention of a symptom associated with metabolic syndrome including, but not limited to, impaired glucose tolerance, hypertension and dyslipidemia and/or dyslipoproteinemia. In some embodiments, the metabolic syndrome is associated with abnormal/altered lyn kinase activity and/or expression

[00219] Metabolic syndrome is characterized by a group of metabolic risk factors in a person. Risk factors that are associated with metabolic syndrome that can be

treated or prevented by administering a composition comprising a compound of the invention include, but are not limited to, central obesity (*i.e.*, excessive fat tissue in and around the abdomen); atherogenic dyslipidemia (blood fat disorders - mainly high triglycerides and low HDL cholesterol - that foster plaque buildups in artery walls); raised blood pressure (130/85 mmHg or higher); insulin resistance or glucose intolerance (the body can't properly use insulin or blood sugar); prothrombotic state (*e.g.*, high fibrinogen or plasminogen activator inhibitor [–1] in the blood); and a proinflammatory state (*e.g.*, elevated high-sensitivity C-reactive protein in the blood).

[00220] The underlying causes of this syndrome are overweight/obesity, physical inactivity and genetic factors. companion animal with metabolic syndrome are at increased risk of coronary heart disease, other diseases related to plaque buildups in artery walls (*e.g.*, stroke and peripheral vascular disease) and type 2 diabetes.

[00221] Metabolic syndrome is closely associated with a generalized metabolic disorder called insulin resistance, in which the body can't use insulin efficiently. This is why the metabolic syndrome is also called the insulin resistance syndrome.

[00222] Some companion animal are genetically predisposed to insulin resistance. Acquired factors, such as excess body fat and physical inactivity, can elicit insulin resistance and the metabolic syndrome in these people. Most companion animal with insulin resistance have central obesity. The biologic mechanisms at the molecular level between insulin resistance and metabolic risk factors aren't fully understood and appear to be complex.

[00223] The compositions of the invention are therefore useful in treating or preventing metabolic syndrome and disorders and risk factors associated with metabolic syndrome.

Treatment or Prevention Type II Diabetes

[00224] As used herein, "treatment or prevention of type II diabetes" encompasses treatment or prevention of a complication associated with type II diabetes including, but not limited to, retinopathy (*i.e.*, blindness); neuropathy (*i.e.*, nerve damage) which leads to foot ulcers, gangrene, and amputations; kidney damage, which leads to dialysis; and cardiovascular disease. In some embodiments, the type

II diabetes is associated with abnormal/altered lyn kinase activity and/or expression.

[00225] Type II diabetes is associated with obesity and with aging. It is a lifestyle-dependent disease, and has a strong genetic component (concordance in twins is 80-90%). The problem seems not so much in insulin production, but that when the insulin reaches its target cells, it doesn't work correctly. Most Type II diabetes patients initially have high insulin levels along with high blood sugar. However, since sugar signals the pancreas to release insulin, Type II diabetics eventually become resistant to that signal and the endocrine-pancreas soon will not make enough insulin. These companion animals end up managing the disease with insulin and they need much higher doses because they are resistant to it.

[00226] When a companion animal takes in a high load of sugar, the sugar stimulates the pancreas to release insulin. The targets for insulin are muscle, fat, and liver cells. These cells have insulin receptor sites on the outside of the cell membrane. For most companion animals, when insulin has bound to the receptors, a cascade of events begins, which leads to sugar being transported from the blood into the interior of the cell. In Type II diabetics, even when insulin is present on the cell membrane, the process doesn't work. The glucose is never taken up into the cell and remains in the bloodstream.

[00227] The liver is responsible for glucose production and insulin is the regulatory agent of production. A high blood sugar content causes the pancreas to release insulin, and the insulin should signal the liver to stop making sugars. But, in diabetics, there's resistance to that signal and the liver keeps producing glucose. Hyperglycemia leads to glucose toxicity.

[00228] It is not high blood sugar that is the disease process of diabetes, but complications from the high blood sugar. A major problem faced by doctors is that some people with high blood sugar feel fine; it's hard to treat diseases that are asymptomatic since most people don't want to take a pill for something that they don't feel bad about. The compositions comprising a compound of the invention are therefore useful in treating or preventing type II diabetes or complications arising from type II diabetes and disorders and risk factors associated with metabolic syndrome. Complications of diabetes include, but are not limited to, diabetic neuropathy, diabetic retinopathy, erectile dysfunction, and kidney disease

and the compounds of the invention are useful in treating or preventing these complications.

Treatment or Prevention of Obesity

[00229] As used herein, "treatment or prevention of obesity" encompasses treatment or prevention of a complication associated with obesity. Complications of obesity include, but are not limited to, hypercholesterolemia, hypertension, dyslipidemia (for example, high total cholesterol or high levels of triglycerides), type 2 diabetes, coronary heart disease, stroke, gallbladder disease, osteoarthritis, sleep apnea and respiratory problems, and some cancers (endometrial, breast, and colon). In some embodiments, the obesity is associated with abnormal/altered lyn kinase activity and/or expression

Other Diseases for Treatment or Prevention

[00230] The present invention provides methods for the treatment or prevention of septicemia, thrombotic disorders, pancreatitis, hypertension, inflammation, and impotence, comprising administering to a patient a therapeutically effective amount of a composition comprising a compound of the invention and a pharmaceutically acceptable vehicle. In some embodiments, these disorders are associated with abnormal/altered lyn kinase activity and/or expression

[00231] As used herein, "treatment or prevention of septicemia" encompasses treatment or prevention of septic shock.

[00232] As used herein, "treatment or prevention of thrombotic disorders" encompasses treatment or prevention of high blood levels of fibrinogen and promotion of fibrinolysis.

[00233] In addition to treating or preventing obesity, the compositions of the invention can be administered to an individual to promote weight reduction of the individual.

Kits of the Invention

[00234] 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.

[00235] In another aspect, the present invention provides a means for communicating information or instructions for one or more of (1) using the polynucleotides of the present invention for detecting the expression of genes differentially expressed in overweight 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 overweight 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 overweight 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 overweight 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 overweight 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 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.

[00236] Disclosed herein are typical illustrative 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

[00237] 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.

[00238] 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.

[00239] 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.

[00240] Preparations: Prepare 50mL polypropylene tubes with 4mL TRIzol® (one tube for each tissue selected for RNA isolation).

[00241] 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 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.

[00242] 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 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.

[00243] 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.

[00244] 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.

[00245] Reagents: 10X PBS, deionized H_2O, absolute ethanol, RNA Storage Solution, β-Mercaptoethanol, RNase Zap®, Buffer RLT, and Buffer RW1 and Buffer RPE (provided in the RNeasy Mini Kit)

[00246] 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.

[00247] 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.

[00248] 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.

[00249] 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

[00250] Using the Agilent 2100 Bioanalyzer and the RNA 6000 Nano Assay, analyze RNA isolated from cultured mammalian cells, lymphocytes or tissues for quality.

[00251] 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.

[00252] 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.

[00253] 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

[00254] 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.

[00255] 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.

[00256] 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.

[00257] Procedure: follow all procedures exactly as described in GeneChip Expression Analysis Technical Manual (Affymetrix Copyright 1999-2003). Use 5 microgram of total RNA for the first strand cDNA synthesis. Use either Peltier Thermal Cycler PTC-200 or heat block for temperature control on reactions and probe denaturing. The quality control is performed using RNA NanoDrop chips with BioAnalyer 2100. Use 100 Format (Midi Array) for the canine genechip.

Example 1

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

[00258] Adipose tissue samples are obtained from 18 (3 lean and 15 fat) or lymphocytes obtained from 44 (12 lean and 32 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 overweight if it has a body condition score of 4 or higher and a total body fat percentage of 30% or higher. All solid tissue samples were snap frozen in liquid nitrogen immediately after removal from the animal. The lymphocytes were isolated using BD Vacutainer® CPT™ Cell Preparation Tube according to manufactuerers instructions and were also snap frozen until needed.

The samples were all analyzed using Affymetrix Canine-2 GeneChips® according to manufacturers recommendations in order to determine which genes are differentially expressed in overweight animals compared to lean animals.

The data was analyzed using Partek® GS (Partek Inc., St. Charles, MO) for Gene Expression Data software (Partek Incorporated, 12747 Olive Blvd., Suite 205, St. Louis, Missouri 63141, U.S.A. http://www.partek.com/partekgs_geneexpression). The Robust Multichip Average (RMA) algorithm (Rafael. A. Irizarry, Benjamin

M. Bolstad, Francois Collin, Leslie M. Cope, Bridget Hobbs and Terence P. Speed (2003), Summaries of Affymetrix GeneChip probe level data *Nucleic Acids Research* 31(4):e15) was used for background adjustment, normalization, and probe-level summarization of the GeneChip® samples. The ANOVA analysis was performed to find significant differentially expressed genes between any two groups with a minimal FDR control at 0.1 (or p-value of 0.1 or 0.05 if power was not sufficient to apply FDR) and a fold change of 1.3 in each direction. Our empirical studies have revealed that the Canine-2 GeneChips® have an associated background noise level of 1.3 fold. Therefore, all analyses presented in this report employed a +/- 1.3 fold cut-off. Furthermore, the false discovery rate threshold of 0.1 (means that 10% of observations are due to chance) was chosen as the minimum level of acceptable statistical significance for studies containing a minimum of 12 animals per group. Studies with smaller numbers of animals do not have enough power to allow for the proper application of the FDR. Results are provided in the tables below.

Table 1:Genes Differentially Expressed in Adipose Tissue in Fat Animals compared to Lean Animals

Fat vs Lean (Adipose Tissue Gene Expression Comparison) allgenelist FC cutoff: 1.3; P-val cutofff: 0.1; Q-val cutoff: 1							
#samples in group-1 (ADP FAT):·15 group-2 (LEAN): 3							
Fold change > 1 implies probes are UP regulated in ADP FAT samples.							
Probe	**P-Value**	**Q-Value**	**Fold-Change**	**Top BLAST Annot.**	**Top Hit Accn.**	**Gene Symbol**	**Gene Desc.**
Cfa.19142.1.S1_s_at	8.81E-02	1.00E+00	1.4	PREDICTED: Equus caballus septin 7 (SEPT7); mRNA	XM_001500153	7-Sep	septin 7
Cfa.6037.1.S1_at	9.81E-02	1.00E+00	0.59	PREDICTED: Canis familiaris similar to Alpha-2-macroglobulin precursor (Alpha-2-M) (LOC477699); mRNA	XM_534893	A2M	alpha-2-macroglobulin
Cfa.6037.1.S1_s_at	5.06E-02	1.00E+00	0.54	PREDICTED: Canis familiaris similar to Alpha-2-macroglobulin precursor (Alpha-2-M) (LOC477699); mRNA	XM_534893	A2M	alpha-2-macroglobulin
Cfa.436.3.S1_a_at	4.36E-02	1.00E+00	0.64	PREDICTED: Canis familiaris similar to alpha/beta hydrolase fold protein; transcript variant 2 (LOC479037); mRNA	XM_536188	ABHD2	abhydrolase domain containing 2
CfaAffx.18000.1.S1_at	5.79E-02	1.00E+00	0.71	PREDICTED: Canis familiaris similar to alpha/beta hydrolase fold protein; transcript variant 3 (LOC479037); mRNA	XM_844639	ABHD2	abhydrolase domain containing 2
CfaAffx.19895.1.S1_s_at	3.87E-02	1.00E+00	0.76	PREDICTED: Canis familiaris similar to Abl-interactor 2 (Abelson interactor 2) (Abi-2) (Abl binding protein 3) (AblBP3) (Arg binding protein 1) (ArgBP1) (LOC488485); mRNA	XM_545606	ABI2	abl interactor 2
CfaAffx.7032.1.S1_at	4.16E-02	1.00E+00	0.75	PREDICTED: Canis familiaris similar to ankyrin repeat and BTB (POZ) domain containing 1 isoform 2 (LOC609299); mRNA	XM_846538	ABTB1	ankyrin repeat and BTB (POZ) domain containing 1
CfaAffx.17376.1.S1_s_at	6.34E-02	1.00E+00	0.34	Homo sapiens cDNA FLJ60371 complete cds; highly similar to Acetyl-CoA carboxylase 2 (EC 6.4.1.2)	AK302502	ACACB	acetyl-Coenzyme A carboxylase beta
CfaAffx.29929.1.S1_s_at	6.27E-02	1.00E+00	1.41	PREDICTED: Canis familiaris similar to Cytosolic acyl coenzyme A thioester hydrolase (Long chain acyl-CoA thioester hydrolase) (CTE-II) (CTE-IIa) (Brain acyl-CoA hydrolase) (LOC479589); mRNA	XM_536727	ACOT7	acyl-CoA thioesterase 7

Table 1:Genes Differentially Expressed in Adipose Tissue in Fat Animals compared to Lean Animals

Cfa.14387.1.A1_s_at	7.17E-02	1.00E+00	0.52	PREDICTED: Canis familiaris similar to acid phosphatase 6; lysophosphatidic (LOC475822); mRNA	XM_533030	ACP6	acid phosphatase 6, lysophosphatidic
Cfa.11382.1.A1_s_at	2.33E-02	1.00E+00	0.53	PREDICTED: Canis familiaris similar to F46E10.1a (LOC480551); mRNA	XM_537673	ACSF2	acyl-CoA synthetase family member 2
Cfa.11382.1.A1_at	6.66E-02	1.00E+00	0.63	PREDICTED: Canis familiaris similar to F46E10.1a (LOC480551); mRNA	XM_537673	ACSF2	acyl-CoA synthetase family member 2
Cfa.18640.1.S1_s_at	4.29E-02	1.00E+00	1.33	PREDICTED: Canis familiaris similar to Long-chain-fatty-acid -CoA ligase 5 (Long-chain acyl-CoA synthetase 5) (LACS 5); transcript variant 5 (LOC477820); mRNA	XM_859627	ACSL5	acyl-CoA synthetase long-chain family member 5
Cfa.17404.1.S1_s_at	3.27E-02	1.00E+00	1.33	PREDICTED: Canis familiaris similar to Long-chain-fatty-acid -CoA ligase 5 (Long-chain acyl-CoA synthetase 5) (LACS 5); transcript variant 5 (LOC477820); mRNA	XM_859627	ACSL5	acyl-CoA synthetase long-chain family member 5
CfaAffx.4436.1.S1_at	4.61E-02	1.00E+00	0.77	PREDICTED: Canis familiaris similar to ARP1 actin-related protein 1 homolog B; centractin beta (LOC611680); mRNA	XM_849380	ACTR1B	ARP1 actin-related protein 1 homolog B, centractin beta (yeast)
Cfa.17603.1.S1_at	9.62E-02	1.00E+00	0.72	PREDICTED: Canis familiaris similar to amino-terminal enhancer of split isoform a (LOC485064); mRNA	XM_542182	AES	amino-terminal enhancer of split
Cfa.19737.1.S1_at	5.56E-02	1.00E+00	1.33	Homo sapiens aryl hydrocarbon receptor; mRNA (cDNA clone MGC:87401 IMAGE:30342582); complete cds	BC070080	AHR	aryl hydrocarbon receptor

Table 1:Genes Differentially Expressed in Adipose Tissue in Fat Animals compared to Lean Animals

Cfa.6363.1.A1_s_at	6.38E-02	1.00E+00	0.75	PREDICTED: Macaca mulatta v-akt murine thymoma viral oncogene homolog 3 (AKT3); mRNA	XM_001104624	AKT3	v-akt murine thymoma viral oncogene homolog 3
Cfa.4557.1.S1_at	7.98E-03	1.00E+00	0.76	PREDICTED: Canis familiaris protein kinase B gamma-like protein; transcript variant 1 (AKT3); mRNA	XM_547496	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)
CfaAffx.24220.1.S1_at	1.43E-02	1.00E+00	0.66	PREDICTED: Canis familiaris protein kinase B gamma-like protein; transcript variant 3 (AKT3); mRNA	XM_858162	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)
CfaAffx.22870.1.S1_s_at	4.57E-03	1.00E+00	0.73	PREDICTED: Canis familiaris alkaline phosphatase (ALP); mRNA	XM_535374	ALPL	alkaline phosphatase, liver/bone/kidney
CfaAffx.10568.1.S1_s_at	8.45E-02	1.00E+00	0.75	PREDICTED: Canis familiaris similar to T12A2.1 (LOC475432); mRNA	XM_532656	AMDHD1	amidohydrolase domain containing 1
Cfa.14585.1.S1_at	6.21E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to MASK-4E-BP3 protein; transcript variant 1 (LOC612748); mRNA	XM_535210	ANKHD1	ankyrin repeat and KH domain containing 1
CfaAffx.9676.1.S1_s_at	3.61E-02	1.00E+00	0.67	PREDICTED: Canis familiaris similar to MASK-4E-BP3 protein; transcript variant 1 (LOC612748); mRNA	XM_535210	ANKHD1	ankyrin repeat and KH domain containing 1
Cfa.1079.1.S1_at	4.84E-02	1.00E+00	1.66	PREDICTED: Equus caballus ankyrin repeat domain 26; transcript variant 1 (ANKRD26); mRNA	XM_001495349	ANKRD26	ankyrin repeat domain 26

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Cfa.19611.1.S1_a_at	4.41E-02	1.00E+00	1.62	Bos taurus ankyrin repeat domain 29; mRNA (cDNA clone MGC:152539 IMAGE:8185222); complete cds	BC149707	ANKRD29	ankyrin repeat domain 29
CfaAffx.27839.1.S1_s_at	1.36E-02	1.00E+00	1.94	PREDICTED: Canis familiaris similar to ankyrin repeat domain 29 (LOC606927); mRNA	XM_843406	ANKRD29	ankyrin repeat domain 29
CfaAffx.28621.1.S1_at	7.16E-02	1.00E+00	0.52	PREDICTED: Canis familiaris hypothetical LOC480209 (LOC480209); mRNA	XM_537333	APCDD1	adenomatosis polyposis coli down-regulated 1
Cfa.1417.1.S1_at	9.62E-02	1.00E+00	1.54	PREDICTED: Canis familiaris similar to Apolipoprotein D precursor (Apo-D) (ApoD); transcript variant 1 (LOC478604); mRNA	XM_535780	APOD	apolipoprotein D
Cfa.21549.1.S1_at	7.65E-02	1.00E+00	0.65	PREDICTED: Canis familiaris similar to Aquaporin 3 (LOC611792); mRNA	XM_849503	AQP3	aquaporin 3 (Gill blood group)
Cfa.21549.1.S1_s_at	7.57E-02	1.00E+00	0.49	PREDICTED: Canis familiaris similar to Aquaporin 3 (LOC611792); mRNA	XM_849503	AQP3	aquaporin 3 (Gill blood group)
Cfa.11933.1.A1_at	7.36E-02	1.00E+00	1.63	PREDICTED: Canis familiaris similar to Rho-GTPase-activating protein 9 (LOC474413); mRNA	XM_531645	ARHGAP9	Rho GTPase activating protein 9
CfaAffx.18645.1.S1_at	7.92E-02	1.00E+00	0.64	PREDICTED: Pan troglodytes ADP-ribosylation factor-like 4C; transcript variant 2 (ARL4C); mRNA	XM_001151934	ARL4C	ADP-ribosylation factor-like 4C
CfaAffx.12981.1.S1_s_at	8.12E-02	1.00E+00	0.64	PREDICTED: Canis familiaris similar to Aryl hydrocarbon receptor nuclear translocator-like protein 1 (Brain and muscle ARNT-like 1) (Member of PAS protein 3) (Basic-helix-loop-helix-PAS orphan MOP3) (bHLH-PAS protein JAP3); transcript variant 3 (LOC476860); mRNA	XM_859290	ARNTL	aryl hydrocarbon receptor nuclear translocator-like
CfaAffx.23219.1.S1_s_at	7.86E-02	1.00E+00	0.68	PREDICTED: Canis familiaris similar to arrestin domain containing 2 isoform 2; transcript variant 3 (LOC609489); mRNA	XM_860432	ARRDC2	arrestin domain containing 2
CfaAffx.3339.1.S1_at	9.06E-02	1.00E+00	0.76	PREDICTED: Canis familiaris similar to alkaline ceramidase 2 (LOC481553); mRNA	XM_538674	ASAH3L	N-acylsphingosine amidohydrolase 3-like

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CfaAffx.26949.1.S1_at	7.35E-02	1.00E+00	0.55	PREDICTED: Canis familiaris similar to ankyrin repeat and SOCS box-containing protein 2 (predicted); transcript variant 1 (LOC490836); mRNA	XM_547958	ASB2	ankyrin repeat and SOCS box containing 2
Cfa.10230.1.A1_at	7.69E-02	1.00E+00	1.35	PREDICTED: Canis familiaris similar to ATPase; aminophospholipid transporter (APLT); class I; type 8A; member 1; transcript variant 2 (LOC607976); mRNA	XM_853476	ATP8A1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1
Cfa.16355.1.S1_s_at	9.25E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to Serine/threonine-protein kinase 12 (Aurora- and Ipl1-like midbody-associated protein 1) (AIM-1) (Aurora/IPL1-related kinase 2) (Aurora-related kinase 2) (STK-1) (Aurora-B); transcript variant 4 (LOC479492); mRNA	XM_854991	AURKB	aurora kinase B
CfaAffx.17802.1.S1_at	9.59E-02	1.00E+00	1.3	PREDICTED: Canis familiaris similar to Beta-1;4-galactosyltransferase 5 (Beta-1;4-GalTase 5) (Beta4Gal-T5) (b4Gal-T5) (UDP-galactose:beta-N-acetylglucosamine beta-1;4-galactosyltransferase 5) (UDP-Gal:beta-GlcNAc beta-1;4-galactosyltransferase 5) (Beta-1;4-GalT II)... (LOC485920); mRNA	XM_543044	B4GALT5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5
CfaAffx.6868.1.S1_at	5.74E-02	1.00E+00	0.73	PREDICTED: Canis familiaris similar to BMP and activin membrane-bound inhibitor homolog precursor (Putative transmembrane protein NMA) (Non-metastatic gene A protein); transcript variant 1 (LOC487081); mRNA	XM_544209	BAMBI	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)
CfaAffx.1768.1.S1_s_at	5.53E-02	1.00E+00	1.46	PREDICTED: Canis familiaris similar to HLA-B associated transcript 2; transcript variant 2 (LOC481713); mRNA	XM_844311	BAT2	HLA-B associated transcript 2
Cfa.110.1.S1_s_at	3.91E-02	1.00E+00	0.69	Canis lupus familiaris bcl-2 mRNA for Bcl-2; partial cds	AB116145	BCL2	B-cell CLL/lymphoma 2

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Cfa.10375.2.A1_at	9.45E-02	1.00E+00	0.74	Homo sapiens B-cell CLL/lymphoma 2 (BCL2); nuclear gene encoding mitochondrial protein; transcript variant alpha; mRNA	NM_000633	BCL2	B-cell CLL/lymphoma 2
Cfa.7221.1.A1_at	2.03E-02	1.00E+00	0.73	Bos taurus BCL2-like 1; mRNA (cDNA clone MGC:139852 IMAGE:8284203); complete cds	BC133281	BCL2L1	BCL2-like 1
CfaAffx.24480.1.S1_at	5.83E-02	1.00E+00	1.35	PREDICTED: Canis familiaris similar to B-cell CLL/lymphoma 6; member B (zinc finger protein) (LOC489459); mRNA	XM_546577	BCL6B	B-cell CLL/lymphoma 6, member B (zinc finger protein)
Cfa.7153.1.A1_s_at	4.00E-02	1.00E+00	0.41	PREDICTED: Canis familiaris similar to Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A); transcript variant 1 (LOC477162); mRNA	XM_534351	BMP2	bone morphogenetic protein 2
CfaAffx.20448.1.S1_at	9.88E-02	1.00E+00	0.76	PREDICTED: Canis familiaris similar to Zinc finger protein basonuclin 1 (LOC488756); mRNA	XM_545874	BNC1	basonuclin 1
CfaAffx.28168.1.S1_at	6.80E-02	1.00E+00	0.69	PREDICTED: Canis familiaris similar to BTB/POZ domain containing protein 6 (Lens BTB domain protein); transcript variant 2 (LOC611389); mRNA	XM_863593	BTBD6	BTB (POZ) domain containing 6
CfaAffx.13161.1.S1_s_at	2.64E-02	1.00E+00	0.58	PREDICTED: Canis familiaris similar to BTG3 protein (Tob5 protein) (Abundant in neuroepithelium area protein); transcript variant 2 (LOC487695); mRNA	XM_544819	BTG3	BTG family, member 3
Cfa.10545.2.S1_s_at	4.00E-02	1.00E+00	0.72	PREDICTED: Canis familiaris similar to Brix domain containing protein 1; transcript variant 2 (LOC475029); mRNA	XM_849359	BXDC1	brix domain containing 1
Cfa.11274.1.A1_at	8.77E-02	1.00E+00	0.71	PREDICTED: Macaca mulatta similar to immunoglobulin superfamily; member 4A isoform a; transcript variant 3 (LOC695983); mRNA	XM_001089381	CADM1	cell adhesion molecule 1
Cfa.3402.2.A1_at	8.07E-02	1.00E+00	1.51	PREDICTED: Canis familiaris similar to calumenin precursor; transcript variant 4 (LOC475201); mRNA	XM_853521	CALU	calumenin
CfaAffx.28438.1.S1_at	8.34E-02	1.00E+00	0.75	PREDICTED: Equus caballus caspase recruitment domain family; member 6 (CARD6); mRNA	XM_001916765	CARD6	caspase recruitment domain family, member 6

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CfaAffx.30657.1.S1_at	8.73E-02	1.00E+00	0.48	similar to Kynurenine--oxoglutarate transaminase I (Kynurenine aminotransferase I) (KATI) (Glutamine--phenylpyruvate transaminase) (Glutamine transaminase K) (GTK) (Cysteine-S-conjugate beta-lyase) (LOC491310); mRNA	XM_548431	CCBL1	cysteine conjugate-beta lyase, cytoplasmic
CfaAffx.30657.1.S1_s_at	8.36E-02	1.00E+00	0.55	similar to Kynurenine--oxoglutarate transaminase I (Kynurenine aminotransferase I) (KATI) (Glutamine--phenylpyruvate transaminase) (Glutamine transaminase K) (GTK) (Cysteine-S-conjugate beta-lyase) (LOC491310); mRNA	XM_548431	CCBL1	cysteine conjugate-beta lyase, cytoplasmic
CfaAffx.1376.1.S1_s_at	8.32E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to CG10874-PA; isoform A (LOC476220); mRNA	XM_533425	CCDC28A	coiled-coil domain containing 28A
Cfa.9084.1.A1_at	6.79E-02	1.00E+00	1.58	PREDICTED: Canis familiaris similar to Coiled-coil domain containing protein 3 precursor (LOC607593); mRNA	XM_844332	CCDC3	coiled-coil domain containing 3
Cfa.13025.1.A1_at	6.76E-02	1.00E+00	1.33	Bos taurus coiled-coil domain containing 88C; mRNA (cDNA clone MGC:160122 IMAGE:8520598); complete cds	BC149856	CCDC88C	coiled-coil domain containing 88C
CfaAffx.18573.1.S1_s_at	9.67E-02	1.00E+00	0.63	PREDICTED: Canis familiaris similar to cyclin D-type binding-protein 1; transcript variant 1 (LOC607896); mRNA	XM_844654	CCNDBP1	cyclin D-type binding-protein 1
CfaAffx.21302.1.S1_s_at	6.08E-02	1.00E+00	1.56	Canis familiaris CC chemokine receptor 5 (CCR5) mRNA; complete cds	AY904725	CCR5	chemokine (C-C motif) receptor 5
Cfa.3629.2.S1_s_at	9.68E-02	1.00E+00	1.42	Canis familiaris B7-2 protein (CD86) mRNA; complete cds	AF106826	CD86	CD86 molecule
CfaAffx.8676.1.S1_at	1.50E-02	1.00E+00	1.54	similar to Complement component C1q receptor precursor (Complement component 1; q subcomponent; receptor 1) (C1qRp) (C1qR(p)) (C1q/MBL/SPA receptor) (CD93 antigen) (CDw93) (LOC606923); mRNA	XM_843403	CD93	CD93 molecule

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Cfa.11357.1.S1_at	6.86E-02	1.00E+00	0.72	PREDICTED: Canis familiaris similar to Cdc42 effector protein 3 (LOC475726); mRNA	XM_532935	CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3
Cfa.8928.1.A1_at	6.09E-02	1.00E+00	1.31	Pongo abelii mRNA; cDNA DKFZp459I233 (from clone DKFZp459I233)	CR861291	CDC42SE2	CDC42 small effector 2
Cfa.20814.1.S1_s_at	8.31E-03	1.00E+00	1.74	Bos taurus cadherin 13; H-cadherin (heart); mRNA (cDNA clone MGC:128634 IMAGE:7986572); complete cds	BC107535	CDH13	cadherin 13, H-cadherin (heart)
Cfa.5459.1.A1_at	7.98E-02	1.00E+00	1.55	PREDICTED: Pan troglodytes cadherin 13; transcript variant 2 (CDH13); mRNA	XM_001149502	CDH13	cadherin 13, H-cadherin (heart)
Cfa.16772.1.A1_at	1.66E-03	1.00E+00	0.44	Bos taurus cyclin-dependent kinase inhibitor 2B (p15; inhibits CDK4); mRNA (cDNA clone MGC:128299 IMAGE:7947847); complete cds	BC105392	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)
CfaAffx.1755.1.S1_at	1.38E-02	1.00E+00	1.35	Homo sapiens mRNA; cDNA DKFZp686I06246 (from clone DKFZp686I06246)	CR627324	CEP120	centrosomal protein 120kDa
Cfa.15651.1.A1_at	9.43E-02	1.00E+00	0.72	Canis familiaris cingulin mRNA; complete cds	DQ910799	CGN	cingulin
CfaAffx.14841.1.S1_at	9.37E-02	1.00E+00	0.75	PREDICTED: Canis familiaris similar to CG10365-PA; isoform A (LOC487504); mRNA	XM_544628	CHAC1	ChaC, cation transport regulator homolog 1 (E. coli)
CfaAffx.14841.1.S1_s_at	2.38E-02	1.00E+00	0.46	PREDICTED: Canis familiaris similar to CG10365-PA; isoform A (LOC487504); mRNA	XM_544628	CHAC1	ChaC, cation transport regulator homolog 1 (E. coli)
CfaAffx.24023.1.S1_at	2.80E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to SR-related CTD associated factor 6 (LOC610237); mRNA	XM_847680	CHERP	calcium homeostasis endoplasmic reticulum protein

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Cfa.6922.1.A1_s_at	6.63E-02	1.00E+00	0.7	PREDICTED: Canis familiaris similar to lens intrinsic membrane protein 2; 19kDa (LOC476399); mRNA	XM_533602	CLDND2	claudin domain containing 2
Cfa.10901.1.A1_at	2.54E-02	1.00E+00	1.34	Pongo abelii mRNA; cDNA DKFZp469F1421 (from clone DKFZp469F1421)	CR857228	CNP	2',3'-cyclic nucleotide 3' phosphodiesterase
CfaAffx.24152.1.S1_s_at	3.54E-03	1.00E+00	1.38	PREDICTED: Canis familiaris similar to 2;3-cyclic-nucleotide 3-phosphodiesterase (CNP) (CNPase) (LOC607694); mRNA	XM_844467	CNP	2',3'-cyclic nucleotide 3' phosphodiesterase
CfaAffx.4930.1.S1_s_at	9.13E-02	1.00E+00	0.61	PREDICTED: Equus caballus collagen; type XII; alpha 1 (COL12A1); mRNA	XM_001914742	COL12A1	collagen, type XII, alpha 1
CfaAffx.4939.1.S1_s_at	9.93E-02	1.00E+00	0.58	PREDICTED: Canis familiaris similar to alpha 1 type XII collagen short isoform precursor; transcript variant 2 (LOC481881); mRNA	XM_862338	COL12A1	collagen, type XII, alpha 1
Cfa.10374.1.A1_at	8.23E-02	1.00E+00	0.69	PREDICTED: Canis familiaris similar to alpha 1 type XII collagen short isoform precursor; transcript variant 3 (LOC481881); mRNA	XM_862345	COL12A1	collagen, type XII, alpha 1
Cfa.14626.3.S1_at	9.62E-02	1.00E+00	1.94	PREDICTED: Canis familiaris similar to Collagen alpha 1(III) chain precursor; transcript variant 3 (LOC478835); mRNA	XM_857812	COL3A1	collagen, type III, alpha 1
CfaAffx.13076.1.S1_at	4.64E-02	1.00E+00	2.3	PREDICTED: Canis familiaris similar to Mast cell carboxypeptidase A precursor (MC-CPA) (Carboxypeptidase A3) (LOC485707); mRNA	XM_542828	CPA3	carboxypeptidase A3 (mast cell)
Cfa.1286.1.A1_at	8.81E-02	1.00E+00	0.56	PREDICTED: Macaca mulatta carnitine palmitoyltransferase 1A (CPT1A); mRNA	XM_001101846	CPT1A	carnitine palmitoyltransferase 1A
Cfa.101.1.S1_s_at	9.54E-02	1.00E+00	0.62	PREDICTED: Canis familiaris carnitine palmitoyl transferase I isoform (CPT1); mRNA	XM_533208	CPT1A	carnitine palmitoyltransferase 1A (liver)
CfaAffx.5470.1.S1_s_at	3.88E-02	1.00E+00	0.76	PREDICTED: Canis familiaris similar to serine carboxypeptidase vitellogenic-like (LOC611483); mRNA	XM_849152	CPVL	carboxypeptidase, vitellogenic-like

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Cfa.12544.1.A1_at	8.74E-02	1.00E+00	1.6	Sus scrofa mRNA; clone:OVRM10164F12; expressed in ovary	AK236216	CR956367.2	prostate transmembrane protein, androgen induced 1
CfaAffx.9880.1.S1_at	6.72E-02	1.00E+00	0.58	PREDICTED: Canis familiaris similar to CG4774-PA; isoform A; transcript variant 2 (LOC607530); mRNA	XM_844822	CRLS1	cardiolipin synthase 1
CfaAffx.7365.1.S1_at	6.35E-02	1.00E+00	0.45	PREDICTED: Canis familiaris similar to cystatin 9-like precursor (LOC485559); mRNA	XM_542677	CST9L	cystatin 9-like
CfaAffx.31268.1.S1_s_at	8.98E-02	1.00E+00	0.76	PREDICTED: Canis familiaris similar to cystathionase isoform 1 (LOC479991); mRNA	XM_537115	CTH	cystathionase (cystathionine gamma-lyase)
Cfa.3883.1.S1_at	4.51E-02	1.00E+00	0.65	Canis familiaris cytochrome P-450 IIB (P450IIB) mRNA; complete cds	M92447	CYPIIB11	cytochrome P450 2B11
Cfa.2772.2.S1_s_at	8.13E-02	1.00E+00	1.44	PREDICTED: Canis familiaris similar to neural stem cell-derived dendrite regulator; transcript variant 1 (LOC479756); mRNA	XM_536885	DAGLB	diacylglycerol lipase, beta
Cfa.2772.1.A1_at	5.13E-02	1.00E+00	1.63	PREDICTED: Canis familiaris similar to neural stem cell-derived dendrite regulator; transcript variant 2 (LOC479756); mRNA	XM_856253	DAGLB	diacylglycerol lipase, beta
Cfa.3648.1.S1_s_at	2.11E-02	1.00E+00	0.5	Canis lupus familiaris CAN2DD mRNA for dimeric dihydrodiol dehydrogenase; complete cds	AB021930	DHDH	dihydrodiol dehydrogenase (dimeric)
Cfa.4679.1.A1_s_at	6.30E-02	1.00E+00	1.41	PREDICTED: Canis familiaris similar to dicer1; transcript variant 4 (LOC480426); mRNA	XM_863433	DICER1	dicer 1, ribonuclease type III
CfaAffx.942.1.S1_at	8.04E-02	1.00E+00	1.45	PREDICTED: Canis familiaris similar to squamous cell carcinoma antigen recognized by T cells 2 (LOC483944); mRNA	XM_541064	DSEL	dermatan sulfate epimerase-like
CfaAffx.395.1.S1_at	1.64E-02	1.00E+00	0.77	PREDICTED: Canis familiaris similar to Dual specificity protein phosphatase 18 (Low molecular weight dual specificity phosphatase 20) (LOC486357); mRNA	XM_543483	DUSP18	dual specificity phosphatase 18

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Cfa.16990.1.S1_at	3.22E-04	1.00E+00	1.65	PREDICTED: Canis familiaris similar to Dysferlin (Dystrophy associated fer-1-like protein) (Fer-1 like protein 1) (LOC483121); mRNA	XM_540237	DYSF	dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive)
CfaAffx.14261.1.S1_s_at	3.36E-02	1.00E+00	1.31	PREDICTED: Canis familiaris similar to Dysferlin (Dystrophy associated fer-1-like protein) (Fer-1 like protein 1) (LOC483121); mRNA	XM_540237	DYSF	dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive)
Cfa.16878.1.S1_s_at	1.09E-02	1.00E+00	1.34	PREDICTED: Canis familiaris similar to CG6311-PB; transcript variant 2 (LOC487647); mRNA	XM_861987	EDC3	enhancer of mRNA decapping 3 homolog (S. cerevisiae)
Cfa.16710.1.S1_at	5.08E-03	1.00E+00	0.45	PREDICTED: Equus caballus eukaryotic translation elongation factor 1 alpha 2 (EEF1A2); mRNA	XM_001915406	EEF1A2	eukaryotic translation elongation factor 1 alpha 2
Cfa.16710.1.S1_s_at	5.01E-03	1.00E+00	0.71	Oryctolagus cuniculus elongation factor 1 A2 (EEF1A-2) mRNA; complete cds	AF035178	EEF1A-2	elongation factor 1 A2
Cfa.1829.1.S1_at	7.29E-02	1.00E+00	1.32	Bos taurus EGF; latrophilin and seven transmembrane domain containing 1; mRNA (cDNA clone MGC:140518 IMAGE:8201146); complete cds	BC123530	ELTD1	EGF, latrophilin and seven transmembrane domain containing 1
Cfa.21260.1.S1_s_at	2.27E-02	1.00E+00	1.49	PREDICTED: Canis familiaris similar to Epithelial membrane protein-1 (EMP-1) (Tumor-associated membrane protein) (LOC486676); mRNA	XM_543803	EMP1	epithelial membrane protein 1

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CfaAffx.20391.1.S1_at	4.71E-02	1.00E+00	1.42	PREDICTED: Canis familiaris similar to Epithelial membrane protein-1 (EMP-1) (Tumor-associated membrane protein) (LOC486676); mRNA	XM_543803	EMP1	epithelial membrane protein 1
CfaAffx.24909.1.S1_s_at	8.24E-02	1.00E+00	1.37	Canis familiaris EMR3 mRNA; complete cds	DQ227277	EMR3	egf-like module containing, mucin-like, hormone receptor-like 3
CfaAffx.30665.1.S1_at	9.32E-02	1.00E+00	0.77	PREDICTED: Canis familiaris similar to Endonuclease G; mitochondrial precursor (Endo G) (LOC608916); mRNA	XM_846067	ENDOG	endonuclease G
CfaAffx.13375.1.S1_at	3.19E-02	1.00E+00	0.67	PREDICTED: Canis familiaris similar to Ectonucleoside triphosphate diphosphohydrolase 1 (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell activation antigen) (Ecto-apyrase) (CD39 antigen) (LOC486810); mRNA	XM_543939	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1
CfaAffx.29840.1.S1_at	6.62E-02	1.00E+00	0.71	PREDICTED: Canis familiaris similar to ectonucleoside triphosphate diphosphohydrolase 2 isoform 2; transcript variant 1 (LOC491241); mRNA	XM_548362	ENTPD2	ectonucleoside triphosphate diphosphohydrolase 2
CfaAffx.4798.1.S1_s_at	5.19E-02	1.00E+00	0.69	PREDICTED: Canis familiaris similar to Endothelial PAS domain protein 1 (EPAS-1) (Member of PAS protein 2) (MOP2) (Hypoxia-inducible factor 2 alpha) (HIF-2 alpha) (HIF2 alpha) (HIF-1 alpha-like factor) (HLF) (LOC474578); mRNA	XM_531807	EPAS1	endothelial PAS domain protein 1
Cfa.17625.1.S1_at	2.51E-02	1.00E+00	0.72	PREDICTED: Canis familiaris similar to Endothelial PAS domain protein 1 (EPAS-1) (Member of PAS protein 2) (MOP2) (Hypoxia-inducible factor 2 alpha) (HIF-2 alpha) (HIF2 alpha) (HIF-1 alpha-like factor) (HLF) (LOC474578); mRNA	XM_531807	EPAS1	endothelial PAS domain protein 1
CfaAffx.13881.1.S1_at	8.61E-02	1.00E+00	1.33	PREDICTED: Canis familiaris similar to endoplasmic reticulum protein 29 precursor (LOC477482); mRNA	XM_848584	ERP29	endoplasmic reticulum protein 29

Table 1:Genes Differentially Expressed in Adipose Tissue in Fat Animals compared to Lean Animals

CfaAffx.2850.1.S1_s_at	7.59E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to fructose-1;6-bisphosphatase 1; transcript variant 1 (LOC476299); mRNA	XM_533503	FBP1	fructose-1,6-bisphosphatase 1
Cfa.17541.1.S1_s_at	5.85E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to fructose-1;6-bisphosphatase 1; transcript variant 4 (LOC476299); mRNA	XM_850754	FBP1	fructose-1,6-bisphosphatase 1
Cfa.663.1.A1_at	2.82E-02	1.00E+00	0.69	PREDICTED: Pan troglodytes F-box only protein 32; transcript variant 1 (FBXO32); mRNA	XM_001149252	FBXO32	F-box protein 32
Cfa.12623.1.A1_at	6.00E-03	1.00E+00	0.66	PREDICTED: Canis familiaris similar to F-box only protein 32 isoform 1; transcript variant 3 (LOC475091); mRNA	XM_856632	FBXO32	F-box protein 32
CfaAffx.2404.1.S1_at	1.77E-02	1.00E+00	0.7	PREDICTED: Canis familiaris similar to F-box only protein 32 isoform 1; transcript variant 4 (LOC475091); mRNA	XM_856659	FBXO32	F-box protein 32
CfaAffx.2404.1.S1_s_at	2.13E-03	1.00E+00	0.68	PREDICTED: Canis familiaris similar to F-box only protein 32 isoform 1; transcript variant 5 (LOC475091); mRNA	XM_856687	FBXO32	F-box protein 32
Cfa.20844.1.S1_at	5.20E-02	1.00E+00	0.73	PREDICTED: Pan troglodytes similar to F-box protein 44; transcript variant 9 (LOC457952); mRNA	XM_514390	FBXO44	F-box protein 44
CfaAffx.25843.1.S1_at	8.34E-02	1.00E+00	0.7	PREDICTED: Canis familiaris similar to Fibroblast growth factor-18 precursor (FGF-18) (zFGF5) (LOC611641); mRNA	XM_849332	FGF18	fibroblast growth factor 18
CfaAffx.2909.1.S1_at	5.22E-02	1.00E+00	0.36	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	XM_538880	FKBP5	FK506 binding protein 5
Cfa.12375.1.A1_at	5.99E-02	1.00E+00	0.38	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	XM_538880	FKBP5	FK506 binding protein 5
CfaAffx.8655.1.S1_at	1.40E-02	1.00E+00	0.45	PREDICTED: Canis familiaris similar to fibronectin type III domain containing 4 (LOC483014); mRNA	XM_540129	FNDC4	fibronectin type III domain containing 4

Table 1:Genes Differentially Expressed in Adipose Tissue in Fat Animals compared to Lean Animals

CfaAffx.24709.1.S1_at	2.19E-02	1.00E+00	0.76	PREDICTED: Canis familiaris similar to Forkhead box protein K1 (Myocyte nuclear factor) (MNF) (LOC489885); mRNA	XM_547003	FOXK1	forkhead box K1
Cfa.19616.1.S1_at	5.75E-02	1.00E+00	0.72	Homo sapiens forkhead box O1 (FOXO1); mRNA	NM_002015	FOXO1	forkhead box O1
CfaAffx.8025.1.S1_s_at	6.29E-02	1.00E+00	0.76	PREDICTED: Canis familiaris similar to FERM domain containing 4A (LOC607414); mRNA	XM_844066	FRMD4A	FERM domain containing 4A
Cfa.204.1.S1_s_at	7.98E-02	1.00E+00	0.58	Canis familiaris glucose-6-phosphatase mRNA; complete cds	U91844	G6PC	glucose-6-phosphatase, catalytic subunit
Cfa.10130.1.A1_at	6.99E-02	1.00E+00	0.75	PREDICTED: Canis familiaris similar to gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1; transcript variant 1 (LOC612919); mRNA	XM_848051	GABARAPL1	GABA(A) receptor-associated protein like 1
CfaAffx.9797.1.S1_s_at	8.91E-02	1.00E+00	0.56	PREDICTED: Canis familiaris similar to UDP-N-acetyl-alpha-D-galactosamine:polypeptide N acetylgalactosaminyltransferase-like 2 (LOC477056); mRNA	XM_534252	GALNTL2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2
CfaAffx.15423.1.S1_at	3.87E-03	1.00E+00	0.61	PREDICTED: Canis familiaris similar to glucose-fructose oxidoreductase domain containing 1 (LOC488222); mRNA	XM_545344	GFOD1	glucose-fructose oxidoreductase domain containing 1
CfaAffx.22871.1.S1_at	8.84E-02	1.00E+00	0.56	Rattus norvegicus glutamate receptor; ionotropic; AMPA4 (Gria4); transcript variant 3; mRNA	NM_001113185	Gria4	glutamate receptor, ionotropic, AMPA4
CfaAffx.5303.1.S1_at	1.88E-02	1.00E+00	0.7	PREDICTED: Canis familiaris similar to G-rich RNA sequence binding factor 1 (LOC475170); mRNA	XM_532402	GRSF1	G-rich RNA sequence binding factor 1

Table 1:Genes Differentially Expressed in Adipose Tissue in Fat Animals compared to Lean Animals

Cfa.253.1.S1_at	4.75E-02	1.00E+00	1.39	Homo sapiens guanylate cyclase 1; soluble; beta 3; mRNA (cDNA clone MGC:51012 IMAGE:5264160); complete cds	BC047620	GUCY1B3	guanylate cyclase 1, soluble, beta 3
Cfa.3045.1.A1_s_at	7.26E-02	1.00E+00	0.67	PREDICTED: Canis familiaris similar to 2-hydroxyphytanoyl-CoA lyase (2-HPCL) (LOC477060); mRNA	XM_534256	HACL1	2-hydroxyacyl-CoA lyase 1
CfaAffx.6846.1.S1_at	5.12E-02	1.00E+00	0.76	PREDICTED: Canis familiaris similar to HMG-box transcription factor 1; transcript variant 8 (LOC475886); mRNA	XM_852649	HBP1	HMG-box transcription factor 1
CfaAffx.7431.1.S1_at	5.23E-03	1.00E+00	0.4	PREDICTED: Canis familiaris similar to hypoxia-inducible factor-3 alpha isoform a (LOC476429); mRNA	XM_533636	HIF3A	hypoxia inducible factor 3, alpha subunit
CfaAffx.7434.1.S1_at	2.01E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to hypoxia-inducible factor-3 alpha isoform a (LOC476429); mRNA	XM_533636	HIF3A	hypoxia inducible factor 3, alpha subunit
CfaAffx.7437.1.S1_s_at	2.73E-02	1.00E+00	0.49	PREDICTED: Canis familiaris similar to hypoxia-inducible factor-3 alpha isoform a (LOC476429); mRNA	XM_533636	HIF3A	hypoxia inducible factor 3, alpha subunit
Cfa.4558.1.S1_s_at	6.43E-02	1.00E+00	0.64	Canis familiaris crossbreed B high mobility group HMGA1A mRNA; complete cds	AY366391	HMGA1	high mobility group AT-hook 1
CfaAffx.10319.1.S1_s_at	5.55E-02	1.00E+00	1.36	PREDICTED: Canis familiaris similar to heterogeneous nuclear ribonucleoprotein L-like (LOC475729); mRNA	XM_532938	HNRPLL	heterogeneous nuclear ribonucleoprotein L-like
Cfa.8017.1.A1_at	9.93E-02	1.00E+00	1.46	PREDICTED: Canis familiaris similar to Hook homolog 2 (h-hook2) (hHK2) (LOC484928); mRNA	XM_542044	HOOK2	hook homolog 2 (Drosophila)
Cfa.17416.1.S1_s_at	6.90E-02	1.00E+00	0.63	PREDICTED: Canis familiaris similar to hippocalcin-like 1 (LOC609787); mRNA	XM_847124	HPCAL1	hippocalcin-like 1
CfaAffx.12647.1.S1_at	3.78E-02	1.00E+00	0.7	PREDICTED: Canis familiaris similar to 15-hydroxyprostaglandin dehydrogenase [NAD+] (PGDH) (Prostaglandin dehydrogenase 1) (LOC486073); mRNA	XM_543199	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)

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CfaAffx.11565.1.S1_s_at	9.11E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to Serine protease hepsin (Transmembrane protease; serine 1) (LOC484583); mRNA	XM_541697	HPN	hepsin (transmembrane protease, serine 1)
Cfa.3599.1.S1_s_at	4.58E-02	1.00E+00	0.77	Canis familiaris ras p21 (H-ras) mRNA; partial cds	U62092	HRAS	v-Ha-ras Harvey rat sarcoma viral oncogene homolog
Cfa.13172.1.S1_at	4.81E-02	1.00E+00	0.66	Canis familiaris 3-beta-hydroxysteroid dehydrogenase mRNA; complete cds	AY739720	HSD3B1	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1
CfaAffx.15407.1.S1_at	7.81E-02	1.00E+00	1.56	PREDICTED: Canis familiaris similar to HIV-1 Tat interactive protein 2; 30kDa (LOC476886); mRNA	XM_534088	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa
CfaAffx.15407.1.S1_s_at	8.99E-02	1.00E+00	1.44	PREDICTED: Canis familiaris similar to HIV-1 Tat interactive protein 2; 30kDa (LOC476886); mRNA	XM_534088	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa
CfaAffx.5506.1.S1_at	3.28E-03	1.00E+00	1.32	PREDICTED: Canis familiaris similar to 5-hydroxytryptamine 1E receptor (5-HT-1E) (Serotonin receptor 1E) (5-HT1E) (S31) (LOC481907); mRNA	XM_539028	HTR1E	5-hydroxytryptamine (serotonin) receptor 1E
Cfa.6077.1.S1_at	4.41E-02	1.00E+00	0.65	PREDICTED: Canis familiaris hypothetical protein LOC608547; transcript variant 3 (LOC608547); mRNA	XM_856580	HVCN1	hydrogen voltage-gated channel 1
CfaAffx.13473.1.S1_s_at	7.75E-02	1.00E+00	0.71	PREDICTED: Canis familiaris hypothetical protein LOC608547; transcript variant 3 (LOC608547); mRNA	XM_856580	HVCN1	hydrogen voltage-gated channel 1
CfaAffx.8742.1.S1_s_at	7.52E-02	1.00E+00	0.63	PREDICTED: Canis familiaris similar to hydroxypyruvate isomerase homolog (LOC482531); mRNA	XM_539648	HYI	hydroxypyruvate isomerase homolog (E. coli)

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CfaAffx.4263.1.S1_s_at	1.36E-02	1.00E+00	1.41	PREDICTED: Canis familiaris similar to islet cell autoantigen 1 isoform 1; transcript variant 6 (LOC475242); mRNA	XM_856689	ICA1	islet cell autoantigen 1, 69kDa
Cfa.16440.1.S1_at	9.85E-02	1.00E+00	1.58	PREDICTED: Canis familiaris similar to Interferon-induced 35 kDa protein (IFP 35) (LOC490954); mRNA	XM_548077	IFI35	interferon-induced protein 35
Cfa.18820.1.S1_at	8.81E-02	1.00E+00	1.38	PREDICTED: Canis familiaris similar to Interferon-induced 35 kDa protein (IFP 35) (LOC490954); mRNA	XM_548077	IFI35	interferon-induced protein 35
CfaAffx.5908.1.S1_at	7.92E-02	1.00E+00	0.52	PREDICTED: Canis familiaris similar to interferon-related developmental regulator 1; transcript variant 1 (LOC482408); mRNA	XM_539525	IFRD1	interferon-related developmental regulator 1
CfaAffx.20601.1.S1_at	9.46E-02	1.00E+00	1.34	PREDICTED: Canis familiaris similar to CG7832-PA (LOC488489); mRNA	XM_545610	INO80D	INO80 complex subunit D
CfaAffx.27879.1.S1_s_at	3.81E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to Insulin receptor precursor (IR) (CD220 antigen) (LOC484990); mRNA	XM_542108	INSR	insulin receptor
Cfa.15284.1.A1_s_at	9.31E-02	1.00E+00	0.75	PREDICTED: Canis familiaris similar to Ras GTPase-activating-like protein IQGAP1 (p195) (LOC479050); mRNA	XM_536199	IQGAP1	IQ motif containing GTPase activating protein 1
CfaAffx.19884.1.S1_s_at	8.47E-02	1.00E+00	0.72	PREDICTED: Canis familiaris similar to Ras GTPase-activating-like protein IQGAP1 (p195) (LOC479050); mRNA	XM_536199	IQGAP1	IQ motif containing GTPase activating protein 1
CfaAffx.8531.1.S1_at	7.53E-02	1.00E+00	1.37	PREDICTED: Canis familiaris similar to IMMUNE-RESPONSIVE PROTEIN 1 (LOC485496); mRNA	XM_542615	IRG1	immunoresponsive 1 homolog (mouse)
CfaAffx.28187.1.S1_at	5.19E-02	1.00E+00	0.73	PREDICTED: Canis familiaris similar to Integrin alpha-2 precursor (Platelet membrane glycoprotein Ia) (GPIa) (Collagen receptor) (VLA-2 alpha chain) (CD49b) (LOC489208); mRNA	XM_546326	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)
CfaAffx.22104.1.S1_at	4.44E-02	1.00E+00	0.69	PREDICTED: Canis familiaris similar to integrin; alpha D precursor (LOC607096); mRNA	XM_843683	ITGAD	integrin, alpha D

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CfaAffx.28297.1.S1_at	3.97E-02	1.00E+00	0.66	PREDICTED: Canis familiaris similar to Variable ABnormal morphology family member (vab-19); transcript variant 2 (LOC476723); mRNA	XM_849162	KANK3	KN motif and ankyrin repeat domains 3
Cfa.15973.1.A1_at	7.96E-03	1.00E+00	1.31	PREDICTED: Canis familiaris similar to KH domain containing; RNA binding; signal transduction associated 1; transcript variant 1 (LOC487316); mRNA	XM_544442	KHDRBS1	KH domain containing, RNA binding, signal transduction associated 1
Cfa.15156.1.A1_at	1.55E-02	1.00E+00	1.32	Homo sapiens KIAA0494 (KIAA0494); mRNA	NM_014774	KIAA0494	KIAA0494
Cfa.19444.1.S1_at	8.25E-02	1.00E+00	1.38	PREDICTED: Macaca mulatta KIT ligand (KITLG); mRNA	XM_001101381	KITLG	KIT ligand
CfaAffx.29994.1.S1_at	1.70E-02	1.00E+00	0.75	PREDICTED: Canis familiaris similar to kelch-like 21 (LOC489634); mRNA	XM_546754	KLHL21	kelch-like 21 (Drosophila)
CfaAffx.7408.1.S1_s_at	4.18E-02	1.00E+00	1.31	PREDICTED: Canis familiaris similar to karyopherin (importin) alpha 3 (predicted) (LOC476909); mRNA	XM_534112	KPNA3	karyopherin alpha 3 (importin alpha 4)
CfaAffx.2542.1.S1_at	9.56E-02	1.00E+00	0.56	PREDICTED: Equus caballus laminin; alpha 2 (merosin; congenital muscular dystrophy) (LAMA2); mRNA	XM_001503221	LAMA2	laminin, alpha 2 (merosin, congenital muscular dystrophy)
Cfa.13909.1.A1_s_at	4.79E-02	1.00E+00	0.77	PREDICTED: Canis familiaris similar to Laminin beta-1 chain precursor (Laminin B1 chain); transcript variant 1 (LOC475882); mRNA	XM_533089	LAMB1	laminin, beta 1
Cfa.18473.1.S1_s_at	2.77E-02	1.00E+00	0.76	PREDICTED: Canis familiaris similar to Laminin beta-1 chain precursor (Laminin B1 chain); transcript variant 2 (LOC475882); mRNA	XM_851951	LAMB1	laminin, beta 1
Cfa.21547.1.S1_s_at	6.72E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to Laminin beta-1 chain precursor (Laminin B1 chain); transcript variant 2 (LOC475882); mRNA	XM_851951	LAMB1	laminin, beta 1

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Cfa.18707.1.S1_s_at	8.90E-03	1.00E+00	0.64	PREDICTED: Canis familiaris similar to Laminin beta-1 chain precursor (Laminin B1 chain); transcript variant 2 (LOC475882); mRNA	XM_851951	LAMB1	laminin, beta 1
CfaAffx.8900.1.S1_at	8.78E-02	1.00E+00	1.31	PREDICTED: Canis familiaris similar to limb-bud and heart (LOC611237); mRNA	XM_848875	LBH	limb bud and heart development homolog (mouse)
CfaAffx.31053.1.S1_at	3.41E-02	1.00E+00	1.42	PREDICTED: Canis familiaris similar to LIM homeobox protein 6 isoform 1 (LOC491354); mRNA	XM_548475	LHX6	LIM homeobox 6
Cfa.2706.1.S1_s_at	1.64E-02	1.00E+00	0.65	Canis familiaris leukemia inhibitory factor receptor mRNA; complete cds	AY745241	LIFR	leukemia inhibitory factor receptor alpha
CfaAffx.16627.1.S1_at	4.93E-02	1.00E+00	0.64	PREDICTED: Equus caballus leiomodin 1 (smooth muscle) (LMOD1); mRNA	XM_001495117	LMOD1	leiomodin 1 (smooth muscle)
Cfa.20295.1.S1_at	3.17E-02	1.00E+00	1.85	PREDICTED: Monodelphis domestica similar to transmembrane protease; serine 11c (LOC100012939); mRNA	XM_001367282	LOC100012939	similar to transmembrane protease, serine 11c
CfaAffx.12934.1.S1_s_at	6.82E-02	1.00E+00	1.6	PREDICTED: Equus caballus similar to Double-stranded RNA-binding protein Staufen homolog 2 (LOC100051157); mRNA	XM_001491834	LOC100051157	similar to Double-stranded RNA-binding protein Staufen homolog 2
CfaAffx.21779.1.S1_at	6.23E-02	1.00E+00	1.41	PREDICTED: Equus caballus similar to calcium-binding tyrosine-phosphorylation regulated protein (LOC100051654); mRNA	XM_001493606	LOC100051654	similar to calcium-binding tyrosine-phosphorylation regulated protein
CfaAffx.10935.1.S1_at	3.53E-02	1.00E+00	0.69	PREDICTED: Equus caballus similar to CAP-Gly domain-containing linker protein 3 (Cytoplasmic linker protein 170 related 59 kDa protein) (CLIPR-59) (CLIP-170-related 59 kDa protein) (LOC100051864); mRNA	XM_001493639	LOC100051864	similar to CLIP-170-related protein

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Cfa.1936.1.S1_at	2.42E-02	1.00E+00	0.65	PREDICTED: Equus caballus similar to Putative glycerophosphodiester phosphodiesterase 5 (LOC100051946); mRNA	XM_001915486	LOC100051946	hypothetical LOC100051946
Cfa.4113.1.S1_at	8.29E-02	1.00E+00	0.67	PREDICTED: Equus caballus similar to macrophage migration inhibitory factor (LOC100053618); mRNA	XM_001489611	LOC100053618	similar to macrophage migration inhibitory factor
Cfa.19016.1.S1_at	1.50E-02	1.00E+00	2.61	PREDICTED: Equus caballus similar to 1700123O20Rik protein (LOC100055817); mRNA	XM_001494306	LOC100055817	similar to 1700123O20Rik protein
Cfa.11008.1.A1_at	5.74E-02	1.00E+00	0.58	PREDICTED: Equus caballus similar to odd homeobox 1 protein (LOC100058285); mRNA	XM_001491312	LOC100058285	similar to odd homeobox 1 protein
CfaAffx.28176.1.S1_at	6.47E-02	1.00E+00	1.37	PREDICTED: Equus caballus similar to Protein Njmu-R1 (LOC100058439); mRNA	XM_001504001	LOC100058439	similar to Protein Njmu-R1
CfaAffx.14997.1.S1_s_at	7.22E-02	1.00E+00	1.3	PREDICTED: Equus caballus similar to signal sequence receptor; alpha (translocon-associated protein alpha) (LOC100061378); mRNA	XM_001493337	LOC100061378	hypothetical protein LOC100061378
Cfa.19492.1.A1_at	7.80E-02	1.00E+00	1.31	PREDICTED: Equus caballus similar to Kelch-like protein 5 (LOC100064472); mRNA	XM_001917431	LOC100064472	hypothetical LOC100064472
CfaAffx.17336.1.S1_s_at	6.87E-02	1.00E+00	0.31	PREDICTED: Equus caballus similar to Acetyl-CoA carboxylase 2 (ACC-beta) (LOC100066740); mRNA	XM_001496930	LOC100066740	similar to Acetyl-CoA carboxylase 2
CfaAffx.4594.1.S1_s_at	7.56E-02	1.00E+00	0.75	PREDICTED: Bos taurus similar to zinc finger protein 570 (LOC100138971); mRNA	XM_001789965	LOC100138971	similar to zinc finger protein 570
CfaAffx.3283.1.S1_at	4.91E-02	1.00E+00	0.67	PREDICTED: Sus scrofa similar to triggering receptor expressed on myeloid cells 2 (LOC100153525); mRNA	XM_001924346	LOC100153525	similar to triggering receptor expressed on myeloid cells 2

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CfaAffx.14304.1.S1_at	8.46E-02	1.00E+00	0.62	PREDICTED: Sus scrofa similar to solute carrier family 24 member 6 (LOC100157056); mRNA	XM_001924244	LOC100157056	similar to solute carrier family 24 member 6
Cfa.12840.1.A1_at	4.03E-02	1.00E+00	0.68	Homo sapiens cDNA clone IMAGE:5171802	BC034770	LOC285847	hypothetical protein LOC285847
CfaAffx.732.1.S1_at	4.78E-02	1.00E+00	0.47	PREDICTED: Pan troglodytes similar to Hypothetical zinc finger-like protein (LOC468909); mRNA	XR_023751	LOC468909	similar to Hypothetical zinc finger-like protein
CfaAffx.732.1.S1_x_at	5.04E-02	1.00E+00	0.51	PREDICTED: Pan troglodytes similar to Hypothetical zinc finger-like protein (LOC468909); mRNA	XR_023751	LOC468909	similar to Hypothetical zinc finger-like protein
Cfa.1647.1.A1_at	5.97E-02	1.00E+00	1.53	PREDICTED: Pan troglodytes similar to Cache domain containing 1 (LOC469343); mRNA	XR_024086	LOC469343	similar to Cache domain containing 1
CfaAffx.2389.1.S1_s_at	6.09E-02	1.00E+00	1.48	PREDICTED: Pan troglodytes hypothetical LOC472115 (LOC472115); mRNA	XM_527494	LOC472115	hypothetical LOC472115
CfaAffx.5916.1.S1_s_at	9.87E-02	1.00E+00	1.4	PREDICTED: Canis familiaris similar to collagen; type XXVII; alpha 1 (LOC474811); mRNA	XM_532042	LOC474811	similar to collagen, type XXVII, alpha 1
Cfa.5277.1.A1_s_at	5.31E-02	1.00E+00	0.46	PREDICTED: Canis familiaris hypothetical LOC474886; transcript variant 2 (LOC474886); mRNA	XM_532120	LOC474886	hypothetical LOC474886
Cfa.12537.1.A1_at	3.61E-02	1.00E+00	0.62	PREDICTED: Canis familiaris hypothetical LOC475300 (LOC475300); mRNA	XM_532531	LOC475300	hypothetical LOC475300

Table 1:Genes Differentially Expressed in Adipose Tissue in Fat Animals compared to Lean Animals

CfaAffx.1319.1.S1_s_at	4.85E-02	1.00E+00	0.71	PREDICTED: Canis familiaris similar to L-lactate dehydrogenase B chain (LDH-B) (LDH heart subunit) (LDH-H); transcript variant 1 (LOC476213); mRNA	XM_533418	LOC476213	similar to L-lactate dehydrogenase B chain (LDH-B) (LDH heart subunit) (LDH-H)
CfaAffx.8020.1.S1_at	2.43E-02	1.00E+00	0.75	PREDICTED: Canis familiaris hypothetical LOC476444 (LOC476444); mRNA	XM_533650	LOC476444	hypothetical LOC476444
Cfa.10960.2.A1_a_at	8.88E-02	1.00E+00	1.37	PREDICTED: Canis familiaris similar to CDK2 (cyclin-dependent kinase 2)-associated protein 1 (LOC477452); mRNA	XM_534650	LOC477452	similar to CDK2 (cyclin-dependent kinase 2)-associated protein 1
CfaAffx.14325.1.S1_at	1.32E-02	1.00E+00	0.66	PREDICTED: Canis familiaris similar to F09B12.3 (LOC477493); mRNA	XM_534691	LOC477493	similar to F09B12.3
CfaAffx.20586.1.S1_s_at	9.00E-02	1.00E+00	1.4	PREDICTED: Canis familiaris similar to N-chimaerin (NC) (N-chimerin) (Alpha chimerin) (A-chimaerin) (Rho-GTPase-activating protein 2); transcript variant 3 (LOC478805); mRNA	XM_856276	LOC478805	similar to N-chimaerin (NC) (N-chimerin) (Alpha chimerin) (A-chimaerin) (Rho-GTPase-activating protein 2)
CfaAffx.29155.1.S1_s_at	3.96E-02	1.00E+00	0.64	PREDICTED: Canis familiaris hypothetical LOC479382 (LOC479382); mRNA	XM_536520	LOC479382	hypothetical LOC479382

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Cfa.20794.1.S1_at	1.12E-02	1.00E+00	1.35	PREDICTED: Canis familiaris similar to fusion (involved in t(12;16) in malignant liposarcoma) (predicted); transcript variant 1 (LOC479778); mRNA	XM_536905	LOC479778	similar to fusion (involved in t(12;16) in malignant liposarcoma) (predicted)
Cfa.20794.1.S1_s_at	1.62E-02	1.00E+00	1.45	PREDICTED: Canis familiaris similar to fusion (involved in t(12;16) in malignant liposarcoma) (predicted); transcript variant 7 (LOC479778); mRNA	XM_851770	LOC479778	similar to fusion (involved in t(12;16) in malignant liposarcoma) (predicted)
Cfa.19285.1.S1_at	4.69E-02	1.00E+00	0.66	PREDICTED: Canis familiaris similar to Protein C9orf72 homolog; transcript variant 1 (LOC481569); mRNA	XM_538691	LOC481569	similar to Protein C9orf72 homolog
CfaAffx.3482.1.S1_s_at	7.50E-02	1.00E+00	0.6	PREDICTED: Canis familiaris similar to Protein C9orf72 homolog; transcript variant 4 (LOC481569); mRNA	XM_860140	LOC481569	similar to Protein C9orf72 homolog
CfaAffx.3351.1.S1_s_at	9.01E-03	1.00E+00	0.75	PREDICTED: Canis familiaris similar to cysteine and histidine rich 1 isoform 1 (LOC482097); mRNA	XM_539218	LOC482097	similar to cysteine and histidine rich 1 isoform 1
CfaAffx.8785.1.S1_s_at	2.96E-02	1.00E+00	0.73	PREDICTED: Canis familiaris similar to KIAA0467 protein (LOC482532); mRNA	XM_539649	LOC482532	similar to KIAA0467 protein
Cfa.13287.1.A1_s_at	1.40E-02	1.00E+00	1.32	PREDICTED: Canis familiaris similar to CG33154-PB; isoform B (LOC482583); mRNA	XM_539700	LOC482583	similar to CG33154-PB, isoform B
CfaAffx.18336.1.S1_at	2.95E-02	1.00E+00	1.37	PREDICTED: Canis familiaris hypothetical LOC483182 (LOC483182); mRNA	XM_540300	LOC483182	hypothetical LOC483182

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CfaAffx.11212.1.S1_s_at	5.47E-02	1.00E+00	0.42	PREDICTED: Canis familiaris similar to regeneration associated muscle protease isoform b (LOC483426); mRNA	XM_540544	LOC483426	similar to regeneration associated muscle protease isoform b
CfaAffx.6973.1.S1_s_at	3.59E-02	1.00E+00	1.54	PREDICTED: Canis familiaris similar to Caspase recruitment domain protein 8 (Apoptotic protein NDPP1) (DACAR) (CARD-inhibitor of NF-kappaB activating ligand) (CARDINAL) (Tumor-up-regulated CARD-containing antagonist of CASP9) (TUCAN) (LOC484411); mRNA	XM_541526	LOC484411	similar to Caspase recruitment domain protein 8 (Apoptotic protein NDPP1) (DACAR) (CARD-inhibitor of NF-kappaB activating ligand) (CARDINAL) (Tumor-up-regulated CARD-containing antagonist of CASP9) (TUCAN)
CfaAffx.8507.1.S1_at	3.52E-02	1.00E+00	0.75	PREDICTED: Canis familiaris similar to cytochrome P450; family 2; subfamily S; polypeptide 1 (LOC484491); mRNA	XM_541605	LOC484491	similar to cytochrome P450, family 2, subfamily S, polypeptide 1
Cfa.20718.1.S1_s_at	7.10E-02	1.00E+00	0.65	PREDICTED: Canis familiaris similar to Protein KIAA1434 (LOC485778); mRNA	XM_542901	LOC485778	similar to Protein KIAA1434
CfaAffx.24113.1.S1_s_at	2.28E-02	1.00E+00	0.71	PREDICTED: Canis familiaris similar to CXYorf1-related protein (LOC486746); mRNA	XM_543873	LOC486746	similar to CXYorf1-related protein

Table 1:Genes Differentially Expressed in Adipose Tissue in Fat Animals compared to Lean Animals

Cfa.9684.1.A1_at	7.59E-03	1.00E+00	1.5	PREDICTED: Canis familiaris similar to zinc finger protein 423 (LOC487291); mRNA	XM_544417	LOC487291	similar to zinc finger protein 423
CfaAffx.27578.1.S1_at	7.51E-02	1.00E+00	0.69	PREDICTED: Canis familiaris hypothetical LOC490496 (LOC490496); mRNA	XM_547618	LOC490496	hypothetical LOC490496
CfaAffx.27590.1.S1_s_at	3.42E-02	1.00E+00	0.75	PREDICTED: Canis familiaris hypothetical LOC490496 (LOC490496); mRNA	XM_547618	LOC490496	hypothetical LOC490496
CfaAffx.26453.1.S1_s_at	3.56E-02	1.00E+00	0.76	PREDICTED: Canis familiaris similar to chromosome 14 open reading frame 145 (LOC490814); mRNA	XM_547936	LOC490814	similar to chromosome 14 open reading frame 145
CfaAffx.27114.1.S1_s_at	2.10E-02	1.00E+00	0.68	PREDICTED: Canis familiaris similar to CPG2 protein (LOC490843); mRNA	XM_547965	LOC490843	similar to CPG2 protein
CfaAffx.22739.1.S1_at	6.71E-02	1.00E+00	1.98	PREDICTED: Canis familiaris similar to ankyrin repeat domain 26 (LOC491592); mRNA	XM_548713	LOC491592	similar to ankyrin repeat domain 26
CfaAffx.17428.1.S1_at	5.44E-02	1.00E+00	0.7	PREDICTED: Canis familiaris similar to family with sequence similarity 20; member C (LOC491596); mRNA	XM_548717	LOC491596	similar to family with sequence similarity 20, member C
CfaAffx.19097.1.S1_at	7.65E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to tensin-like SH2 domain containing 1 (LOC491620); mRNA	XM_843449	LOC491620	similar to tensin-like SH2 domain containing 1
Cfa.3959.1.A1_at	8.27E-02	1.00E+00	0.73	Bos taurus hypothetical LOC506309; mRNA (cDNA clone MGC:166209 IMAGE:8570991); complete cds	BC150106	LOC506309	hypothetical LOC506309

Table 1:Genes Differentially Expressed in Adipose Tissue in Fat Animals compared to Lean Animals

CfaAffx.12843.1.S1_s_at	9.69E-03	1.00E+00	1.33	PREDICTED: Bos taurus similar to olfactory receptor; family 5; subfamily M; member 10 (LOC513474); mRNA	XM_591159	LOC513474	similar to olfactory receptor, family 5, subfamily M, member 10
CfaAffx.19610.1.S1_at	2.64E-02	1.00E+00	1.77	PREDICTED: Canis familiaris similar to immunity-related GTPase family; cinema 1 (LOC606875); mRNA	XM_843352	LOC606875	similar to immunity-related GTPase family, cinema 1
CfaAffx.14433.1.S1_at	9.15E-02	1.00E+00	0.68	PREDICTED: Canis familiaris similar to dual specificity phosphatase 22 (LOC606970); mRNA	XM_843466	LOC606970	similar to dual specificity phosphatase 22
Cfa.19016.1.S1_s_at	1.73E-02	1.00E+00	2.07	PREDICTED: Canis familiaris similar to Protein C14orf119 (LOC607014); mRNA	XM_843279	LOC607014	similar to Protein C14orf119
Cfa.18258.1.S1_a_at	6.36E-02	1.00E+00	0.66	PREDICTED: Canis familiaris similar to downregulated in renal cell carcinoma (LOC607380); mRNA	XM_844019	LOC607380	similar to downregulated in renal cell carcinoma
Cfa.18258.2.S1_s_at	1.68E-02	1.00E+00	0.65	PREDICTED: Canis familiaris similar to downregulated in renal cell carcinoma (LOC607380); mRNA	XM_844019	LOC607380	similar to downregulated in renal cell carcinoma
Cfa.12385.1.A1_at	9.95E-02	1.00E+00	1.73	PREDICTED: Canis familiaris hypothetical protein LOC607395 (LOC607395); mRNA	XM_852878	LOC607395	hypothetical protein LOC607395
CfaAffx.8051.1.S1_at	9.28E-02	1.00E+00	0.49	PREDICTED: Canis familiaris similar to phytanoyl-CoA hydroxylase precursor (LOC607509); mRNA	XM_844206	LOC607509	similar to phytanoyl-CoA hydroxylase precursor
CfaAffx.14751.1.S1_at	6.32E-02	1.00E+00	0.67	PREDICTED: Canis familiaris hypothetical protein LOC608512 (LOC608512); mRNA	XM_845563	LOC608512	hypothetical protein LOC608512

Table 1:Genes Differentially Expressed in Adipose Tissue in Fat Animals compared to Lean Animals

CfaAffx.2096.1.S1_at	4.92E-02	1.00E+00	0.75	PREDICTED: Canis familiaris similar to CG11755-PA (LOC608872); mRNA	XM_846008	LOC608872	similar to CG11755-PA
CfaAffx.16276.1.S1_at	2.03E-02	1.00E+00	1.36	PREDICTED: Canis familiaris similar to Protein KIAA0152 precursor; transcript variant 1 (LOC609274); mRNA	XM_846298	LOC609274	similar to Protein KIAA0152 precursor
CfaAffx.15112.1.S1_at	5.12E-02	1.00E+00	1.32	PREDICTED: Canis familiaris hypothetical protein LOC609688 (LOC609688); mRNA	XM_847001	LOC609688	hypothetical protein LOC609688
Cfa.19768.1:S1_at	5.05E-02	1.00E+00	2.07	PREDICTED: Canis familiaris similar to ankyrin repeat domain 26 (LOC609691); mRNA	XM_847004	LOC609691	similar to ankyrin repeat domain 26
Cfa.15094.2.S1_a_at	5.09E-02	1.00E+00	1.86	PREDICTED: Canis familiaris similar to expressed in non-metastatic cells 1; protein (NM23A) (nucleoside diphosphate kinase) (LOC609873); mRNA	XM_847625	LOC609873	similar to expressed in non-metastatic cells 1, protein (NM23A) (nucleoside diphosphate kinase)
Cfa.6530.1.A1_at	2.89E-02	1.00E+00	1.31	PREDICTED: Canis familiaris similar to opposite strand transcription unit to Stag3; transcript variant 1 (LOC609909); mRNA	XM_847394	LOC609909	similar to opposite strand transcription unit to Stag3
CfaAffx.19396.1.S1_s_at	3.35E-02	1.00E+00	1.38	PREDICTED: Canis familiaris similar to opposite strand transcription unit to Stag3; transcript variant 2 (LOC609909); mRNA	XM_860682	LOC609909	similar to opposite strand transcription unit to Stag3
Cfa.20088.1.S1_at	7.21E-02	1.00E+00	1.49	PREDICTED: Canis familiaris hypothetical protein LOC610260 (LOC610260); partial mRNA	XM_847712	LOC610260	hypothetical protein LOC610260

Table 1:Genes Differentially Expressed in Adipose Tissue in Fat Animals compared to Lean Animals

							similar to Cytochrome P450 27, mitochondrial precursor (Cytochrome P-450C27/25) (Sterol 26-hydroxylase) (Sterol 27-hydroxylase) (Vitamin D(3) 25-hydroxylase) (5-beta-cholestane-3-alpha,7-alpha,12-alpha-triol 27-hydroxylase)
CfaAffx.22992.1.S1_at	4.05E-02	1.00E+00	0.64	PREDICTED: Canis familiaris similar to Cytochrome P450 27; mitochondrial precursor (Cytochrome P-450C27/25) (Sterol 26-hydroxylase) (Sterol 27-hydroxylase) (Vitamin D(3) 25-hydroxylase) (5-beta-cholestane-3-alpha;7-alpha;12-alpha-triol 27-hydroxylase) (LOC610489); mRNA	XM_848001	LOC610489	
CfaAffx.13327.1.S1_s_at	5.98E-02	1.00E+00	0.69	PREDICTED: Canis familiaris similar to Cytochrome c oxidase polypeptide Va; mitochondrial precursor (LOC610768); mRNA	XM_848859	LOC610768	similar to Cytochrome c oxidase polypeptide Va, mitochondrial precursor
CfaAffx.5042.1.S1_s_at	7.52E-03	1.00E+00	0.68	PREDICTED: Canis familiaris similar to CG9166-PA (LOC611116); mRNA	XM_848757	LOC611116	similar to CG9166-PA
CfaAffx.31158.1.S1_at	1.33E-03	1.00E+00	0.75	PREDICTED: Canis familiaris similar to CG11125-PA (LOC611150); mRNA	XM_848794	LOC611150	similar to CG11125-PA
Cfa.14385.1.S1_s_at	5.07E-02	1.00E+00	0.67	PREDICTED: Canis familiaris similar to Hypothetical UPF0195 protein CGI-128 (LOC611301); mRNA	XM_848951	LOC611301	similar to Hypothetical UPF0195 protein CGI-128

Table 1:Genes Differentially Expressed in Adipose Tissue in Fat Animals compared to Lean Animals

Cfa.14385.2.S1_s_at	4.38E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to Hypothetical UPF0195 protein CGI-128 (LOC611301); mRNA	XM_848951	LOC611301	similar to Hypothetical UPF0195 protein CGI-128
CfaAffx.31224.1.S1_s_at	3.39E-02	1.00E+00	0.68	PREDICTED: Canis familiaris similar to Hypothetical UPF0195 protein CGI-128 (LOC611301); mRNA	XM_848951	LOC611301	similar to Hypothetical UPF0195 protein CGI-128
Cfa.14385.2.S1_x_at	1.13E-02	1.00E+00	0.65	PREDICTED: Canis familiaris similar to Hypothetical UPF0195 protein CGI-128 (LOC611301); mRNA	XM_848951	LOC611301	similar to Hypothetical UPF0195 protein CGI-128
CfaAffx.15695.1.S1_at.	5.13E-02	1.00E+00	0.69	PREDICTED: Canis familiaris similar to ovary-specific MOB-like protein (LOC611494); mRNA	XM_849165	LOC611494	similar to ovary-specific MOB-like protein
CfaAffx.15732.1.S1_at	4.04E-02	1.00E+00	0.59	PREDICTED: Canis familiaris similar to Interferon-inducible protein (LOC611537); mRNA	XM_849217	LOC611537	similar to Interferon-inducible protein
CfaAffx.25700.1.S1_s_at	6.72E-04	1.00E+00	0.67	PREDICTED: Canis familiaris similar to 60S ribosomal protein L26-like 1 (LOC611570); mRNA	XM_849254	LOC611570	similar to 60S ribosomal protein L26-like 1
Cfa.4706.1.A1_at	8.56E-02	1.00E+00	0.77	PREDICTED: Canis familiaris similar to 60S ribosomal protein L26-like 1 (LOC611570); mRNA	XM_849254	LOC611570	similar to 60S ribosomal protein L26-like 1
CfaAffx.10678.1.S1_at	2.87E-02	1.00E+00	0.76	PREDICTED: Canis familiaris hypothetical protein LOC611604 (LOC611604); mRNA	XM_849285	LOC611604	hypothetical protein LOC611604
CfaAffx.12328.1.S1_at	7.18E-02	1.00E+00	0.72	PREDICTED: Canis familiaris similar to atonal homolog 8 (LOC612024); mRNA	XM_849751	LOC612024	similar to atonal homolog 8

Table 1:Genes Differentially Expressed in Adipose Tissue in Fat Animals compared to Lean Animals

Cfa.12014.1.A1_a_at	2.68E-02	1.00E+00	1.3	PREDICTED: Canis familiaris similar to Cytoplasmic dynein light chain (T-complex testis-specific protein 1 homolog) (Protein CW-1) (LOC612201); mRNA	XM_849938	LOC612201	similar to Cytoplasmic dynein light chain (T-complex testis-specific protein 1 homolog) (Protein CW-1)
CfaAffx.1907.1.S1_s_at	2.59E-02	1.00E+00	1.39	PREDICTED: Canis familiaris similar to Cytoplasmic dynein light chain (T-complex testis-specific protein 1 homolog) (Protein CW-1) (LOC612201); mRNA	XM_849938	LOC612201	similar to Cytoplasmic dynein light chain (T-complex testis-specific protein 1 homolog) (Protein CW-1)
Cfa.5178.1.S1_at	5.21E-02	1.00E+00	1.81	PREDICTED: Canis familiaris hypothetical protein LOC612422 (LOC612422); mRNA	XM_863647	LOC612422	hypothetical protein LOC612422
CfaAffx.131.1.S1_at	9.71E-02	1.00E+00	1.36	PREDICTED: Canis familiaris hypothetical protein LOC612530 (LOC612530); mRNA	XM_850260	LOC612530	hypothetical protein LOC612530
CfaAffx.26144.1.S1_at	5.62E-02	1.00E+00	0.58	PREDICTED: Macaca mulatta similar to KIBRA protein (LOC698875); mRNA	XM_001091174	LOC698875	similar to KIBRA protein
CfaAffx.29319.1.S1_at	8.25E-03	1.00E+00	0.73	PREDICTED: Macaca mulatta similar to calmodulin-like 6 (LOC703514); mRNA	XM_001096624	LOC703514	similar to calmodulin-like 6
Cfa.7478.1.A1_s_at	7.56E-02	1.00E+00	0.41	PREDICTED: Macaca mulatta similar to acetyl-Coenzyme A carboxylase beta (LOC706909); mRNA	XR_013022	LOC706909	similar to acetyl-Coenzyme A carboxylase beta

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CfaAffx.7975.1.S1_at	1.35E-02	1.00E+00	1.68	PREDICTED: Macaca mulatta similar to zinc finger protein 227 (LOC713327); mRNA	XM_001102642	LOC713327	similar to zinc finger protein 227
Cfa.13913.1.A1_at	8.82E-02	1.00E+00	1.32	PREDICTED: Macaca mulatta similar to Nck-associated protein 5 (LOC713453); mRNA	XM_001102812	LOC713453	similar to Nck-associated protein 5
Cfa.16284.1.S1_at	7.62E-02	1.00E+00	0.71	PREDICTED: Macaca mulatta similar to muscle specific ring finger protein 1 (LOC713802); mRNA	XM_001108306	LOC713802	similar to muscle specific ring finger protein 1
Cfa.6429.1.A1_at	2.56E-02	1.00E+00	0.64	PREDICTED: Macaca mulatta similar to Protein KIAA1434 (LOC719117); mRNA	XR_014093	LOC719117	similar to Protein KIAA1434
CfaAffx.17461.1.S1_s_at	6.82E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to low density lipoprotein receptor-related protein 10 precursor (LOC608002); mRNA	XM_537364	LRP10	low density lipoprotein receptor-related protein 10
Cfa.16962.1.S1_s_at	5.09E-02	1.00E+00	0.68	PREDICTED: Canis familiaris similar to latent transforming growth factor beta binding protein 2; transcript variant 1 (LOC490784); mRNA	XM_547906	LTBP2	latent transforming growth factor beta binding protein 2
CfaAffx.25922.1.S1_s_at	7.43E-02	1.00E+00	0.61	PREDICTED: Canis familiaris similar to latent transforming growth factor beta binding protein 2; transcript variant 3 (LOC490784); mRNA	XM_862924	LTBP2	latent transforming growth factor beta binding protein 2
CfaAffx.25362.1.S1_at	3.93E-02	1.00E+00	0.73	PREDICTED: Canis familiaris similar to Mitotic spindle assembly checkpoint protein MAD2B (MAD2-like 2) (LOC487443); mRNA	XM_544568	MAD2L2	MAD2 mitotic arrest deficient-like 2 (yeast)
Cfa.2264.1.S1_at	9.59E-02	1.00E+00	1.41	PREDICTED: Canis familiaris similar to melanoma antigen family D; 1 isoform b; transcript variant 1 (LOC480923); mRNA	XM_538044	MAGED1	melanoma antigen family D, 1

Table 1:Genes Differentially Expressed in Adipose Tissue in Fat Animals compared to Lean Animals

Cfa.3975.2.A1_at	6.28E-02	1.00E+00	1.34	PREDICTED: Canis familiaris similar to Melanoma-associated antigen D2 (MAGE-D2 antigen) (MAGE-D) (Breast cancer associated gene 1 protein) (BCG-1) (11B6) (Hepatocellular carcinoma associated protein JCL-1); transcript variant 11 (LOC480934); mRNA	XM_859782	MAGED2	melanoma antigen family D, 2
Cfa.21536.1.S1_at	3.42E-02	1.00E+00	1.33	PREDICTED: Canis familiaris similar to Melanoma-associated antigen D2 (MAGE-D2 antigen) (MAGE-D) (Breast cancer associated gene 1 protein) (BCG-1) (11B6) (Hepatocellular carcinoma associated protein JCL-1); transcript variant 11 (LOC480934); mRNA	XM_859782	MAGED2	melanoma antigen family D, 2
Cfa.2709.1.A1_at	6.75E-02	1.00E+00	1.75	PREDICTED: Pan troglodytes microtubule-associated protein 1B (MAP1B); mRNA	XM_517716	MAP1B	microtubule-associated protein 1B
CfaAffx.14768.1.S1_at	5.60E-02	1.00E+00	0.72	PREDICTED: Canis familiaris similar to C-jun-amino-terminal kinase interacting protein 1 (JNK-interacting protein 1) (JIP 1) (JNK MAP kinase scaffold protein 1) (Islet-brain-1) (IB-1) (Mitogen-activated protein kinase 8-interacting protein 1) (LOC483640); mRNA	XM_540760	MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1
Cfa.10212.1.A1_at	3.17E-02	1.00E+00	0.7	PREDICTED: Canis familiaris similar to microtubule-associated protein; RP/EB family; member 3; transcript variant 3 (LOC475694); mRNA	XM_854788	MAPRE3	microtubule-associated protein, RP/EB family, member 3
CfaAffx.21136.1.S1_s_at	9.18E-02	1.00E+00	0.67	PREDICTED: Canis familiaris similar to Microtubule-associated protein tau (Neurofibrillary tangle protein) (Paired helical filament-tau) (PHF-tau); transcript variant 3 (LOC480488); mRNA	XM_855209	MAPT	microtubule-associated protein tau
Cfa.10118.1.A1_at	9.32E-02	1.00E+00	0.73	PREDICTED: Canis familiaris similar to minichromosome maintenance protein 8 isoform 1; transcript variant 1 (LOC477163); mRNA	XM_534352	MCM8	minichromosome maintenance complex component 8

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CfaAffx.11578.1.S1_at	8.16E-02	1.00E+00	0.72	PREDICTED: Canis familiaris similar to MER receptor tyrosine kinase precursor (LOC483060); mRNA	XM_540175	MERTK	c-mer proto-oncogene tyrosine kinase
CfaAffx.16056.1.S1_s_at	1.46E-03	1.00E+00	0.71	PREDICTED: Canis familiaris similar to methyltransferase 5 domain containing 1 (LOC476897); mRNA	XM_534100	METT5D1	methyltransferase 5 domain containing 1
CfaAffx.16052.1.S1_at	7.57E-03	1.00E+00	0.7	PREDICTED: Canis familiaris similar to methyltransferase 5 domain containing 1 (LOC476897); mRNA	XM_534100	METT5D1	methyltransferase 5 domain containing 1
CfaAffx.17981.1.S1_s_at	7.51E-02	1.00E+00	0.68	PREDICTED: Canis familiaris similar to pP47 protein (LOC488730); mRNA	XM_545848	MFGE8	milk fat globule-EGF factor 8 protein
CfaAffx.17995.1.S1_at	3.12E-02	1.00E+00	1.5	PREDICTED: Canis familiaris similar to midline 1 isoform alpha; transcript variant 5 (LOC491737); mRNA	XM_851199	MID1	midline 1 (Opitz/BBB syndrome)
CfaAffx.30572.1.S1_at	9.46E-02	1.00E+00	0.76	PREDICTED: Canis familiaris similar to Malonyl-CoA decarboxylase; mitochondrial precursor (MCD) (LOC489688); mRNA	XM_847059	MLYCD	malonyl-CoA decarboxylase
Cfa.8997.1.A1_at	3.67E-02	1.00E+00	0.65	PREDICTED: Canis familiaris similar to ZK546.17 (LOC482514); mRNA	XM_539631	MMACHC	methylmalonic aciduria (cobalamin deficiency) cblC type, with homocystinuria
CfaAffx.23178.1.S1_at	3.36E-02	1.00E+00	0.64	PREDICTED: Canis familiaris similar to matrix metalloproteinase 27 (LOC489430); mRNA	XM_546548	MMP27	matrix metallopeptidase 27
CfaAffx.3467.1.S1_at	5.63E-02	1.00E+00	0.65	PREDICTED: Canis familiaris similar to MOB1; Mps One Binder kinase activator-like 2B (LOC474735); mRNA	XM_531966	MOBKL2B	MOB1, Mps One Binder kinase activator-like 2B (yeast)

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CfaAffx.12433.1.S1_s_at	2.76E-02	1.00E+00	0.76	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein S36 (LOC478085); mRNA	XM_535262	MRPS36	mitochondrial ribosomal protein S36
CfaAffx.25424.1.S1_at	7.82E-02	1.00E+00	1.32	PREDICTED: Canis familiaris similar to Moesin (Membrane-organizing extension spike protein); transcript variant 2 (LOC491924); mRNA	XM_843243	MSN	moesin
Cfa.542.1.A1_at	5.64E-02	1.00E+00	1.36	PREDICTED: Canis familiaris similar to Sialidase 1 precursor (Lysosomal sialidase) (N-acetyl-alpha-neuraminidase 1) (Acetylneuraminyl hydrolase) (G9 sialidase) (LOC481717); mRNA	XM_538838	NEU1	sialidase 1 (lysosomal sialidase)
CfaAffx.17532.1.S1_s_at	2.87E-03	1.00E+00	0.43	PREDICTED: Canis familiaris similar to X-linked neuroligin 4; transcript variant 1 (LOC607406); mRNA	XM_843264	NLGN4X	neuroligin 4, X-linked
CfaAffx.26479.1.S1_x_at	5.30E-02	1.00E+00	1.86	Canis lupus familiaris nm23-C1 mRNA for NM23-C1; complete cds	AB207044	NME1	non-metastatic cells 1, protein (NM23A) expressed in
Cfa.15094.1.S1_a_at	2.87E-02	1.00E+00	2.2	PREDICTED: Canis familiaris similar to expressed in non-metastatic cells 1; protein (NM23A) (nucleoside diphosphate kinase) (LOC476767); mRNA	XM_533973	NME1-NME2	NME1-NME2
Cfa.18171.1.S1_at	2.59E-02	1.00E+00	1.33	PREDICTED: Canis familiaris similar to nucleolar protein 3 (LOC611249); mRNA	XM_848890	NOL3	nucleolar protein 3 (apoptosis repressor with CARD domain)
Cfa.11099.1.A1_at	3.12E-02	1.00E+00	0.72	Bos taurus nuclear receptor binding factor 2; mRNA (cDNA clone MGC:143396 IMAGE:8142759); complete cds	BC123769	NRBF2	nuclear receptor binding factor 2
Cfa.2717.1.A1_a_at	3.48E-02	1.00E+00	0.69	trkC {alternatively spliced} [human; brain; mRNA; 2225 nt]	S76476	NTRK3	neurotrophic tyrosine kinase, receptor, type 3

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Cfa.2717.2.A1_at	5.44E-02	1.00E+00	0.65	PREDICTED: Macaca mulatta similar to neurotrophic tyrosine kinase; receptor; type 3 isoform c precursor; transcript variant 6 (NTRK3); mRNA	XM_001087841	NTRK3	neurotrophic tyrosine kinase, receptor, type 3
CfaAffx.13803.1.S1_at	6.40E-02	1.00E+00	1.31	PREDICTED: Canis familiaris similar to Nucleobindin 2 precursor (DNA-binding protein NEFA) (Gastric cancer antigen Zg4); transcript variant 7 (LOC476876); mRNA	XM_859996	NUCB2	nucleobindin 2
CfaAffx.21366.1.S1_s_at	2.20E-02	1.00E+00	0.75	PREDICTED: Canis familiaris similar to oxysterol-binding protein-like protein 6 isoform a; transcript variant 1 (LOC478816); mRNA	XM_535978	OSBPL6	oxysterol binding protein-like 6
Cfa.5284.1.A1_at	9.31E-02	1.00E+00	1.34	PREDICTED: Canis familiaris similar to phosphoprotein associated with glycosphingolipid microdomains 1 (LOC610895); mRNA	XM_848462	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1
CfaAffx.18467.1.S1_s_at	8.37E-02	1.00E+00	0.72	PREDICTED: Canis familiaris similar to mitochondrial phosphoenolpyruvate carboxykinase 2 isoform 1 precursor; transcript variant 7 (LOC480255); mRNA	XM_854642	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
Cfa.8974.1.A1_s_at	6.02E-02	1.00E+00	2.63	PREDICTED: Canis familiaris similar to proprotein convertase subtilisin/kexin type 1 preproprotein; transcript variant 4 (LOC479149); mRNA	XM_843544	PCSK1	proprotein convertase subtilisin/kexin type 1
Cfa.643.1.A1_at	4.87E-02	1.00E+00	0.67	PREDICTED: Pan troglodytes phosphodiesterase 3A; cGMP-inhibited (PDE3A); mRNA	XM_520783	PDE3A	phosphodiesterase 3A, cGMP-inhibited
Cfa.7017.1.A1_s_at	8.45E-02	1.00E+00	0.63	PREDICTED: Canis familiaris similar to platelet-derived growth factor; D polypeptide (LOC479460); mRNA	XM_536595	PDGFD	platelet derived growth factor D
Cfa.17829.1.S1_s_at	7.11E-02	1.00E+00	0.7	PREDICTED: Canis familiaris similar to pyruvate dehydrogenase kinase; isoenzyme 2 (LOC491075); mRNA	XM_548195	PDK2	pyruvate dehydrogenase kinase, isozyme 2

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CfaAffx.25948.1.S1_at	7.97E-02	1.00E+00	0.75	PREDICTED: Canis familiaris similar to pyruvate dehydrogenase kinase; isoenzyme 2 (LOC491075); mRNA	XM_548195	PDK2	pyruvate dehydrogenase kinase, isozyme 2
CfaAffx.4097.1.S1_s_at	3.06E-02	1.00E+00	0.36	PREDICTED: Canis familiaris similar to [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; mitochondrial precursor (Pyruvate dehydrogenase kinase isoform 4) (LOC482310); mRNA	XM_539427	PDK4	pyruvate dehydrogenase kinase, isozyme 4
CfaAffx.25273.1.S1_at	8.10E-02	1.00E+00	0.75	PREDICTED: Canis familiaris similar to MEGF10 protein (LOC490403); mRNA	XM_547524	PEAR1	platelet endothelial aggregation receptor 1
CfaAffx.25273.1.S1_s_at	4.68E-02	1.00E+00	0.73	PREDICTED: Canis familiaris similar to MEGF10 protein (LOC490403); mRNA	XM_547524	PEAR1	platelet endothelial aggregation receptor 1
CfaAffx.23485.1.S1_at	6.36E-02	1.00E+00	0.76	PREDICTED: Canis familiaris similar to 6-phosphogluconolactonase (LOC610090); mRNA	XM_847489	PGLS	6-phosphogluconolactonase
Cfa.14949.1.A1_s_at	1.93E-02	1.00E+00	0.68	PREDICTED: Canis familiaris similar to PHD finger protein 15; transcript variant 7 (LOC481508); mRNA	XM_857072	PHF15	PHD finger protein 15
Cfa.5653.1.A1_at	3.05E-02	1.00E+00	1.44	PREDICTED: Canis familiaris similar to Phosphorylase b kinase alpha regulatory chain; liver isoform (Phosphorylase kinase alpha L subunit); transcript variant 1 (LOC480857); mRNA	XM_537974	PHKA2	phosphorylase kinase, alpha 2 (liver)
CfaAffx.20064.1.S1_s_at	6.65E-02	1.00E+00	1.32	PREDICTED: Canis familiaris similar to Phosphorylase b kinase alpha regulatory chain; liver isoform (Phosphorylase kinase alpha L subunit); transcript variant 4 (LOC480857); mRNA	XM_853325	PHKA2	phosphorylase kinase, alpha 2 (liver)
Cfa.15689.1.A1_at	6.48E-02	1.00E+00	0.42	PREDICTED: Canis familiaris similar to phytanoyl-CoA hydroxylase precursor (LOC478001); mRNA	XM_844220	PHYH	phytanoyl-CoA 2-hydroxylase

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Cfa.1864.1.A1 at	6.61E-02	1.00E+00	0.7	PREDICTED: Equus caballus phosphatidylinositol-4-phosphate 5-kinase; type I; beta (PIP5K1B); mRNA	XM_001489746	PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta
CfaAffx.5584.1.S1_at	3.01E-02	1.00E+00	0.55	PREDICTED: Canis familiaris hypothetical LOC481916 (LOC481916); mRNA	XM_539037	PM20D2	peptidase M20 domain containing 2
CfaAffx.18740.1.S1_s_at	9.16E-02	1.00E+00	1.49	PREDICTED: Canis familiaris similar to Transmembrane prostate androgen-induced protein (Solid tumor-associated 1 protein) (LOC485945); mRNA	XM_543070	PMEPA1	prostate transmembrane protein, androgen induced 1
CfaAffx.25777.1.S1_at	5.07E-02	1.00E+00	0.77	PREDICTED: Canis familiaris similar to Paraneoplastic antigen Ma1 (Neuron- and testis-specific protein 1) (37 kDa neuronal protein) (LOC490774); mRNA	XM_547896	PNMA1	paraneoplastic antigen MA1
CfaAffx.15010.1.S1_at	8.46E-02	1.00E+00	0.6	PREDICTED: Canis familiaris similar to patatin-like phospholipase domain containing 2 (LOC611403); mRNA	XM_849071	PNPLA2	patatin-like phospholipase domain containing 2
CfaAffx.21675.1.S1_at	4.99E-02	1.00E+00	0.64	PREDICTED: Canis familiaris similar to inorganic pyrophosphatase (LOC479238); mRNA	XM_536380	PPA1	pyrophosphatase (inorganic) 1
Cfa.9464.1.S1_at	7.89E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to inorganic pyrophosphatase (LOC479238); mRNA	XM_536380	PPA1	pyrophosphatase (inorganic) 1
CfaAffx.21675.1.S1_s_at	5.41E-02	1.00E+00	0.66	PREDICTED: Canis familiaris similar to inorganic pyrophosphatase (LOC479238); mRNA	XM_536380	PPA1	pyrophosphatase (inorganic) 1
Cfa.11731.1.A1_at	7.14E-02	1.00E+00	0.74	Bos taurus phosphatidic acid phosphatase type 2 domain containing 3; mRNA (cDNA clone MGC:143389 IMAGE:8141929); complete cds	BC123770	PPAPDC3	phosphatidic acid phosphatase type 2 domain containing 3

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Cfa.11839.1.A1_s_at	1.33E-02	1.00E+00	0.56	PREDICTED: Canis familiaris similar to pyruvate dehydrogenase phosphatase precursor (LOC477941); mRNA	XM_535129	PPM2C	protein phosphatase 2C, magnesium-dependent, catalytic subunit
Cfa.11839.1.A1_at	5.91E-03	1.00E+00	0.51	PREDICTED: Canis familiaris similar to pyruvate dehydrogenase phosphatase precursor (LOC477941); mRNA	XM_535129	PPM2C	protein phosphatase 2C, magnesium-dependent, catalytic subunit
CfaAffx.14411.1.S1_at	4.69E-03	1.00E+00	0.53	PREDICTED: Canis familiaris similar to pyruvate dehydrogenase phosphatase precursor (LOC477941); mRNA	XM_535129	PPM2C	protein phosphatase 2C, magnesium-dependent, catalytic subunit
CfaAffx.18658.1.S1_at	2.97E-03	1.00E+00	1.39	PREDICTED: Canis familiaris similar to protein phosphatase 1 regulatory inhibitor subunit 8 isoform alpha; transcript variant 1 (LOC487340); mRNA	XM_544466	PPP1R8	protein phosphatase 1, regulatory (inhibitor) subunit 8
CfaAffx.15427.1.S1_at	6.93E-02	1.00E+00	0.77	PREDICTED: Canis familiaris similar to HMT1 hnRNP methyltransferase-like 3; transcript variant 1 (LOC476887); mRNA	XM_534089	PRMT3	protein arginine methyltransferase 3
Cfa.6910.1.A1_at	3.99E-02	1.00E+00	1.31	PREDICTED: Canis familiaris similar to Ribose-phosphate pyrophosphokinase II (Phosphoribosyl pyrophosphate synthetase II) (PRS-II); transcript variant 5 (LOC476855); mRNA	XM_851577	PRPS2	phosphoribosyl pyrophosphate synthetase 2
CfaAffx.19134.1.S1_at	1.66E-02	1.00E+00	0.71	Pan troglodytes protease; serine; 12 (neurotrypsin; motopsin) (PRSS12); mRNA	NM_001071807	PRSS12	protease, serine, 12 (neurotrypsin, motopsin)

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CfaAffx.10730.1.S1_at	5.23E-02	1.00E+00	0.73	PREDICTED: Canis familiaris similar to phosphatidylserine synthase 2 (LOC483401); mRNA	XM_540520	PTDSS2	phosphatidylserine synthase 2
Cfa.3452.1.S1_s_at	5.39E-02	1.00E+00	1.54	Canis familiaris prostaglandin E2 receptor EP4 subtype mRNA; complete cds	AF177934	PTGER4	prostaglandin E receptor 4 (subtype EP4)
CfaAffx.6541.1.S1_s_at	4.44E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1 (LOC475014); mRNA	XM_532250	QRSL1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1
Cfa.20264.1.S1_s_at	6.60E-02	1.00E+00	0.75	PREDICTED: Canis familiaris similar to RAN binding protein 9 (LOC478728); mRNA	XM_535893	RANBP9	RAN binding protein 9
Cfa.21620.1.S1_at	2.52E-02	1.00E+00	1.49	Homo sapiens Rap guanine nucleotide exchange factor (GEF) 5; mRNA (cDNA clone MGC:26203 IMAGE:4811483); complete cds	BC039203	RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5
CfaAffx.4051.1.S1_s_at	5.58E-02	1.00E+00	0.76	PREDICTED: Canis familiaris similar to RNA cyclase homolog (LOC484183); mRNA	XM_541299	RCL1	RNA terminal phosphate cyclase-like 1
Cfa.20008.1.S1_at	8.25E-02	1.00E+00	1.37	PREDICTED: Canis familiaris similar to Retinol dehydrogenase 11 (Retinal reductase 1) (RalR1) (Prostate short-chain dehydrogenase/reductase 1) (Androgen-regulated short-chain dehydrogenase/reductase 1) (HCV core-binding protein HCBP12) (LOC480366); mRNA	XM_849261	RDH11	retinol dehydrogenase 11 (all-trans/9 cis/11-cis)
Cfa.9467.1.A1_at	3.69E-02	1.00E+00	1.59	PREDICTED: Canis familiaris similar to reelin isoform b; transcript variant 1 (LOC483273); mRNA	XM_540392	RELN	reelin
Cfa.3701.1.S1_at	7.10E-02	1.00E+00	0.63	Pongo abelii mRNA; cDNA DKFZp469I191 (from clone DKFZp469I191)	CR926484	REN	renin
Cfa.470.1.A1_at	1.32E-02	1.00E+00	0.42	PREDICTED: Canis familiaris similar to DNA repair protein REV1 (Rev1-like terminal deoxycytidyl transferase) (Alpha integrin binding protein 80) (AIBP80) (LOC481337); mRNA	XM_538458	REV1	REV1 homolog (S. cerevisiae)

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Cfa.17646.1.S1_s_at	6.57E-02	1.00E+00	0.66	PREDICTED: Canis familiaris similar to raft-linking protein (LOC485653); mRNA	XM_542773	RFTN1	raftlin, lipid raft linker 1
CfaAffx.9766.1.S1_at	3.10E-02	1.00E+00	0.65	PREDICTED: Canis familiaris similar to raft-linking protein (LOC485653); mRNA	XM_542773	RFTN1	raftlin, lipid raft linker 1
Cfa.995.1.S1_s_at	3.91E-02	1.00E+00	0.72	PREDICTED: Canis familiaris similar to CG3295-PA; transcript variant 2 (LOC475760); mRNA	XM_847036	RMND5A	required for meiotic nuclear division 5 homolog A (S. cerevisiae)
CfaAffx.5868.1.S1_at	2.57E-03	1.00E+00	0.73	PREDICTED: Bos taurus similar to mKIAA0161 protein (RNF144A); mRNA	XM_870498	RNF144A	ring finger protein 144A
CfaAffx.6394.1.S1_at	6.97E-02	1.00E+00	0.58	PREDICTED: Canis familiaris similar to ring finger protein 150 (LOC607611); mRNA	XM_844361	RNF150	ring finger protein 150
Cfa.155.1.S1_s_at	8.18E-02	1.00E+00	0.63	TPA_inf: Canis familiaris RTN1-C (RTN1) mRNA; complete cds	BK001793	RTN1	reticulon 1
CfaAffx.30603.1.S1_at	6.19E-02	1.00E+00	1.48	PREDICTED: Canis familiaris similar to endothelial differentiation; sphingolipid G-protein-coupled receptor; 1 (EDG1); mRNA	XM_547259	S1PR1	sphingosine-1-phosphate receptor 1
CfaAffx.25247.1.S1_at	6.89E-02	1.00E+00	0.75	PREDICTED: Bos taurus similar to sterile alpha motif domain containing 1 (SAMD1); mRNA	XM_001250641	SAMD1	sterile alpha motif domain containing 1
CfaAffx.11400.1.S1_at	6.66E-02	1.00E+00	0.24	Homo sapiens clone DNA66675 HLAR698 (UNQ698) mRNA; complete cds	AY358701	SBSN	suprabasin
Cfa.11487.1.A1_at	6.39E-02	1.00E+00	0.76	PREDICTED: Pan troglodytes serologically defined colon cancer antigen 8; transcript variant 4 (SDCCAG8); mRNA	XM_525116	SDCCAG8	serologically defined colon cancer antigen 8
Cfa.19483.1.S1_s_at	9.82E-02	1.00E+00	1.36	PREDICTED: Canis familiaris similar to splicing factor 3b; subunit 3; transcript variant 1 (LOC479659); mRNA	XM_536791	SF3B3	splicing factor 3b, subunit 3, 130kDa
Cfa.12118.1.A1_at	1.60E-02	1.00E+00	0.65	Bos taurus sphingosine-1-phosphate lyase 1; mRNA (cDNA clone MGC:140361 IMAGE:8188064); complete cds	BC140468	SGPL1	sphingosine-1-phosphate lyase 1

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CfaAffx.18664.1.S1_at	9.17E-02	1.00E+00	0.66	PREDICTED: Canis familiaris similar to SH3-domain binding protein 4 (LOC486172); mRNA	XM_543298	SH3BP4	SH3-domain binding protein 4
CfaAffx.9996.1.S1_at	2.80E-02	1.00E+00	1.4	PREDICTED: Canis familiaris similar to SH3 domain-binding protein 5 (SH3 domain-binding protein that preferentially associates with BTK) (LOC485657); mRNA	XM_542777	SH3BP5	SH3-domain binding protein 5 (BTK-associated)
CfaAffx.13680.1.S1_s_at	9.34E-03	1.00E+00	0.72	PREDICTED: Canis familiaris similar to shroom (LOC478438); mRNA	XM_844910	SHROOM3	shroom family member 3
Cfa.21475.1.S1_at	2.78E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to SID1 transmembrane family; member 2 (LOC489391); mRNA	XM_546509	SIDT2	SID1 transmembrane family, member 2
CfaAffx.16900.1.S1_s_at	9.11E-03	1.00E+00	0.74	PREDICTED: Canis familiaris similar to Solute carrier family 12; member 7 (Electroneutral potassium-chloride cotransporter 4) (K-Cl cotransporter 4) (LOC488069); mRNA	XM_545193	SLC12A7	solute carrier family 12 (potassium/chloride transporters), member 7
Cfa.19806.1.S1_s_at	7.93E-02	1.00E+00	0.73	PREDICTED: Canis familiaris similar to Monocarboxylate transporter 1 (MCT 1); transcript variant 3 (LOC475856); mRNA	XM_857592	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)
Cfa.16871.1.S1_at	5.07E-02	1.00E+00	0.54	PREDICTED: Canis familiaris similar to solute carrier family 27 (fatty acid transporter); member 6 (LOC474666); mRNA	XM_531894	SLC27A6	solute carrier family 27 (fatty acid transporter), member 6

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CfaAffx.2004.1.S1_s_at	1.11E-02	1.00E+00	0.48	PREDICTED: Canis familiaris similar to solute carrier family 27 (fatty acid transporter); member 6 (LOC474666); mRNA	XM_531894	SLC27A6	solute carrier family 27 (fatty acid transporter), member 6
CfaAffx.16375.1.S1_s_at	8.39E-03	1.00E+00	0.66	PREDICTED: Canis familiaris similar to solute carrier family 37 member 1 (LOC487780); mRNA	XM_544905	SLC37A1	solute carrier family 37 (glycerol-3-phosphate transporter), member 1
CfaAffx.23808.1.S1_at	1.75E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to solute carrier family 3 (activators of dibasic and neutral amino acid transport); member 2 isoform a (LOC483777); mRNA	XM_540898	SLC3A2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2
CfaAffx.17822.1.S1_at	1.36E-02	1.00E+00	0.75	PREDICTED: Canis familiaris similar to Large neutral amino acids transporter small subunit 2 (L-type amino acid transporter 2) (hLAT2); transcript variant 7 (LOC490608); mRNA	XM_853554	SLC7A8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8
Cfa.16330.1.S1_s_at	3.80E-02	1.00E+00	0.69	Canis familiaris prostaglandin transporter mRNA; complete cds	AY879310	SLCO2A1	solute carrier organic anion transporter family, member 2A1

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							SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1
Cfa.1931.1.A1_at	5.58E-02	1.00E+00	1.37	PREDICTED: Canis familiaris similar to SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a1 isoform a; transcript variant 19 (LOC481046); mRNA	XM_860493	SMARCA1	
CfaAffx.21915.1.S1_at	6.28E-02	1.00E+00	0.69	PREDICTED: Canis familiaris similar to SNF1-like kinase 2 (LOC489410); mRNA	XM_546528	SNF1LK2	SNF1-like kinase 2
CfaAffx.21458.1.S1_at	5.37E-02	1.00E+00	0.64	PREDICTED: Canis familiaris similar to Sterol O-acyltransferase 1 (Cholesterol acyltransferase 1) (Acyl coenzyme A:cholesterol acyltransferase 1) (ACAT-1) (LOC490325); mRNA	XM_547445	SOAT1	sterol O-acyltransferase 1
CfaAffx.14389.1.S1_at	6.96E-02	1.00E+00	1.55	PREDICTED: Canis familiaris similar to SON DNA-binding protein isoform A; transcript variant 4 (LOC478406); mRNA	XM_851635	SON	SON DNA binding protein
CfaAffx.1703.1.S1_x_at	9.64E-02	1.00E+00	1.99	PREDICTED: Canis familiaris similar to SON DNA-binding protein isoform A; transcript variant 14 (LOC478406); mRNA	XM_852093	SON	SON DNA binding protein
Cfa.17029.1.S1_at	4.04E-02	1.00E+00	0.69	PREDICTED: Canis familiaris similar to SH3 domain protein 4 (LOC477383); mRNA	XM_534577	SORBS3	sorbin and SH3 domain containing 3
CfaAffx.18082.1.S1_s_at	1.01E-02	1.00E+00	0.67	PREDICTED: Canis familiaris similar to SRY (sex determining region Y)-box 5 isoform a; transcript variant 10 (LOC486635); mRNA	XM_860888	SOX5	SRY (sex determining region Y)-box 5
CfaAffx.27328.1.S1_s_at	1.00E-02	1.00E+00	1.38	PREDICTED: Canis familiaris similar to SPARC precursor (Secreted protein acidic and rich in cysteine) (Osteonectin) (ON) (Basement-membrane protein 40) (BM-40) (LOC612159); mRNA	XM_849889	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)

Table 1:Genes Differentially Expressed in Adipose Tissue in Fat Animals compared to Lean Animals

Cfa.20143.1.S1_at	9.41E-02	1.00E+00	1.46	PREDICTED: Canis familiaris similar to atlastin; transcript variant 1 (LOC480318); mRNA	XM_537440	SPG3A	spastic paraplegia 3A (autosomal dominant)
Cfa.4966.1.A1_s_at	9.23E-02	1.00E+00	0.68	Homo sapiens sparc/osteonectin; cwcv and kazal-like domains proteoglycan (testican) 2 (SPOCK2); transcript variant 2; mRNA	NM_014767	SPOCK2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2
CfaAffx.25530.1.S1_at	2.75E-03	1.00E+00	0.69	Bos taurus spondin 2; extracellular matrix protein; mRNA (cDNA clone MGC:138085 IMAGE:8086057); complete cds	BC113291	SPON2	spondin 2, extracellular matrix protein
Cfa.16366.1.A1_at	8.37E-02	1.00E+00	1.47	Homo sapiens ST8 alpha-N-acetyl-neuraminide alpha-2;8-sialyltransferase 4 (ST8SIA4); transcript variant 1; mRNA	NM_005668	ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4
Cfa.20754.1.S1_at	8.30E-02	1.00E+00	1.33	PREDICTED: Canis familiaris similar to Signal transducer and activator of transcription 1-alpha/beta (Transcription factor ISGF-3 components p91/p84); transcript variant 4 (LOC488449); mRNA	XM_850863	STAT1	signal transducer and activator of transcription 1, 91kDa
Cfa.11720.1.A1_at	4.02E-02	1.00E+00	1.34	PREDICTED: Canis familiaris similar to serine/threonine kinase 35 (LOC609432); mRNA	XM_846689	STK35	serine/threonine kinase 35
Cfa.17400.1.S1_s_at	9.89E-02	1.00E+00	0.7	PREDICTED: Canis familiaris similar to Dual specificity protein phosphatase 24 (Map kinase phosphatase-like protein MK-STYX) (Dual specificity phosphatase inhibitor MK-STYX); transcript variant 3 (LOC489817); mRNA	XM_853119	STYXL1	serine/threonine/tyrosine interacting-like 1
CfaAffx.12846.1.S1_s_at	6.03E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to succinate-CoA ligase; GDP-forming; alpha subunit (LOC475775); mRNA	XM_532985	SUCLG1	succinate-CoA ligase, alpha subunit

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Cfa.11749.1.A1_at	7.63E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to Sulfite oxidase; mitochondrial precursor (LOC481103); mRNA	XM_538224	SUOX	sulfite oxidase
CfaAffx.1103.1.S1_at	5.10E-02	1.00E+00	0.73	PREDICTED: Canis familiaris similar to Sulfite oxidase; mitochondrial precursor (LOC481103); mRNA	XM_538224	SUOX	sulfite oxidase
CfaAffx.6930.1.S1_s_at	2.24E-02	1.00E+00	0.63	PREDICTED: Canis familiaris similar to supervillin isoform 1; transcript variant 2 (LOC477965); mRNA	XM_844807	SVIL	supervillin
Cfa.19132.1.S1_s_at	4.56E-02	1.00E+00	0.7	PREDICTED: Canis familiaris similar to supervillin isoform 1; transcript variant 4 (LOC477965); mRNA	XM_855044	SVIL	supervillin
Cfa.9691.1.A1_at	8.37E-02	1.00E+00	0.77	PREDICTED: Canis familiaris similar to spectrin repeat containing; nuclear envelope 2 isoform e; transcript variant 1 (LOC490729); mRNA	XM_547851	SYNE2	spectrin repeat containing, nuclear envelope 2
Cfa.4844.1.A1_at	1.29E-02	1.00E+00	1.51	Porcine mRNA for transforming growth factor-beta 3 (TGF-beta 3)	X14150	TGFB3	transforming growth factor, beta 3
CfaAffx.26179.1.S1_s_at	1.37E-02	1.00E+00	1.33	PREDICTED: Canis familiaris similar to Transforming growth factor beta 3 precursor (TGF-beta 3); transcript variant 5 (LOC490796); mRNA	XM_863112	TGFB3	transforming growth factor, beta 3
CfaAffx.8681.1.S1_s_at	2.38E-02	1.00E+00	0.75	Canis lupus familiaris TM mRNA for thrombomodulin; complete cds	AB193481	THBD	thrombomodulin
CfaAffx.13216.1.S1_s_at	5.50E-02	1.00E+00	1.87	PREDICTED: Canis familiaris similar to Transmembrane 4 L6 family member 1 (Tumor-associated antigen L6) (Membrane component; surface marker 1) (M3S1) (LOC477107); mRNA	XM_534302	TM4SF18	transmembrane 4 L six family member 18
Cfa.17747.1.S1_s_at	4.64E-02	1.00E+00	0.72	PREDICTED: Canis familiaris similar to RECS1 protein homolog (LOC610419); mRNA	XM_847923	TMBIM1	transmembrane BAX inhibitor motif containing 1
Cfa.13654.1.A1_s_at	3.82E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to RECS1 protein homolog (LOC610419); mRNA	XM_847923	TMBIM1	transmembrane BAX inhibitor motif containing 1

Table 1:Genes Differentially Expressed in Adipose Tissue in Fat Animals compared to Lean Animals

CfaAffx.22563.1.S1_at	2.34E-02	1.00E+00	0.72	PREDICTED: Canis familiaris similar to RECS1 protein homolog (LOC610419); mRNA	XM_847923	TMBIM1	transmembrane BAX inhibitor motif containing 1
Cfa.7109.1.A1_at	1.49E-02	1.00E+00	1.3	PREDICTED: Canis familiaris similar to transmembrane emp24 protein transport domain containing 9; transcript variant 1 (LOC481444); mRNA	XM_538565	TMED9	transmembrane emp24 protein transport domain containing 9
CfaAffx.1310.1.S1_at	4.56E-03	1.00E+00	1.51	PREDICTED: Canis familiaris similar to transmembrane emp24 protein transport domain containing 9; transcript variant 1 (LOC481444); mRNA	XM_538565	TMED9	transmembrane emp24 protein transport domain containing 9
CfaAffx.4729.1.S1_at	3.53E-02	1.00E+00	2.29	PREDICTED: Canis familiaris similar to transmembrane protein with EGF-like and two follistatin-like domains 1; transcript variant 2 (LOC612942); mRNA	XM_862118	TMEFF1	transmembrane protein with EGF-like and two follistatin-like domains 1
Cfa.1794.1.S1_at	6.31E-02	1.00E+00	0.69	PREDICTED: Canis familiaris similar to BE10.2 (LOC475247); mRNA	XM_532481	TMEM195	transmembrane protein 195
CfaAffx.10111.1.S1_at	8.52E-02	1.00E+00	1.31	PREDICTED: Canis familiaris similar to CG4050-PA; isoform A (LOC475421); mRNA	XM_532644	TMTC3	transmembrane and tetratricopeptide repeat containing 3
CfaAffx.3284.1.S1_at	1.01E-02	1.00E+00	0.5	PREDICTED: Canis familiaris similar to Triggering receptor expressed on myeloid cells 2 precursor (Triggering receptor expressed on monocytes 2) (TREM-2) (LOC608965); mRNA	XM_846138	TREM2	triggering receptor expressed on myeloid cells 2

Table 1:Genes Differentially Expressed in Adipose Tissue in Fat Animals compared to Lean Animals

CfaAffx.3283.1.S1_s_at	2.89E-02	1.00E+00	0.51	PREDICTED: Canis familiaris similar to Triggering receptor expressed on myeloid cells 2 precursor (Triggering receptor expressed on monocytes 2) (TREM-2) (LOC608965); mRNA	XM_846138	TREM2	triggering receptor expressed on myeloid cells 2
Cfa.5715.1.S1_at	7.39E-02	1.00E+00	0.73	PREDICTED: Canis familiaris similar to triggering receptor expressed on myeloid cells-like 1 (LOC474898); mRNA	XM_532133	TREML1	triggering receptor expressed on myeloid cells-like 1
CfaAffx.22480.1.S1_at	9.75E-02	1.00E+00	0.69	PREDICTED: Canis familiaris similar to tRNA splicing 2 phosphotransferase 1 (LOC483765); mRNA	XM_540886	TRPT1	tRNA phosphotransferase 1
CfaAffx.22480.1.S1_s_at	7.29E-02	1.00E+00	0.62	PREDICTED: Canis familiaris similar to tRNA splicing 2 phosphotransferase 1 (LOC483765); mRNA	XM_540886	TRPT1	tRNA phosphotransferase 1
CfaAffx.24324.1.S1_s_at	1.90E-03	1.00E+00	0.74	PREDICTED: Canis familiaris similar to tetraspanin 14 (LOC610573); mRNA	XM_848106	TSPAN14	tetraspanin 14
Cfa.13544.1.A1_at	3.65E-02	1.00E+00	1.41	Homo sapiens clone PP1057 unknown mRNA	AF217967	TSPAN9	tetraspanin 9
Cfa.14054.1.A1_s_at	5.62E-02	1.00E+00	0.66	PREDICTED: Canis familiaris similar to Y54G11A.7; transcript variant 2 (LOC474465); mRNA	XM_851458	TTC38	tetratricopeptide repeat domain 38
CfaAffx.24911.1.S1_s_at	4.83E-02	1.00E+00	1.35	PREDICTED: Canis familiaris similar to Tubulin alpha-8 chain (Alpha-tubulin 8) (LOC486762); mRNA	XM_543889	TUBA8	tubulin, alpha 8
Cfa.11276.1.S1_at	4.30E-02	1.00E+00	1.37	PREDICTED: Canis familiaris similar to tubulin; beta 2 (LOC478701); mRNA	XM_535868	TUBB2A	tubulin, beta 2A
CfaAffx.9291.1.S1_s_at	1.63E-02	1.00E+00	0.42	Canis lupus familiaris ucp2 mRNA for uncoupling protein 2; complete cds	AB020887	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)
CfaAffx.28986.1.S1_s_at	3.28E-02	1.00E+00	0.76	similar to Ubiquitin carboxyl-terminal hydrolase 24 (Ubiquitin thiolesterase 24) (Ubiquitin-specific processing protease 24) (Deubiquitinating enzyme 24) (LOC479558); mRNA	XM_536697	USP24	ubiquitin specific peptidase 24

Table 1:Genes Differentially Expressed in Adipose Tissue in Fat Animals compared to Lean Animals

Cfa.16692.1.S1_s_at	4.39E-02	1.00E+00	0.71	similar to Ubiquitin carboxyl-terminal hydrolase 24 (Ubiquitin thiolesterase 24) (Ubiquitin-specific processing protease 24) (Deubiquitinating enzyme 24) (LOC479558); mRNA	XM_536697	USP24	ubiquitin specific peptidase 24
CfaAffx.19310.1.S1_s_at	2.74E-02	1.00E+00	0.62	PREDICTED: Canis familiaris similar to ubiquitin specific protease 53 (LOC487923); mRNA	XM_545046	USP53	ubiquitin specific peptidase 53
CfaAffx.8845.1.S1_s_at	3.20E-02	1.00E+00	0.66	PREDICTED: Canis familiaris similar to vasoactive intestinal peptide receptor 2 (LOC611663); mRNA	XM_849361	VIPR2	vasoactive intestinal peptide receptor 2
Cfa.3482.1.S1_at	9.43E-02	1.00E+00	1.55	Canis familiaris TIFF66 mRNA; complete cds	U39663	VNN1	vanin 1
CfaAffx.1247.1.S1_s_at	4.47E-02	1.00E+00	1.8	Canis familiaris TIFF66 mRNA; complete cds	U39663	VNN1	vanin 1
CfaAffx.22068.1.S1_s_at	7.57E-02	1.00E+00	1.77	Canis familiaris TIFF66 mRNA; complete cds	U39663	VNN1	vanin 1
CfaAffx.24331.1.S1_at	1.69E-02	1.00E+00	0.6	PREDICTED: Canis familiaris similar to TGF-beta resistance-associated protein (LOC487562); mRNA	XM_544687	WDR72	WD repeat domain 72
CfaAffx.24332.1.S1_s_at	6.86E-02	1.00E+00	0.71	PREDICTED: Canis familiaris similar to TGF-beta resistance-associated protein (LOC487562); mRNA	XM_544687	WDR72	WD repeat domain 72
CfaAffx.15356.1.S1_at	1.55E-02	1.00E+00	0.73	PREDICTED: Canis familiaris similar to YY1 associated factor 2 isoform a (LOC609790); mRNA	XM_847127	YAF2	YY1 associated factor 2
CfaAffx.10465.1.S1_s_at	2.02E-02	1.00E+00	1.31	PREDICTED: Canis familiaris similar to smooth muscle cell associated protein 5 (LOC478048); mRNA	XM_535226	YIPF5	Yip1 domain family, member 5
CfaAffx.12550.1.S1_at	5.61E-03	1.00E+00	0.73	PREDICTED: Canis familiaris similar to yippee-like 4 (LOC610168); mRNA	XM_847589	YPEL4	yippee-like 4 (Drosophila)
CfaAffx.20922.1.S1_at	7.15E-02	1.00E+00	0.56	PREDICTED: Canis familiaris similar to promyelocytic leukemia zinc finger protein; transcript variant 2 (LOC489398); mRNA	XM_845250	ZBTB16	zinc finger and BTB domain containing 16

Table 1:Genes Differentially Expressed in Adipose Tissue in Fat Animals compared to Lean Animals

CfaAffx.6587.1.S1_at	6.66E-02	1.00E+00	1.33	PREDICTED: Canis familiaris similar to Zinc finger FYVE domain containing protein 9 (Mothers against decapentaplegic homolog interacting protein) (Madh-interacting protein) (Smad anchor for receptor activation) (Receptor activation anchor) (hSARA) (Novel serine protease) (NSP...; transcript variant 1 (LOC475352); mRNA	XM_532576	ZFYVE9	zinc finger, FYVE domain containing 9
CfaAffx.7931.1.S1_s_at	8.47E-02	1.00E+00	0.75	Bos taurus zinc finger protein 180; mRNA (cDNA clone MGC:151525 IMAGE:8097646); complete cds	BC149088	ZNF180	zinc finger protein 180
CfaAffx.7983.1.S1_s_at	7.11E-03	1.00E+00	1.64	PREDICTED: Canis familiaris similar to zinc finger protein 227 (LOC484460); mRNA	XM_850112	ZNF227	zinc finger protein 227
CfaAffx.26487.1.S1_s_at	4.20E-02	1.00E+00	0.69	PREDICTED: Canis familiaris similar to zinc finger protein 617 (LOC611075); mRNA	XM_848708	ZNF564	zinc finger protein 564
Cfa.12414.1.A1_s_at	5.90E-02	1.00E+00	0.72	PREDICTED: Canis familiaris similar to zinc finger protein 622; transcript variant 2 (LOC479383); mRNA	XM_863227	ZNF622	zinc finger protein 622
CfaAffx.29168.1.S1_s_at	4.34E-02	1.00E+00	0.74	PREDICTED: Canis familiaris similar to zinc finger protein 622; transcript variant 3 (LOC479383); mRNA	XM_863237	ZNF622	zinc finger protein 622
Cfa.11779.1.A1_at	8.46E-02	1.00E+00	0.73	PREDICTED: Canis familiaris hypothetical LOC479517; transcript variant 1 (LOC479517); mRNA	XM_536655	ZSWIM7	zinc finger, SWIM-type containing 7
Cfa.11779.1.A1_s_at	1.03E-02	1.00E+00	0.72	PREDICTED: Canis familiaris hypothetical LOC479517; transcript variant 1 (LOC479517); mRNA	XM_536655	ZSWIM7	zinc finger, SWIM-type containing 7

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Fat vs Lean (Whole Blood Gene Expression Comparison) allgenelist FC cutoff: 1.3; P-val cutofff:							
#samples in group-1 (FAT): 32 group-2 (LEAN): 12							
Fold change > 1 implies probes are UP regulated in FAT samples.							
Probe	**P-Value**	**Q-Value**	**Fold-Change**	**Top BLAST Annot.**	**Top Hit Accn.**	**Gene Symbol**	**Gene Desc.**
CfaAffx.14897.1.S1_at	5.05E-03	1.77E-02	0.75	PREDICTED: Canis familiaris similar to axotrophin; transcript variant 1 (LOC478763); mRNA	XM_535929		membrane-associated ring finger (C3HC4) 7
Cfa.10982.1.A1_at	5.26E-03	1.79E-02	0.71	PREDICTED: Canis familiaris similar to Septin-2 (NEDD5 protein homolog) (LOC487886); mRNA	XM_846816	2-Sep	septin 2
CfaAffx.20073.1.S1_s_at	5.48E-04	1.02E-02	0.76	PREDICTED: Canis familiaris similar to Septin-2 (NEDD5 protein homolog) (LOC487886); mRNA	XM_846816	2-Sep	septin 2
CfaAffx.30993.1.S1_s_at	9.84E-04	1.16E-02	0.73	Canis lupus familiaris 15 kDa selenoprotein (SEP15); mRNA	NM_001114760	15-Sep	15 kDa selenoprotein
CfaAffx.30994.1.S1_s_at	8.25E-03	2.12E-02	0.73	Homo sapiens 15 kDa selenoprotein (SEP15); transcript variant 2; mRNA	NM_203341	15-Sep	15 kDa selenoprotein
Cfa.2510.1.S1_at	2.82E-03	1.48E-02	0.74	PREDICTED: Pan troglodytes aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase (AASDHPPT); mRNA	XM_508734	AASDHPPT	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase
Cfa.19800.1.S1_s_at	2.28E-05	7.55E-03	0.7	familiaris similar to ATP-binding cassette sub-family E member 1 (RNase L inhibitor) (Ribonuclease 4 inhibitor) (RNS4I); transcript variant 1 (LOC475454); mRNA	XM_532679	ABCE1	ATP-binding cassette, sub-family E (OABP), member 1
CfaAffx.1556.1.S1_at	1.90E-02	3.07E-02	1.47	PREDICTED: Canis familiaris similar to ATP-binding cassette; sub-family F; member 1 (ATP-binding cassette 50) (TNF-alpha stimulated ABC protein) (LOC474826); mRNA	XM_532056	ABCF1	ATP-binding cassette, sub-family F (GCN20), member 1
CfaAffx.27934.1.S1_s_at	2.81E-03	1.48E-02	0.7	PREDICTED: Canis familiaris similar to alpha/beta hydrolase domain containing protein 3 (LOC480177); mRNA	XM_537301	ABHD3	abhydrolase domain containing 3

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.14958.1.S1_s_at	2.63E-03	1.45E-02	1.3	PREDICTED: Canis familiaris similar to ABI gene family; member 3 (NESH) binding protein isoform 2 (LOC478544); mRNA	XM_535721	ABI3BP	ABI gene family, member 3 (NESH) binding protein
Cfa.6351.1.S1_a_at	2.54E-02	3.53E-02	0.76	familiaris similar to 3-ketoacyl-CoA thiolase; peroxisomal precursor (Beta-ketothiolase) (Acetyl-CoA acyltransferase) (Peroxisomal 3-oxoacyl-CoA thiolase); transcript variant 1 (LOC477023); mRNA	XM_534222	ACAA1	acetyl-Coenzyme A acyltransferase 1
Cfa.1502.1.S1_at	3.49E-02	4.18E-02	0.76	PREDICTED: Canis familiaris similar to Acetyl-CoA acetyltransferase; mitochondrial precursor (Acetoacetyl-CoA thiolase) (T2) (LOC489421); mRNA	XM_546539	ACAT1	acetyl-Coenzyme A acetyltransferase 1
CfaAffx.22504.1.S1_s_at	9.45E-04	1.16E-02	0.73	PREDICTED: Canis familiaris similar to Acetyl-CoA acetyltransferase; mitochondrial precursor (Acetoacetyl-CoA thiolase) (T2) (LOC489421); mRNA	XM_546539	ACAT1	acetyl-Coenzyme A acetyltransferase 1
CfaAffx.2011.1.S1_s_at	6.63E-04	1.06E-02	0.77	PREDICTED: Canis familiaris similar to Acetyl-CoA acetyltransferase; cytosolic (Cytosolic acetoacetyl-CoA thiolase) (Acetyl CoA transferase-like protein) (LOC484063); mRNA	XM_541180	ACAT2	acetyl-Coenzyme A acetyltransferase 2
Cfa.5146.1.A1_s_at	4.39E-03	1.69E-02	0.76	PREDICTED: Canis familiaris similar to acyl-Coenzyme A binding domain containing 6 (LOC480029); mRNA	XM_537152	ACBD6	acyl-Coenzyme A binding domain containing 6
Cfa.16841.1.S1_at	3.87E-03	1.63E-02	0.74	PREDICTED: Canis familiaris similar to ATP citrate lyase isoform 2; transcript variant 17 (LOC607852); mRNA	XM_856258	ACLY	ATP citrate lyase
Cfa.11699.1.A1_at	5.17E-02	5.20E-02	0.75	PREDICTED: Canis familiaris similar to Cytosolic acyl coenzyme A thioester hydrolase (Long chain acyl-CoA thioester hydrolase) (CTE-II) (CTE-IIa) (Brain acyl-CoA hydrolase) (LOC479589); mRNA	XM_536727	ACOT7	acyl-CoA thioesterase 7

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.29929.1.S1_at	3.35E-02	4.08E-02	0.68	PREDICTED: Canis familiaris similar to Cytosolic acyl coenzyme A thioester hydrolase (Long chain acyl-CoA thioester hydrolase) (CTE-II) (CTE-IIa) (Brain acyl-CoA hydrolase) (LOC479589); mRNA	XM_536727	ACOT7	acyl-CoA thioesterase 7
CfaAffx.29929.1.S1_s_at	3.80E-02	4.38E-02	0.7	PREDICTED: Canis familiaris similar to Cytosolic acyl coenzyme A thioester hydrolase (Long chain acyl-CoA thioester hydrolase) (CTE-II) (CTE-IIa) (Brain acyl-CoA hydrolase) (LOC479589); mRNA	XM_536727	ACOT7	acyl-CoA thioesterase 7
Cfa.14057.1.A1_s_at	5.13E-03	1.78E-02	0.77	PREDICTED: Canis familiaris similar to acyl-CoA synthetase long-chain family member 3; transcript variant 1 (LOC478927); mRNA	XM_536086	ACSL3	acyl-CoA synthetase long-chain family member 3
CfaAffx.24825.1.S1_s_at	2.62E-03	1.44E-02	0.71	PREDICTED: Canis familiaris similar to acyl-CoA synthetase long-chain family member 3; transcript variant 2 (LOC478927); mRNA	XM_846524	ACSL3	acyl-CoA synthetase long-chain family member 3
CfaAffx.27683.1.S1_s_at	2.60E-02	3.57E-02	0.71	PREDICTED: Canis familiaris similar to acyl-CoA synthetase long-chain family member 4 isoform 2; transcript variant 1 (LOC481018); mRNA	XM_538140	ACSL4	acyl-CoA synthetase long-chain family member 4
CfaAffx.23489.1.S1_at	2.85E-03	1.48E-02	0.67	PREDICTED: Canis familiaris similar to Actin-related protein 10 (hARP11); transcript variant 2 (LOC480337); mRNA	XM_846850	ACTR10	actin-related protein 10 homolog (S. cerevisiae)
Cfa.3302.2.S1_at	1.67E-02	2.89E-02	0.74	Bos taurus ARP2 actin-related protein 2 homolog (yeast); mRNA (cDNA clone MGC:166374 IMAGE:8470421); complete cds	BC151356	ACTR2	ARP2 actin-related protein 2 homolog (yeast)
Cfa.20888.1.S1_s_at	1.10E-04	8.90E-03	0.67	PREDICTED: Canis familiaris similar to actin-related protein 2 isoform a; transcript variant 1 (LOC481396); mRNA	XM_538516	ACTR2	ARP2 actin-related protein 2 homolog (yeast)
CfaAffx.5751.1.S1_at	3.32E-04	9.28E-03	0.7	PREDICTED: Canis familiaris similar to actin-related protein 2 isoform a; transcript variant 2 (LOC481396); mRNA	XM_847614	ACTR2	ARP2 actin-related protein 2 homolog (yeast)

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.14947.1.S1_at	5.33E-02	5.29E-02	0.77	PREDICTED: Canis familiaris similar to adenosine deaminase; adenosine aminohydrolase; ADA; transcript variant 1 (ADA-like); mRNA	XM_534428	ADA	adenosine deaminase
CfaAffx.14951.1.S1_s_at	3.16E-03	1.53E-02	0.75	PREDICTED: Canis familiaris similar to adenosine deaminase; adenosine aminohydrolase; ADA; transcript variant 1 (ADA-like); mRNA	XM_534428	ADA	adenosine deaminase
Cfa.19869.1.S1_s_at	5.81E-04	1.03E-02	1.32	PREDICTED: Canis familiaris similar to adenylate cyclase 2; transcript variant 2 (LOC478624); mRNA	XM_851103	ADCY2	adenylate cyclase 2 (brain)
Cfa.21375.1.S1_s_at	1.16E-03	1.21E-02	0.74	PREDICTED: Canis familiaris similar to ALL1 fused gene from 5q31; transcript variant 5 (LOC474678); mRNA	XM_856180	AFF4	AF4/FMR2 family, member 4
Cfa.19807.1.S1_at	2.20E-03	1.37E-02	0.76	full-length cDNA clone CS0DK011YN13 of HeLa cells Cot 25-normalized of Homo sapiens (human)	CR592694	AGA	aspartylglucosaminidase
Cfa.5288.1.A1_s_at	1.13E-03	1.20E-02	0.73	Bos taurus 1-acylglycerol-3-phosphate O-acyltransferase 3 (AGPAT3); mRNA; incomplete 5-prime cds	BT025436	AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3
Cfa.13638.1.A1_at	2.99E-03	1.51E-02	0.74	PREDICTED: Pan troglodytes alkyldihydroxyacetone phosphate synthase; transcript variant 3 (AGPS); mRNA	XM_001154211	AGPS	alkylglycerone phosphate synthase
Cfa.19737.1.S1_at	1.78E-02	2.97E-02	0.75	Homo sapiens aryl hydrocarbon receptor; mRNA (cDNA clone MGC:87401 IMAGE:30342582); complete cds	BC070080	AHR	aryl hydrocarbon receptor
Cfa.14366.1.S1_s_at	5.83E-02	5.55E-02	0.75	PREDICTED: Canis familiaris similar to allograft inflammatory factor 1 isoform 3; transcript variant 1 (LOC474841); mRNA	XM_532072	AIF1	allograft inflammatory factor 1
Cfa.1525.1.A1_s_at	3.82E-03	1.63E-02	0.77	PREDICTED: Canis familiaris similar to programmed cell death 8 isoform 3; transcript variant 2 (LOC481048); mRNA	XM_860655	AIFM1	apoptosis-inducing factor, mitochondrion-associated, 1
Cfa.6359.1.A1_at	6.29E-04	1.05E-02	0.76	PREDICTED: Canis familiaris similar to Adenylate kinase isoenzyme 2; mitochondrial (ATP-AMP transphosphorylase); transcript variant 2 (LOC478145); mRNA	XM_858927	AK2	adenylate kinase 2

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.27724.1.S1_at	3.66E-03	1.61E-02	0.77	PREDICTED: Canis familiaris similar to A-kinase anchor protein 10 precursor (LOC609073); mRNA	XM_846274	AKAP10	A kinase (PRKA) anchor protein 10
Cfa.2653.1.S1_at	2.46E-03	1.41E-02	0.74	PREDICTED: Canis familiaris similar to pyrroline-5-carboxylate synthetase isoform 1 (LOC477781); mRNA	XM_534976	ALDH18A1	aldehyde dehydrogenase 18 family, member A1
Cfa.403.1.A1_at	6.09E-03	1.88E-02	0.67	PREDICTED: Canis familiaris similar to antiquitin (LOC481486); mRNA	XM_538607	ALDH7A1	aldehyde dehydrogenase 7 family, member A1
Cfa.403.1.A1_s_at	6.52E-04	1.06E-02	0.72	PREDICTED: Canis familiaris similar to antiquitin (LOC481486); mRNA	XM_538607	ALDH7A1	aldehyde dehydrogenase 7 family, member A1
Cfa.11280.1.A1_s_at	6.62E-03	1.94E-02	0.72	PREDICTED: Equus caballus asparagine-linked glycosylation 11 homolog (S. cerevisiae; alpha-1;2-mannosyltransferase) (ALG11); mRNA	XM_001487974	ALG11	asparagine-linked glycosylation 11 homolog (S. cerevisiae, alpha-1,2-mannosyltransferase)
Cfa.16818.1.S1_s_at	5.15E-04	1.01E-02	0.7	PREDICTED: Canis familiaris similar to Dolichyl-phosphate beta-glucosyltransferase (DolP-glucosyltransferase); transcript variant 5 (LOC477301); mRNA	XM_851876	ALG5	asparagine-linked glycosylation 5 homolog (S. cerevisiae, dolichyl-phosphate beta-glucosyltransferase)
CfaAffx.28557.1.S1_s_at	3.74E-04	9.61E-03	0.73	PREDICTED: Canis familiaris similar to ankyrin repeat domain 12; transcript variant 2 (LOC480205); mRNA	XM_854453	ANKRD12	ankyrin repeat domain 12
CfaAffx.12205.1.S1_s_at	2.27E-02	3.33E-02	0.75	PREDICTED: Canis familiaris similar to ankyrin repeat domain 37 (LOC475627); mRNA	XM_532841	ANKRD37	ankyrin repeat domain 37
CfaAffx.4452.1.S1_at	1.02E-04	8.90E-03	0.64	PREDICTED: Canis familiaris similar to ankyrin repeat domain 39 (LOC474568); mRNA	XM_531796	ANKRD39	ankyrin repeat domain 39
CfaAffx.7148.1.S1_at	1.44E-03	1.25E-02	0.77	PREDICTED: Canis familiaris similar to fetal globin inducing factor (LOC485125); mRNA	XM_542243	ANKRD49	ankyrin repeat domain 49

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.31.1.S1_s_at	1.94E-02	3.11E-02	0.73	Canis familiaris inhibitor-1 of protein phosphatase type 2A mRNA; complete cds	AY162293	ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A
CfaAffx.13980.1.S1_at	1.95E-02	3.11E-02	0.7	PREDICTED: Canis familiaris similar to Annexin A3 (Annexin III) (Lipocortin III) (Placental anticoagulant protein III) (PAP-III) (35-alpha calcimedin) (Inositol 1;2-cyclic phosphate 2-phosphohydrolase) (LOC478447); mRNA	XM_535624	ANXA3	annexin A3
Cfa.12149.1.S1_at	7.03E-02	6.17E-02	0.76	PREDICTED: Canis familiaris similar to Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I) (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha) (Anchorin CII) (LOC476094); mRNA	XM_533303	ANXA5	annexin A5
Cfa.229.1.S1_at	1.39E-02	2.66E-02	0.75	PREDICTED: Canis familiaris similar to amine oxidase (flavin containing) domain 2 isoform a; transcript variant 2 (LOC478193); mRNA	XM_861517	AOF2	amine oxidase (flavin containing) domain 2
Cfa.10636.1.S1_s_at	4.95E-03	1.76E-02	0.77	PREDICTED: Canis familiaris similar to adaptor-related protein complex 1; gamma 1 subunit isoform a; transcript variant 3 (LOC479666); mRNA	XM_857437	AP1G1	adaptor-related protein complex 1, gamma 1 subunit
Cfa.15765.1.A1_at	1.14E-03	1.20E-02	0.76	familiaris similar to Adapter-related protein complex 3 mu 1 subunit (Mu-adaptin 3A) (AP-3 adapter complex mu3A subunit) (LOC489052); mRNA	XM_546170	AP3M1	adaptor-related protein complex 3, mu 1 subunit
CfaAffx.23575.1.S1_at	1.94E-04	9.06E-03	0.72	familiaris similar to Adapter-related protein complex 3 mu 1 subunit (Mu-adaptin 3A) (AP-3 adapter complex mu3A subunit) (LOC489052); mRNA	XM_546170	AP3M1	adaptor-related protein complex 3, mu 1 subunit
Cfa.1256.1.A1_s_at	1.80E-03	1.30E-02	0.75	Canis familiaris heat shock protein Apg-2 (Apg-2) mRNA; complete cds	AY911512	APG-2	heat shock protein Apg-2

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Cfa.6362.1.A1_at	2.92E-02	3.80E-02	1.44	Canis familiaris heat shock protein Apg-2 (Apg-2) mRNA; complete cds	AY911512	APG-2	heat shock protein Apg-2
CfaAffx.15873.1.S1_s_at	1.50E-02	2.75E-02	0.72	PREDICTED: Canis familiaris similar to amyloid beta (A4) precursor-like protein 2; transcript variant 23 (LOC479393); mRNA	XM_851642	APLP2	amyloid beta (A4) precursor-like protein 2
Cfa.3891.1.S1_at	2.58E-03	1.44E-02	1.4	Dog apolipoprotein C-III mRNA; complete cds	M17178	APOC3	apolipoprotein C-III
Cfa.3891.1.S1_x_at	1.03E-02	2.33E-02	1.31	Dog apolipoprotein C-III mRNA; complete cds	M17178	APOC3	apolipoprotein C-III
Cfa.2457.1.S1_at	3.04E-02	3.88E-02	0.76	PREDICTED: Pan troglodytes amyloid beta precursor protein-binding protein 2 (APPBP2); mRNA	XM_001136833	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2
Cfa.21549.1.S1_s_at	7.17E-02	6.24E-02	0.72	PREDICTED: Canis familiaris similar to Aquaporin 3 (LOC611792); mRNA	XM_849503	AQP3	aquaporin 3 (Gill blood group)
CfaAffx.25331.1.S1_at	2.36E-02	3.39E-02	0.69	PREDICTED: Canis familiaris similar to aquaporin 9 (LOC487576); mRNA	XM_544701	AQP9	aquaporin 9
CfaAffx.4964.1.S1_s_at	3.38E-03	1.56E-02	0.77	PREDICTED: Canis familiaris similar to ADP-ribosylation factor-1 (LOC474591); mRNA	XM_531820	ARF1	ADP-ribosylation factor 1
Cfa.2289.1.S1_at	5.39E-02	5.31E-02	0.76	Homo sapiens ADP-ribosylation factor 6 (ARF6); mRNA	NM_001663	ARF6	ADP-ribosylation factor 6
Cfa.10772.1.A1_at	1.00E-03	1.17E-02	0.74	PREDICTED: Canis familiaris similar to ADP-ribosylation factor GTPase activating protein 3; transcript variant 5 (LOC474477); mRNA	XM_852321	ARFGAP3	ADP-ribosylation factor GTPase activating protein 3
Cfa.17093.1.S1_at	1.10E-03	1.20E-02	0.71	PREDICTED: Canis familiaris similar to ADP-ribosylation factor GTPase activating protein 3; transcript variant 5 (LOC474477); mRNA	XM_852321	ARFGAP3	ADP-ribosylation factor GTPase activating protein 3
CfaAffx.2327.1.S1_s_at	4.26E-05	7.55E-03	0.67	PREDICTED: Canis familiaris similar to ADP-ribosylation factor GTPase activating protein 3; transcript variant 5 (LOC474477); mRNA	XM_852321	ARFGAP3	ADP-ribosylation factor GTPase activating protein 3
CfaAffx.17840.1.S1_s_at	2.38E-02	3.41E-02	0.73	PREDICTED: Canis familiaris similar to AT rich interactive domain 4B isoform 1; transcript variant 3 (LOC488959); mRNA	XM_843623	ARID4B	AT rich interactive domain 4B (RBP1-like)

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CfaAffx.17879.1.S1_s_at	2.82E-02	3.72E-02	0.76	PREDICTED: Canis familiaris similar to AT rich interactive domain 4B isoform 1; transcript variant 3 (LOC488959); mRNA	XM_843623	ARID4B	AT rich interactive domain 4B (RBP1-like)
CfaAffx.11375.1.S1_s_at	1.30E-03	1.23E-02	0.73	PREDICTED: Canis familiaris similar to ADP-ribosylation factor-like 1; transcript variant 1 (LOC612931); mRNA	XM_847897	ARL1	ADP-ribosylation factor-like 1
Cfa.20059.1.A1_at	1.36E-03	1.23E-02	0.75	PREDICTED: Canis familiaris similar to ADP-ribosylation factor-like 6 interacting protein 5 (LOC476559); mRNA	XM_533764	ARL6IP5	ADP-ribosylation-like factor 6 interacting protein 5
Cfa.1737.1.A1_at	4.56E-03	1.72E-02	0.72	Bos taurus armadillo repeat containing 1; mRNA (cDNA clone MGC:127965 IMAGE:7954315); complete cds	BC103407	ARMC1	armadillo repeat containing 1
CfaAffx.27095.1.S1_s_at	1.77E-04	9.00E-03	0.73	PREDICTED: Canis familiaris similar to ALEX3 protein (LOC492022); mRNA	XM_549142	ARMCX3	armadillo repeat containing, X-linked 3
Cfa.20824.1.S1_at	2.50E-03	1.43E-02	0.74	PREDICTED: Canis familiaris similar to ARMET protein precursor (Arginine-rich protein) (LOC608421); mRNA	XM_845447	ARMET	arginine-rich, mutated in early stage tumors
CfaAffx.23231.1.S1_at	3.26E-03	1.55E-02	0.73	PREDICTED: Canis familiaris similar to actin related protein 2/3 complex subunit 1A (LOC479745); mRNA	XM_536873	ARPC1A	actin related protein 2/3 complex, subunit 1A, 41kDa
Cfa.17137.1.S1_at	6.68E-04	1.07E-02	0.74	PREDICTED: Canis familiaris similar to actin related protein 2/3 complex; subunit 5-like; transcript variant 1 (LOC612856); mRNA	XM_846253	ARPC5L	actin related protein 2/3 complex, subunit 5-like
CfaAffx.30958.1.S1_s_at	1.66E-03	1.28E-02	0.67	PREDICTED: Canis familiaris similar to actin related protein 2/3 complex; subunit 5-like; transcript variant 2 (LOC612856); mRNA	XM_858438	ARPC5L	actin related protein 2/3 complex, subunit 5-like
Cfa.1326.1.S1_at	9.63E-02	7.42E-02	0.72	PREDICTED: Canis familiaris similar to N-acylsphingosine amidohydrolase (acid ceramidase) 1 preproprotein isoform a (LOC482897); mRNA	XM_540012	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1
CfaAffx.5053.1.S1_at	4.63E-02	4.88E-02	1.37	Arabidopsis thaliana unknown protein (AT3G13510) mRNA; complete cds	NM_112197	AT3G13510	hypothetical protein

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.2390.1.S1_at	1.55E-03	1.26E-02	0.65	PREDICTED: Canis familiaris similar to two AAA domain containing protein; transcript variant 2 (LOC475090); mRNA	XM_845427	ATAD2	ATPase family, AAA domain containing 2
Cfa.16352.1.S1_at	1.45E-02	2.70E-02	0.75	Homo sapiens mRNA for KIAA1240 protein; partial cds	AB033066	ATAD2B	ATPase family, AAA domain containing 2B
Cfa.3397.1.A1_s_at	6.36E-03	1.91E-02	0.76	PREDICTED: Canis familiaris similar to Autophagy protein 5-like (APG5-like) (Apoptosis-specific protein); transcript variant 1 (LOC610868); mRNA	XM_849201	ATG5	ATG5 autophagy related 5 homolog (S. cerevisiae)
Cfa.3397.1.A1_at	4.32E-03	1.68E-02	0.74	PREDICTED: Canis familiaris similar to Autophagy protein 5-like (APG5-like) (Apoptosis-specific protein); transcript variant 3 (LOC610868); mRNA	XM_863268	ATG5	ATG5 autophagy related 5 homolog (S. cerevisiae)
CfaAffx.18231.1.S1_at	3.94E-04	9.61E-03	0.7	Homo sapiens cDNA FLJ56374 complete cds; highly similar to Probable phospholipid-transporting ATPase IF(EC 3.6.3.1)	AK304855	ATP11B	ATPase, class VI, type 11B
Cfa.19636.1.S1_s_at	9.14E-06	6.68E-03	0.73	[illegible] familiaris similar to Potential phospholipid-transporting ATPase IF (ATPase class I type 11B) (ATPase IR) (LOC478644); mRNA	XM_535816	ATP11B	ATPase, class VI, type 11B
CfaAffx.18234.1.S1_s_at	8.11E-05	8.77E-03	0.72	familiaris similar to Potential phospholipid-transporting ATPase IF (ATPase class I type 11B) (ATPase IR) (LOC478644); mRNA	XM_535816	ATP11B	ATPase, class VI, type 11B
Cfa.19006.1.S1_s_at	1.08E-02	2.37E-02	0.76	PREDICTED: Canis familiaris similar to calcium-transporting ATPase 2C1 isoform 1a; transcript variant 12 (LOC477066); mRNA	XM_858740	ATP2C1	ATPase, Ca++ transporting, type 2C, member 1
CfaAffx.10126.1.S1_at	6.16E-04	1.05E-02	0.75	PREDICTED: Canis familiaris similar to calcium-transporting ATPase 2C1 isoform 1a; transcript variant 12 (LOC477066); mRNA	XM_858740	ATP2C1	ATPase, Ca++ transporting, type 2C, member 1
Cfa.990.1.S1_s_at	8.57E-06	6.68E-03	0.73	familiaris similar to ATP synthase; H+ transporting; mitochondrial F1 complex; gamma subunit isoform H (heart) precursor; transcript variant 1 (LOC478009); mRNA	XM_535193	ATP5C1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1

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CfaAffx.30193.1.S1_s_at	3.54E-05	7.55E-03	0.71	PREDICTED: Canis familiaris similar to ATP synthase B chain; mitochondrial precursor (LOC479901); mRNA	XM_537027	ATP5F1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1
Cfa.685.1.S1_s_at	8.57E-04	1.13E-02	0.69	PREDICTED: Canis familiaris similar to ATP synthase; H+ transporting; mitochondrial F0 complex; subunit c; isoform 1; transcript variant 2 (LOC491061); mRNA	XM_846891	ATP5G1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subunit 9)
CfaAffx.2478 4.1.S1_s_at	1.12E-03	1.20E-02	0.75	PREDICTED: Canis familiaris similar to ATPase; H+ transporting; V1 subunit E isoform 1; transcript variant 4 (LOC477740); mRNA	XM_863074	ATP6V1E1	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1
Cfa.1409.1.A1_at	2.14E-03	1.37E-02	0.74	PREDICTED: Canis familiaris similar to ATPase; H+ transporting; V1 subunit F (LOC475199); mRNA	XM_532431	ATP6V1F	ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F
CfaAffx.11312.1.S1_s_at	1.00E-03	1.17E-02	0.67	PREDICTED: Canis familiaris similar to ATPase; H+ transporting; lysosomal 50/57kDa; V1 subunit H; transcript variant 1 (LOC486953); mRNA	XM_544082	ATP6V1H	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H
CfaAffx.26396.1.S1_s_at	2.07E-04	9.06E-03	1.4	PREDICTED: Canis familiaris similar to transcriptional regulator ATRX isoform 1; transcript variant 7 (LOC480963); mRNA	XM_855075	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)
Cfa.19626.1.A1_at	1.65E-02	2.88E-02	0.75	PREDICTED: Pan troglodytes similar to AZI2 protein; transcript variant 5 (LOC460239); mRNA	XM_001166320	AZI2	5-azacytidine induced 2
Cfa.4399.1.S1_at	1.10E-02	2.38E-02	0.76	PREDICTED: Canis familiaris similar to ornithine decarboxylase antizyme inhibitor; transcript variant 10 (LOC475058); mRNA	XM_853643	AZIN1	antizyme inhibitor 1
CfaAffx.144.1.S1_s_at	3.42E-03	1.57E-02	0.75	PREDICTED: Canis familiaris similar to barrier to autointegration factor 1 (LOC611961); mRNA	XM_849683	BANF1	barrier to autointegration factor 1
Cfa.16811.1.S1_at	5.43E-02	5.33E-02	0.74	PREDICTED: Canis familiaris similar to HLA-B associated transcript 4 (LOC481714); mRNA	XM_538835	BAT4	HLA-B associated transcript 4

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.20602.1.S1_s_at	4.68E-03	1.73E-02	0.74	PREDICTED: Canis familiaris similar to bromodomain adjacent to zinc finger domain; 1A isoform a; transcript variant 9 (LOC480287); mRNA	XM_856678	BAZ1A	bromodomain adjacent to zinc finger domain, 1A
CfaAffx.7103.1.S1_at	2.90E-02	3.78E-02	0.77	PREDICTED: Canis familiaris similar to Bardet Biedl syndrome 7 protein isoform b; transcript variant 4 (LOC476092); mRNA	XM_852128	BBS7	Bardet-Biedl syndrome 7
Cfa.20742.1.S1_s_at	5.32E-02	5.28E-02	0.73	PREDICTED: Canis familiaris similar to B-cell receptor-associated protein BAP29 isoform d (LOC475884); mRNA	XM_533092	BCAP29	B-cell receptor-associated protein 29
Cfa.3943.1.A1_a_at	8.94E-03	2.20E-02	0.73	PREDICTED: Canis familiaris similar to Breast carcinoma amplified sequence 2 homolog (DNA amplified in mammary carcinoma-1 protein) (LOC475805); mRNA	XM_533014	BCAS2	breast carcinoma amplified sequence 2
CfaAffx.21575.1.S1_s_at	2.81E-02	3.72E-02	0.75	PREDICTED: Canis familiaris similar to Bcl-2-related protein A1 (BFL-1 protein) (Hemopoietic-specific early response protein) (GRS protein) (LOC488770); mRNA	XM_545888	BCL2A1	BCL2-related protein A1
Cfa.11173.1.A1_s_at	4.27E-02	4.67E-02	0.73	PREDICTED: Canis familiaris similar to transcription factor-like nuclear regulator (LOC478090); mRNA	XM_535267	BDP1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB
Cfa.10514.1.S1_at	1.52E-03	1.26E-02	0.76	PREDICTED: Canis familiaris similar to Biliverdin reductase A precursor (Biliverdin-IX alpha-reductase) (BVR A) (LOC475867); mRNA	XM_533075	BLVRA	biliverdin reductase A
Cfa.13165.1.A1_s_at	2.13E-02	3.24E-02	0.75	Brugia malayi PHD-finger family protein partial mRNA	XM_001900228	Bm1_44005	PHD-finger family protein
CfaAffx.18770.1.S1_s_at	3.45E-02	4.16E-02	0.76	PREDICTED: Canis familiaris similar to Cytoplasmic tyrosine-protein kinase BMX (Bone marrow tyrosine kinase gene in chromosome X protein) (Epithelial and endothelial tyrosine kinase) (ETK) (NTK38) (LOC491750); mRNA	XM_548870	BMX	BMX non-receptor tyrosine kinase

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.25505.1.S1_s_at	7.24E-04	1.08E-02	0.72	Bos taurus cDNA clone IMAGE:8094530	BC148951	BNIP2	BCL2/adenovirus E1B 19kDa interacting protein 2
Cfa.11221.1.A1_at	3.97E-04	9.61E-03	0.67	PREDICTED: Canis familiaris similar to 3(2);5-bisphosphate nucleotidase 1 (Bisphosphate 3-nucleotidase 1) (PAP-inositol-1;4-phosphatase) (PIP) (LOC608525); mRNA	XM_845576	BPNT1	3'(2'), 5'-bisphosphate nucleotidase 1
CfaAffx.15480.1.S1_s_at	4.83E-03	1.75E-02	0.72	PREDICTED: Canis familiaris similar to bromodomain containing 7 (LOC478130); mRNA	XM_535306	BRD7	bromodomain containing 7
Cfa.14120.1.A1_s_at	1.88E-02	3.06E-02	0.74	PREDICTED: Canis familiaris similar to brain and reproductive organ-expressed protein; transcript variant 1 (LOC475711); mRNA	XM_532918	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)
Cfa.10573.1.A1_at	1.43E-02	2.70E-02	0.75	PREDICTED: Canis familiaris similar to Brain protein I3 (pRGR2) (LOC608902); mRNA	XM_846053	BRI3	brain protein I3
Cfa.13282.1.S1_s_at	2.95E-04	9.25E-03	0.73	PREDICTED: Canis familiaris similar to Brain protein 44 (LOC480086); mRNA	XM_537209	BRP44	brain protein 44
Cfa.11093.1.S1_at	1.07E-04	8.90E-03	0.76	PREDICTED: Canis familiaris similar to Brain protein 44-like protein; transcript variant 5 (LOC609356); mRNA	XM_858018	BRP44L	brain protein 44-like
CfaAffx.227.1.S1_s_at	4.82E-04	1.00E-02	0.75	PREDICTED: Canis familiaris similar to Brain protein 44-like protein; transcript variant 5 (LOC609356); mRNA	XM_858018	BRP44L	brain protein 44-like
CfaAffx.11934.1.S1_at	1.14E-03	1.20E-02	0.7	PREDICTED: Canis familiaris similar to TATA-binding-protein-associated factor 172 (TBP-associated factor 172) (TAF-172) (TAF(II)170) (B-TFIID transcription factor-associated 170 kDa subunit) (LOC486800); mRNA	XM_543929	BTAF1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (Mot1 homolog, S. cerevisiae)
Cfa.16454.1.S1_at	6.43E-02	5.87E-02	0.77	PREDICTED: Canis familiaris similar to Bruton agammaglobulinemia tyrosine kinase; transcript variant 6 (LOC492019); mRNA	XM_856682	BTK	Bruton agammaglobulinemia tyrosine kinase

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.23181.1.S1_x_at	3.14E-03	1.53E-02	0.76	PREDICTED: Canis familiaris similar to G10 protein homolog (EDG-2); transcript variant 1 (LOC479743); mRNA	XM_536871	BUD31	BUD31 homolog (S. cerevisiae)
Cfa.673.1.S1_at	9.07E-03	2.21E-02	0.77	PREDICTED: Canis familiaris similar to RNA processing factor 1 (LOC479972); mRNA	XM_537096	BXDC5	brix domain containing 5
Cfa.673.2.S1_s_at	6.08E-03	1.88E-02	0.77	PREDICTED: Canis familiaris similar to RNA processing factor 1 (LOC479972); mRNA	XM_537096	BXDC5	brix domain containing 5
Cfa.3834.1.S1_at	9.31E-02	7.27E-02	0.76	C.familiaris mRNA for complement C5a receptor	X65860	C5AR1	complement component 5a receptor 1
CfaAffx.13131.1.S1_s_at	6.72E-03	1.95E-02	0.72	PREDICTED: Bos taurus chromosome 12 open reading frame 62 ortholog (C5H12orf62); mRNA	XM_001250167	C5H12orf62	chromosome 12 open reading frame 62 ortholog
Cfa.4155.1.A1_at	5.26E-02	5.25E-02	0.76	Homo sapiens chromosome 5 open reading frame 33 (C5orf33); transcript variant 2; mRNA	NM_153013	C5orf33	chromosome 5 open reading frame 33
Cfa.240.1.A1_at	1.80E-02	3.00E-02	0.77	Bos taurus chromosome 5 open reading frame 15 ortholog; mRNA (cDNA clone MGC:127320 IMAGE:7948853); complete cds	BC102841	C7H5ORF15	chromosome 5 open reading frame 15 ortholog
Cfa.18190.1.S1_at	3.34E-03	1.56E-02	0.76	Homo sapiens chromosome 7 open reading frame 23; mRNA (cDNA clone MGC:4175 IMAGE:3634983); complete cds	BC002837	C7orf23	chromosome 7 open reading frame 23
Cfa.3420.1.A1_at	4.53E-03	1.71E-02	0.76	PREDICTED: Pan troglodytes calcium binding protein 39 (CAB39); mRNA	XM_526055	CAB39	calcium binding protein 39
CfaAffx.16790.1.S1_s_at	4.88E-02	5.03E-02	0.76	PREDICTED: Canis familiaris similar to Calcium binding protein 39 (Mo25 protein); transcript variant 4 (LOC477403); mRNA	XM_856073	CAB39	calcium binding protein 39
Cfa.4277.2.S1_at	5.98E-05	8.40E-03	0.75	PREDICTED: Canis familiaris similar to calreticulin; transcript variant 1 (LOC476694); mRNA	XM_533899	CALR	calreticulin
Cfa.3402.1.S1_at	2.11E-03	1.36E-02	0.77	PREDICTED: Canis familiaris similar to calumenin precursor; transcript variant 4 (LOC475201); mRNA	XM_853521	CALU	calumenin
CfaAffx.3375.1.S1_s_at	3.65E-05	7.55E-03	0.74	PREDICTED: Canis familiaris similar to calumenin precursor; transcript variant 4 (LOC475201); mRNA	XM_853521	CALU	calumenin

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.3402.3.S1_a_at	2.73E-05	7.55E-03	0.74	PREDICTED: Canis familiaris similar to calumenin precursor; transcript variant 8 (LOC475201); mRNA	XM_853685	CALU	calumenin
Cfa.1566.1.A1_at	1.28E-02	2.55E-02	0.75	PREDICTED: Canis familiaris similar to TIP120 protein; transcript variant 5 (LOC474437); mRNA	XM_531667	CAND1	cullin-associated and neddylation-dissociated 1
CfaAffx.1565.1.S1_s_at	4.65E-04	9.90E-03	0.74	PREDICTED: Canis familiaris similar to TIP120 protein; transcript variant 6 (LOC474437); mRNA	XM_855867	CAND1	cullin-associated and neddylation-dissociated 1
Cfa.3766.1.S2_at	4.93E-03	1.75E-02	0.71	Pongo abelii mRNA; cDNA DKFZp459P042 (from clone DKFZp459P042)	CR861420	CANX	calnexin
Cfa.20167.1.S1_at	6.87E-04	1.07E-02	0.75	PREDICTED: Canis familiaris similar to capping protein (actin filament) muscle Z-line; alpha 1; transcript variant 5 (LOC475857); mRNA	XM_857739	CAPZA1	capping protein (actin filament) muscle Z-line, alpha 1
CfaAffx.20828.1.S1_s_at	5.38E-04	1.02E-02	0.72	PREDICTED: Canis familiaris similar to capping protein (actin filament) muscle Z-line; alpha 1; transcript variant 5 (LOC475857); mRNA	XM_857739	CAPZA1	capping protein (actin filament) muscle Z-line, alpha 1
Cfa.16612.1.S1_s_at	6.21E-04	1.05E-02	0.67	Canis lupus familiaris capping protein (actin filament) muscle Z-line; alpha 2 (CAPZA2); mRNA	NM_001012995	CAPZA2	capping protein (actin filament) muscle Z-line, alpha 2
Cfa.6332.1.A1_at	8.61E-04	1.13E-02	0.7	PREDICTED: Canis familiaris similar to CG8257-PA (LOC476983); mRNA	XM_534184	CARS2	cysteinyl-tRNA synthetase 2, mitochondrial (putative)
CfaAffx.12454.1.S1_s_at	3.75E-03	1.62E-02	0.71	Canis lupus familiaris mRNA for caspase-3; complete cds	AB085580	CASP3	caspase 3, apoptosis-related cysteine peptidase
Cfa.3589.1.S1_s_at	5.74E-02	5.50E-02	0.75	Canis familiaris caspase-1-like protein mRNA; complete cds	AF135967	CASP4	caspase 4, apoptosis-related cysteine peptidase
CfaAffx.2035.1.S1_s_at	2.17E-03	1.37E-02	0.76	PREDICTED: Canis familiaris similar to chromobox homolog 3; transcript variant 5 (LOC482015); mRNA	XM_859382	CBX3	chromobox homolog 3 (HP1 gamma homolog, Drosophila)

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.10657.1.A1_at	3.38E-03	1.56E-02	0.75	PREDICTED: Canis familiaris similar to Ymer protein long isoform (LOC478675); mRNA	XM_535844	CCDC50	coiled-coil domain containing 50
CfaAffx.25466.1.S1_s_at	2.44E-04	9.06E-03	0.66	PREDICTED: Canis familiaris similar to Protein AD-016; transcript variant 1 (LOC475444); mRNA	XM_532668	CCDC53	coiled-coil domain containing 53
Cfa.9407.1.A1_s_at	9.35E-04	1.16E-02	0.75	PREDICTED: Canis familiaris similar to CG15881-PA; isoform A (LOC478583); mRNA	XM_535759	CCDC58	coiled-coil domain containing 58
Cfa.14257.1.A1_at	6.95E-05	8.42E-03	1.32	PREDICTED: Canis familiaris similar to coiled-coil domain containing 8 (LOC484430); mRNA	XM_541545	CCDC8	coiled-coil domain containing 8
CfaAffx.29399.1.S1_s_at	1.14E-02	2.42E-02	0.73	PREDICTED: Canis familiaris similar to cyclin L2 isoform 1; transcript variant 3 (LOC479570); mRNA	XM_843460	CCNL2	cyclin L2
CfaAffx.24405.1.S1_at	5.17E-03	1.79E-02	0.67	PREDICTED: Canis familiaris similar to cell cycle progression 1 isoform 2; transcript variant 3 (LOC487566); mRNA	XM_858478	CCPG1	cell cycle progression 1
CfaAffx.7895.1.S1_s_at	1.84E-03	1.31E-02	0.74	PREDICTED: Canis familiaris similar to chaperonin containing TCP1; subunit 3 isoform c; transcript variant 3 (LOC480123); mRNA	XM_859172	CCT3	chaperonin containing TCP1, subunit 3 (gamma)
Cfa.1588.1.S1_at	3.31E-03	1.55E-02	0.76	PREDICTED: Canis familiaris similar to T-complex protein 1; delta subunit (TCP-1-delta) (CCT-delta) (A45) (LOC482271); mRNA	XM_539390	CCT4	chaperonin containing TCP1, subunit 4 (delta)
CfaAffx.5572.1.S1_at	2.66E-05	7.55E-03	0.76	PREDICTED: Canis familiaris similar to T-complex protein 1; delta subunit (TCP-1-delta) (CCT-delta) (A45) (LOC482271); mRNA	XM_539390	CCT4	chaperonin containing TCP1, subunit 4 (delta)
CfaAffx.5572.1.S1_s_at	9.87E-05	8.90E-03	0.75	PREDICTED: Canis familiaris similar to T-complex protein 1; delta subunit (TCP-1-delta) (CCT-delta) (A45) (LOC482271); mRNA	XM_539390	CCT4	chaperonin containing TCP1, subunit 4 (delta)
Cfa.18708.1.S1_s_at	7.45E-04	1.09E-02	0.71	PREDICTED: Canis familiaris similar to T-complex protein 1; epsilon subunit (TCP-1-epsilon) (CCT-epsilon); transcript variant 1 (LOC606873); mRNA	XM_843210	CCT5	chaperonin containing TCP1, subunit 5 (epsilon)
CfaAffx.15808.1.S1_s_at	3.60E-04	9.61E-03	0.73	PREDICTED: Canis familiaris similar to T-complex protein 1; epsilon subunit (TCP-1-epsilon) (CCT-epsilon); transcript variant 1 (LOC606873); mRNA	XM_843210	CCT5	chaperonin containing TCP1, subunit 5 (epsilon)

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Cfa.1285.1.A1_at	2.24E-02	3.31E-02	0.73	Homo sapiens partial mRNA for chaperonin subunit 6A (CCT6A gene)	AM295155	CCT6A	chaperonin containing TCP1, subunit 6A (zeta 1)
CfaAffx.13783.1.S1_s_at	2.55E-05	7.55E-03	0.71	familiaris similar to T-complex protein 1; theta subunit (TCP-1-theta) (CCT-theta); transcript variant 1 (LOC478399); mRNA	XM_535576	CCT8	chaperonin containing TCP1, subunit 8 (theta)
Cfa.7303.1.A1_a_at	1.13E-02	2.41E-02	1.33	Canis lupus familiaris CD163v3 mRNA; complete cds	DQ060837	CD163	CD163 molecule
Cfa.3619.1.S1_s_at	1.46E-02	2.72E-02	0.73	Canis familiaris hematopoietic antigen CD38 mRNA; complete cds	AF117714	CD38	CD38 molecule
Cfa.1961.1.S1_at	1.39E-02	2.66E-02	0.71	Homo sapiens cDNA FLJ39351 fis; clone PEBLM2001072	AK096670	CD47	CD47 molecule
Cfa.654.1.A1_a_at	1.36E-02	2.63E-02	0.71	Canis lupus familiaris CD47 molecule (CD47); mRNA	NM_001080721	CD47	CD47 molecule
Cfa.14560.1.S1_at	3.54E-04	9.56E-03	0.75	PREDICTED: Canis familiaris similar to B-lymphocyte activation marker BLAST-1 precursor (BCM1 surface antigen) (Leucocyte antigen MEM-102) (TCT.1) (Antigen CD48) (LOC488642); mRNA	XM_545759	CD48	CD48 molecule
CfaAffx.19527.1.S1_s_at	1.38E-03	1.24E-02	0.76	PREDICTED: Canis familiaris similar to B-lymphocyte activation marker BLAST-1 precursor (BCM1 surface antigen) (Leucocyte antigen MEM-102) (TCT.1) (Antigen CD48) (LOC488642); mRNA	XM_545759	CD48	CD48 molecule
Cfa.838.1.A1_at	5.04E-03	1.77E-02	0.69	PREDICTED: Canis familiaris similar to CD59 antigen p18-20 (LOC475945); mRNA	XM_533156	CD59	CD59 molecule, complement regulatory protein
CfaAffx.8125.1.S1_s_at	1.96E-03	1.33E-02	0.75	PREDICTED: Canis familiaris similar to D123 gene product (LOC478005); mRNA	XM_535189	CDC123	cell division cycle 123 homolog (S. cerevisiae)
Cfa.1040.1.A1_at	5.12E-03	1.78E-02	0.75	PREDICTED: Canis familiaris similar to CDC16 homolog; transcript variant 1 (LOC607100); mRNA	XM_843484	CDC16	cell division cycle 16 homolog (S. cerevisiae)
CfaAffx.10703.1.S1_at	8.98E-03	2.20E-02	0.74	PREDICTED: Canis familiaris similar to CDC16 homolog; transcript variant 1 (LOC607100); mRNA	XM_843484	CDC16	cell division cycle 16 homolog (S. cerevisiae)

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Cfa.489.1.S1_s_at	3.68E-03	1.61E-02	0.73	PREDICTED: Canis familiaris similar to cell division cycle 37 homolog (S. cerevisiae)-like 1 (LOC476341); mRNA	XM_533542	CDC37L1	cell division cycle 37 homolog (S. cerevisiae)-like 1
Cfa.163.1.A1_s_at	1.42E-02	2.68E-02	0.77	PREDICTED: Canis familiaris similar to CDC5-like (LOC474921); mRNA	XM_532156	CDC5L	CDC5 cell division cycle 5-like (S. pombe)
Cfa.20147.1.S1_s_at	6.17E-03	1.89E-02	0.76	PREDICTED: Canis familiaris similar to CDC5-like (LOC474921); mRNA	XM_532156	CDC5L	CDC5 cell division cycle 5-like (S. pombe)
CfaAffx.12456.1.S1_s_at	1.13E-03	1.20E-02	0.67	PREDICTED: Canis familiaris similar to Cell division protein kinase 7 (CDK-activating kinase) (CAK) (TFIIH basal transcription factor complex kinase subunit) (39 kDa protein kinase) (P39 Mo15) (STK1) (CAK1); transcript variant 1 (LOC608441); mRNA	XM_845331	CDK7	cyclin-dependent kinase 7
CfaAffx.12648.1.S1_at	1.73E-04	9.00E-03	0.67	PREDICTED: Canis familiaris similar to collaborates/cooperates with ARF (alternate reading frame) protein (LOC607991); mRNA	XM_844869	CDKN2AIP	CDKN2A interacting protein
Cfa.19151.1.A1_at	2.02E-02	3.16E-02	0.76	PREDICTED: Canis familiaris hypothetical LOC481507 (LOC481507); mRNA	XM_538628	CDKN2AIPNL	CDKN2A interacting protein N-terminal like
Cfa.20967.1.S1_s_at	4.42E-03	1.70E-02	0.77	PREDICTED: Canis familiaris similar to CCAAT/enhancer binding protein zeta; transcript variant 2 (LOC483035); mRNA	XM_858367	CEBPZ	CCAAT/enhancer binding protein zeta
CfaAffx.30235.1.S1_s_at	1.32E-03	1.23E-02	0.76	PREDICTED: Canis familiaris similar to choline/ethanolaminephosphotransferase; transcript variant 4 (LOC612948); mRNA	XM_860637	CEPT1	choline/ethanolamine phosphotransferase 1
Cfa.15821.1.S1_at	1.17E-03	1.21E-02	1.36	Canis lupus familiaris cauxin mRNA for carboxylesterase-like urinary excreted protein; complete cds	AB186392	CES7	carboxylesterase 7
CfaAffx.12484.1.S1_s_at	1.07E-02	2.36E-02	0.76	PREDICTED: Canis familiaris similar to CGG triplet repeat binding protein 1 (LOC478375); mRNA	XM_535549	CGGBP1	CGG triplet repeat binding protein 1
CfaAffx.7939.1.S1_at	9.84E-04	1.16E-02	1.32	PREDICTED: Canis familiaris similar to cell growth regulator with EF hand domain 1 (LOC483006); mRNA	XM_540121	CGREF1	cell growth regulator with EF-hand domain 1

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Cfa.5198.1.A1_s_at	4.14E-04	9.68E-03	0.73	PREDICTED: Canis familiaris similar to coiled-coil-helix-coiled-coil-helix domain containing 1 (LOC609960); mRNA	XM_847315	CHCHD1	coiled-coil-helix-coiled-coil-helix domain containing 1
CfaAffx.15927.1.S1_s_at	2.38E-04	9.06E-03	0.7	PREDICTED: Canis familiaris similar to Coiled-coil-helix-coiled-coil-helix domain containing protein 2 (HCV NS2 trans-regulated protein) (NS2TP) (LOC479702); mRNA	XM_536830	CHCHD2	coiled-coil-helix-coiled-coil-helix domain containing 2
Cfa.13515.1.S1_at	3.96E-04	9.61E-03	0.73	PREDICTED: Canis familiaris similar to Coiled-coil-helix-coiled-coil-helix domain containing protein 3; transcript variant 2 (LOC607574); mRNA	XM_843362	CHCHD3	coiled-coil-helix-coiled-coil-helix domain containing 3
CfaAffx.2860.1.S1_s_at	2.50E-05	7.55E-03	0.63	PREDICTED: Canis familiaris similar to Coiled-coil-helix-coiled-coil-helix domain containing protein 3; transcript variant 2 (LOC607574); mRNA	XM_843362	CHCHD3	coiled-coil-helix-coiled-coil-helix domain containing 3
CfaAffx.12401.1.S1_at	3.59E-03	1.60E-02	0.7	PREDICTED: Canis familiaris similar to chromodomain helicase DNA binding protein 1; transcript variant 1 (LOC488891); mRNA	XM_546008	CHD1	chromodomain helicase DNA binding protein 1
CfaAffx.12405.1.S1_s_at	7.37E-03	2.02E-02	0.74	PREDICTED: Canis familiaris similar to chromodomain helicase DNA binding protein 1; transcript variant 6 (LOC488891); mRNA	XM_851226	CHD1	chromodomain helicase DNA binding protein 1
Cfa.447.1.S1_at	2.12E-02	3.23E-02	0.75	PREDICTED: Pan troglodytes cysteine-rich hydrophobic domain 2; transcript variant 2 (CHIC2); mRNA	XM_001145791	CHIC2	cysteine-rich hydrophobic domain 2
CfaAffx.7350.1.S1_s_at	8.81E-04	1.13E-02	0.74	PREDICTED: Canis familiaris similar to cysteine and histidine-rich domain (CHORD)-containing; zinc-binding protein 1 (LOC476773); mRNA	XM_533979	CHORDC1	cysteine and histidine-rich domain (CHORD)-containing 1
Cfa.21493.1.S1_at	2.44E-02	3.46E-02	0.76	PREDICTED: Canis familiaris similar to Churchill protein; transcript variant 1 (LOC609942); mRNA	XM_847755	CHURC1	churchill domain containing 1
CfaAffx.24801.1.S1_s_at	1.07E-02	2.36E-02	0.76	PREDICTED: Canis familiaris similar to Churchill protein; transcript variant 1 (LOC609942); mRNA	XM_847755	CHURC1	churchill domain containing 1
CfaAffx.29825.1.S1_s_at	2.61E-02	3.58E-02	0.75	PREDICTED: Canis familiaris similar to cold inducible RNA binding protein; transcript variant 1 (LOC476755); mRNA	XM_533961	CIRBP	cold inducible RNA binding protein

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.4292.1.A1_at	3.89E-02	4.44E-02	0.63	PREDICTED: Canis familiaris similar to cold inducible RNA binding protein; transcript variant 4 (LOC476755); mRNA	XM_863509	CIRBP	cold inducible RNA binding protein
Cfa.4292.2.A1_a_at	2.10E-02	3.21E-02	0.72	PREDICTED: Canis familiaris similar to cold inducible RNA binding protein; transcript variant 4 (LOC476755); mRNA	XM_863509	CIRBP	cold inducible RNA binding protein
Cfa.10250.1.A1_at	1.10E-02	2.39E-02	0.74	PREDICTED: Canis familiaris similar to Protein C10orf70 (LOC479212); mRNA	XM_536355	CISD1	CDGSH iron sulfur domain 1
CfaAffx.26219.1.S1_s_at	3.70E-04	9.61E-03	0.74	PREDICTED: Canis familiaris similar to Cyclin-dependent kinases regulatory subunit 1 (CKS-1) (Sid 1334) (LOC612237); mRNA	XM_849974	CKS1B	CDC28 protein kinase regulatory subunit 1B
Cfa.10770.1.S1_s_at	8.85E-03	2.19E-02	0.76	full-length cDNA clone CS0CAP004YD01 of Thymus of Homo sapiens (human)	CR601576	CKS2	CDC28 protein kinase regulatory subunit 2
Cfa.9474.1.A1_at	3.35E-03	1.56E-02	0.62	PREDICTED: Canis familiaris similar to myeloid inhibitory C-type lectin-like receptor isoform alpha (LOC477697); mRNA	XM_534891	CLEC12A	C-type lectin domain family 12, member A
Cfa.9474.1.A1_s_at	1.35E-02	2.63E-02	0.75	PREDICTED: Canis familiaris similar to myeloid inhibitory C-type lectin-like receptor isoform alpha (LOC477697); mRNA	XM_534891	CLEC12A	C-type lectin domain family 12, member A
CfaAffx.8533.1.S1_s_at	8.38E-03	2.14E-02	0.74	Canis familiaris mRNA for ceroid-lipofuscinosis; neuronal 5 (cln5 gene)	AJ875417	cln5	ceroid-lipofuscinosis, neuronal 5
Cfa.14535.1.S1_s_at	3.93E-03	1.64E-02	0.62	PREDICTED: Canis familiaris similar to ATP-dependent Clp protease ATP-binding subunit ClpX-like; mitochondrial precursor; transcript variant 3 (LOC609344); mRNA	XM_860781	CLPX	ClpX caseinolytic peptidase X homolog (E. coli)
CfaAffx.4312.1.S1_s_at	1.23E-02	2.52E-02	0.69	PREDICTED: Canis familiaris similar to clathrin; light polypeptide A isoform a; transcript variant 6 (LOC474765); mRNA	XM_861732	CLTA	clathrin, light chain (Lca)
CfaAffx.25055.1.S1_s_at	2.30E-03	1.39E-02	0.75	PREDICTED: Canis familiaris similar to Protein HSPC163 homolog (LOC480116); mRNA	XM_537238	CNIH4	cornichon homolog 4 (Drosophila)

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CfaAffx.5770.1.S1_s_at	2.87E-03	1.49E-02	0.75	familiaris similar to CCR4-NOT transcription complex; subunit 4 isoform a; transcript variant 10 (LOC482708); mRNA	XM_854588	CNOT4	CCR4-NOT transcription complex, subunit 4
CfaAffx.5774.1.S1_s_at	7.08E-04	1.08E-02	0.74	familiaris similar to CCR4-NOT transcription complex; subunit 4 isoform a; transcript variant 10 (LOC482708); mRNA	XM_854588	CNOT4	CCR4-NOT transcription complex, subunit 4
Cfa.18438.1.S1_s_at	5.28E-03	1.80E-02	0.75	PREDICTED: Canis familiaris similar to CCR4-NOT transcription complex subunit 7 (CCR4-associated factor 1) (CAF1); transcript variant 5 (LOC482895); mRNA	XM_850922	CNOT7	CCR4-NOT transcription complex, subunit 7
Cfa.9466.1.A1_s_at	5.64E-04	1.03E-02	0.71	PREDICTED: Canis familiaris similar to MIR-interacting saposin-like protein precursor (Transmembrane protein 4) (Putative secreted protein ZSIG9); transcript variant 1 (LOC607115); mRNA	XM_843770	CNPY2	canopy 2 homolog (zebrafish)
CfaAffx.31045.1.S1_at	2.82E-03	1.48E-02	1.32	PREDICTED: Canis familiaris similar to collagen; type XXIV; alpha 1 (LOC479965); mRNA	XM_537089	COL24A1	collagen, type XXIV, alpha 1
Cfa.2334.1.S1_at	1.66E-02	2.89E-02	0.76	Homo sapiens collagen; type IV; alpha 3 (Goodpasture antigen) binding protein (COL4A3BP); transcript variant 2; mRNA	NM_031361	COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein
CfaAffx.1259.1.S1_at	2.23E-02	3.31E-02	0.76	PREDICTED: Canis familiaris similar to COMM domain containing protein 10 (LOC474635); mRNA	XM_531865	COMMD10	COMM domain containing 10
CfaAffx.7152.1.S1_s_at	3.52E-03	1.59E-02	0.74	PREDICTED: Canis familiaris similar to COMM domain containing 3; transcript variant 1 (LOC477977); mRNA	XM_535162	COMMD3	COMM domain containing 3
Cfa.17817.1.S1_s_at	1.31E-03	1.23E-02	0.74	PREDICTED: Canis familiaris similar to coatomer protein complex; subunit beta (LOC476866); mRNA	XM_534069	COPB1	coatomer protein complex, subunit beta 1
Cfa.18869.1.S1_s_at	1.83E-05	7.55E-03	0.68	PREDICTED: Canis familiaris similar to coatomer protein complex; subunit beta (LOC476866); mRNA	XM_534069	COPB1	coatomer protein complex, subunit beta 1

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Cfa.18764.1.S1_s_at	8.28E-05	8.77E-03	0.72	PREDICTED: Canis familiaris similar to coatomer protein complex; subunit beta 2 (beta prime) (LOC477088); mRNA	XM_534283	COPB2	coatomer protein complex, subunit beta 2 (beta prime)
Cfa.20115.1.S1_s_at	4.89E-03	1.75E-02	0.73	PREDICTED: Canis familiaris similar to coatomer protein complex; subunit beta 2 (beta prime) (LOC477088); mRNA	XM_534283	COPB2	coatomer protein complex, subunit beta 2 (beta prime)
Cfa.3255.1.A1_s_at	8.00E-04	1.10E-02	0.76	PREDICTED: Canis familiaris similar to coatomer protein complex; subunit beta 2 (beta prime) (LOC477088); mRNA	XM_534283	COPB2	coatomer protein complex, subunit beta 2 (beta prime)
CfaAffx.12255.1.S1_s_at	2.38E-03	1.40E-02	0.7	PREDICTED: Canis familiaris similar to coatomer protein complex; subunit beta 2 (beta prime) (LOC477088); mRNA	XM_534283	COPB2	coatomer protein complex, subunit beta 2 (beta prime)
Cfa.2267.1.S1_s_at	3.69E-04	9.61E-03	0.73	PREDICTED: Canis familiaris similar to COP9 signalosome subunit 4; transcript variant 2 (LOC478455); mRNA	XM_854195	COPS4	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis)
Cfa.11305.1.A1_s_at	3.93E-04	9.61E-03	0.72	PREDICTED: Canis familiaris similar to COP9 signalosome complex subunit 5 (Signalosome subunit 5) (SGN5) (Jun activation domain-binding protein 1) (Kip1 C-terminus interacting protein 2); transcript variant 1 (LOC477901); mRNA	XM_535093	COPS5	COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis)
Cfa.19331.1.S1_at	1.62E-02	2.85E-02	0.76	PREDICTED: Canis familiaris coenzyme Q3 (COQ3); mRNA	XM_532241	COQ3	coenzyme Q3 homolog, methyltransferase (S. cerevisiae)
Cfa.1515.1.A1_at	7.54E-03	2.04E-02	0.73	PREDICTED: Canis familiaris similar to CG30493-PB; transcript variant 1 (LOC478110); mRNA	XM_535284	COQ9	coenzyme Q9 homolog (S. cerevisiae)

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.29503.1.S1_at	2.51E-03	1.43E-02	1.31	Canis lupus familiaris 1P2 olfactory receptor protein (OR1P2) mRNA; complete cds	EF451962	cOR1P2	cOR1P2 olfactory receptor family 1 subfamily P-like
Cfa.50.1.S1_s_at	2.63E-03	1.45E-02	0.76	PREDICTED: Canis familiaris cOR2W9 olfactory receptor family 2 subfamily W-like (cOR2W9); mRNA	XM_849461	cOR2W9	cOR2W9 olfactory receptor family 2 subfamily W-like
CfaAffx.19098.1.S1_at	1.28E-02	2.55E-02	1.3	PREDICTED: Canis familiaris cOR52A8 olfactory receptor family 52 subfamily A-like (cOR52A8); mRNA	XM_847813	cOR52A8	cOR52A8 olfactory receptor family 52 subfamily A-like
CfaAffx.17612.1.S1_s_at	4.58E-04	9.87E-03	1.31	C.familiaris mRNA for TPCR79 protein	X89665	cOR8G8P	cOR8G8P olfactory receptor family 8 subfamily G pseudogene
CfaAffx.14186.1.S1_at	3.58E-03	1.60E-02	1.33	PREDICTED: Canis familiaris cOR8S17 olfactory receptor family 8 subfamily S-like (cOR8S17); mRNA	XM_543703	cOR8S17	cOR8S17 olfactory receptor family 8 subfamily S-like
Cfa.4546.1.S1_s_at	1.46E-03	1.25E-02	0.76	Canis familiaris cytochrome c oxidase copper chaperone (COX17) mRNA; complete cds	AY603041	COX17	COX17 homolog, cytochrome c oxidase assembly protein (yeast)
Cfa.11403.1.A1_at	2.27E-04	9.06E-03	0.73	PREDICTED: Canis familiaris similar to Neighbor of COX4 (LOC479624); mRNA	XM_536760	COX4NB	COX4 neighbor
CfaAffx.30489.1.S1_s_at	2.79E-03	1.48E-02	0.74	PREDICTED: Canis familiaris similar to Neighbor of COX4 (LOC479624); mRNA	XM_536760	COX4NB	COX4 neighbor
CfaAffx.13068.1.S1_s_at	2.25E-04	9.06E-03	1.34	Canis lupus familiaris ZAP47 mRNA for zymogen granule membrane associated protein; complete cds	D78348	CPB1	carboxypeptidase B1 (tissue)
CfaAffx.17069.1.S1_s_at	6.85E-03	1.97E-02	0.76	PREDICTED: Canis familiaris similar to cleavage and polyadenylation specific factor 2; transcript variant 1 (LOC480230); mRNA	XM_537353	CPSF2	cleavage and polyadenylation specific factor 2, 100kDa

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Cfa.8873.1.A1_at	5.47E-03	1.82E-02	0.72	PREDICTED: Canis familiaris similar to cleavage and polyadenylation specific factor 2; transcript variant 3 (LOC480230); mRNA	XM_851321	CPSF2	cleavage and polyadenylation specific factor 2, 100kDa
CfaAffx.17079.1.S1_s_at	2.57E-03	1.44E-02	0.7	PREDICTED: Canis familiaris similar to cleavage and polyadenylation specific factor 2; transcript variant 4 (LOC480230); mRNA	XM_851362	CPSF2	cleavage and polyadenylation specific factor 2, 100kDa
Cfa.12286.1.A1_at	7.38E-03	2.02E-02	0.71	PREDICTED: Canis familiaris similar to cleavage and polyadenylation specific factor 6; 68 kD subunit (LOC474441); mRNA	XM_531671	CPSF6	cleavage and polyadenylation specific factor 6, 68kDa
CfaAffx.1594.1.S1_s_at	7.97E-04	1.10E-02	0.72	PREDICTED: Canis familiaris similar to cleavage and polyadenylation specific factor 6; 68 kD subunit (LOC474441); mRNA	XM_531671	CPSF6	cleavage and polyadenylation specific factor 6, 68kDa
Cfa.15225.1.S1_a_at	1.43E-02	2.69E-02	0.76	familiaris similar to Carnitine O-palmitoyltransferase II; mitochondrial precursor (CPT II) (LOC489585); mRNA	XM_546705	CPT2	carnitine palmitoyltransferase II
Cfa.12544.1.A1_at	2.35E-03	1.40E-02	0.77	Sus scrofa mRNA; clone:OVRM10164F12; expressed in ovary	AK236216	CR956367.2	prostate transmembrane protein, androgen induced 1
CfaAffx.30984.1.S1_s_at	6.38E-03	1.91E-02	1.37	PREDICTED: Canis familiaris similar to crumbs homolog 2 (LOC491341); mRNA	XM_548462	CRB2	crumbs homolog 2 (Drosophila)
Cfa.2596.1.S1_at	3.99E-03	1.64E-02	0.76	PREDICTED: Canis familiaris similar to CG4774-PA; isoform A; transcript variant 2 (LOC607530); mRNA	XM_844822	CRLS1	cardiolipin synthase 1
CfaAffx.8952.1.S1_s_at	5.92E-03	1.86E-02	0.71	familiaris similar to Crooked neck-like protein 1 (Crooked neck homolog) (hCrn); transcript variant 5 (LOC477137); mRNA	XM_851428	CRNKL1	crooked neck pre-mRNA splicing factor-like 1 (Drosophila)
Cfa.2895.1.S1_at	5.23E-03	1.79E-02	0.67	PREDICTED: Equus caballus CSE1 chromosome segregation 1-like (yeast) (CSE1L); mRNA	XM_001503546	CSE1L	CSE1 chromosome segregation 1-like (yeast)
CfaAffx.11464.1.S1_at	8.40E-04	1.12E-02	0.74	PREDICTED: Bos taurus similar to chondroitin beta1;4 N-acetylgalactosaminyltransferase 2; transcript variant 1 (LOC509328); mRNA	XM_586267	CSGALNACT2	chondroitin sulfate N-acetylgalactosaminyltransferase 2

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.15058.1.S1_s_at	5.49E-03	1.82E-02	0.76	PREDICTED: Canis familiaris similar to casein kinase 1; alpha 1 isoform 1; transcript variant 15 (LOC479331); mRNA	XM_862678	CSNK1A1	casein kinase 1, alpha 1
Cfa.2931.1.S1_at	1.89E-03	1.32E-02	0.77	PREDICTED: Canis familiaris similar to casein kinase 1; alpha 1 isoform 1; transcript variant 15 (LOC479331); mRNA	XM_862678	CSNK1A1	casein kinase 1, alpha 1
Cfa.347.1.S1_s_at	7.60E-04	1.09E-02	0.76	PREDICTED: Canis familiaris similar to Y47D9A.2a; transcript variant 6 (LOC487531); mRNA	XM_855627	CTDSPL2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2
Cfa.12490.1.A1_at	3.65E-02	4.28E-02	0.75	PREDICTED: Canis familiaris similar to Cathepsin Z precursor (Cathepsin X) (Cathepsin P) (LOC611983); mRNA	XM_849702	CTSZ	cathepsin Z
CfaAffx.18934.1.S1_at	1.25E-02	2.53E-02	0.73	PREDICTED: Canis familiaris similar to Cathepsin Z precursor (Cathepsin X) (Cathepsin P) (LOC611983); mRNA	XM_849702	CTSZ	cathepsin Z
Cfa.20001.1.S1_s_at	1.25E-02	2.53E-02	0.71	PREDICTED: Canis familiaris similar to Cullin-1 (CUL-1); transcript variant 5 (LOC475512); mRNA	XM_851039	CUL1	cullin 1
Cfa.6461.1.A1_at	5.62E-03	1.83E-02	0.77	PREDICTED: Canis familiaris similar to Cullin-1 (CUL-1); transcript variant 5 (LOC475512); mRNA	XM_851039	CUL1	cullin 1
Cfa.657.1.A1_s_at	1.79E-03	1.30E-02	0.76	PREDICTED: Canis familiaris similar to Cullin-3 (CUL-3); transcript variant 1 (LOC477392); mRNA	XM_534586	CUL3	cullin 3
Cfa.1816.1.A1_at	2.27E-02	3.33E-02	0.71	PREDICTED: Canis familiaris similar to Copper homeostasis protein cutC homolog (LOC477793); mRNA	XM_534987	CUTC	cutC copper transporter homolog (E. coli)
CfaAffx.14982.1.S1_at	2.23E-03	1.37E-02	0.76	PREDICTED: Canis familiaris similar to Copper homeostasis protein cutC homolog (LOC477793); mRNA	XM_534987	CUTC	cutC copper transporter homolog (E. coli)

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CfaAffx.24352.1.S1_at	2.55E-02	3.54E-02	0.77	familiaris similar to Small inducible cytokine B16 precursor (Transmembrane chemokine CXCL16) (SR-PSOX) (Scavenger receptor for phosphatidylserine and oxidized low density lipoprotein) (LOC607514); mRNA	XM_844211	CXCL16	chemokine (C-X-C motif) ligand 16
Cfa.20770.1.S1_s_at	5.28E-03	1.80E-02	0.75	TPA_inf: Canis lupus familiaris cyba mRNA for predicted cytochrome b-245; alpha polypeptide; complete cds	BR000286	CYBA	cytochrome b-245, alpha polypeptide
Cfa.379.1.S1_at	2.07E-04	9.06E-03	0.69	PREDICTED: Canis familiaris similar to Cytochrome c; somatic (LOC475258); mRNA	XM_532493	CYCS	cytochrome c, somatic
CfaAffx.5204.1.S1_s_at	2.95E-04	9.25E-03	0.7	PREDICTED: Canis familiaris similar to Cytochrome c; somatic (LOC475258); mRNA	XM_532493	CYCS	cytochrome c, somatic
Cfa.13343.1.A1_at	1.49E-03	1.25E-02	1.35	Canis familiaris cytochrome P450 4A38 (CYP4A38) mRNA; complete cds	DQ138951	CYP4A38	cytochrome P450 4A38
Cfa.3883.1.S1_at	1.11E-03	1.20E-02	1.37	Canis familiaris cytochrome P-450 IIB (P450IIB) mRNA; complete cds	M92447	CYPIIB11	cytochrome P450 2B11
Cfa.20092.1.S1_s_at	2.82E-03	1.48E-02	0.67	familiaris similar to Dual adapter for phosphotyrosine and 3-phosphotyrosine and 3-phosphoinositide (hDAPP1) (B cell adapter molecule of 32 kDa) (B lymphocyte adapter protein Bam32) (LOC478491); mRNA	XM_535669	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides
Cfa.20254.1.S1_at	2.04E-03	1.35E-02	0.75	PREDICTED: Canis familiaris similar to Aspartyl-tRNA synthetase (Aspartate--tRNA ligase) (AspRS); transcript variant 4 (LOC476132); mRNA	XM_851746	DARS	aspartyl-tRNA synthetase
CfaAffx.3674.1.S1_s_at	2.62E-03	1.44E-02	0.7	PREDICTED: Canis familiaris similar to activator of S phase kinase (LOC475219); mRNA	XM_532451	DBF4	DBF4 homolog (S. cerevisiae)
Cfa.15548.1.A1_at	3.75E-03	1.62E-02	0.75	PREDICTED: Macaca mulatta DNA-crosslink repair gene SNM1 (DCLRE1A); mRNA	XM_001090942	DCLRE1A	DNA cross-link repair 1A (PSO2 homolog, S. cerevisiae)
Cfa.16555.1.S1_at	2.51E-02	3.51E-02	0.74	PREDICTED: Canis familiaris similar to MAD homolog 4 interacting transcription coactivator 1; transcript variant 1 (LOC607346); mRNA	XM_844390	DCP1A	DCP1 decapping enzyme homolog A (S. cerevisiae)

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Cfa.1807.1.S1_at	2.30E-04	9.06E-03	0.71	PREDICTED: Canis familiaris similar to dynactin 3 isoform 2; transcript variant 1 (LOC474750); mRNA	XM_531981	DCTN3	dynactin 3 (p22)
CfaAffx.3820.1.S1_s_at	1.14E-04	8.90E-03	0.74	PREDICTED: Canis familiaris similar to dynactin 3 isoform 2; transcript variant 1 (LOC474750); mRNA	XM_531981	DCTN3	dynactin 3 (p22)
CfaAffx.10737.1.S1_s_at	6.39E-04	1.05E-02	0.77	PREDICTED: Canis familiaris similar to Dynactin subunit 6 (Dynactin subunit p27) (WS-3 protein) (LOC475600); mRNA	XM_532816	DCTN6	dynactin 6
Cfa.5351.1.A1_at	1.08E-03	1.20E-02	0.73	PREDICTED: Pan troglodytes DDHD domain containing 2 (DDHD2); mRNA	XM_519711	DDHD2	DDHD domain containing 2
CfaAffx.6502.1.S1_s_at	2.17E-04	9.06E-03	0.73	PREDICTED: Canis familiaris similar to DEAD (Asp-Glu-Ala-Asp) box polypeptide 1; transcript variant 2 (LOC475671); mRNA	XM_843772	DDX1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1
Cfa.17424.1.S1_s_at	8.76E-03	2.18E-02	0.75	PREDICTED: Canis familiaris similar to Probable RNA-dependent helicase p72 (DEAD-box protein p72) (DEAD-box protein 17); transcript variant 10 (LOC474508); mRNA	XM_855514	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17
Cfa.11665.1.A1_at	3.66E-04	9.61E-03	0.75	PREDICTED: Canis familiaris similar to DDX19 like protein; transcript variant 1 (LOC479658); mRNA	XM_536790	DDX19A	DEAD (Asp-Glu-Ala-As) box polypeptide 19A
Cfa.5340.1.A1_s_at	6.24E-03	1.89E-02	0.71	PREDICTED: Canis familiaris similar to DEAD (Asp-Glu-Ala-Asp) box polypeptide 39 isoform 1 (LOC476689); mRNA	XM_533895	DDX39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
CfaAffx.25064.1.S1_at	9.61E-04	1.16E-02	0.74	PREDICTED: Canis familiaris similar to DEAD (Asp-Glu-Ala-Asp) box polypeptide 39 isoform 1 (LOC476689); mRNA	XM_533895	DDX39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
CfaAffx.2200 6.1.S1_s_at	9.94E-03	2.30E-02	0.7	PREDICTED: Canis familiaris similar to DEAD-box protein 3; X-chromosomal (Helicase-like protein 2) (HLP2) (DEAD-box; X isoform); transcript variant 4 (LOC480886); mRNA	XM_856207	DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked

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Cfa.19989.1.S1_s_at	6.74E-03	1.95E-02	0.75	PREDICTED: Canis familiaris similar to DEAD-box protein 3; X-chromosomal (Helicase-like protein 2) (HLP2) (DEAD-box; X isoform); transcript variant 8 (LOC480886); mRNA	XM_856356	DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked
CfaAffx.20479.1.S1_s_at	5.06E-04	1.00E-02	0.75	PREDICTED: Canis familiaris similar to DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 isoform 2; transcript variant 2 (LOC477691); mRNA	XM_861747	DDX47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47
CfaAffx.21291.1.S1_s_at	1.45E-02	2.70E-02	0.76	PREDICTED: Canis familiaris similar to nucleolar protein GU2; transcript variant 4 (LOC612801); mRNA	XM_855730	DDX50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50
CfaAffx.12074.1.S1_s_at	1.76E-03	1.30E-02	0.74	PREDICTED: Canis familiaris similar to coated vesicle membrane protein; transcript variant 2 (LOC486246); mRNA	XM_852856	DDX55	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55
CfaAffx.3613.1.S1_at	3.75E-02	4.34E-02	0.73	PREDICTED: Equus caballus DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 (DDX58); mRNA	XM_001497845	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
CfaAffx.14220.1.S1_s_at	4.42E-03	1.70E-02	0.75	PREDICTED: Canis familiaris similar to 2;4-dienoyl-CoA reductase; mitochondrial precursor (2;4-dienoyl-CoA reductase [NADPH]) (4-enoyl-CoA reductase [NADPH]) (LOC477938); mRNA	XM_535127	DECR1	2,4-dienoyl CoA reductase 1, mitochondrial
Cfa.10449.1.A1_s_at	6.60E-04	1.06E-02	0.71	PREDICTED: Canis familiaris similar to Putative deoxyribose-phosphate aldolase (Phosphodeoxyriboaldolase) (Deoxyriboaldolase) (DERA) (LOC477684); mRNA	XM_534879	DERA	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)
CfaAffx.19551.1.S1_at	8.60E-04	1.13E-02	1.31	Drosophila erecta GG20584 (Dere\GG20584); mRNA	XM_001975357	Dere\GG20584	GG20584 gene product from transcript GG20584-RA
CfaAffx.2368.1.S1_s_at	1.07E-03	1.20E-02	0.75	PREDICTED: Canis familiaris similar to Der1-like domain family; member 1 (LOC475086); mRNA	XM_532320	DERL1	Der1-like domain family, member 1

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Cfa.3368.1.S1_at	4.91E-03	1.75E-02	0.73	PREDICTED: Canis familiaris similar to Der1-like domain family; member 2; transcript variant 1 (LOC606991); mRNA	XM_843261	DERL2	Der1-like domain family, member 2
CfaAffx.23819.1.S1_at	2.82E-03	1.48E-02	0.77	PREDICTED: Canis familiaris similar to Der1-like domain family; member 2; transcript variant 1 (LOC606991); mRNA	XM_843261	DERL2	Der1-like domain family, member 2
Cfa.11317.1.A1_s_at	5.27E-03	1.79E-02	0.77	familiaris similar to Putative pre-mRNA splicing factor RNA helicase (DEAH box protein 15); transcript variant 9 (LOC488856); mRNA	XM_858970	DHX15	DEAH (Asp-Glu-Ala-His) box polypeptide 15
Cfa.2263.1.A1_s_at	4.26E-03	1.68E-02	0.76	PREDICTED: Canis familiaris similar to DEAH (Asp-Glu-Ala-His) box polypeptide 29 (LOC478060); mRNA	XM_535238	DHX29	DEAH (Asp-Glu-Ala-His) box polypeptide 29
Cfa.1875.1.S1_at	1.11E-02	2.40E-02	0.75	PREDICTED: Canis familiaris similar to disrupted in renal carcinoma 2 (LOC478588); mRNA	XM_535764	DIRC2	disrupted in renal carcinoma 2
CfaAffx.8460.1.S1_s_at	6.77E-04	1.07E-02	0.68	PREDICTED: Canis familiaris similar to KIAA1008 (LOC485491); mRNA	XM_542610	DIS3	DIS3 mitotic control homolog (S. cerevisiae)
Cfa.429.1.A1_at	2.67E-02	3.62E-02	0.75	PREDICTED: Canis familiaris similar to CG6413-PA (LOC478346); mRNA	XM_535520	DIS3L	DIS3 mitotic control homolog (S. cerevisiae)-like
Cfa.862.1.S1_s_at	1.75E-02	2.95E-02	0.69	Canis lupus familiaris dihydrolipoamide dehydrogenase (DLD); mRNA	NM_001003294	DLD	dihydrolipoamide dehydrogenase
CfaAffx.14460.1.S1_s_at	6.18E-02	5.73E-02	1.31	PREDICTED: Canis familiaris similar to Dimethylglycine dehydrogenase; mitochondrial precursor (ME2GLYDH) (LOC488935); mRNA	XM_546052	DMGDH	dimethylglycine dehydrogenase
Cfa.20980.1.S1_s_at	1.49E-02	2.74E-02	0.74	PREDICTED: Canis familiaris similar to DnaJ homolog subfamily B member 11 precursor (ER-associated dnaJ protein 3) (ErJ3) (ER-associated Hsp40 co-chaperone) (hDj9) (PWP1-interacting protein 4) (LOC478664); mRNA	XM_535834	DNAJB11	DnaJ (Hsp40) homolog, subfamily B, member 11

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CfaAffx.22335.1.S1_s_at	1.51E-02	2.75E-02	0.67	PREDICTED: Canis familiaris similar to DnaJ (Hsp40) homolog; subfamily B; member 12; transcript variant 6 (LOC489039); mRNA	XM_856892	DNAJB12	DnaJ (Hsp40) homolog, subfamily B, member 12
Cfa.406.1.S1_at	5.56E-03	1.82E-02	0.71	PREDICTED: Pan troglodytes similar to DnaJ (Hsp40) homolog; subfamily B; member 14; transcript variant 3 (LOC471258); mRNA	XM_001167856	DNAJB14	DnaJ (Hsp40) homolog, subfamily B, member 14
Cfa.10963.1.A1_s_at	1.43E-03	1.25E-02	0.77	PREDICTED: Canis familiaris similar to DnaJ (Hsp40) homolog; subfamily B; member 14 isoform 2 (LOC487875); mRNA	XM_544997	DNAJB14	DnaJ (Hsp40) homolog, subfamily B, member 14
Cfa.3079.1.S1_at	6.55E-03	1.94E-02	0.76	PREDICTED: Canis familiaris similar to DnaJ (Hsp40) homolog; subfamily B; member 6 isoform a; transcript variant 3 (LOC608937); mRNA	XM_856569	DNAJB6	DnaJ (Hsp40) homolog, subfamily B, member 6
Cfa.17880.2.S1_s_at	1.18E-03	1.21E-02	0.73	PREDICTED: Canis familiaris similar to DnaJ (Hsp40) homolog; subfamily B; member 9 (LOC475286); mRNA	XM_532518	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9
CfaAffx.22084.1.S1_s_at	5.87E-03	1.86E-02	0.77	PREDICTED: Canis familiaris similar to DnaJ (Hsp40) homolog; subfamily C; member 10; transcript variant 1 (LOC478826); mRNA	XM_535988	DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10
CfaAffx.1082.1.S1_s_at	1.11E-03	1.20E-02	0.73	PREDICTED: Canis familiaris similar to dopamine receptor interacting protein (LOC474392); mRNA	XM_531625	DNAJC14	DnaJ (Hsp40) homolog, subfamily C, member 14
CfaAffx.1085.1.S1_s_at	2.30E-02	3.35E-02	0.69	PREDICTED: Canis familiaris similar to dopamine receptor interacting protein (LOC474392); mRNA	XM_531625	DNAJC14	DnaJ (Hsp40) homolog, subfamily C, member 14
Cfa.7675.1.A1_at	2.63E-03	1.45E-02	0.74	PREDICTED: Canis familiaris similar to DNAJ domain-containing (LOC476930); mRNA	XM_534131	DNAJC15	DnaJ (Hsp40) homolog, subfamily C, member 15
Cfa.16320.1.A1_s_at	1.96E-03	1.33E-02	0.68	PREDICTED: Canis familiaris similar to DnaJ (Hsp40) homolog; subfamily C; member 3 (LOC476966); mRNA	XM_534166	DNAJC3	DnaJ (Hsp40) homolog, subfamily C, member 3
Cfa.7924.1.A1_s_at	7.41E-02	6.34E-02	0.76	PREDICTED: Canis familiaris similar to DnaJ (Hsp40) homolog; subfamily C; member 7; transcript variant 2 (LOC480519); mRNA	XM_537639	DNAJC7	DnaJ (Hsp40) homolog, subfamily C, member 7

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Cfa.1508.1.A1_at	2.08E-02	3.20E-02	0.77	PREDICTED: Canis familiaris similar to Deoxyribonuclease I-like 1 precursor (DNase I-like 1) (Muscle-specific DNase I-like) (DNase X) (XIB); transcript variant 1 (LOC492250); mRNA	XM_549370	DNASE1L1	deoxyribonuclease I-like 1
Cfa.4392.1.S1_at	1.22E-03	1.22E-02	0.7	PREDICTED: Canis familiaris similar to Deoxyribonuclease II alpha precursor (DNase II alpha) (Acid DNase) (Lysosomal DNase II) (LOC476697); mRNA	XM_533902	DNASE2	deoxyribonuclease II, lysosomal
CfaAffx.28094.1.S1_s_at	4.17E-03	1.67E-02	0.76	PREDICTED: Canis familiaris similar to dedicator of cytokinesis 11; transcript variant 1 (LOC492089); mRNA	XM_549211	DOCK11	dedicator of cytokinesis 11
CfaAffx.14677.1.S1_at	9.21E-04	1.15E-02	0.73	PREDICTED: Canis familiaris similar to Downstream neighbor of Son protein (B17) (LOC478407); mRNA	XM_535584	DONSON	downstream neighbor of SON
CfaAffx.30709.1.S1_s_at	1.95E-02	3.11E-02	0.77	PREDICTED: Canis familiaris similar to Dihydropyrimidine dehydrogenase [NADP+] precursor (DPD) (DHPDHase) (Dihydrouracil dehydrogenase) (Dihydrothymine dehydrogenase) (LOC479935); mRNA	XM_537061	DPYD	dihydropyrimidine dehydrogenase
CfaAffx.26960.1.S1_at	4.94E-07	6.68E-03	1.33	Homo sapiens cDNA FLJ75585 complete cds; highly similar to Homo sapiens dystrophin related protein 2 (DRP2); mRNA	AK289825	DRP2	dystrophin related protein 2
Cfa.12509.1.A1_s_at	1.07E-02	2.36E-02	0.75	PREDICTED: Canis familiaris similar to squamous cell carcinoma antigen recognized by T cells 2 (LOC476271); mRNA	XM_533477	DSE	dermatan sulfate epimerase
Cfa.8933.1.A1_at	2.45E-02	3.46E-02	0.77	PREDICTED: Canis familiaris similar to dual specificity phosphatase 6 isoform a; transcript variant 1 (LOC482594); mRNA	XM_539711	DUSP6	dual specificity phosphatase 6
Cfa.4000.1.A1_s_at	4.93E-03	1.75E-02	0.73	PREDICTED: Canis familiaris similar to Deoxyuridine 5-triphosphate nucleotidohydrolase; mitochondrial precursor (dUTPase) (dUTP pyrophosphatase) (LOC609526); mRNA	XM_846796	DUT	deoxyuridine triphosphatase

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.18048.1.S1_at	3.56E-04	9.58E-03	1.38	Drosophila virilis GJ11817 (Dvir\GJ11817); mRNA	XM_002051476	Dvir\GJ11817	GJ11817 gene product from transcript GJ11817-RA
CfaAffx.9020.1.S1_s_at	2.49E-04	9.06E-03	0.7	Bos taurus dynein, cytoplasmic 1, light intermediate chain 1; mRNA (cDNA clone MGC:137616 IMAGE:8162469); complete cds	BC112621	DYNC1LI1	dynein, cytoplasmic 1, light intermediate chain 1
Cfa.11109.1.A1_at	1.01E-03	1.17E-02	0.7	PREDICTED: Macaca mulatta dynein; cytoplasmic; light intermediate polypeptide 2 (DYNC1LI2); mRNA	XM_001085468	DYNC1LI2	dynein, cytoplasmic 1, light intermediate chain 2
CfaAffx.13960.1.S1_s_at	8.95E-03	2.20E-02	0.71	PREDICTED: Canis familiaris similar to RIKEN cDNA 1810011O16; transcript variant 4 (LOC490647); mRNA	XM_856354	EAPP	E2F-associated phosphoprotein
Cfa.212.1.A1_s_at	3.60E-02	4.25E-02	0.73	Canis lupus familiaris RCAS1 mRNA for receptor binding cancer antigen; complete cds	AB083366	EBAG9	estrogen receptor binding site associated, antigen, 9
Cfa.3338.1.A1_at	1.56E-02	2.80E-02	0.68	PREDICTED: Canis familiaris similar to Probable rRNA processing protein EBP2 (EBNA1 binding protein 2) (Nucleolar protein p40) (LOC475391); mRNA	XM_848382	EBNA1BP2	EBNA1 binding protein 2
Cfa.3338.1.A1_s_at	2.56E-03	1.44E-02	0.74	PREDICTED: Canis familiaris similar to Probable rRNA processing protein EBP2 (EBNA1 binding protein 2) (Nucleolar protein p40) (LOC475391); mRNA	XM_848382	EBNA1BP2	EBNA1 binding protein 2
Cfa.2077.1.A1_at	9.76E-04	1.16E-02	0.6	PREDICTED: Canis familiaris similar to SGT1 protein (hSGT1) (Suppressor of GCR2) (LOC479244); mRNA	XM_536386	ECD	ecdysoneless homolog (Drosophila)
Cfa.14431.1.A1_at	4.94E-03	1.75E-02	0.74	PREDICTED: Canis familiaris similar to ER degradation-enhancing-mannosidase-like protein 2; transcript variant 2 (LOC477209); mRNA	XM_859088	EDEM2	ER degradation enhancer, mannosidase alpha-like 2
Cfa.2977.1.A1_s_at	2.23E-02	3.31E-02	0.77	PREDICTED: Canis familiaris similar to ER degradation-enhancing-mannosidase-like protein 2; transcript variant 9 (LOC477209); mRNA	XM_859274	EDEM2	ER degradation enhancer, mannosidase alpha-like 2
Cfa.19497.1.S1_at	2.11E-03	1.36E-02	0.71	PREDICTED: Pan troglodytes early endosome antigen 1; 162kD (EEA1); mRNA	XM_522610	EEA1	early endosome antigen 1

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Cfa.10198.1.A1_s_at	2.21E-03	1.37E-02	0.76	familiaris similar to embryonic ectoderm development; transcript variant 4 (LOC476779); mRNA	XM_852571	EED	embryonic ectoderm development
CfaAffx.2866.1.S1_s_at	3.61E-03	1.60E-02	0.75	PREDICTED: Canis familiaris similar to eukaryotic translation elongation factor 1 delta; transcript variant 1 (LOC475115); mRNA	XM_532345	EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
Cfa.11745.1.A1_s_at	2.11E-04	9.06E-03	0.68	PREDICTED: Canis familiaris similar to Eukaryotic translation elongation factor 1 epsilon-1 (Multisynthetase complex auxiliary component p18) (Elongation factor p18) (LOC478717); mRNA	XM_535882	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1
CfaAffx.28979.1.S1_at	2.46E-03	1.41E-02	1.45	PREDICTED: Canis familiaris hypothetical LOC480634 (LOC480634); mRNA	XM_537754	EFCAB5	EF-hand calcium binding domain 5
Cfa.18530.1.S1_s_at	1.12E-02	2.40E-02	0.76	PREDICTED: Canis familiaris similar to EF hand domain family; member A1 (LOC486044); mRNA	XM_543170	EFHA1	EF-hand domain family, member A1
CfaAffx.18906.1.S1_at	4.84E-03	1.75E-02	0.71	PREDICTED: Canis familiaris similar to Translation initiation factor eIF-2B epsilon subunit (eIF-2B GDP-GTP exchange factor); transcript variant 3 (LOC488103); mRNA	XM_852430	EIF2B5	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa
Cfa.19645.1.S1_s_at	9.66E-04	1.16E-02	0.72	PREDICTED: Canis familiaris similar to Eukaryotic translation initiation factor 2 subunit 1 (Eukaryotic translation initiation factor 2 alpha subunit) (eIF-2-alpha) (EIF-2alpha) (EIF-2A) (LOC480361); mRNA	XM_537485	EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa
Cfa.304.1.A1_s_at	2.38E-04	9.06E-03	0.71	PREDICTED: Canis familiaris similar to Eukaryotic translation initiation factor 2 subunit 2 (Eukaryotic translation initiation factor 2 beta subunit) (eIF-2-beta); transcript variant 7 (LOC477197); mRNA	XM_858344	EIF2S2	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa

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Cfa.14462.2.S1_s_at	4.07E-04	9.68E-03	0.72	familiaris similar to eukaryotic translation initiation factor 3; subunit 6 (predicted); transcript variant 2 (LOC475070); mRNA	XM_532304	EIF3E	eukaryotic translation initiation factor 3, subunit E
CfaAffx.1984.1.S1_s_at	4.14E-03	1.67E-02	0.73	eukaryotic translation initiation factor 3; subunit 6 (predicted); transcript variant 4 (LOC475070); mRNA	XM_854853	EIF3E	eukaryotic translation initiation factor 3, subunit E
CfaAffx.2153.1.S1_s_at	3.35E-04	9.28E-03	0.75	PREDICTED: Canis familiaris similar to eukaryotic translation initiation factor 3; subunit 3 gamma; 40kDa; transcript variant 6 (LOC475081); mRNA	XM_855836	EIF3H	eukaryotic translation initiation factor 3, subunit H
Cfa.1036.1.S1_at	3.90E-04	9.61E-03	0.69	PREDICTED: Canis familiaris similar to Eukaryotic translation initiation factor 3 subunit 2 (eIF-3 beta) (eIF3 p36) (eIF3i) (TGF-beta receptor interacting protein 1) (TRIP-1) (LOC478152); mRNA	XM_535328	EIF3I	eukaryotic translation initiation factor 3, subunit I
CfaAffx.16721.1.S1_s_at	8.60E-06	6.68E-03	0.72	PREDICTED: Canis familiaris similar to Eukaryotic translation initiation factor 3 subunit 2 (eIF-3 beta) (eIF3 p36) (eIF3i) (TGF-beta receptor interacting protein 1) (TRIP-1) (LOC478152); mRNA	XM_535328	EIF3I	eukaryotic translation initiation factor 3, subunit I
Cfa.11166.2.S1_s_at	4.05E-04	9.68E-03	0.74	PREDICTED: Canis familiaris similar to Eukaryotic translation initiation factor 3 subunit 1 (eIF-3 alpha) (LOC487532); mRNA	XM_544656	EIF3J	eukaryotic translation initiation factor 3, subunit J
CfaAffx.11955.1.S1_s_at	1.64E-03	1.28E-02	0.77	PREDICTED: Canis familiaris similar to B5 receptor (LOC475950); mRNA	XM_533160	EIF3M	eukaryotic translation initiation factor 3, subunit M
Cfa.1317.1.A1_at	2.30E-03	1.39E-02	0.73	PREDICTED: Pan troglodytes eukaryotic translation initiation factor 4 gamma; 3 (EIF4G3); mRNA	XM_001165083	EIF4G3	eukaryotic translation initiation factor 4 gamma, 3
CfaAffx.27903.1.S1_s_at	5.88E-04	1.03E-02	0.74	familiaris similar to eukaryotic translation initiation factor 5; transcript variant 5 (LOC480442); mRNA	XM_863519	EIF5	eukaryotic translation initiation factor 5

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Cfa.15358.1.A1_at	7.88E-04	1.10E-02	0.63	PREDICTED: Canis familiaris similar to RNA polymerase II elongation factor ELL2; transcript variant 1 (LOC488899); mRNA	XM_546016	ELL2	elongation factor, RNA polymerase II, 2
Cfa.17202.1.S1_at	4.69E-03	1.73E-02	0.74	Bos taurus ELOVL family member 5; elongation of long chain fatty acids (FEN1/Elo2; SUR4/Elo3-like; yeast); mRNA (cDNA clone MGC:128086 IMAGE:7988977); complete cds	BC105391	ELOVL5	ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)
CfaAffx.4290.1.S1_s_at	5.85E-02	5.56E-02	0.74	Pongo abelii mRNA; cDNA DKFZp469M0522 (from clone DKFZp469M0522)	CR857140	ELOVL5	ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)
Cfa.10492.1.A1_at	3.35E-03	1.56E-02	0.75	PREDICTED: Canis familiaris similar to elongator protein 2 (LOC480158); mRNA	XM_537281	ELP2	elongation protein 2 homolog (S. cerevisiae)
CfaAffx.22271.1.S1_s_at	8.63E-04	1.13E-02	0.7	PREDICTED: Canis familiaris similar to Probable ribosome biogenesis protein NEP1 (C2f protein); transcript variant 2 (LOC477708); mRNA	XM_848280	EMG1	EMG1 nucleolar protein homolog (S. cerevisiae)
CfaAffx.3948.1.S1_at	1.60E-02	2.84E-02	0.77	PREDICTED: Canis familiaris similar to ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function) (LOC481824); mRNA	XM_538945	ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function)
CfaAffx.31149.1.S1_at	3.65E-04	9.61E-03	0.73	PREDICTED: Mus musculus similar to nuclear transport factor 2 (LOC100043462); mRNA	XM_001480585	ENSMUSG00000071497	predicted gene, ENSMUSG00000071497
Cfa.4059.1.A1_at	9.53E-02	7.38E-02	1.42	PREDICTED: Canis familiaris similar to Mammalian ependymin related protein-1 precursor (MERP-1) (UCC1 protein) (LOC609403); mRNA	XM_846651	EPDR1	ependymin related protein 1 (zebrafish)
Cfa.222.1.S1_s_at	1.77E-04	9.00E-03	0.72	PREDICTED: Canis familiaris similar to glutamyl-prolyl tRNA synthetase; transcript variant 2 (LOC478962); mRNA	XM_844375	EPRS	glutamyl-prolyl-tRNA synthetase

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CfaAffx.12177.1.S1_s_at	2.01E-02	3.15E-02	0.77	PREDICTED: Canis familiaris similar to ERBB2 interacting protein isoform 7 (LOC478082); mRNA	XM_535260	ERBB2IP	erbb2 interacting protein
CfaAffx.12926.1.S1_s_at	3.88E-03	1.63E-02	0.75	PREDICTED: Canis familiaris similar to Serologically defined breast cancer antigen NY-BR-84; transcript variant 3 (LOC477212); mRNA	XM_859489	ERGIC3	ERGIC and golgi 3
Cfa.11513.2.A1_at	2.52E-04	9.06E-03	0.66	PREDICTED: Canis familiaris similar to Enhancer of rudimentary homolog (LOC480371); mRNA	XM_537493	ERH	enhancer of rudimentary homolog (Drosophila)
CfaAffx.25345.1.S1_s_at	1.17E-04	8.90E-03	0.71	PREDICTED: Canis familiaris similar to Enhancer of rudimentary homolog (LOC480371); mRNA	XM_537493	ERH	enhancer of rudimentary homolog (Drosophila)
Cfa.3168.1.A1_at	5.00E-03	1.76E-02	0.73	PREDICTED: Canis familiaris similar to endoplasmic reticulum protein 29 precursor (LOC477482); mRNA	XM_848584	ERP29	endoplasmic reticulum protein 29
CfaAffx.7652.1.S1_s_at	2.05E-03	1.35E-02	0.72	PREDICTED: Canis familiaris similar to esterase D/formylglutathione hydrolase; transcript variant 1 (LOC607116); mRNA	XM_843276	ESD	esterase D/formylglutathione hydrolase
CfaAffx.5785.1.S1_at	1.78E-03	1.30E-02	0.71	PREDICTED: Canis familiaris similar to ETAA16 protein (LOC474621); mRNA	XM_531851	ETAA1	Ewing tumor-associated antigen 1
Cfa.10372.1.S1_at	1.26E-03	1.23E-02	0.69	PREDICTED: Equus caballus eukaryotic translation termination factor 1 (ETF1); mRNA	XM_001502537	ETF1	eukaryotic translation termination factor 1
Cfa.15333.1.S1_s_at	8.20E-04	1.10E-02	0.7	PREDICTED: Canis familiaris similar to Electron transfer flavoprotein alpha-subunit; mitochondrial precursor (Alpha-ETF); transcript variant 1 (LOC610134); mRNA	XM_848294	ETFA	electron-transfer-flavoprotein, alpha polypeptide
Cfa.20483.1.S1_s_at	4.91E-03	1.75E-02	0.69	PREDICTED: Canis familiaris similar to Electron transfer flavoprotein alpha-subunit; mitochondrial precursor (Alpha-ETF); transcript variant 2 (LOC610134); mRNA	XM_862172	ETFA	electron-transfer-flavoprotein, alpha polypeptide
Cfa.6564.1.S1_s_at	1.12E-03	1.20E-02	0.71	PREDICTED: Canis familiaris similar to electron-transfer-flavoprotein; beta polypeptide isoform 1; transcript variant 1 (LOC476400); mRNA	XM_533603	ETFB	electron-transfer-flavoprotein, beta polypeptide

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Cfa.11262.1.A1_at	1.53E-02	2.76E-02	0.74	PREDICTED: Canis familiaris similar to Electron transfer flavoprotein-ubiquinone oxidoreductase; mitochondrial precursor (ETF-QO) (ETF-ubiquinone oxidoreductase) (ETF dehydrogenase) (Electron-transferring-flavoprotein dehydrogenase); transcript variant 1 (LOC475480); mRNA	XM_532703	ETFDH	electron-transferring-flavoprotein dehydrogenase
CfaAffx.18327.1.S1_at	3.70E-03	1.61E-02	0.75	PREDICTED: Canis familiaris similar to exocyst complex 84-kDa subunit (LOC488973); mRNA	XM_546091	EXOC8	exocyst complex component 8
Cfa.2745.1.A1_s_at	5.98E-03	1.87E-02	0.74	PREDICTED: Canis familiaris similar to Exosome complex exonuclease RRP42 (Ribosomal RNA processing protein 42) (Exosome component 7) (p8); transcript variant 1 (LOC476654); mRNA	XM_533858	EXOSC7	exosome component 7
Cfa.19340.1.S1_s_at	4.18E-03	1.67E-02	0.75	PREDICTED: Canis familiaris similar to Exosome complex exonuclease RRP43 (Ribosomal RNA processing protein 43) (Exosome component 8) (p9) (Opa-interacting protein 2); transcript variant 1 (LOC477300); mRNA	XM_534492	EXOSC8	exosome component 8
CfaAffx.10167.1.S1_at	1.25E-03	1.23E-02	0.7	PREDICTED: Canis familiaris similar to Exosome complex exonuclease RRP43 (Ribosomal RNA processing protein 43) (Exosome component 8) (p9) (Opa-interacting protein 2); transcript variant 1 (LOC477300); mRNA	XM_534492	EXOSC8	exosome component 8
Cfa.11712.1.A1_at	2.53E-02	3.52E-02	0.76	PREDICTED: Canis familiaris similar to Exostosin-1 (Glucuronosyl-N-acetylglucosaminyl-proteoglycan/N-acetylglucosaminyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase) (Putative tumor suppressor protein EXT1) (Multiple exostoses protein 1); transcript variant 2 (LOC482024); mRNA	XM_856004	EXT1	exostoses (multiple) 1

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Cfa.19919.1.S1_at	4.68E-02	4.91E-02	0.74	familiaris similar to Exostosin-like 2 (Glucuronyl-galactosyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase) (Alpha-1;4-N-acetylhexosaminyltransferase EXTL2) (Alpha-GalNAcT EXTL2) (EXT-related protein 2) (LOC479925); mRNA	XM_537051	EXTL2	exostoses (multiple)-like 2
CfaAffx.1916.1.S1_at	3.45E-02	4.16E-02	0.75	PREDICTED: Canis familiaris similar to Ezrin (p81) (Cytovillin) (Villin-2); transcript variant 5 (LOC484056); mRNA	XM_857339	EZR	ezrin
Cfa.15480.2.A1_s_at	8.70E-03	2.17E-02	1.4	Sus scrofa prothrombin mRNA; complete cds	EF692642	F2	coagulation factor II
CfaAffx.11994.1.S1_at	9.05E-03	2.21E-02	1.47	PREDICTED: Canis familiaris fatty acid binding protein (FABP); mRNA	XM_532966	FABP1	fatty acid binding protein 1, liver
CfaAffx.109.1.S1_s_at	5.45E-02	5.34E-02	0.75	PREDICTED: Canis familiaris similar to Fatty acid-binding protein; epidermal (E-FABP) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP) (LOC477923); mRNA	XM_535112	FABP5L2	fatty acid binding protein 5-like 2
CfaAffx.12220.1.S1_at	3.12E-02	3.93E-02	0.75	PREDICTED: Canis familiaris similar to Fas apoptotic inhibitory molecule 1 (rFAIM) (LOC485687); mRNA	XM_542807	FAIM	Fas apoptotic inhibitory molecule
Cfa.2943.1.A1_at	1.02E-02	2.32E-02	0.74	Bos taurus family with sequence similarity 122B; mRNA (cDNA clone MGC:155300 IMAGE:8504472); complete cds	BC133383	FAM122B	family with sequence similarity 122B
CfaAffx.18805.1.S1_s_at	1.28E-02	2.56E-02	0.76	Pongo abelii mRNA; cDNA DKFZp459C1125 (from clone DKFZp459C1125)	CR859515	FAM126B	family with sequence similarity 126, member B
Cfa.1879.1.S1_s_at	2.30E-03	1.39E-02	0.72	PREDICTED: Canis familiaris similar to male sterility domain containing 2; transcript variant 1 (LOC476863); mRNA	XM_534066	FAR1	fatty acyl CoA reductase 1
Cfa.4911.1.A1_at	4.87E-04	1.00E-02	0.76	PREDICTED: Canis familiaris similar to Phenylalanyl-tRNA synthetase beta chain (Phenylalanine--tRNA ligase beta chain) (PheRS); transcript variant 3 (LOC478926); mRNA	XM_858952	FARSB	phenylalanyl-tRNA synthetase, beta subunit
Cfa.8841.1.A1_s_at	6.91E-03	1.97E-02	0.75	PREDICTED: Canis familiaris similar to fibrillarin (LOC476460); mRNA	XM_533671	FBL	fibrillarin

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Cfa.18553.1.S1_s_at	4.13E-03	1.67E-02	0.75	PREDICTED: Canis familiaris similar to F-box and leucine-rich repeat protein 5 isoform 1 (LOC479085); mRNA	XM_536232	FBXL5	F-box and leucine-rich repeat protein 5
CfaAffx.23557.1.S1_s_at	2.40E-03	1.40E-02	0.75	PREDICTED: Canis familiaris similar to F-box and leucine-rich repeat protein 5 isoform 1 (LOC479085); mRNA	XM_536232	FBXL5	F-box and leucine-rich repeat protein 5
CfaAffx.25379.1.S1_at	5.59E-02	5.42E-02	1.4	PREDICTED: Canis familiaris similar to F-box only protein 2 (LOC478231); mRNA	XM_535406	FBXO2	F-box protein 2
Cfa.5036.1.A1_s_at	2.32E-04	9.06E-03	0.75	PREDICTED: Canis familiaris similar to F-box only protein 22 isoform a (LOC487672); mRNA	XM_544796	FBXO22	F-box protein 22
Cfa.19659.1.A1_at	1.69E-02	2.91E-02	0.75	PREDICTED: Pan troglodytes hypothetical protein LOC735792 (LOC735792); mRNA	XM_001135277	FBXO28	F-box protein 28
Cfa.19071.1.S1_s_at	2.23E-02	3.31E-02	0.76	PREDICTED: Canis familiaris similar to F-box only protein 4 isoform 1 (LOC489220); mRNA	XM_546338	FBXO4	F-box protein 4
Cfa.173.1.A1_s_at	9.18E-03	2.22E-02	0.77	PREDICTED: Canis familiaris high affinity IgG Fc gamma receptor 1 (FCGAMMARI); mRNA	XM_850458	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)
Cfa.2873.1.A1_at	5.75E-04	1.03E-02	0.76	Homo sapiens KIAA0396 mRNA; partial cds	AB007856	FEM1B	fem-1 homolog b (C. elegans)
Cfa.1780.1.S1_at	6.67E-03	1.95E-02	0.73	PREDICTED: Canis familiaris similar to flap structure-specific endonuclease 1; transcript variant 1 (LOC476063); mRNA	XM_533271	FEN1	flap structure-specific endonuclease 1
Cfa.7269.1.A1_a_at	2.71E-02	3.65E-02	0.77	PREDICTED: Canis familiaris similar to fasciculation and elongation protein zeta 2 (zygin II); transcript variant 3 (LOC483031); mRNA	XM_858068	FEZ2	fasciculation and elongation protein zeta 2 (zygin II)
Cfa.11696.1.A1_s_at	3.53E-03	1.59E-02	0.75	PREDICTED: Canis familiaris similar to Fumarate hydratase; mitochondrial precursor (Fumarase); transcript variant 3 (LOC480092); mRNA	XM_857911	FH	fumarate hydratase
CfaAffx.24074.1.S1_at	2.68E-04	9.11E-03	0.72	PREDICTED: Canis familiaris similar to Fumarate hydratase; mitochondrial precursor (Fumarase); transcript variant 3 (LOC480092); mRNA	XM_857911	FH	fumarate hydratase

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Cfa.4181.1.A1_s_at	7.33E-04	1.08E-02	0.75	PREDICTED: Canis familiaris similar to FK506-binding protein 2 precursor (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (13 kDa FKBP) (FKBP-13); transcript variant 2 (LOC483764); mRNA	XM_848202	FKBP2	FK506 binding protein 2, 13kDa
Cfa.4497.1.S1_at	8.58E-02	6.93E-02	1.31	PREDICTED: Canis familiaris similar to FK506-binding protein 8 (LOC484819); mRNA	XM_541935	FKBP8	FK506 binding protein 8, 38kDa
CfaAffx.22733.1.S1_s_at	7.05E-02	6.18E-02	1.42	PREDICTED: Canis familiaris similar to FK506-binding protein 8 (LOC484819); mRNA	XM_541935	FKBP8	FK506 binding protein 8, 38kDa
CfaAffx.1629.1.S1_s_at	1.28E-02	2.55E-02	0.77	PREDICTED: Canis familiaris similar to Flotillin-1; transcript variant 6 (LOC474831); mRNA	XM_852118	FLOT1	flotillin 1
CfaAffx.9682.1.S1_s_at	8.81E-05	8.90E-03	1.32	PREDICTED: Canis familiaris similar to formin-like 2 isoform B (LOC476151); mRNA	XM_533358	FMNL2	formin-like 2
CfaAffx.20168.1.S1_s_at	6.95E-02	6.13E-02	1.33	PREDICTED: Canis familiaris similar to fructosamine 3 kinase (LOC608337); mRNA	XM_845329	FN3K	fructosamine 3 kinase
CfaAffx.13224.1.S1_at	7.10E-05	8.52E-03	1.34	PREDICTED: Canis familiaris similar to formin binding protein 4 (LOC483619); mRNA	XM_540739	FNBP4	formin binding protein 4
CfaAffx.9617.1.S1_s_at	5.31E-02	5.28E-02	0.77	PREDICTED: Canis familiaris similar to Folate receptor beta precursor (FR-beta) (Folate receptor 2) (Folate receptor; fetal/placental) (Placental folate-binding protein) (FBP) (LOC476816); mRNA	XM_534020	FOLR2	folate receptor 2 (fetal)
CfaAffx.11576.1.S1_at	2.55E-03	1.44E-02	0.76	PREDICTED: Canis familiaris similar to FRG1 protein (FSHD region gene 1 protein) (LOC482899); mRNA	XM_540014	FRG1	FSHD region gene 1
Cfa.14681.1.A1_s_at	2.80E-04	9.14E-03	1.36	PREDICTED: Canis familiaris similar to fibronectin type III and SPRY domain containing 1; transcript variant 2 (LOC476743); mRNA	XM_533948	FSD1	fibronectin type III and SPRY domain containing 1
CfaAffx.31175.1.S1_at	3.33E-03	1.55E-02	1.6	PREDICTED: Canis familiaris similar to Far upstream element binding protein 1 (FUSE binding protein 1) (FBP) (DNA helicase V) (HDH V); transcript variant 6 (LOC490201); mRNA	XM_862632	FUBP1	far upstream element (FUSE) binding protein 1

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.31174.1.S1_at	3.72E-02	4.33E-02	0.76	familiaris similar to Far upstream element binding protein 1 (FUSE binding protein 1) (FBP) (DNA helicase V) (HDH V); transcript variant 20 (LOC490201); mRNA	XM_862753	FUBP1	far upstream element (FUSE) binding protein 1
Cfa.19777.1.S1_s_at	1.69E-03	1.29E-02	0.72	PREDICTED: Canis familiaris similar to fragile X mental retardation-related protein 1 isoform b; transcript variant 12 (LOC478642); mRNA	XM_851395	FXR1	fragile X mental retardation, autosomal homolog 1
CfaAffx.27301.1.S1_s_at	1.36E-04	8.90E-03	0.76	PREDICTED: Canis familiaris similar to Ras-GTPase-activating protein binding protein 1 (GAP SH3-domain binding protein 1) (G3BP-1) (DNA helicase VIII) (HDH-VIII); transcript variant 3 (LOC479322); mRNA	XM_862269	G3BP1	GTPase activating protein (SH3 domain) binding protein 1
CfaAffx.13299.1.S1_s_at	4.61E-03	1.72E-02	0.77	PREDICTED: Canis familiaris similar to Ras-GTPase activating protein SH3 domain-binding protein 2 isoform a; transcript variant 7 (LOC478429); mRNA	XM_851019	G3BP2	GTPase activating protein (SH3 domain) binding protein 2
Cfa.20087.1.S1_s_at	2.07E-02	3.19E-02	0.76	PREDICTED: Canis familiaris similar to polypeptide N-acetylgalactosaminyltransferase 3; transcript variant 1 (LOC478774); mRNA	XM_535940	GALNT3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc T3)
CfaAffx.17476.1.S1_at	3.84E-02	4.41E-02	0.73	PREDICTED: Canis familiaris similar to polypeptide N-acetylgalactosaminyltransferase 3; transcript variant 2 (LOC478774); mRNA	XM_853627	GALNT3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc T3)
CfaAffx.30916.1.S1_at	7.42E-03	2.02E-02	0.68	PREDICTED: Canis familiaris similar to GTPase activating protein and VPS9 domains 1; transcript variant 3 (LOC480725); mRNA	XM_858142	GAPVD1	GTPase activating protein and VPS9 domains 1
Cfa.3929.1.A1_a_at	9.85E-04	1.16E-02	0.74	PREDICTED: Canis familiaris similar to Glycyl-tRNA synthetase (Glycine-tRNA ligase) (GlyRS) (LOC475268); mRNA	XM_532502	GARS	glycyl-tRNA synthetase

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Cfa.3954.1.S1_at	3.13E-03	1.53E-02	0.74	familiaris similar to NipSnap2 protein (Glioblastoma amplified sequence); transcript variant 1 (LOC479700); mRNA	XM_536828	GBAS	glioblastoma amplified sequence
CfaAffx.30939.1.S1_at	9.04E-02	7.15E-02	0.67	PREDICTED: Canis familiaris similar to guanylate nucleotide binding protein 4 (LOC490169); mRNA	XM_547290	GBP6	guanylate binding protein family, member 6
Cfa.19511.1.A1_at	6.37E-04	1.05E-02	0.7	familiaris similar to ganglioside induced differentiation associated protein 2; transcript variant 1 (LOC475812); mRNA	XM_533021	GDAP2	ganglioside induced differentiation associated protein 2
CfaAffx.15531.1.S1_at	1.00E-03	1.17E-02	0.67	familiaris similar to ganglioside induced differentiation associated protein 2; transcript variant 1 (LOC475812); mRNA	XM_533021	GDAP2	ganglioside induced differentiation associated protein 2
Cfa.5628.1.A1_at	1.02E-02	2.32E-02	1.47	familiaris similar to growth differentiation factor 3 precursor (LOC477702); mRNA	XM_534896	GDF3	growth differentiation factor 3
Cfa.7399.1.A1_a_at	8.68E-04	1.13E-02	0.72	PREDICTED: Canis familiaris similar to glucosamine-fructose-6-phosphate aminotransferase (LOC474624); mRNA	XM_531854	GFPT1	glutamine-fructose-6-phosphate transaminase 1
Cfa.7399.2.A1_a_at	7.83E-03	2.07E-02	0.73	PREDICTED: Canis familiaris similar to glucosamine-fructose-6-phosphate aminotransferase (LOC474624); mRNA	XM_531854	GFPT1	glutamine-fructose-6-phosphate transaminase 1
CfaAffx.13567.1.S1_s_at	1.57E-02	2.80E-02	0.77	PREDICTED: Canis familiaris similar to geranylgeranyl diphosphate synthase 1 (LOC479198); mRNA	XM_536340	GGPS1	geranylgeranyl diphosphate synthase 1
Cfa.1271.1.S1_at	1.29E-04	8.90E-03	0.75	PREDICTED: Canis familiaris similar to Growth hormone inducible transmembrane protein (Dermal papilla derived protein 2); transcript variant 3 (LOC479266); mRNA	XM_846854	GHITM	growth hormone inducible transmembrane protein
CfaAffx.9546.1.S1_at	1.18E-02	2.46E-02	0.76	PREDICTED: Canis familiaris similar to SLD5 (LOC482843); mRNA	XM_539958	GINS4	GINS complex subunit 4 (Sld5 homolog)

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Cfa.1560.3.A1_s_at	2.26E-02	3.33E-02	0.68	familiaris similar to G protein-coupled receptor kinase-interactor 2 isoform 1; transcript variant 1 (LOC477520); mRNA	XM_534715	GIT2	G protein-coupled receptor kinase interactor 2
Cfa.1560.3.A1_at	1.34E-02	2.61E-02	0.71	familiaris similar to G protein-coupled receptor kinase-interactor 2 isoform 1; transcript variant 10 (LOC477520); mRNA	XM_858931	GIT2	G protein-coupled receptor kinase interactor 2
Cfa.12018.1.A1_at	5.96E-02	5.62E-02	0.76	familiaris similar to glycerol kinase isoform 2; transcript variant 2 (LOC480872); mRNA	XM_844916	GK	glycerol kinase
Cfa.11691.1.A1_at	7.60E-02	6.44E-02	1.37	familiaris similar to glucocorticoid induced transcript 1 (LOC612938); mRNA	XM_847809	GLCCI1	glucocorticoid induced transcript 1
Cfa.1970.1.S1_at	1.85E-02	3.04E-02	0.76	PREDICTED: Pan troglodytes D-glucuronyl C5-epimerase; transcript variant 1 (GLCE); mRNA	XM_001174876	GLCE	glucuronic acid epimerase
CfaAffx.4299.1.S1_s_at	5.02E-02	5.11E-02	0.75	familiaris similar to chromosome 9 open reading frame 19 (LOC611995); mRNA	XM_849719	GLIPR2	GLI pathogenesis-related 2
CfaAffx.3130.1.S1_s_at	9.46E-05	8.90E-03	0.7	PREDICTED: Canis familiaris similar to glyoxylase 1 (LOC474894); mRNA	XM_532129	GLO1	glyoxalase I
CfaAffx.29198.1.S1_s_at	2.40E-02	3.43E-02	0.75	familiaris similar to CG1532-PA; transcript variant 1 (LOC480640); mRNA	XM_537759	GLOD4	glyoxalase domain containing 4
Cfa.325.1.A1_s_at	5.11E-04	1.00E-02	0.7	familiaris similar to glutaredoxin 2 isoform 1 (LOC478956); mRNA	XM_536114	GLRX2	glutaredoxin 2
Cfa.9878.1.S1_at	2.78E-03	1.48E-02	0.77	PREDICTED: Canis familiaris similar to Thioredoxin-like 2 protein (PKC-interacting cousin of thioredoxin) (PKCq-interacting protein) (PKC-theta-interacting protein) (LOC477869); mRNA	XM_535061	GLRX3	glutaredoxin 3
Cfa.1020.1.A1_at	1.69E-03	1.29E-02	0.66	PREDICTED: Canis familiaris similar to germ cell-less protein; transcript variant 1 (LOC481414); mRNA	XM_538534	GMCL1	germ cell-less homolog 1 (Drosophila)
Cfa.1740.1.S1_at	5.64E-04	1.03E-02	0.71	Pongo abelii mRNA; cDNA DKFZp459J101 (from clone DKFZp459J101)	CR860440	GMFB	glia maturation factor, beta

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Cfa.19948.1.S1_s_at	1.63E-03	1.28E-02	0.71	PREDICTED: Canis familiaris similar to Guanine nucleotide-binding protein G(k); alpha subunit (G(i) alpha-3) (LOC611810); mRNA	XM_849521	GNAI3	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3
CfaAffx.30335.1.S1_at	1.16E-02	2.44E-02	0.77	PREDICTED: Canis familiaris similar to Guanine nucleotide-binding protein G(k); alpha subunit (G(i) alpha-3) (LOC611810); mRNA	XM_849521	GNAI3	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3
Cfa.1666.1.S1_at	2.86E-02	3.75E-02	0.74	PREDICTED: Canis familiaris similar to glucosamine-phosphate N-acetyltransferase 1 (LOC480325); mRNA	XM_537448	GNPNAT1	glucosamine-phosphate N-acetyltransferase 1
CfaAffx.17247.1.S1_at	1.59E-03	1.26E-02	0.75	familiaris similar to Golgi autoantigen; golgin subfamily A member 5 (Golgin-84) (RET-fused gene 5 protein) (Ret-II protein) (LOC480233); mRNA	XM_537356	GOLGA5	golgi autoantigen, golgin subfamily a, 5
Cfa.1625.1.A1_at	1.15E-02	2.43E-02	0.74	PREDICTED: Canis familiaris similar to Golgi phosphoprotein 3 (Coat-protein GPP34) (Trans-Golgi protein GMx33) (LOC489241); mRNA	XM_546359	GOLPH3	golgi phosphoprotein 3 (coat-protein)
CfaAffx.29053.1.S1_at	3.11E-02	3.93E-02	0.72	PREDICTED: Canis familiaris similar to golgi SNAP receptor complex member 1 isoform 2 (LOC491185); mRNA	XM_548305	GOSR1	golgi SNAP receptor complex member 1
CfaAffx.29053.1.S1_s_at	4.90E-04	1.00E-02	0.73	PREDICTED: Canis familiaris similar to golgi SNAP receptor complex member 1 isoform 2 (LOC491185); mRNA	XM_548305	GOSR1	golgi SNAP receptor complex member 1
Cfa.761.1.A1_at	9.14E-03	2.22E-02	0.77	PREDICTED: Macaca mulatta glycerol-3-phosphate dehydrogenase 2 (mitochondrial); transcript variant 1 (GPD2); mRNA	XM_001086842	GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)

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Cfa.12478.1.S1_at	3.10E-03	1.53E-02	0.65	PREDICTED: Canis familiaris similar to putative NFkB activating protein 373 isoform 1; transcript variant 3 (LOC611491); mRNA	XM_862872	GPR177	G protein-coupled receptor 177
CfaAffx.26530.1.S1_at	1.99E-02	3.14E-02	0.73	PREDICTED: Canis familiaris similar to G protein-coupled receptor 65 (LOC490821); mRNA	XM_547943	GPR65	G protein-coupled receptor 65
Cfa.3254.1.S1_at	5.15E-04	1.01E-02	1.38	Mus musculus glutamate receptor; ionotropic; NMDA2B (epsilon 2) (Grin2b); mRNA	NM_008171	Grin2b	glutamate receptor, ionotropic, NMDA2B (epsilon 2)
Cfa.1176.1.S1_at	7.40E-03	2.02E-02	0.75	PREDICTED: Canis familiaris similar to G-rich RNA sequence binding factor 1 (LOC475170); mRNA	XM_532402	GRSF1	G-rich RNA sequence binding factor 1
Cfa.20162.1.S1_s_at	4.43E-04	9.78E-03	0.76	PREDICTED: Canis familiaris similar to G1 to S phase transition protein 1 homolog (GTP-binding protein GST1-HS); transcript variant 2 (LOC479846); mRNA	XM_858262	GSPT1	G1 to S phase transition 1
Cfa.5851.1.A1_a_at	1.01E-02	2.31E-02	0.77	PREDICTED: Canis familiaris similar to peptide chain release factor 3; transcript variant 1 (LOC480921); mRNA	XM_538042	GSPT2	G1 to S phase transition 2
CfaAffx.16567.1.S1_s_at	2.25E-03	1.38E-02	0.72	PREDICTED: Canis familiaris similar to glutathione-S-transferase omega 1; transcript variant 1 (LOC477813); mRNA	XM_535007	GSTO1	glutathione S-transferase omega 1
CfaAffx.10698.1.S1_s_at	2.99E-03	1.51E-02	0.76	PREDICTED: Canis familiaris similar to Transcription initiation factor IIE beta subunit (TFIIE-beta) (LOC475597); mRNA	XM_532814	GTF2E2	general transcription factor IIE, polypeptide 2, beta 34kDa
CfaAffx.6808.1.S1_at	2.80E-04	9.14E-03	0.72	PREDICTED: Canis familiaris hypothetical LOC481961 (LOC481961); mRNA	XM_539082	GTF3C6	general transcription factor IIIC, polypeptide 6, alpha 35kDa

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

				PREDICTED: Canis familiaris similar to Trifunctional enzyme beta subunit; mitochondrial precursor (TP-beta); transcript variant 4 (LOC607926); mRNA			hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit
CfaAffx.7396.1.S1_at	1.28E-03	1.23E-02	0.76		XM_854527	HADHB	
Cfa.10971.1.S1_at	4.27E-03	1.68E-02	0.7	PREDICTED: Canis familiaris similar to hepatitis B virus x-interacting protein (LOC479907); mRNA	XM_537033	HBXIP	hepatitis B virus x interacting protein
CfaAffx.30266.1.S1_s_at	5.69E-04	1.03E-02	0.73	PREDICTED: Canis familiaris similar to hepatitis B virus x-interacting protein (LOC479907); mRNA	XM_537033	HBXIP	hepatitis B virus x interacting protein
CfaAffx.332.1.S1_at	3.83E-02	4.39E-02	0.76	PREDICTED: Canis familiaris similar to HMBA-inducible (LOC606811); mRNA	XM_843229	HEXIM1	hexamethylene bis-acetamide inducible 1
Cfa.126.1.S1_s_at	9.55E-05	8.90E-03	0.65	Canis familiaris hypoxia-inducible factor 1 alpha subunit mRNA; partial cds	AY455802	HIF1A	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
CfaAffx.24079.1.S1_s_at	4.71E-03	1.73E-02	0.73	PREDICTED: Canis familiaris hypoxia-inducible factor 1; alpha subunit; transcript variant 10 (HIF1A); mRNA	XM_860420	HIF1A	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
Cfa.10927.1.A1_s_at	2.53E-03	1.43E-02	0.71	PREDICTED: Canis familiaris similar to histidine triad nucleotide binding protein 1 (LOC474667); mRNA	XM_531895	HINT1	histidine triad nucleotide binding protein 1

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Cfa.17194.1.S1_s_at	5.38E-04	1.02E-02	0.77	PREDICTED: Canis familiaris similar to Homeodomain-interacting protein kinase 3 (Homolog of protein kinase YAK1) (Fas-interacting serine/threonine-protein kinase) (FIST) (Androgen receptor-interacting nuclear protein kinase) (ANPK); transcript variant 1 (LOC475947); mRNA	XM_533158	HIPK3	homeodomain interacting protein kinase 3
Cfa.18297.1.S1_at	6.99E-02	6.15E-02	0.72	Canis lupus familiaris major histocompatibility complex; class II; DM alpha (HLA-DMA); mRNA	NM_001048099	HLA-DMA	major histocompatibility complex, class II, DM alpha
Cfa.11398.1.A1_at	7.06E-04	1.08E-02	0.74	PREDICTED: Canis familiaris similar to Hydroxymethylglutaryl-CoA synthase; cytoplasmic (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase) (LOC479344); mRNA	XM_536483	HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)
CfaAffx.5250.1.S1_s_at	1.82E-03	1.31E-02	0.75	[illegible] familiaris similar to heterogeneous nuclear ribonucleoprotein A2/B1 isoform 2; transcript variant 1 (LOC475260); mRNA	XM_532495	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1
Cfa.10247.1.S1_at	6.64E-02	5.97E-02	0.74	[illegible] familiaris similar to heterogeneous nuclear ribonucleoprotein A2/B1 isoform 2; transcript variant 6 (LOC475260); mRNA	XM_858843	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1
Cfa.717.1.A1_s_at	3.94E-03	1.64E-02	0.68	[illegible] familiaris similar to heterogeneous nuclear ribonucleoprotein A3; transcript variant 11 (LOC608074); mRNA	XM_856952	HNRNPA3	heterogeneous nuclear ribonucleoprotein A3
Cfa.4338.1.S1_at	5.71E-03	1.84E-02	0.74	[illegible] familiaris similar to heterogeneous nuclear ribonucleoprotein A3; transcript variant 13 (LOC608074); mRNA	XM_857010	HNRNPA3	heterogeneous nuclear ribonucleoprotein A3
Cfa.15024.1.S1_at	6.85E-03	1.97E-02	0.76	[illegible] familiaris similar to heterogeneous nuclear ribonucleoprotein C isoform b; transcript variant 25 (LOC475399); mRNA	XM_858823	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)
Cfa.15024.2.S1_s_at	2.03E-02	3.16E-02	0.73	familiaris similar to heterogeneous nuclear ribonucleoprotein C isoform b; transcript variant 25 (LOC475399); mRNA	XM_858823	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)

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CfaAffx.14121.1.S1_s_at	1.16E-02	2.44E-02	0.73	Homo sapiens cDNA FLJ54150 complete cds; highly similar to Heterogeneous nuclear ribonucleoprotein D0	AK300149	HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)
Cfa.7431.2.A1_a_at	1.14E-02	2.42E-02	0.74	PREDICTED: Canis familiaris similar to heterogeneous nuclear ribonucleoprotein D isoform c; transcript variant 11 (LOC478450); mRNA	XM_852864	HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)
CfaAffx.1450.1.S1_s_at	2.12E-02	3.23E-02	0.75	PREDICTED: Canis familiaris similar to Heterogeneous nuclear ribonucleoprotein H (hnRNP H); transcript variant 14 (LOC481455); mRNA	XM_851737	HNRNPH1	heterogeneous nuclear ribonucleoprotein H1 (H)
Cfa.17447.1.S1_s_at	1.90E-03	1.32E-02	0.72	PREDICTED: Canis familiaris similar to Heterogeneous nuclear ribonucleoprotein H (hnRNP H) (FTP-3); transcript variant 2 (LOC480989); mRNA	XM_845526	HNRNPH2	heterogeneous nuclear ribonucleoprotein H2 (H')
CfaAffx.27083.1.S1_at	2.17E-03	1.37E-02	0.69	PREDICTED: Canis familiaris similar to Heterogeneous nuclear ribonucleoprotein H (hnRNP H) (FTP-3); transcript variant 6 (LOC480989); mRNA	XM_856931	HNRNPH2	heterogeneous nuclear ribonucleoprotein H2 (H')
Cfa.18334.1.S1_s_at	1.28E-02	2.55E-02	0.77	PREDICTED: Canis familiaris similar to heterogeneous nuclear ribonucleoprotein H3 isoform a; transcript variant 2 (LOC479227); mRNA	XM_844897	HNRNPH3	heterogeneous nuclear ribonucleoprotein H3 (2H9)
CfaAffx.14135.1.S1_s_at	1.15E-02	2.42E-02	0.75	PREDICTED: Canis familiaris similar to heterogeneous nuclear ribonucleoprotein D-like; transcript variant 10 (LOC476976); mRNA	XM_853232	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like
CfaAffx.10319.1.S1_s_at	1.38E-02	2.65E-02	0.73	PREDICTED: Canis familiaris similar to heterogeneous nuclear ribonucleoprotein L-like (LOC475729); mRNA	XM_532938	HNRPLL	heterogeneous nuclear ribonucleoprotein L-like
Cfa.11277.1.A1_at	1.39E-03	1.24E-02	0.68	PREDICTED: Canis familiaris similar to Ribonuclease UK114 (14.5 kDa translational inhibitor protein) (p14.5) (UK114 antigen homolog); transcript variant 1 (LOC475043); mRNA	XM_532278	HRSP12	heat-responsive protein 12

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Cfa.4491.1.S1_at	1.84E-03	1.31E-02	0.76	PREDICTED: Canis familiaris similar to 3-hydroxyacyl-CoA dehydrogenase type II (Type II HADH) (Endoplasmic reticulum-associated amyloid beta-peptide binding protein) (Short-chain type dehydrogenase/reductase XH98G2); transcript variant 1 (LOC480930); mRNA	XM_538051	HSD17B10	hydroxysteroid (17-beta) dehydrogenase 10
CfaAffx.24950.1.S1_s_at	2.07E-03	1.35E-02	0.71	PREDICTED: Canis familiaris similar to 3-hydroxyacyl-CoA dehydrogenase type II (Type II HADH) (Endoplasmic reticulum-associated amyloid beta-peptide binding protein) (Short-chain type dehydrogenase/reductase XH98G2); transcript variant 1 (LOC480930); mRNA	XM_538051	HSD17B10	hydroxysteroid (17-beta) dehydrogenase 10
Cfa.441.1.A1_at	3.68E-03	1.61E-02	0.77	PREDICTED: Canis familiaris similar to steroid dehydrogenase homolog; transcript variant 1 (LOC475939); mRNA	XM_533148	HSD17B12	hydroxysteroid (17-beta) dehydrogenase 12
Cfa.10807.1.S1_at	1.70E-02	2.91E-02	0.77	PREDICTED: Canis familiaris similar to hydroxysteroid dehydrogenase like 2; transcript variant 2 (LOC474804); mRNA	XM_848518	HSDL2	hydroxysteroid dehydrogenase like 2
CfaAffx.12023.1.S1_at	1.24E-02	2.52E-02	0.72	Canis familiaris GRP94 mRNA; complete cds	U01153	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1
Cfa.9260.1.S1_at	2.29E-03	1.39E-02	0.77	PREDICTED: Canis familiaris similar to 60 kDa heat shock protein; mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein) (HuCHA60); transcript variant 1 (LOC478854); mRNA	XM_536016	HSPD1	heat shock 60kDa protein 1 (chaperonin)

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CfaAffx.16986.1.S1_s_at	2.83E-03	1.48E-02	0.7	PREDICTED: Canis familiaris similar to 60 kDa heat shock protein; mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein) (HuCHA60); transcript variant 1 (LOC478854); mRNA	XM_536016	HSPD1	heat shock 60kDa protein 1 (chaperonin)
Cfa.2783.1.A1_at	5.27E-03	1.79E-02	0.73	PREDICTED: Canis familiaris similar to Heat-shock protein 105 kDa (Heat shock 110 kDa protein) (Antigen NY-CO-25) (LOC477322); mRNA	XM_534515	HSPH1	heat shock 105kDa/110kDa protein 1
Cfa.11015.1.A1_at	1.33E-03	1.23E-02	0.69	PREDICTED: Canis familiaris similar to HUS1 checkpoint protein (LOC606789); mRNA	XM_843198	HUS1	HUS1 checkpoint homolog (S. pombe)
CfaAffx.6003.1.S1_s_at	1.25E-02	2.53E-02	0.76	PREDICTED: Canis familiaris hypothetical protein LOC609656 (LOC609656); mRNA	XM_846956	IAH1	isoamyl acetate-hydrolyzing esterase 1 homolog (S. cerevisiae)
Cfa.278.2.S1_a_at	6.18E-03	1.89E-02	0.71	PREDICTED: Canis familiaris similar to isocitrate dehydrogenase 2 (NADP+); mitochondrial (LOC479043); mRNA	XM_536192	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial
CfaAffx.29440.1.S1_at	1.89E-02	3.06E-02	0.74	PREDICTED: Canis familiaris similar to Isocitrate dehydrogenase [NAD] subunit gamma; mitochondrial precursor (Isocitric dehydrogenase) (NAD(+)-specific ICDH); transcript variant 7 (LOC481081); mRNA	XM_862250	IDH3G	isocitrate dehydrogenase 3 (NAD+) gamma
Cfa.16440.1.S1_at	1.08E-02	2.37E-02	0.7	PREDICTED: Canis familiaris similar to Interferon-induced 35 kDa protein (IFP 35) (LOC490954); mRNA	XM_548077	IFI35	interferon-induced protein 35
Cfa.19476.1.S1_s_at	3.40E-03	1.57E-02	0.74	PREDICTED: Canis familiaris similar to interferon-alpha receptor 1 precursor (LOC609830); mRNA	XM_847173	IFNAR1	interferon (alpha, beta and omega) receptor 1
CfaAffx.5908.1.S1_at	2.62E-03	1.44E-02	0.64	PREDICTED: Canis familiaris similar to interferon-related developmental regulator 1; transcript variant 1 (LOC482408); mRNA	XM_539525	IFRD1	interferon-related developmental regulator 1

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.25616.1.S1_at	7.20E-03	2.00E-02	0.68	PREDICTED: Canis familiaris similar to Immunoglobulin-binding protein 1 (CD79a-binding protein 1) (B cell signal transduction molecule alpha 4) (Alpha 4 protein); transcript variant 1 (LOC480950); mRNA	XM_538070	IGBP1	immunoglobulin (CD79A) binding protein 1
CfaAffx.25616.1.S1_s_at	2.54E-03	1.44E-02	0.7	PREDICTED: Canis familiaris similar to Immunoglobulin-binding protein 1 (CD79a-binding protein 1) (B cell signal transduction molecule alpha 4) (Alpha 4 protein); transcript variant 1 (LOC480950); mRNA	XM_538070	IGBP1	immunoglobulin (CD79A) binding protein 1
Cfa.12360.1.A1_at	4.83E-03	1.75E-02	0.76	Homo sapiens inositol hexaphosphate kinase 2; mRNA (cDNA clone IMAGE:3533563)	BC001864	IHPK2	inositol hexaphosphate kinase 2
Cfa.4946.1.A1_s_at	8.62E-03	2.17E-02	0.73	Homo sapiens inositol hexakisphosphate kinase 2 (IP6K2); transcript variant 4; mRNA	NM_001005911	IHPK2	inositol hexaphosphate kinase 2
Cfa.10903.1.A1_s_at	2.29E-02	3.35E-02	0.72	PREDICTED: Canis familiaris similar to RED protein (LOC607109); mRNA	XM_843700	IK	IK cytokine, down-regulator of HLA II
Cfa.4778.1.A1_at	5.52E-03	1.82E-02	0.71	Canis familiaris interleukin 10 receptor beta mRNA; partial cds	DQ195086	IL10RB	interleukin 10 receptor, beta
Cfa.40.1.S1_s_at	8.27E-03	2.12E-02	0.75	Canis familiaris mRNA for interferon gamma inducing factor (IL-18)	Y11133	IL18	interleukin 18 (interferon-gamma-inducing factor)
Cfa.3180.1.S1_at	5.90E-02	5.59E-02	0.77	familiaris similar to Mitochondrial inner membrane protein (Mitofilin) (p87/89) (Proliferation-inducing gene 4 protein); transcript variant 1 (LOC475764); mRNA	XM_532974	IMMT	inner membrane protein, mitochondrial (mitofilin)
CfaAffx.12210.1.S1_s_at	8.91E-04	1.14E-02	0.72	familiaris similar to Mitochondrial inner membrane protein (Mitofilin) (p87/89) (Proliferation-inducing gene 4 protein); transcript variant 1 (LOC475764); mRNA	XM_532974	IMMT	inner membrane protein, mitochondrial (mitofilin)
Cfa.18298.1.S1_at	4.12E-02	4.57E-02	0.75	PREDICTED: Canis familiaris similar to CG1120-PA; transcript variant 1 (LOC475565); mRNA	XM_532785	INTS10	integrator complex subunit 10

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CfaAffx.14816.1.S1_s_at	2.59E-02	3.56E-02	0.75	Homo sapiens mRNA; cDNA DKFZp686P06215 (from clone DKFZp686P06215)	BX538203	INTS8	integrator complex subunit 8
Cfa.16494.1.S1_at	1.51E-03	1.25E-02	0.73	PREDICTED: Equus caballus iron-responsive element binding protein 2 (IREB2); mRNA	XM_001488966	IREB2	iron-responsive element binding protein 2
CfaAffx.2007.1.S1_s_at	3.25E-02	4.02E-02	0.75	Bos taurus isochorismatase domain containing 1; mRNA (cDNA clone MGC:148632 IMAGE:8271882); complete cds	BC148130	ISOC1	isochorismatase domain containing 1
CfaAffx.21882.1.S1_at	1.87E-03	1.32E-02	0.73	PREDICTED: Canis familiaris similar to Integrin alpha-4 precursor (Integrin alpha-IV) (VLA-4) (CD49d) (LOC488429); mRNA	XM_545551	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)
CfaAffx.5987.1.S1_s_at	1.24E-03	1.23E-02	0.77	familiaris similar to Integrin beta-1 binding protein 1 (Integrin cytoplasmic domain-associated protein 1) (ICAP-1) (LOC475660); mRNA	XM_532868	ITGB1BP1	integrin beta 1 binding protein 1
Cfa.6183.1.A1_at	1.90E-02	3.07E-02	1.43	PREDICTED: Canis familiaris similar to jagunal homolog 1 (LOC484661); mRNA	XM_541776	JAGN1	jagunal homolog 1 (Drosophila)
CfaAffx.12161.1.S1_s_at	4.34E-03	1.69E-02	0.74	PREDICTED: Canis familiaris similar to jumonji domain containing 1A; transcript variant 1 (LOC475763); mRNA	XM_532973	JMJD1A	jumonji domain containing 1A
Cfa.17114.1.S1_at	1.23E-02	2.51E-02	0.74	PREDICTED: Canis familiaris similar to phosphatidylserine receptor; transcript variant 2 (LOC483335); mRNA	XM_843987	JMJD6	jumonji domain containing 6
Cfa.511.1.S1_at	1.27E-02	2.54E-02	0.76	PREDICTED: Pan troglodytes kelch repeat and BTB (POZ) domain containing 7 (KBTBD7); mRNA	XM_522666	KBTBD7	kelch repeat and BTB (POZ) domain containing 7
CfaAffx.16854.1.S1_at	1.87E-04	9.00E-03	0.68	PREDICTED: Canis familiaris similar to KH domain containing; RNA binding; signal transduction associated 1; transcript variant 1 (LOC487316); mRNA	XM_544442	KHDRBS1	KH domain containing, RNA binding, signal transduction associated 1

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Cfa.9538.1.S1_at	2.06E-03	1.35E-02	0.67	PREDICTED: Pan troglodytes similar to KIAA0143 protein (KIAA0143); mRNA	XR_022810	KIAA0143	similar to KIAA0143 protein
Cfa.19624.1.S1_at	1.51E-02	2.75E-02	0.74	Homo sapiens KIAA0247; mRNA (cDNA clone MGC:71667 IMAGE:30344263); complete cds	BC064697	KIAA0247	KIAA0247
Cfa.1688.1.S1_at	7.07E-03	1.99E-02	0.75	Homo sapiens mRNA for KIAA1712 protein; partial cds	AB051499	KIAA1712	KIAA1712
Cfa.1938.1.A1_at	3.12E-02	3.93E-02	0.76	Homo sapiens kinase D-interacting substrate; 220kDa (KIDINS220); mRNA	NM_020738	KIDINS220	kinase D-interacting substrate of 220 kDa
CfaAffx.12118.1.S1_s_at	2.29E-02	3.35E-02	0.73	PREDICTED: Canis familiaris similar to kinesin family member 11 (LOC477769); mRNA	XM_534964	KIF11	kinesin family member 11
Cfa.922.1.A1_at	4.26E-03	1.68E-02	0.73	familiaris similar to Kinesin heavy chain (Ubiquitous kinesin heavy chain) (UKHC); transcript variant 6 (LOC477968); mRNA	XM_854433	KIF5B	kinesin family member 5B
CfaAffx.7041.1.S1_s_at	8.49E-05	8.80E-03	0.69	familiaris similar to Kinesin heavy chain (Ubiquitous kinesin heavy chain) (UKHC); transcript variant 6 (LOC477968); mRNA	XM_854433	KIF5B	kinesin family member 5B
CfaAffx.8480.1.S1_s_at	1.20E-02	2.47E-02	0.67	PREDICTED: Canis familiaris similar to HsKin17 protein; transcript variant 1 (LOC478010); mRNA	XM_535194	KIN	KIN, antigenic determinant of recA protein homolog (mouse)
Cfa.933.1.S1_s_at	2.25E-04	9.06E-03	0.67	PREDICTED: Canis familiaris similar to Kelch domain containing protein 2 (Hepatocellular carcinoma-associated antigen 33) (Host cell factor homolog LCP) (LOC480314); mRNA	XM_537436	KLHDC2	kelch domain containing 2
Cfa.15714.1.A1_at	5.21E-03	1.79E-02	0.75	familiaris similar to Plasma kallikrein precursor (Plasma prekallikrein) (Kininogenin) (Fletcher factor) (LOC475624); mRNA	XM_532838	KLKB1	kallikrein B, plasma (Fletcher factor) 1
Cfa.14036.1.A1_at	1.50E-02	2.74E-02	0.75	PREDICTED: Canis familiaris similar to kynurenine 3-monooxygenase (LOC480093); mRNA	XM_537216	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)

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Cfa.14036.1.A1_s_at	1.52E-02	2.76E-02	0.73	PREDICTED: Canis familiaris similar to kynurenine 3-monooxygenase (LOC480093); mRNA	XM_537216	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)
CfaAffx.375.1.S1_at	1.41E-03	1.24E-02	0.76	PREDICTED: Canis familiaris similar to Importin alpha-4 subunit (Karyopherin alpha-4 subunit) (Qip1 protein); transcript variant 2 (LOC478680); mRNA	XM_845438	KPNA4	karyopherin alpha 4 (importin alpha 3)
Cfa.5370.1.A1_s_at	3.60E-03	1.60E-02	0.71	PREDICTED: Canis familiaris similar to karyopherin beta 1; transcript variant 5 (LOC491042); mRNA	XM_859343	KPNB1	karyopherin (importin) beta 1
Cfa.16644.1.S1_at	1.19E-03	1.21E-02	0.72	Homo sapiens v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog (KRAS); transcript variant a; mRNA	NM_033360	KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
CfaAffx.24495.1.S1_s_at	8.16E-04	1.10E-02	1.36	PREDICTED: Canis familiaris similar to type I hair keratin KA27 (LOC490989); mRNA	XM_548112	KRT34	keratin 34
Cfa.9971.1.S1_at	1.24E-02	2.52E-02	0.71	PREDICTED: Canis familiaris similar to lactamase; beta 2; transcript variant 1 (LOC486990); mRNA	XM_544119	LACTB2	lactamase, beta 2
Cfa.9971.2.S1_s_at	4.87E-03	1.75E-02	0.64	PREDICTED: Canis familiaris similar to lactamase; beta 2; transcript variant 3 (LOC486990); mRNA	XM_854407	LACTB2	lactamase, beta 2
Cfa.2472.1.S1_at	1.05E-02	2.34E-02	0.76	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2); transcript variant B; mRNA	NM_013995	LAMP2	lysosomal-associated membrane protein 2
Cfa.10080.1.A1_at	2.57E-02	3.55E-02	0.75	familiaris similar to Lysosome-associated membrane glycoprotein 2 precursor (LAMP-2) (CD107b antigen); transcript variant 1 (LOC481037); mRNA	XM_538159	LAMP2	lysosomal-associated membrane protein 2
CfaAffx.28310.1.S1_at	5.66E-02	5.45E-02	0.74	familiaris similar to Lysosome-associated membrane glycoprotein 2 precursor (LAMP-2) (CD107b antigen); transcript variant 3 (LOC481037); mRNA	XM_859449	LAMP2	lysosomal-associated membrane protein 2
CfaAffx.18306.1.S1_at	1.50E-03	1.25E-02	0.74	PREDICTED: Canis familiaris similar to lysosomal-associated membrane protein 3 (LOC607186); mRNA	XM_843796	LAMP3	lysosomal-associated membrane protein 3
Cfa.285.2.S1_s_at	2.14E-02	3.25E-02	0.65	PREDICTED: Canis familiaris similar to leucine aminopeptidase (LOC479081); mRNA	XM_536228	LAP3	leucine aminopeptidase 3

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.14608.1.A1_at	1.50E-02	2.75E-02	0.69	PREDICTED: Bos taurus similar to la related protein (LARP1); mRNA	XM_582017	LARP1	La ribonucleoprotein domain family, member 1
CfaAffx.30748.1.S1_at	6.69E-02	6.00E-02	0.72	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	XM_857229	LCN2	lipocalin 2
Cfa.21232.1.S1_s_at	4.38E-03	1.69E-02	0.73	PREDICTED: Canis familiaris similar to Lymphocyte cytosolic protein 2 (SH2 domain-containing leucocyte protein of 76 kDa) (SLP-76 tyrosine phosphoprotein) (SLP76); transcript variant 1 (LOC489126); mRNA	XM_546244	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)
Cfa.9446.1.A1_s_at	3.47E-03	1.58E-02	0.75	PREDICTED: Canis familiaris similar to senescence downregulated leo1-like; transcript variant 4 (LOC478310); mRNA	XM_858008	LEO1	Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)
Cfa.10550.2.S1_at	1.88E-04	9.00E-03	0.64	PREDICTED: Canis familiaris similar to LETM1 domain containing 1 isoform 1; transcript variant 1 (LOC607861); mRNA	XM_845192	LETMD1	LETM1 domain containing 1
Cfa.11075.2.A1_s_at	1.69E-03	1.29E-02	0.68	PREDICTED: Canis familiaris similar to galectin 8 isoform a (LOC479193); mRNA	XM_536335	LGALS8	lectin, galactoside-binding, soluble, 8
Cfa.14080.1.A1_at	6.99E-04	1.08E-02	1.32	PREDICTED: Canis familiaris similar to Leucine-rich repeat-containing G-protein coupled receptor 4 precursor (G-protein coupled receptor 48) (LOC476896); mRNA	XM_534098	LGR4	leucine-rich repeat-containing G protein-coupled receptor 4
Cfa.2087.1.A1_at	2.86E-03	1.48E-02	0.61	PREDICTED: Canis familiaris similar to ligatin; transcript variant 1 (LOC478951); mRNA	XM_536109	LGTN	ligatin

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.11 12.1.S1 s at	2.40E-02	3.42E-02	0.68	PREDICTED: Canis familiaris similar to ERGIC-53 protein precursor (ER-Golgi intermediate compartment 53 kDa protein) (Lectin; mannose-binding 1) (Gp58) (Intracellular mannose specific lectin MR60) (LOC476186); mRNA	XM 5333 90	LMAN1	lectin, mannose-binding, 1
Cfa.16359. 1.S1 at	1.73E-02	2.93E-02	0.75	Oryctolagus cuniculus mannosyl-oligosaccharide alpha-1;2-mannosidase mRNA; partial cds	U04301	LOC100 009182	mannosyl-oligosaccharide alpha-1,2-mannosidase
CfaAffx.30 639.1.S1 a t	1.45E-03	1.25E-02	1.32	PREDICTED: Monodelphis domestica similar to early growth response 3 (LOC100033116); mRNA	XM 0013 81959	LOC100 033116	similar to early growth response 3
CfaAffx.28 002.1.S1 a t	1.84E-02	3.03E-02	0.74	PREDICTED: Equus caballus Rho-associated coiled coil containing protein kinase 1 (LOC100034056); mRNA	XM 0019 15218	LOC100 034056	Rho-associated coiled coil containing protein kinase 1
CfaAffx.28 599.1.S1 s at	7.94E-03	2.08E-02	0.75	PREDICTED: Equus caballus similar to Nuclear distribution protein nudE homolog 1 (NudE) (LOC100050421); mRNA	XM 0019 16795	LOC100 050421	similar to Nuclear distribution protein nudE homolog 1 (NudE)
CfaAffx.38 38.1.S1 s at	3.97E-03	1.64E-02	0.69	PREDICTED: Equus caballus similar to HCOBP; transcript variant 2 (LOC100050598); mRNA	XM 0014 90056	LOC100 050598	similar to COBW domain containing protein
CfaAffx.17 45.1.S1 x at	2.90E-03	1.49E-02	1.4	PREDICTED: Equus caballus similar to olfactory receptor; family 6; subfamily C; member 1 (LOC100051018); mRNA	XM 0015 04709	LOC100 051018	similar to olfactory receptor, family 6, subfamily C, member 1
CfaAffx.19 128.1.S1 s at	3.76E-02	4.35E-02	0.72	PREDICTED: Equus caballus similar to Synaptonemal complex protein 2 (SCP-2) (Synaptonemal complex lateral element protein) (hsSCP2) (LOC100051057); mRNA	XM 0019 15153	LOC100 051057	similar to Synaptonemal complex protein 2 (SCP-2) (Synaptonemal complex lateral element protein) (hsSCP2)

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.22919.1.S1_at	2.49E-02	3.50E-02	0.74	PREDICTED: Equus caballus hypothetical LOC100051235 (LOC100051235); mRNA	XM_001489111	LOC100051235	hypothetical LOC100051235
Cfa.16441.1.A1_at	1.43E-04	8.90E-03	0.65	PREDICTED: Equus caballus similar to arginine and glutamate rich 1 (LOC100051338); mRNA	XM_001493829	LOC100051338	similar to arginine and glutamate rich 1
Cfa.14225.1.A1_s_at	6.72E-02	6.02E-02	0.76	PREDICTED: Equus caballus similar to protein phosphatase 1; regulatory subunit 15A (LOC100051382); mRNA	XM_001489532	LOC100051382	similar to protein phosphatase 1, regulatory subunit 15A
Cfa.10188.1.S1_at	9.57E-04	1.16E-02	0.74	PREDICTED: Equus caballus similar to proteasome (prosome; macropain) 26S subunit; non-ATPase; 14 (LOC100051409); mRNA	XM_001493620	LOC100051409	similar to proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
Cfa.10853.1.A1_at	1.62E-02	2.85E-02	0.77	PREDICTED: Equus caballus similar to 1-phosphatidylinositol-4;5-bisphosphate phosphodiesterase beta-1 (Phosphoinositide phospholipase C) (Phospholipase C-beta-1) (PLC-beta-1) (PLC-I) (PLC-154) (LOC100051558); mRNA	XM_001493603	LOC100051558	similar to 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 1 (Phosphoinositide phospholipase C) (Phospholipase C-beta-1) (PLC-beta-1) (PLC-I) (PLC-154)
Cfa.16981.1.S1_s_at	6.31E-05	8.40E-03	0.71	PREDICTED: Equus caballus similar to Ubiquitin carboxyl-terminal hydrolase isozyme L3 (UCH-L3) (Ubiquitin thioesterase L3) (LOC100052000); mRNA	XM_001488246	LOC100052000	similar to Ubiquitin carboxyl-terminal hydrolase isozyme L3 (UCH-L3) (Ubiquitin thioesterase L3)
CfaAffx.1703.1.S1_s_at	7.56E-02	6.42E-02	0.73	PREDICTED: Equus caballus similar to SON DNA binding protein; isoform f (predicted) (LOC100052256); mRNA	XM_001915560	LOC100052256	similar to SON DNA binding protein, isoform f (predicted)

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.11138.1.S1_s_at	1.91E-03	1.32E-02	0.74	PREDICTED: Equus caballus similar to TNF receptor-associated factor 6 (LOC100052296); mRNA	XM_001914936	LOC100052296	similar to TNF receptor-associated factor 6
Cfa.464.1.S1_a_at	6.26E-02	5.78E-02	0.71	PREDICTED: Equus caballus similar to methyltransferase like 6 (LOC100052536); mRNA	XM_001496483	LOC100052536	similar to methyltransferase like 6
Cfa.10870.1.S1_at	2.03E-03	1.35E-02	0.74	PREDICTED: Equus caballus similar to ADP-ribosylation factor-like protein 1 (LOC100052976); mRNA	XM_001496831	LOC100052976	similar to ADP-ribosylation factor-like protein 1
CfaAffx.2241.1.S1_at	5.62E-05	8.24E-03	1.34	PREDICTED: Equus caballus similar to WD repeat domain 27 (LOC100053367); mRNA	XM_001915187	LOC100053367	hypothetical LOC100053367
CfaAffx.16527.1.S1_at	1.42E-02	2.69E-02	0.74	PREDICTED: Equus caballus similar to dual adaptor of phosphotyrosine and 3-phosphoinositides (LOC100053857); mRNA	XM_001498521	LOC100053857	hypothetical protein LOC100053857
Cfa.15046.1.A1_at	2.37E-02	3.40E-02	0.75	PREDICTED: Equus caballus similar to solute carrier family 30 (zinc transporter); member 1 (LOC100054805); mRNA	XM_001489279	LOC100054805	hypothetical protein LOC100054805
CfaAffx.18191.1.S1_s_at	1.34E-02	2.61E-02	0.72	PREDICTED: Equus caballus similar to interferon-inducible protein 203 (LOC100057060); mRNA	XM_001490548	LOC100057060	similar to interferon activated gene 203
Cfa.10611.1.A1_at	3.03E-03	1.51E-02	0.77	PREDICTED: Equus caballus similar to armadillo repeat containing; X-linked 3; transcript variant 1 (LOC100057749); mRNA	XM_001494074	LOC100057749	hypothetical protein LOC100057749
Cfa.15795.1.A1_s_at	6.69E-02	6.00E-02	1.38	PREDICTED: Equus caballus similar to putative MIP-1beta protein (LOC100057859); mRNA	XM_001503888	LOC100057859	similar to putative MIP-1beta protein
Cfa.3071.1.S1_at	2.82E-02	3.72E-02	0.66	PREDICTED: Equus caballus similar to cdc2/CDC28-like protein kinase 4 (LOC100058051); mRNA	XM_001501953	LOC100058051	similar to cdc2/CDC28-like protein kinase 4
Cfa.14999.1.A1_at	1.33E-03	1.23E-02	0.64	PREDICTED: Equus caballus similar to interferon regulatory factor 2 binding protein 2 (LOC100059147); mRNA	XM_001916562	LOC100059147	hypothetical LOC100059147

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.14999.1.A1_s_at	2.01E-03	1.35E-02	0.69	PREDICTED: Equus caballus similar to interferon regulatory factor 2 binding protein 2 (LOC100059147); mRNA	XM_001916562	LOC100059147	hypothetical LOC100059147
Cfa.1748.1.S1_at	6.73E-03	1.95E-02	0.74	PREDICTED: Equus caballus similar to Dimethyladenosine transferase (LOC100059778); mRNA	XM_001493893	LOC100059778	similar to Dimethyladenosine transferase
CfaAffx.20711.1.S1_at	5.11E-02	5.16E-02	0.71	PREDICTED: Equus caballus similar to inhibitor-2 (LOC100060058); mRNA	XM_001500822	LOC100060058	similar to inhibitor-2
Cfa.16638.1.S1_at	6.58E-05	8.40E-03	0.73	PREDICTED: Equus caballus similar to translocase of inner mitochondrial membrane 13 (LOC100060448); mRNA	XM_001494016	LOC100060448	hypothetical protein LOC100060448
Cfa.1295.1.S1_at	4.30E-04	9.78E-03	0.69	PREDICTED: Equus caballus similar to signal sequence receptor; alpha (translocon-associated protein alpha) (LOC100061378); mRNA	XM_001493337	LOC100061378	hypothetical protein LOC100061378
Cfa.16541.1.S1_at	8.86E-03	2.19E-02	0.71	PREDICTED: Equus caballus similar to PEST proteolytic signal containing nuclear protein; transcript variant 1 (LOC100061942); mRNA	XM_001503437	LOC100061942	similar to PEST proteolytic signal containing nuclear protein
Cfa.2411.1.A1_at	2.64E-02	3.59E-02	0.75	PREDICTED: Equus caballus similar to mCG12474 (LOC100062680); mRNA	XM_001494169	LOC100062680	hypothetical protein LOC100062680
Cfa.12874.1.A1_at	2.95E-03	1.50E-02	0.72	PREDICTED: Equus caballus similar to AF4/FMR2 family member 4 (ALL1-fused gene from chromosome 5q31) (Major CDK9 elongation factor-associated protein) (LOC100063038); mRNA	XM_001504421	LOC100063038	similar to AF5q31 protein
Cfa.9741.2.A1_at	3.96E-03	1.64E-02	0.66	PREDICTED: Equus caballus similar to casein kinase II alpha subunit (LOC100063080); mRNA	XM_001494444	LOC100063080	similar to casein kinase II alpha subunit
Cfa.9847.1.A1_at	4.95E-04	1.00E-02	0.73	PREDICTED: Equus caballus hypothetical LOC100064702 (LOC100064702); mRNA	XM_001504598	LOC100064702	hypothetical protein LOC100064702

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.5595.1.A1_at	3.46E-03	1.58E-02	0.76	PREDICTED: Equus caballus similar to cofactor A (LOC100065465); mRNA	XM_001504660	LOC100065465	similar to cofactor A
Cfa.2674.1.S1_at	5.52E-04	1.02E-02	0.74	PREDICTED: Equus caballus similar to rab11 (LOC100066116); mRNA	XM_001496510	LOC100066116	similar to rab11
Cfa.18972.1.S1_s_at	9.64E-03	2.27E-02	0.74	PREDICTED: Equus caballus similar to splicing factor YT521-B; transcript variant 2 (LOC100066303); mRNA	XM_001501526	LOC100066303	hypothetical protein LOC100066303
Cfa.19409.1.S1_at	4.07E-05	7.55E-03	0.7	PREDICTED: Equus caballus similar to N-acetylgalactosaminyltransferase 7 (Protein-UDP acetylgalactosaminyltransferase 7) (UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 7) (Polypeptide GalNAc transferase 7) (GalNAc-T7) (pp-GaNTase 7) (LOC100066545); mRNA	XM_001915557	LOC100066545	hypothetical LOC100066545
Cfa.6274.1.S1_s_at	1.02E-04	8.90E-03	0.73	PREDICTED: Equus caballus similar to Proteasome subunit beta type-7 (LOC100067317); mRNA	XM_001502120	LOC100067317	similar to proteasome beta 7 subunit proprotein
CfaAffx.16690.1.S1_at	2.89E-03	1.49E-02	0.68	PREDICTED: Equus caballus similar to B-cell scaffold protein with ankyrin repeats (LOC100067773); mRNA	XM_001497747	LOC100067773	similar to B-cell scaffold protein with ankyrin repeats 1
Cfa.10920.1.S1_x_at	1.77E-04	9.00E-03	0.68	PREDICTED: Equus caballus similar to Acyl carrier protein; mitochondrial precursor (ACP) (NADH-ubiquinone oxidoreductase 9.6 kDa subunit) (CI-SDAP) (LOC100069079); mRNA	XM_001498903	LOC100069079	similar to Acyl carrier protein, Mitochondrial (ACP) (5partial)
CfaAffx.4335.1.S1_at	4.56E-04	9.87E-03	1.34	PREDICTED: Equus caballus similar to chromosome 6 open reading frame 142 (LOC100069574); mRNA	XM_001499311	LOC100069574	similar to chromosome 6 open reading frame 142
CfaAffx.4335.1.S1_x_at	3.28E-04	9.28E-03	1.32	PREDICTED: Equus caballus similar to chromosome 6 open reading frame 142 (LOC100069574); mRNA	XM_001499311	LOC100069574	similar to chromosome 6 open reading frame 142

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.23811.1.S1_at	3.60E-03	1.60E-02	0.71	PREDICTED: Equus caballus similar to Vesicle transport protein USE1 (USE1-like protein) (Putative MAPK-activating protein PM26) (Protein p31) (LOC100070008); mRNA	XM_001503032	LOC100070008	hypothetical protein LOC100070008
CfaAffx.16114.1.S1_s_at	1.30E-02	2.57E-02	1.33	PREDICTED: Equus caballus similar to zinc finger protein 362 (LOC100070027); mRNA	XM_001499712	LOC100070027	hypothetical protein LOC100070027
Cfa.2265.1.A1_at	1.11E-02	2.40E-02	0.75	PREDICTED: Equus caballus similar to SYNCRIP protein; transcript variant 2 (LOC100070472); mRNA	XM_001915136	LOC100070472	similar to synaptotagmin binding, cytoplasmic RNA interacting protein
Cfa.277.1.S1_at	2.38E-03	1.40E-02	0.75	PREDICTED: Equus caballus similar to splicing factor; arginine/serine-rich 6 (LOC100070669); mRNA	XM_001500335	LOC100070669	similar to splicing factor, arginine/serine-rich 6
CfaAffx.11227.1.S1_at	3.99E-02	4.50E-02	0.75	PREDICTED: Equus caballus similar to eukaryotic translation initiation factor 3; subunit 5 epsilon; 47kDa (LOC100070877); mRNA	XM_001500555	LOC100070877	similar to hCG1784554
CfaAffx.26862.1.S1_at	1.25E-03	1.23E-02	0.73	PREDICTED: Equus caballus similar to RAD51 homolog C (LOC100070966); mRNA	XM_001500643	LOC100070966	similar to RAD51 homolog C
Cfa.2073.1.S1_at	7.72E-03	2.06E-02	0.71	PREDICTED: Equus caballus similar to Translocation protein SEC63 homolog (LOC100072096); mRNA	XM_001501960	LOC100072096	similar to SEC63 homolog (S. cerevisiae)
CfaAffx.6163.1.S1_at	4.69E-03	1.73E-02	0.62	PREDICTED: Equus caballus similar to Protein disulfide-isomerase A6 precursor (Protein disulfide isomerase P5) (Thioredoxin domain-containing protein 7) (LOC100072358); mRNA	XM_001502274	LOC100072358	similar to Protein disulfide-isomerase A6 precursor (Protein disulfide isomerase P5) (Thioredoxin domain-containing protein 7)

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.9496.1.S1_at	2.84E-02	3.73E-02	0.72	PREDICTED: Equus caballus hypothetical LOC100072521 (LOC100072521); mRNA	XM_001502483	LOC100072521	hypothetical LOC100072521
Cfa.1403.1.S2_s_at	3.09E-04	9.27E-03	0.76	PREDICTED: Equus caballus similar to protein phosphatase 2; catalytic subunit; alpha (LOC100072780); mRNA	XM_001917927	LOC100072780	similar to protein phosphatase 2, catalytic subunit, alpha
CfaAffx.2393.1.S1_at	4.53E-03	1.71E-02	0.76	PREDICTED: Equus caballus similar to protein phosphatase 2; catalytic subunit; alpha (LOC100072780); mRNA	XM_001917927	LOC100072780	similar to protein phosphatase 2, catalytic subunit, alpha
Cfa.5559.1.A1_a_at	8.21E-03	2.12E-02	1.34	Xenopus tropicalis hypothetical protein LOC100135097; mRNA (cDNA clone MGC:172910 IMAGE:7694930); complete cds	BC155703	LOC100135097	hypothetical protein LOC100135097
CfaAffx.25830.1.S1_at	2.56E-03	1.44E-02	0.76	PREDICTED: Bos taurus similar to Ubiquitin-conjugating enzyme E2 Z (Ubiquitin-protein ligase Z) (Ubiquitin carrier protein Z) (Uba6-specific E2 conjugating enzyme 1) (Use1) (LOC100138178); mRNA	XM_001789275	LOC100138178	similar to Ubiquitin-conjugating enzyme E2 Z (Ubiquitin-protein ligase Z) (Ubiquitin carrier protein Z) (Uba6-specific E2 conjugating enzyme 1) (Use1)
Cfa.10131.1.S1_s_at	1.10E-02	2.38E-02	1.31	PREDICTED: Equus caballus similar to HLA-B associated transcript 1 (LOC100146384); mRNA	XM_001917617	LOC100146384	similar to HLA-B associated transcript 1
Cfa.1992.1.S1_at	8.07E-03	2.10E-02	0.72	PREDICTED: Sus scrofa similar to zinc finger and BTB domain containing 1 (LOC100152273); mRNA	XM_001925789	LOC100152273	similar to zinc finger and BTB domain containing 1
Cfa.3312.1.S1_at	4.95E-02	5.07E-02	0.71	PREDICTED: Sus scrofa similar to polyglutamine-containing protein (LOC100152768); mRNA	XM_001928316	LOC100152768	similar to polyglutamine-containing protein
CfaAffx.26442.1.S1_at	1.23E-03	1.23E-02	0.72	PREDICTED: Sus scrofa similar to TIPIN protein (LOC100153268); mRNA	XM_001925231	LOC100153268	similar to TIPIN protein

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.8929.1.A1_at	4.64E-03	1.73E-02	0.75	PREDICTED: Sus scrofa similar to Presqualene diphosphate phosphatase (Phosphatidic acid phosphatase type 2 domain-containing protein 2) (PPAP2 domain-containing protein 2) (LOC100153280); mRNA	XM_001926782	LOC100153280	similar to Presqualene diphosphate phosphatase (Phosphatidic acid phosphatase type 2 domain-containing protein 2) (PPAP2 domain-containing protein 2)
Cfa.8215.1.A1_at	1.07E-03	1.20E-02	0.7	PREDICTED: Sus scrofa similar to DNA-damage-inducible transcript 4 protein (Protein regulated in development and DNA damage response 1) (REDD-1) (HIF-1 responsive protein RTP801) (LOC100153821); mRNA	XM_001925275	LOC100153821	similar to DNA-damage-inducible transcript 4 protein (Protein regulated in development and DNA damage response 1) (REDD-1) (HIF-1 responsive protein RTP801)
Cfa.12793.1.A1_at	9.32E-03	2.23E-02	0.73	PREDICTED: Sus scrofa similar to cell division cycle associated 7; transcript variant 1 (LOC100154583); mRNA	XM_001928628	LOC100154583	similar to cell division cycle associated 7
Cfa.9507.1.A1_at	1.85E-02	3.04E-02	0.74	PREDICTED: Sus scrofa similar to nuclear undecaprenyl pyrophosphate synthase 1 homolog (LOC100154658); mRNA	XM_001928072	LOC100154658	similar to nuclear undecaprenyl pyrophosphate synthase 1 homolog
Cfa.19021.2.S1_a_at	3.91E-02	4.45E-02	0.76	PREDICTED: Sus scrofa similar to Plastin-2 (L-plastin) (Lymphocyte cytosolic protein 1) (LCP-1) (LC64P); transcript variant 2 (LOC100156254); mRNA	XM_001929145	LOC100156254	similar to Plastin-2 (L-plastin) (Lymphocyte cytosolic protein 1) (LCP-1) (LC64P)

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Cfa.1029.1.A1_at	3.52E-04	9.50E-03	0.65	PREDICTED: Sus scrofa similar to vesicle trafficking protein sec22b (LOC100157002); mRNA	XM_001928686	LOC100157002	similar to vesicle trafficking protein sec22b
Cfa.11703.1.A1_at	6.63E-04	1.06E-02	0.74	Sus scrofa mRNA; clone:AMP010019E02; expressed in alveolar macrophage	AK230638	LOC100157274	similar to Phosphatidylinositol transfer protein beta isoform (PtdIns transfer protein beta) (PtdInsTP) (PI-TP-beta)
Cfa.9211.1.A1_at	4.63E-03	1.72E-02	0.75	PREDICTED: Sus scrofa similar to ATPase family; AAA domain containing 1 (LOC100157471); mRNA	XM_001927977	LOC100157471	similar to ATPase family, AAA domain containing 1
Cfa.17118.1.S1_at	4.47E-03	1.70E-02	0.73	PREDICTED: Sus scrofa similar to FGFR1 oncogene partner 2 (LOC100157490); mRNA	XM_001924597	LOC100157490	similar to FGFR1 oncogene partner 2
Cfa.569.1.S1_at	2.08E-02	3.21E-02	0.74	PREDICTED: Sus scrofa similar to amine oxidase (flavin containing) domain 1 (LOC100158047); mRNA	XM_001927844	LOC100158047	similar to amine oxidase (flavin containing) domain 1
CfaAffx.1432.1.S1_at	6.17E-04	1.05E-02	1.31	PREDICTED: Rattus norvegicus hypothetical LOC363725 (LOC363725); mRNA	XR_008227	LOC363725	hypothetical LOC363725
CfaAffx.25106.1.S1_s_at	8.17E-03	2.11E-02	0.76	Homo sapiens hypothetical protein LOC389203; mRNA (cDNA clone IMAGE:4521185); partial cds	BC032431	LOC389203	hypothetical gene supported by BC032431
Cfa.1161.1.S1_at	5.40E-02	5.32E-02	0.76	PREDICTED: Pan troglodytes similar to OTU domain containing 6B (LOC464282); mRNA	XR_023126	LOC464282	similar to OTU domain containing 6B
CfaAffx.12773.1.S1_at	2.77E-05	7.55E-03	0.67	PREDICTED: Pan troglodytes hypothetical LOC467645; transcript variant 6 (LOC467645); mRNA	XM_001165269	LOC467645	hypothetical LOC467645
Cfa.2514.1.S1_at	1.90E-03	1.32E-02	0.74	PREDICTED: Pan troglodytes similar to Prenylcysteine oxidase 1 (LOC470398); mRNA	XR_022935	LOC470398	similar to Prenylcysteine oxidase 1

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.3947.1.S1_s_at	4.51E-02	4.80E-02	0.77	PREDICTED: Canis familiaris similar to LIM and senescent cell antigen-like domains 1; transcript variant 6 (LOC474540); mRNA	XM_857968	LOC474540	similar to LIM and senescent cell antigen-like domains 1
CfaAffx.4983.1.S1_s_at	1.74E-04	9.00E-03	0.69	PREDICTED: Canis familiaris similar to chromosome 2 open reading frame 30; transcript variant 1 (LOC474593); mRNA	XM_531822	LOC474593	similar to chromosome 2 open reading frame 30
Cfa.3321.1.S1_at	2.03E-03	1.35E-02	0.72	PREDICTED: Canis familiaris similar to chromosome 2 open reading frame 30; transcript variant 3 (LOC474593); mRNA	XM_859968	LOC474593	similar to chromosome 2 open reading frame 30
CfaAffx.2623.1.S1_s_at	3.46E-03	1.58E-02	0.74	PREDICTED: Canis familiaris similar to Protein C5orf5 (GAP-like protein N61); transcript variant 1 (LOC474690); mRNA	XM_531916	LOC474690	similar to Protein C5orf5 (GAP-like protein N61)
CfaAffx.2621.1.S1_at	2.50E-02	3.50E-02	0.75	PREDICTED: Canis familiaris similar to Protein C5orf5 (GAP-like protein N61); transcript variant 2 (LOC474690); mRNA	XM_845894	LOC474690	similar to Protein C5orf5 (GAP-like protein N61)
Cfa.14572.1.S1_at	2.06E-03	1.35E-02	0.77	PREDICTED: Canis familiaris hypothetical LOC474705 (LOC474705); mRNA	XM_531931	LOC474705	hypothetical LOC474705
Cfa.9913.1.S1_at	9.31E-03	2.23E-02	0.69	PREDICTED: Canis familiaris similar to DnaJ homolog subfamily A member 1 (Heat shock 40 kDa protein 4) (DnaJ protein homolog 2) (HSJ-2) (HSDJ); transcript variant 3 (LOC474739); mRNA	XM_860355	LOC474739	similar to DnaJ homolog subfamily A member 1 (Heat shock 40 kDa protein 4) (DnaJ protein homolog 2) (HSJ-2) (HSDJ)

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.3639.1.S1_s_at	3.42E-03	1.57E-02	0.66	PREDICTED: Canis familiaris similar to DnaJ homolog subfamily A member 1 (Heat shock 40 kDa protein 4) (DnaJ protein homolog 2) (HSJ-2) (HSDJ); transcript variant 3 (LOC474739); mRNA	XM_860355	LOC474739	similar to DnaJ homolog subfamily A member 1 (Heat shock 40 kDa protein 4) (DnaJ protein homolog 2) (HSJ-2) (HSDJ)
Cfa.11753.1.A1_s_at	1.63E-02	2.86E-02	0.7	PREDICTED: Canis familiaris similar to CG12822-PA; isoform A; transcript variant 1 (LOC474773); mRNA	XM_532004	LOC474773	similar to CG12822-PA, isoform A
Cfa.12434.1.A1_at	6.00E-02	5.64E-02	0.68	PREDICTED: Canis familiaris similar to collagen; type XXVII; alpha 1 (LOC474811); mRNA	XM_532042	LOC474811	similar to collagen, type XXVII, alpha 1
Cfa.2864.1.A1_s_at	1.96E-03	1.33E-02	0.71	PREDICTED: Canis familiaris similar to Histone deacetylase 2 (HD2) (LOC475035); mRNA	XM_532270	LOC475035	similar to Histone deacetylase 2 (HD2)
Cfa.20275.1.S1_at	3.89E-04	9.61E-03	0.75	PREDICTED: Canis familiaris similar to Protein KIAA0196; transcript variant 1 (LOC475095); mRNA	XM_532327	LOC475095	similar to Protein KIAA0196
CfaAffx.21467.1.S1_at	5.11E-04	1.00E-02	1.39	PREDICTED: Canis familiaris hypothetical LOC475237 (LOC475237); mRNA	XM_532470	LOC475237	hypothetical LOC475237
CfaAffx.12494.1.S1_s_at	3.11E-03	1.53E-02	0.72	PREDICTED: Canis familiaris similar to CG9882-PA (LOC475460); mRNA	XM_532684	LOC475460	similar to CG9882-PA
CfaAffx.5646.1.S1_s_at	1.74E-03	1.30E-02	0.7	PREDICTED: Canis familiaris similar to H2A histone family; member V isoform 5; transcript variant 1 (LOC475501); mRNA	XM_532724	LOC475501	similar to H2A histone family, member V isoform 5
Cfa.5126.1.A1_s_at	5.84E-04	1.03E-02	0.61	PREDICTED: Canis familiaris similar to splicing factor 3B; 14 kDa subunit (LOC475682); mRNA	XM_532889	LOC475682	similar to splicing factor 3B, 14 kDa subunit
CfaAffx.6865.1.S1_at	6.59E-05	8.40E-03	0.71	PREDICTED: Canis familiaris similar to splicing factor 3B; 14 kDa subunit (LOC475682); mRNA	XM_532889	LOC475682	similar to splicing factor 3B, 14 kDa subunit
Cfa.11769.1.A1_at	1.17E-02	2.44E-02	1.34	PREDICTED: Canis familiaris similar to protein containing single MORN motif in testis (LOC475733); mRNA	XM_532942	LOC475733	similar to protein containing single MORN motif in testis

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.10736.1.S1_s_at	1.18E-03	1.21E-02	0.71	PREDICTED: Canis familiaris similar to cytochrome c oxidase subunit VIIa polypeptide 2 like (LOC475739); mRNA	XM_532946	LOC475739	similar to cytochrome c oxidase subunit VIIa polypeptide 2 like
Cfa.9136.1.A1_s_at	3.04E-03	1.51E-02	0.77	PREDICTED: Canis familiaris similar to protease; serine; 25 isoform 2; transcript variant 1 (LOC475782); mRNA	XM_532992	LOC475782	similar to protease, serine, 25 isoform 2
CfaAffx.28197.1.S1_x_at	3.21E-02	3.99E-02	0.76	PREDICTED: Canis familiaris similar to large subunit ribosomal protein L36a; transcript variant 3 (LOC475808); mRNA	XM_852126	LOC475808	similar to large subunit ribosomal protein L36a
CfaAffx.16936.1.S1_s_at	2.25E-02	3.32E-02	0.77	PREDICTED: Canis familiaris similar to D-3-phosphoglycerate dehydrogenase (3-PGDH) (LOC475815); mRNA	XM_533024	LOC475815	similar to D-3-phosphoglycerate dehydrogenase (3-PGDH)
Cfa.4331.2.S1_at	7.89E-02	6.57E-02	0.75	PREDICTED: Canis familiaris similar to Protein C2orf25; mitochondrial precursor; transcript variant 1 (LOC476145); mRNA	XM_533352	LOC476145	similar to Protein C2orf25, mitochondrial precursor
Cfa.483.1.A1_at	7.50E-03	2.03E-02	0.73	PREDICTED: Canis familiaris hypothetical LOC57614; transcript variant 4 (LOC476181); mRNA	XM_852439	LOC476181	hypothetical LOC476181
Cfa.11029.1.A1_at	3.63E-02	4.27E-02	0.77	PREDICTED: Canis familiaris similar to Protein C6orf115 (LOC476222); mRNA	XM_533427	LOC476222	similar to Protein C6orf115
CfaAffx.267.1.S1_at	1.35E-03	1.23E-02	0.75	PREDICTED: Canis familiaris similar to eukaryotic translation elongation factor 1 alpha 1 (LOC476228); mRNA	XM_849334	LOC476228	hypothetical gene supported by AY195837
CfaAffx.4041.1.S1_s_at	9.74E-03	2.28E-02	0.72	PREDICTED: Canis familiaris similar to adenylate kinase 3 (LOC476342); mRNA	XM_533543	LOC476342	similar to adenylate kinase 3
Cfa.8384.1.A1_at	2.17E-04	9.06E-03	1.32	PREDICTED: Canis familiaris similar to F35A5.1 (LOC476380); mRNA	XM_533583	LOC476380	similar to F35A5.1
CfaAffx.1289.1.S1_s_at	3.20E-03	1.54E-02	0.77	PREDICTED: Canis familiaris similar to ubiquinol-cytochrome c reductase; Rieske iron-sulfur polypeptide 1 (LOC476503); mRNA	XM_533711	LOC476503	similar to ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.2536.1.A1_s_at	3.50E-03	1.58E-02	0.72	PREDICTED: Canis familiaris similar to retinoblastoma-associated protein 140; transcript variant 2 (LOC476580); mRNA	XM_844103	LOC476580	similar to retinoblastoma-associated protein 140
CfaAffx.18576.1.S1_at	4.14E-03	1.67E-02	0.75	PREDICTED: Canis familiaris similar to nuclear protein E3-3 isoform a; transcript variant 1 (LOC476631); mRNA	XM_533836	LOC476631	similar to nuclear protein E3-3 isoform a
CfaAffx.26385.1.S1_at	3.03E-03	1.51E-02	0.74	PREDICTED: Canis familiaris similar to UPF0139 protein CGI-140; transcript variant 1 (LOC476703); mRNA	XM_533908	LOC476703	similar to UPF0139 protein CGI-140
Cfa.15081.1.A1_s_at	9.91E-03	2.30E-02	0.75	PREDICTED: Canis familiaris hypothetical LOC476739 (LOC476739); mRNA	XM_533944	LOC476739	hypothetical LOC476739
Cfa.15734.1.A1_at	4.32E-02	4.70E-02	0.76	PREDICTED: Canis familiaris similar to Oligophrenin 1 (LOC476762); mRNA	XM_533968	LOC476762	similar to Oligophrenin 1
Cfa.5123.1.A1_at	2.27E-02	3.33E-02	0.75	PREDICTED: Canis familiaris similar to eukaryotic translation initiation factor 3; subunit 5 epsilon; 47kDa (LOC476840); mRNA	XM_534044	LOC476840	similar to eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

							similar to Mediator complex subunit 4 (Mediator of RNA polymerase II transcription subunit 4) (Vitamin D3 receptor-interacting protein complex 36 kDa component) (DRIP36) (Activator-recruited cofactor 36 kDa component) (ARC36) (TRAP/SMCC/PC2 subunit...
Cfa.10497.1.A1_at	4.30E-03	1.68E-02	0.74	PREDICTED: Canis familiaris similar to Mediator complex subunit 4 (Mediator of RNA polymerase II transcription subunit 4) (Vitamin D3 receptor-interacting protein complex 36 kDa component) (DRIP36) (Activator-recruited cofactor 36 kDa component) (ARC36) (TRAP/SMCC/PC2 subunit... (LOC476917); mRNA	XM_534120	LOC476917	
Cfa.15101.1.A1_s_at	2.72E-03	1.46E-02	0.76	PREDICTED: Canis familiaris similar to U2-associated SR140 protein (LOC477103); mRNA	XM_534297	LOC477103	similar to U2-associated SR140 protein
Cfa.3236.1.S1_at	1.64E-03	1.28E-02	0.73	PREDICTED: Canis familiaris similar to Selenoprotein T precursor (LOC477113); mRNA	XM_534307	LOC477113	similar to Selenoprotein T precursor
CfaAffx.13369.1.S1_s_at	5.81E-06	6.68E-03	0.72	PREDICTED: Canis familiaris similar to Selenoprotein T precursor (LOC477113); mRNA	XM_534307	LOC477113	similar to Selenoprotein T precursor
CfaAffx.13204.1.S1_s_at	1.02E-03	1.17E-02	0.72	PREDICTED: Canis familiaris similar to CG6878-PA (LOC477215); mRNA	XM_534406	LOC477215	similar to CG6878-PA
Cfa.11288.1.A1_at	6.26E-03	1.90E-02	0.73	PREDICTED: Canis familiaris similar to U11/U12 snRNP 35K isoform a (LOC477450); mRNA	XM_534648	LOC477450	similar to U11/U12 snRNP 35K isoform a
Cfa.11288.1.A1_s_at	3.75E-05	7.55E-03	0.68	PREDICTED: Canis familiaris similar to U11/U12 snRNP 35K isoform a (LOC477450); mRNA	XM_534648	LOC477450	similar to U11/U12 snRNP 35K isoform a
Cfa.1141.1.S1_at	1.15E-02	2.43E-02	0.75	PREDICTED: Canis familiaris hypothetical LOC477476 (LOC477476); mRNA	XM_534674	LOC477476	hypothetical LOC477476

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.10288.1.S1_at	1.26E-04	8.90E-03	0.73	PREDICTED: Canis familiaris similar to DC2 protein; transcript variant 2 (LOC477512); mRNA	XM_846200	LOC477512	similar to DC2 protein
Cfa.242.1.S1_at	7.92E-04	1.10E-02	0.75	PREDICTED: Canis familiaris similar to X-box binding protein 1 (LOC477532); mRNA	XM_849540	LOC477532	similar to X-box binding protein 1
CfaAffx.21661.1.S1_at	4.43E-03	1.70E-02	1.31	PREDICTED: Canis familiaris similar to glutathione S-transferase; theta 3 (LOC477555); mRNA	XM_534750	LOC477555	similar to glutathione S-transferase, theta 3
Cfa.11409.3.S1_s_at	3.00E-03	1.51E-02	0.72	PREDICTED: Canis familiaris hypothetical LOC477569 (LOC477569); mRNA	XM_534764	LOC477569	hypothetical LOC477569
CfaAffx.20702.1.S1_s_at	2.33E-02	3.37E-02	0.75	PREDICTED: Canis familiaris similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP); transcript variant 5 (LOC477645); mRNA	XM_859705	LOC477645	similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP)
Cfa.10773.1.A1_at	4.12E-03	1.66E-02	1.3	PREDICTED: Canis familiaris hypothetical LOC477662 (LOC477662); mRNA	XM_534856	LOC477662	hypothetical LOC477662
Cfa.504.1.S1_at	1.62E-02	2.85E-02	0.76	PREDICTED: Canis familiaris similar to CG6454-PB; isoform B; transcript variant 1 (LOC477671); mRNA	XM_534864	LOC477671	similar to CG6454-PB, isoform B
Cfa.20341.1.S1_s_at	5.30E-03	1.80E-02	0.64	PREDICTED: Canis familiaris hypothetical LOC477837 (LOC477837); mRNA	XM_535029	LOC477837	hypothetical LOC477837

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

							similar to Thioredoxin-dependent peroxide reductase, mitochondrial precursor (Peroxiredoxin 3) (Antioxidant protein 1) (AOP-1) (MER5 protein homolog) (HBC189) (PRX III)
Cfa.19049.1.S1_at	1.07E-02	2.37E-02	0.69	PREDICTED: Canis familiaris similar to Thioredoxin-dependent peroxide reductase; mitochondrial precursor (Peroxiredoxin 3) (Antioxidant protein 1) (AOP-1) (MER5 protein homolog) (HBC189) (PRX III); transcript variant 1 (LOC477839); mRNA	XM_535031	LOC477839	
CfaAffx.12259.1.S1_at	9.10E-04	1.15E-02	0.73	PREDICTED: Canis familiaris similar to Mitochondrial 28S ribosomal protein S22 (S22mt) (MRP-S22) (LOC477924); mRNA	XM_535113	LOC477924	similar to Mitochondrial 28S ribosomal protein S22 (S22mt) (MRP-S22)
CfaAffx.14881.1.S1_s_at	5.72E-04	1.03E-02	0.65	PREDICTED: Canis familiaris similar to ubiquinol-cytochrome c reductase binding protein (LOC477944); mRNA	XM_535132	LOC477944	similar to ubiquinol-cytochrome c reductase binding protein
CfaAffx.6478.1.S1_s_at	1.74E-02	2.95E-02	0.75	PREDICTED: Canis familiaris similar to suppressor of G2 allele of SKP1 (LOC477951); mRNA	XM_535139	LOC477951	similar to suppressor of G2 allele of SKP1
Cfa.11104.1.S1_at	9.05E-02	7.15E-02	0.77	PREDICTED: Canis familiaris similar to phytanoyl-CoA hydroxylase precursor (LOC478000); mRNA	XM_535184	LOC478000	similar to phytanoyl-CoA hydroxylase precursor
Cfa.11121.1.S1_at	5.80E-03	1.85E-02	0.75	PREDICTED: Canis familiaris similar to TGF beta-inducible nuclear protein 1 (L-name related LNR42); transcript variant 1 (LOC478102); mRNA	XM_535277	LOC478102	similar to TGF beta-inducible nuclear protein 1 (L-name related LNR42)

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.11121.3.S1_s_at	5.23E-03	1.79E-02	0.68	PREDICTED: Canis familiaris similar to TGF beta-inducible nuclear protein 1 (L-name related LNR42); transcript variant 1 (LOC478102); mRNA	XM_535277	LOC478102	similar to TGF beta-inducible nuclear protein 1 (L-name related LNR42)
CfaAffx.24175.1.S1_s_at	1.42E-03	1.25E-02	0.64	PREDICTED: Canis familiaris similar to H2A histone family; member Z; transcript variant 1 (LOC478215); mRNA	XM_535390	LOC478215	similar to H2A histone family, member Z
Cfa.2680.1.A1_s_at	1.14E-03	1.20E-02	0.73	PREDICTED: Canis familiaris similar to RIKEN cDNA 2900064A13; transcript variant 1 (LOC478242); mRNA	XM_535417	LOC478242	similar to RIKEN cDNA 2900064A13
CfaAffx.24638.1.S1_x_at	7.34E-04	1.08E-02	0.7	PREDICTED: Canis familiaris similar to ATP synthase; H+ transporting; mitochondrial F0 complex; subunit d isoform a (LOC478252); mRNA	XM_535426	LOC478252	similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d isoform a
CfaAffx.3982.1.S1_x_at	4.21E-05	7.55E-03	0.74	PREDICTED: Canis familiaris similar to ATP synthase; H+ transporting; mitochondrial F0 complex; subunit d isoform a (LOC478252); mRNA	XM_535426	LOC478252	similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d isoform a
CfaAffx.24384.1.S1_s_at	4.24E-03	1.68E-02	0.72	PREDICTED: Canis familiaris similar to ribosomal protein L24-like (LOC478313); mRNA	XM_535488	LOC478313	similar to ribosomal protein L24-like
Cfa.9445.1.A1_at	1.19E-02	2.47E-02	0.69	PREDICTED: Canis familiaris similar to calmodulin-like 4 (LOC478351); mRNA	XM_535525	LOC478351	similar to calmodulin-like 4
Cfa.1395.1.S1_s_at	1.06E-02	2.36E-02	0.74	PREDICTED: Canis familiaris histone H2AF; transcript variant 1 (LOC478493); mRNA	XM_535671	LOC478493	histone H2AF
Cfa.8589.2.S1_a_at	3.42E-04	9.36E-03	0.68	PREDICTED: Canis familiaris similar to ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog; yeast); transcript variant 3 (LOC478495); mRNA	XM_845800	LOC478495	similar to ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)
Cfa.12239.1.S1_at	3.30E-03	1.55E-02	0.73	PREDICTED: Canis familiaris similar to ribosomal protein L34 (LOC478509); mRNA	XM_535688	LOC478509	similar to ribosomal protein L34

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.8972.1.S1_at	5.84E-03	1.85E-02	0.7	PREDICTED: Canis familiaris similar to growth and transformation-dependent protein (LOC478584); mRNA	XM_535760	LOC478584	similar to growth and transformation-dependent protein
CfaAffx.18479.1.S1_s_at	1.48E-04	8.97E-03	0.67	PREDICTED: Canis familiaris similar to growth and transformation-dependent protein (LOC478584); mRNA	XM_535760	LOC478584	similar to growth and transformation-dependent protein
Cfa.12583.1.A1_at	5.39E-03	1.81E-02	0.74	PREDICTED: Canis familiaris similar to Y39A1A.21a (LOC478620); mRNA	XM_535794	LOC478620	similar to Y39A1A.21a
CfaAffx.683.1.S1_s_at	1.50E-03	1.25E-02	0.74	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 5 (LOC478639); mRNA	XM_535812	LOC478639	similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5
Cfa.6063.1.A1_s_at	4.63E-03	1.72E-02	0.76	PREDICTED: Canis familiaris similar to Dynein intermediate chain 2; cytosolic (DH IC-2) (Cytoplasmic dynein intermediate chain 2); transcript variant 1 (LOC478797); mRNA	XM_535961	LOC478797	similar to Dynein intermediate chain 2, cytosolic (DH IC-2) (Cytoplasmic dynein intermediate chain 2)
CfaAffx.19713.1.S1_s_at	4.88E-04	1.00E-02	0.74	PREDICTED: Canis familiaris similar to Dynein intermediate chain 2; cytosolic (DH IC-2) (Cytoplasmic dynein intermediate chain 2); transcript variant 1 (LOC478797); mRNA	XM_535961	LOC478797	similar to Dynein intermediate chain 2, cytosolic (DH IC-2) (Cytoplasmic dynein intermediate chain 2)
CfaAffx.19978.1.S1_at	6.65E-03	1.94E-02	0.75	PREDICTED: Canis familiaris similar to histone aminotransferase 1 (predicted); transcript variant 3 (LOC478799); mRNA	XM_844987	LOC478799	similar to histone aminotransferase 1 (predicted)
CfaAffx.20465.1.S1_s_at	3.50E-03	1.58E-02	0.7	PREDICTED: Canis familiaris similar to CBF1 interacting corepressor isoform 2; transcript variant 2 (LOC478804); mRNA	XM_535968	LOC478804	similar to CBF1 interacting corepressor isoform 2

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.3946.2.S1_a_at	5.38E-04	1.02E-02	0.67	PREDICTED: Canis familiaris similar to solute carrier family 39 (zinc transporter); member 10 (LOC478850); mRNA	XM_536012	LOC478850	similar to solute carrier family 39 (zinc transporter), member 10
CfaAffx.15878.1.S1_s_at	6.45E-05	8.40E-03	0.68	PREDICTED: Canis familiaris similar to solute carrier family 39 (zinc transporter); member 10 (LOC478850); mRNA	XM_536012	LOC478850	similar to solute carrier family 39 (zinc transporter), member 10
CfaAffx.16996.1.S1_x_at	1.68E-02	2.91E-02	0.74	PREDICTED: Canis familiaris similar to heat shock 10kDa protein 1 (chaperonin 10) (LOC478855); mRNA	XM_536017	LOC478855	similar to heat shock 10kDa protein 1 (chaperonin 10)
CfaAffx.20896.1.S1_at	6.02E-03	1.87E-02	0.75	PREDICTED: Canis familiaris similar to B0507.2 (LOC478996); mRNA	XM_536151	LOC478996	similar to B0507.2
CfaAffx.20436.1.S1_s_at	1.76E-02	2.96E-02	0.75	PREDICTED: Canis familiaris similar to Hepatoma-derived growth factor-related protein 3 (HRP-3) (Hepatoma-derived growth factor 2) (LOC479059); mRNA	XM_536208	LOC479059	similar to Hepatoma-derived growth factor-related protein 3 (HRP-3) (Hepatoma-derived growth factor 2)
Cfa.8201.1.A1_at	4.26E-04	9.78E-03	0.76	PREDICTED: Canis familiaris similar to signal recognition particle 19kDa (LOC479138); mRNA	XM_536284	LOC479138	similar to signal recognition particle 19kDa
CfaAffx.25557.1.S1_s_at	2.50E-02	3.50E-02	0.75	PREDICTED: Canis familiaris similar to Activated RNA polymerase II transcriptional coactivator p15 (Positive cofactor 4) (PC4) (p14) (LOC479283); mRNA	XM_536425	LOC479283	similar to Activated RNA polymerase II transcriptional coactivator p15 (Positive cofactor 4) (PC4) (p14)

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.10268.1.A1_s_at	4.63E-03	1.72E-02	0.76	PREDICTED: Canis familiaris similar to Brix domain containing protein 2 (Ribosome biogenesis protein Brix) (LOC479365); mRNA	XM_536504	LOC479365	similar to Brix domain containing protein 2 (Ribosome biogenesis protein Brix)
Cfa.1427.1.A1_s_at	6.94E-02	6.13E-02	0.68	PREDICTED: Canis familiaris similar to Glucose-6-phosphate isomerase (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Neuroleukin) (NLK) (Sperm antigen-36) (SA-36) (LOC479379); mRNA	XM_850413	LOC479379	similar to Glucose-6-phosphate isomerase (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (Neuroleukin) (NLK) (Sperm antigen-36) (SA-36)
CfaAffx.24477.1.S1_s_at	3.19E-03	1.54E-02	0.76	PREDICTED: Canis familiaris similar to CG32955-PD; isoform D; transcript variant 1 (LOC479477); mRNA	XM_536614	LOC479477	similar to CG32955-PD, isoform D
Cfa.18024.1.S1_s_at	5.23E-04	1.01E-02	0.73	PREDICTED: Canis familiaris similar to MAK31-like protein (LOC479488); mRNA	XM_536626	LOC479488	similar to MAK31-like protein
CfaAffx.29250.1.S1_s_at	4.02E-06	6.68E-03	0.73	PREDICTED: Canis familiaris similar to CG4646-PA (LOC479563); mRNA	XM_536703	LOC479563	similar to CG4646-PA
Cfa.3121.2.S1_s_at	1.28E-03	1.23E-02	0.77	PREDICTED: Canis familiaris similar to Cytochrome c oxidase subunit IV isoform 1; mitochondrial precursor (COX IV-1) (Cytochrome c oxidase polypeptide IV) (LOC479623); mRNA	XM_536759	LOC479623	similar to Cytochrome c oxidase subunit IV isoform 1, mitochondrial precursor (COX IV-1) (Cytochrome c oxidase polypeptide IV)
CfaAffx.30964.1.S1_s_at	1.13E-03	1.20E-02	0.72	PREDICTED: Canis familiaris similar to Protein KIAA0174; transcript variant 1 (LOC479667); mRNA	XM_536798	LOC479667	similar to Protein KIAA0174

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.10833.1.A1_s_at	1.26E-02	2.54E-02	0.76	PREDICTED: Canis familiaris similar to CG14977-PA; transcript variant 2 (LOC479736); mRNA	XM_854640	LOC479736	similar to CG14977-PA
Cfa.1043.1.A1_at	5.42E-03	1.81E-02	0.73	PREDICTED: Canis familiaris similar to CG14980-PB; transcript variant 3 (LOC479750); mRNA	XM_856170	LOC479750	similar to CG14980-PB
Cfa.3182.1.A1_at	4.84E-03	1.75E-02	0.77	PREDICTED: Canis familiaris similar to JTV1 (LOC479752); mRNA	XM_536880	LOC479752	similar to JTV1
Cfa.17019.1.S1_s_at	6.23E-02	5.76E-02	0.67	PREDICTED: Canis familiaris similar to ecotropic viral integration site 5 (LOC479950); mRNA	XM_537075	LOC479950	similar to ecotropic viral integration site 5
CfaAffx.15893.1.S1_s_at	1.12E-02	2.41E-02	0.75	PREDICTED: Canis familiaris similar to T-complex protein 1; zeta subunit (TCP-1-zeta) (CCT zeta) (CCT-zeta-1) (LOC480059); mRNA	XM_848687	LOC480059	similar to T-complex protein 1, zeta subunit (TCP-1-zeta) (CCT-zeta) (CCT-zeta-1)
Cfa.1499.1.A1_at	1.21E-02	2.48E-02	0.72	PREDICTED: Canis familiaris similar to Inner membrane protein OXA1L; mitochondrial precursor (Oxidase assembly 1-like protein) (OXA1-like protein) (OXA1Hs) (Hsa); transcript variant 1 (LOC480239); mRNA	XM_537362	LOC480239	similar to Inner membrane protein OXA1L, mitochondrial precursor (Oxidase assembly 1-like protein) (OXA1-like protein) (OXA1Hs) (Hsa)
Cfa.16186.1.A1_at	4.39E-03	1.69E-02	0.7	PREDICTED: Canis familiaris similar to magnesium-dependent phosphatase-1 (LOC480264); mRNA	XM_537388	LOC480264	similar to magnesium-dependent phosphatase-1
CfaAffx.27629.1.S1_s_at	2.02E-04	9.06E-03	0.68	PREDICTED: Canis familiaris similar to heat shock protein 1; alpha; transcript variant 1 (LOC480438); mRNA	XM_537557	LOC480438	similar to heat shock protein 1, alpha
Cfa.293.1.S2_at	3.80E-04	9.61E-03	0.73	PREDICTED: Canis familiaris similar to heat shock protein 1; alpha; transcript variant 3 (LOC480438); mRNA	XM_863495	LOC480438	similar to heat shock protein 1, alpha

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.18054.1.S1_s_at	7.47E-03	2.03E-02	0.72	PREDICTED: Canis familiaris similar to Importin alpha-2 subunit (Karyopherin alpha-2 subunit) (SRP1-alpha) (RAG cohort protein 1); transcript variant 3 (LOC480469); mRNA	XM_856928	LOC480469	similar to Importin alpha-2 subunit (Karyopherin alpha-2 subunit) (SRP1-alpha) (RAG cohort protein 1)
Cfa.1871.1.S1_at	1.31E-02	2.58E-02	0.68	PREDICTED: Canis familiaris similar to ADP-ribosylation factor 2; transcript variant 1 (LOC480487); mRNA	XM_537606	LOC480487	similar to ADP-ribosylation factor 2
CfaAffx.25041.1.S1_s_at	3.68E-03	1.61E-02	0.72	PREDICTED: Canis familiaris similar to chromosome 17 open reading frame 37 (LOC480532); mRNA	XM_537653	LOC480532	similar to chromosome 17 open reading frame 37
Cfa.10996.1.A1_at	1.67E-05	7.55E-03	0.73	PREDICTED: Canis familiaris similar to CG18335-PA (LOC480665); mRNA	XM_537784	LOC480665	similar to CG18335-PA
Cfa.795.1.A1_s_at	3.49E-02	4.19E-02	0.77	PREDICTED: Canis familiaris similar to 60S ribosomal protein L12; transcript variant 4 (LOC480716); mRNA	XM_857732	LOC480716	similar to 60S ribosomal protein L12
Cfa.20174.1.S1_at	1.41E-02	2.68E-02	0.76	PREDICTED: Canis familiaris similar to 78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein) (BiP) (Endoplasmic reticulum lumenal Ca(2+) binding protein grp78); transcript variant 1 (LOC480726); mRNA	XM_537847	LOC480726	similar to 78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein) (BiP) (Endoplasmic reticulum lumenal Ca(2+) binding protein grp78)

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

							similar to 78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein) (BiP) (Endoplasmic reticulum lumenal Ca(2+) binding protein grp78)
CfaAffx.30936.1.S1_s_at	4.68E-03	1.73E-02	0.75	PREDICTED: Canis familiaris similar to 78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain binding protein) (BiP) (Endoplasmic reticulum lumenal Ca(2+) binding protein grp78); transcript variant 1 (LOC480726); mRNA	XM_537847	LOC480726	
CfaAffx.18006.1.S1_s_at	1.90E-03	1.32E-02	0.76	PREDICTED: Canis familiaris similar to Cytochrome c-type heme lyase (CCHL) (Holocytochrome c-type synthase) (LOC480834); mRNA	XM_537950	LOC480834	similar to Cytochrome c-type heme lyase (CCHL) (Holocytochrome c-type synthase)
CfaAffx.330.1.S1_s_at	9.55E-04	1.16E-02	0.77	PREDICTED: Canis familiaris similar to NADH-ubiquinone oxidoreductase MWFE subunit (Complex I-MWFE) (CI-MWFE) (LOC481033); mRNA	XM_538155	LOC481033	similar to NADH-ubiquinone oxidoreductase MWFE subunit (Complex I-MWFE) (CI-MWFE)
CfaAffx.4869.1.S1_s_at	2.13E-03	1.36E-02	0.76	PREDICTED: Canis familiaris similar to nudix (nucleoside diphosphate linked moiety X)-type motif 21 (LOC481880); mRNA	XM_539001	LOC481880	similar to nudix (nucleoside diphosphate linked moiety X)-type motif 21
CfaAffx.7536.1.S1_s_at	3.30E-04	9.28E-03	0.72	PREDICTED: Canis familiaris similar to small nuclear ribonucleoprotein D2 (LOC481991); mRNA	XM_539112	LOC481991	similar to small nuclear ribonucleoprotein D2
CfaAffx.19604.1.S1_x_at	1.54E-03	1.26E-02	0.67	PREDICTED: Canis familiaris similar to CG17059-PA (LOC482354); mRNA	XM_539471	LOC482354	similar to CG17059-PA
CfaAffx.4604.1.S1_at	1.88E-04	9.00E-03	1.31	PREDICTED: Canis familiaris similar to olfactory receptor Olr859 (LOC482435); mRNA	XM_539552	LOC482435	similar to olfactory receptor Olr859

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.10775.1.S1_at	5.20E-03	1.79E-02	0.75	PREDICTED: Canis familiaris similar to IKK interacting protein isoform 2; transcript variant 3 (LOC482619); mRNA	XM_861359	LOC482619	similar to IKK interacting protein isoform 2
CfaAffx.15171.1.S1_s_at	4.36E-03	1.69E-02	0.74	PREDICTED: Canis familiaris similar to FGFR1 oncogene partner 2; transcript variant 5 (LOC483131); mRNA	XM_851911	LOC483131	similar to FGFR1 oncogene partner 2
Cfa.12195.11.A1_at	2.80E-02	3.71E-02	0.74	PREDICTED: Canis familiaris similar to Histone H2B 291B (LOC483164); mRNA	XM_540282	LOC483164	similar to Histone H2B 291B
CfaAffx.17974.1.S1_at	1.15E-02	2.43E-02	0.62	PREDICTED: Canis familiaris similar to H2B histone family; member F (LOC483173); mRNA	XM_540291	LOC483173	similar to H2B histone family, member F
CfaAffx.759.1.S1_at	8.43E-03	2.14E-02	0.76	PREDICTED: Canis familiaris similar to Histone-lysine N-methyltransferase; H3 lysine-9 specific 4 (Histone H3-K9 methyltransferase 4) (H3-K9-HMTase 4) (SET domain bifurcated 1) (ERG-associated protein with SET domain) (ESET) (LOC483186); mRNA	XM_540304	LOC483186	similar to Histone-lysine N-methyltransferase, H3 lysine-9 specific 4 (Histone H3-K9 methyltransferase 4) (H3-K9-HMTase 4) (SET domain bifurcated 1) (ERG-associated protein with SET domain) (ESET)
CfaAffx.1324.1.S1_at	1.89E-02	3.07E-02	0.73	PREDICTED: Canis familiaris similar to DUF729 domain containing 1 (LOC483997); mRNA	XM_541114	LOC483997	similar to DUF729 domain containing 1
CfaAffx.5095.1.S1_at	3.01E-04	9.25E-03	0.73	PREDICTED: Canis familiaris similar to Zinc finger protein 432; transcript variant 8 (LOC484338); mRNA	XM_858041	LOC484338	similar to Zinc finger protein 432
CfaAffx.7460.1.S1_s_at	4.87E-04	1.00E-02	1.35	PREDICTED: Canis familiaris similar to tripartite motif protein 39 (LOC485141); mRNA	XM_542259	LOC485141	similar to tripartite motif protein 39
Cfa.11764.1.A1_at	4.57E-02	4.84E-02	0.76	PREDICTED: Canis familiaris hypothetical LOC55004; transcript variant 1 (LOC485211); mRNA	XM_542329	LOC485211	hypothetical LOC485211

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.10116.1.S1_at	4.62E-05	7.75E-03	1.32	PREDICTED: Canis familiaris similar to olfactory receptor; family 51; subfamily E; member 1 (LOC485235); mRNA	XM_542353	LOC485235	similar to olfactory receptor, family 51, subfamily E, member 1
CfaAffx.291.1.S1_s_at	7.73E-04	1.10E-02	1.36	PREDICTED: Canis familiaris similar to Olfactory receptor 56A4 (LOC485321); mRNA	XM_542439	LOC485321	similar to Olfactory receptor 56A4
CfaAffx.11153.1.S1_at	9.17E-04	1.15E-02	1.36	PREDICTED: Canis familiaris similar to olfactory receptor Olr245 (LOC485372); mRNA	XM_848953	LOC485372	similar to olfactory receptor Olr245
CfaAffx.13549.1.S1_s_at	2.05E-03	1.35E-02	0.75	PREDICTED: Canis familiaris similar to RAB5-interacting protein isoform a (LOC485858); mRNA	XM_542982	LOC485858	similar to RAB5-interacting protein isoform a
CfaAffx.631.1.S1_x_at	1.73E-04	9.00E-03	1.37	PREDICTED: Canis familiaris similar to olfactory receptor Olr1347 (LOC486190); mRNA	XM_543315	LOC486190	similar to olfactory receptor Olr1347
CfaAffx.16483.1.S1_s_at	1.86E-02	3.04E-02	0.67	PREDICTED: Canis familiaris similar to phosphoglycerate kinase 1 (LOC486305); mRNA	XM_849252	LOC486305	similar to phosphoglycerate kinase 1
CfaAffx.18115.1.S1_s_at	2.45E-04	9.06E-03	0.73	PREDICTED: Canis familiaris hypothetical LOC486899 (LOC486899); mRNA	XM_544029	LOC486899	hypothetical LOC486899
CfaAffx.13504.1.S1_s_at	2.40E-03	1.40E-02	0.73	PREDICTED: Canis familiaris similar to transcription factor IIB (LOC487256); mRNA	XM_544382	LOC487256	similar to transcription factor IIB
CfaAffx.16112.1.S1_at	2.77E-03	1.48E-02	1.39	PREDICTED: Canis familiaris similar to eukaryotic translation elongation factor 1 alpha 1; transcript variant 1 (LOC488054); mRNA	XM_545177	LOC488054	similar to eukaryotic translation elongation factor 1 alpha 1
CfaAffx.641.1.S1_at	5.10E-04	1.00E-02	1.44	PREDICTED: Canis familiaris similar to olfactory receptor; family 6; subfamily C; member 2 (LOC488680); mRNA	XM_848408	LOC488680	similar to olfactory receptor, family 6, subfamily C, member 2
CfaAffx.14124.1.S1_s_at	2.99E-03	1.51E-02	0.75	PREDICTED: Canis familiaris similar to WW domain binding protein 11 (LOC488929); mRNA	XM_847719	LOC488929	similar to WW domain binding protein 11

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.8425.1.S1_a_at	5.61E-03	1.83E-02	0.77	PREDICTED: Canis familiaris similar to transforming growth factor beta regulator 1; transcript variant 3 (LOC489312); mRNA	XM_853901	LOC489312	similar to transforming growth factor beta regulator 1
CfaAffx.27443.1.S1_s_at	1.32E-02	2.59E-02	0.74	PREDICTED: Canis familiaris similar to RIKEN cDNA 1810036I24 (LOC489517); mRNA	XM_546636	LOC489517	similar to RIKEN cDNA 1810036I24
Cfa.21283.1.S1_at	4.31E-04	9.78E-03	0.59	PREDICTED: Canis familiaris similar to RS21-C6 protein (LOC489903); mRNA	XM_547022	LOC489903	similar to RS21-C6 protein
CfaAffx.25383.1.S1_at	6.79E-04	1.07E-02	0.73	PREDICTED: Canis familiaris similar to RS21-C6 protein (LOC489903); mRNA	XM_547022	LOC489903	similar to RS21-C6 protein
CfaAffx.29995.1.S1_at	1.79E-02	2.99E-02	0.74	PREDICTED: Canis familiaris similar to CG3337-PA (LOC490089); mRNA	XM_547210	LOC490089	similar to CG3337-PA
CfaAffx.556.1.S1_s_at	3.92E-03	1.64E-02	0.72	PREDICTED: Canis familiaris hypothetical LOC490542 (LOC490542); mRNA	XM_547664	LOC490542	hypothetical LOC490542
CfaAffx.23440.1.S1_s_at	1.71E-03	1.30E-02	0.75	PREDICTED: Canis familiaris similar to Protein C14orf108 homolog; transcript variant 1 (LOC490711); mRNA	XM_547833	LOC490711	similar to Protein C14orf108 homolog
CfaAffx.23866.1.S1_s_at	7.67E-04	1.10E-02	0.76	PREDICTED: Canis familiaris similar to CG2126-PA (LOC490716); mRNA	XM_547838	LOC490716	similar to CG2126-PA
Cfa.15165.1.A1_s_at	3.78E-03	1.62E-02	0.72	PREDICTED: Canis familiaris similar to CG33071-PC; isoform C (LOC490810); mRNA	XM_547932	LOC490810	similar to CG33071-PC, isoform C
CfaAffx.10966.1.S1_s_at	1.31E-02	2.58E-02	0.64	PREDICTED: Canis familiaris similar to LBP-9 (LOC491028); mRNA	XM_548148	LOC491028	similar to LBP-9
CfaAffx.22384.1.S1_s_at	1.99E-02	3.14E-02	0.7	PREDICTED: Canis familiaris similar to Cullin-3 (CUL-3) (LOC491522); mRNA	XM_548643	LOC491522	similar to Cullin-3 (CUL-3)
CfaAffx.19338.1.S1_at	3.92E-05	7.55E-03	1.47	PREDICTED: Canis familiaris similar to olfactory receptor 630 (LOC491639); mRNA	XM_847695	LOC491639	similar to olfactory receptor 630
CfaAffx.20561.1.S1_s_at	9.61E-04	1.16E-02	0.77	PREDICTED: Canis familiaris similar to Y106G6H.15 (LOC491691); mRNA	XM_548812	LOC491691	similar to Y106G6H.15
CfaAffx.22633.1.S1_at	4.21E-04	9.75E-03	1.35	PREDICTED: Canis familiaris similar to Nucleoplasmin 3 (LOC491846); mRNA	XM_850198	LOC491846	similar to Nucleoplasmin 3
Cfa.10416.1.S1_at	4.00E-03	1.64E-02	0.76	PREDICTED: Bos taurus hypothetical LOC509155 (LOC509155); mRNA	XM_586057	LOC509155	hypothetical LOC509155

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.10408.1.S1_at	1.81E-02	3.00E-02	1.34	PREDICTED: Canis familiaris similar to olfactory receptor Olr1002 (LOC606771); mRNA	XM_843161	LOC606771	similar to olfactory receptor Olr1002
CfaAffx.14005.1.S1_at	2.66E-04	9.11E-03	0.76	PREDICTED: Canis familiaris similar to signal sequence receptor; gamma (LOC606868); mRNA	XM_843338	LOC606868	similar to signal sequence receptor, gamma
Cfa.14458.1.S1_s_at	5.74E-03	1.84E-02	0.74	PREDICTED: Canis familiaris similar to thioredoxin-like 5 (LOC607009); mRNA	XM_843522	LOC607009	similar to thioredoxin-like 5
CfaAffx.265.1.S1_s_at	2.86E-02	3.75E-02	0.75	PREDICTED: Canis familiaris similar to Ig lambda chain V-I region BL2 precursor (LOC607020); mRNA	XM_843551	LOC607020	similar to Ig lambda chain V-I region BL2 precursor
Cfa.17890.1.S1_at	4.37E-02	4.72E-02	0.77	PREDICTED: Canis familiaris hypothetical protein LOC607161 (LOC607161); mRNA	XM_843762	LOC607161	hypothetical protein LOC607161
Cfa.729.1.A1_at	2.49E-02	3.49E-02	0.75	PREDICTED: Canis familiaris similar to Prefoldin subunit 5 (C-myc binding protein Mm-1) (Myc modulator 1) (EIG-1); transcript variant 3 (LOC607260); mRNA	XM_853105	LOC607260	similar to Prefoldin subunit 5 (C-myc binding protein Mm-1) (Myc modulator 1) (EIG-1)
Cfa.16324.1.S1_s_at	7.02E-02	6.16E-02	0.75	PREDICTED: Canis familiaris similar to peptidylprolyl isomerase A isoform 1; transcript variant 1 (LOC607390); mRNA	XM_844247	LOC607390	similar to peptidylprolyl isomerase A isoform 1
CfaAffx.12195.1.S1_s_at	3.84E-04	9.61E-03	0.74	PREDICTED: Canis familiaris similar to cell division cycle 42; transcript variant 2 (LOC607429); mRNA	XM_844251	LOC607429	similar to cell division cycle 42
CfaAffx.22275.1.S1_at	1.15E-02	2.42E-02	1.3	PREDICTED: Canis familiaris similar to Ig lambda chain V-IV region Bau (LOC607441); mRNA	XM_844112	LOC607441	similar to Ig lambda chain V-IV region Bau
CfaAffx.11967.1.S1_at	5.24E-03	1.79E-02	0.71	PREDICTED: Canis familiaris similar to cytochrome P450; family 4; subfamily v; polypeptide 2 (LOC607548); mRNA	XM_844271	LOC607548	similar to cytochrome P450, family 4, subfamily v, polypeptide 2
Cfa.15096.1.S1_s_at	1.14E-03	1.20E-02	0.71	PREDICTED: Canis familiaris similar to nucleolar protein 5; transcript variant 6 (LOC607667); mRNA	XM_854035	LOC607667	similar to nucleolar protein 5

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.3436.1.S1_at	2.58E-02	3.56E-02	0.72	PREDICTED: Canis familiaris similar to nucleolar protein 5; transcript variant 6 (LOC607667); mRNA	XM_854035	LOC607667	similar to nucleolar protein 5
Cfa.18525.1.S1_at	9.12E-02	7.18E-02	0.76	PREDICTED: Canis familiaris similar to CG18675-PA; transcript variant 1 (LOC607697); mRNA	XM_843430	LOC607697	similar to CG18675-PA
CfaAffx.8671.1.S1_at	2.75E-02	3.68E-02	0.71	PREDICTED: Canis familiaris similar to chromosome 3 open reading frame 10; transcript variant 2 (LOC607701); mRNA	XM_856399	LOC607701	similar to chromosome 3 open reading frame 10
CfaAffx.8671.1.S1_s_at	1.53E-02	2.77E-02	0.75	PREDICTED: Canis familiaris similar to chromosome 3 open reading frame 10; transcript variant 2 (LOC607701); mRNA	XM_856399	LOC607701	similar to chromosome 3 open reading frame 10
CfaAffx.3096.1.S1_x_at	6.13E-02	5.71E-02	0.73	PREDICTED: Canis familiaris similar to 60S ribosomal protein L37a (LOC607732); mRNA	XM_843618	LOC607732	similar to 60S ribosomal protein L37a
CfaAffx.17330.1.S1_s_at	8.43E-02	6.85E-02	0.76	PREDICTED: Canis familiaris hypothetical protein LOC607913 (LOC607913); mRNA	XM_844768	LOC607913	hypothetical protein LOC607913
Cfa.18383.1.S1_at	8.62E-03	2.17E-02	0.7	PREDICTED: Canis familiaris similar to THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Transcriptional coactivator Aly/REF) (bZIP enhancing factor BEF) (LOC607948); mRNA	XM_844818	LOC607948	similar to THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Transcriptional coactivator Aly/REF) (bZIP enhancing factor BEF)
Cfa.18383.1.S1_s_at	1.40E-02	2.67E-02	0.73	PREDICTED: Canis familiaris similar to THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Transcriptional coactivator Aly/REF) (bZIP enhancing factor BEF) (LOC607948); mRNA	XM_844818	LOC607948	similar to THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Transcriptional coactivator Aly/REF) (bZIP enhancing factor BEF)

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.9765.1.S1_at	3.20E-02	3.98E-02	0.73	PREDICTED: Canis familiaris similar to THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Transcriptional coactivator Aly/REF) (bZIP enhancing factor BEF) (LOC607948); mRNA	XM_844818	LOC607948	similar to THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Transcriptional coactivator Aly/REF) (bZIP enhancing factor BEF)
Cfa.1050.3.S1_at	4.34E-04	9.78E-03	0.71	PREDICTED: Canis familiaris similar to heat shock 70kD protein binding protein; transcript variant 3 (LOC607960); mRNA	XM_844401	LOC607960	similar to heat shock 70kD protein binding protein
CfaAffx.2582.1.S1_s_at	1.34E-02	2.61E-02	0.73	PREDICTED: Canis familiaris similar to heat shock 70kD protein binding protein; transcript variant 4 (LOC607960); mRNA	XM_853827	LOC607960	similar to heat shock 70kD protein binding protein
CfaAffx.6738.1.S1_s_at	1.51E-02	2.75E-02	0.69	PREDICTED: Canis familiaris similar to chaperonin containing TCP1; subunit 2 (LOC607972); mRNA	XM_844841	LOC607972	similar to chaperonin containing TCP1, subunit 2
Cfa.3337.1.A1_at	8.70E-03	2.17E-02	0.64	PREDICTED: Canis familiaris similar to Splicing factor 3A subunit 3 (Spliceosome associated protein 61) (SAP 61) (SF3a60) (LOC607999); mRNA	XM_844887	LOC607999	similar to Splicing factor 3A subunit 3 (Spliceosome associated protein 61) (SAP 61) (SF3a60)
CfaAffx.4578.1.S1_at	7.87E-03	2.07E-02	1.3	PREDICTED: Canis familiaris similar to 40S ribosomal protein S2 (LOC608028); mRNA	XM_844921	LOC608028	similar to 40S ribosomal protein S2
Cfa.12239.1.S1_s_at	9.53E-04	1.16E-02	0.72	PREDICTED: Canis familiaris similar to ribosomal protein L34 (LOC608033); mRNA	XM_845040	LOC608033	similar to ribosomal protein L34
Cfa.18980.2.S1_at	5.06E-03	1.77E-02	1.31	PREDICTED: Canis familiaris similar to Non-muscle caldesmon (CDM) (L-caldesmon); transcript variant 2 (LOC608135); mRNA	XM_854787	LOC608135	similar to Non-muscle caldesmon (CDM) (L-caldesmon)
CfaAffx.747.1.S1_s_at	3.15E-03	1.53E-02	0.57	PREDICTED: Canis familiaris similar to diazepam binding inhibitor (LOC608150); mRNA	XM_845072	LOC608150	similar to diazepam binding inhibitor

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.7581.1.S1_s_at	2.77E-03	1.48E-02	0.75	PREDICTED: Canis familiaris similar to Ssu72 RNA polymerase II CTD phosphatase homolog (LOC608299); mRNA	XM_845279	LOC608299	similar to Ssu72 RNA polymerase II CTD phosphatase homolog
CfaAffx.19568.1.S1_x_at	5.16E-03	1.79E-02	1.33	PREDICTED: Canis familiaris similar to olfactory receptor Olr1347 (LOC608416); mRNA	XM_534623	LOC608416	similar to olfactory receptor Olr1347
Cfa.3342.1.A1_s_at	2.16E-03	1.37E-02	0.74	PREDICTED: Canis familiaris hypothetical protein LOC608597 (LOC608597); mRNA	XM_845666	LOC608597	hypothetical protein LOC608597
CfaAffx.25281.1.S1_at	6.34E-03	1.91E-02	0.73	PREDICTED: Canis familiaris similar to ADP-ribosylation-like factor 12 protein; transcript variant 1 (LOC608600); mRNA	XM_846551	LOC608600	similar to ADP-ribosylation-like factor 12 protein
CfaAffx.2814.1.S1_s_at	1.38E-04	8.90E-03	0.69	PREDICTED: Canis familiaris similar to eukaryotic translation termination factor 1 (predicted); transcript variant 4 (LOC608717); mRNA	XM_858385	LOC608717	similar to eukaryotic translation termination factor 1 (predicted)
Cfa.10101.1.A1_s_at	3.25E-04	9.28E-03	0.69	PREDICTED: Canis familiaris similar to single-stranded DNA binding protein 1 isoform 1 (LOC608727); mRNA	XM_845839	LOC608727	similar to single-stranded DNA binding protein 1 isoform 1
CfaAffx.11168.1.S1_at	4.23E-03	1.68E-02	0.67	PREDICTED: Canis familiaris similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma laminin-binding protein) (NEM/1CHD4) (Multidrug resistance-associated protein MGr1-Ag) (LOC608876); mRNA	XM_846011	LOC608876	similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma laminin-binding protein) (NEM/1CHD4) (Multidrug resistance-associated protein MGr1-Ag)

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

							similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma laminin-binding protein) (NEM/1CHD4) (Multidrug resistance-associated protein MGr1-Ag)
CfaAffx.32 2.1.S1 x a t	2.37E-03	1.40E-02	0.73	PREDICTED: Canis familiaris similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma laminin-binding protein) (NEM/1CHD4) (Multidrug resistance-associated protein MGr1-Ag) (LOC608876); mRNA	XM_846011	LOC608876	
							similar to SET protein (Phosphatase 2A inhibitor I2PP2A) (I-2PP2A) (Template activating factor I) (TAF-I) (HLA-DR associated protein II) (PHAPII) (Inhibitor of granzyme A-activated DNase) (IGAAD)
Cfa.11306. 1.A1 s at	1.09E-02	2.38E-02	0.72	PREDICTED: Canis familiaris similar to SET protein (Phosphatase 2A inhibitor I2PP2A) (I-2PP2A) (Template activating factor I) (TAF-I) (HLA-DR associated protein II) (PHAPII) (Inhibitor of granzyme A-activated DNase) (IGAAD) (LOC608952); mRNA	XM_846114	LOC608952	
CfaAffx.14 119.1.S1 s at	7.77E-04	1.10E-02	0.75	PREDICTED: Canis familiaris similar to CG18041-PA (LOC609028); mRNA	XM_846208	LOC609028	similar to CG18041-PA
CfaAffx.25 848.1.S1 s at	1.33E-04	8.90E-03	0.7	PREDICTED: Canis familiaris similar to prohibitin (LOC609045); mRNA	XM_846232	LOC609045	similar to prohibitin
CfaAffx.26 274.1.S1 a t	2.36E-03	1.40E-02	1.33	PREDICTED: Canis familiaris hypothetical protein LOC609090 (LOC609090); mRNA	XM_846292	LOC609090	hypothetical protein LOC609090
Cfa.17614. 1.S1 at	2.13E-02	3.24E-02	0.72	PREDICTED: Canis familiaris hypothetical protein LOC609096 (LOC609096); mRNA	XM_846301	LOC609096	hypothetical protein LOC609096
CfaAffx.62 87.1.S1 s at	3.17E-03	1.54E-02	0.76	PREDICTED: Canis familiaris hypothetical protein LOC609096 (LOC609096); mRNA	XM_846301	LOC609096	hypothetical protein LOC609096

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.3811.1.S1_at	1.78E-03	1.30E-02	1.33	PREDICTED: Canis familiaris hypothetical protein LOC609117 (LOC609117); mRNA	XM_846320	LOC609117	hypothetical protein LOC609117
CfaAffx.23009.1.S1_s_at	4.10E-02	4.57E-02	1.34	PREDICTED: Canis familiaris similar to NKG2-F type II integral membrane protein (NKG2-F activating NK receptor) (NK cell receptor F) (LOC609192); mRNA	XM_846408	LOC609192	similar to NKG2-F type II integral membrane protein (NKG2-F activating NK receptor) (NK cell receptor F)
Cfa.594.1.A1_at	1.19E-03	1.21E-02	0.77	PREDICTED: Canis familiaris similar to family with sequence similarity 32; member A; like; transcript variant 2 (LOC609217); mRNA	XM_858065	LOC609217	similar to family with sequence similarity 32, member A, like
Cfa.19973.1.S1_at	1.91E-03	1.32E-02	0.68	PREDICTED: Canis familiaris similar to putative 40-2-3 protein (LOC609238); mRNA	XM_846457	LOC609238	similar to putative 40-2-3 protein
CfaAffx.943.1.S1_at	9.87E-02	7.53E-02	0.69	PREDICTED: Canis familiaris similar to 60S ribosomal protein L17 (L23); transcript variant 1 (LOC609261); mRNA	XM_847140	LOC609261	similar to 60S ribosomal protein L17 (L23)
Cfa.13253.1.A1_at	9.00E-03	2.20E-02	0.7	PREDICTED: Canis familiaris similar to Protein KIAA0152 precursor; transcript variant 1 (LOC609274); mRNA	XM_846298	LOC609274	similar to Protein KIAA0152 precursor
CfaAffx.9633.1.S1_s_at	3.45E-03	1.57E-02	0.75	PREDICTED: Canis familiaris similar to heat shock 70kD protein binding protein (LOC609351); mRNA	XM_846598	LOC609351	similar to heat shock 70kD protein binding protein
CfaAffx.20546.1.S1_s_at	2.26E-02	3.33E-02	0.74	PREDICTED: Canis familiaris similar to sorting nexin 6 (LOC609486); mRNA	XM_846746	LOC609486	similar to sorting nexin 6

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.19736.1.S1_s_at	4.27E-03	1.68E-02	0.73	PREDICTED: Canis familiaris similar to TATA box binding protein-like protein 1 (TBP-like protein 1) (TATA box binding protein-related factor 2) (TBP-related factor 2) (21-kDa TBP-like protein); transcript variant 3 (LOC609509); mRNA	XM_861295	LOC609509	similar to TATA box binding protein-like protein 1 (TBP-like protein 1) (TATA box binding protein-related factor 2) (TBP-related factor 2) (21-kDa TBP-like protein)
Cfa.14095.1.S1_s_at	2.95E-03	1.50E-02	0.69	PREDICTED: Canis familiaris similar to CG17680-PA (LOC609643); mRNA	XM_846940	LOC609643	similar to CG17680-PA
Cfa.4311.1.A1_at	1.74E-03	1.30E-02	0.77	PREDICTED: Canis familiaris similar to MHC class II region expressed gene KE2 (LOC609675); mRNA	XM_846463	LOC609675	similar to MHC class II region expressed gene KE2
CfaAffx.313.1.S1_at	6.39E-04	1.05E-02	0.66	PREDICTED: Canis familiaris similar to GC-rich sequence DNA-binding factor homolog (LOC609740); mRNA	XM_847066	LOC609740	similar to GC-rich sequence DNA-binding factor homolog

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

							similar to Proteasome activator complex subunit 1 (Proteasome activator 28-alpha subunit) (PA28alpha) (PA28a) (Activator of multicatalytic protease subunit 1) (11S regulator complex alpha subunit) (REG-alpha) (Interferon gamma up-regulated I-5111 p...
CfaAffx.3927.1.S1_s_at	5.25E-03	1.79E-02	0.62	PREDICTED: Canis familiaris similar to Proteasome activator complex subunit 1 (Proteasome activator 28-alpha subunit) (PA28alpha) (PA28a) (Activator of multicatalytic protease subunit 1) (11S regulator complex alpha subunit) (REG-alpha) (Interferon gamma up-regulated I-5111 p... (LOC609763); mRNA	XM_847095	LOC609763	
Cfa.10530.1.A1_at	6.05E-03	1.87E-02	0.75	PREDICTED: Canis familiaris similar to Alcohol dehydrogenase class III chi chain (Glutathione-dependent formaldehyde dehydrogenase) (FDH) (LOC609781); mRNA	XM_847120	LOC609781	similar to Alcohol dehydrogenase class III chi chain (Glutathione-dependent formaldehyde dehydrogenase) (FDH)
CfaAffx.6601.1.S1_x_at	3.73E-04	9.61E-03	1.56	PREDICTED: Canis familiaris similar to Ferritin light chain 1 (Ferritin L subunit 1) (LOC609811); mRNA	XM_847150	LOC609811	similar to Ferritin light chain 1 (Ferritin L subunit 1)
CfaAffx.27186.1.S1_at	1.34E-03	1.23E-02	1.31	PREDICTED: Canis familiaris similar to nuclear RNA export factor 2 (LOC609814); mRNA	XM_847153	LOC609814	similar to nuclear RNA export factor 2
CfaAffx.26687.1.S1_at	3.09E-03	1.53E-02	1.33	PREDICTED: Canis familiaris similar to olfactory receptor 464 (LOC609961); mRNA	XM_847316	LOC609961	similar to olfactory receptor 464

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.19061.1.S1_s_at	3.78E-05	7.55E-03	0.66	PREDICTED: Canis familiaris similar to Cytochrome c oxidase polypeptide VIIc; mitochondrial precursor (LOC609990); mRNA	XM_847363	LOC609990	similar to Cytochrome c oxidase polypeptide VIIc, mitochondrial precursor
Cfa.10041.1.S1_s_at	7.86E-03	2.07E-02	0.72	PREDICTED: Canis familiaris similar to Transcription initiation factor TFIID subunit 12 (Transcription initiation factor TFIID 20/15 kDa subunits) (TAFII-20/TAFII 15) (TAFII20/TAFII15); transcript variant 2 (LOC609994); mRNA	XM_847249	LOC609994	similar to Transcription initiation factor TFIID subunit 12 (Transcription initiation factor TFIID 20/15 kDa subunits) (TAFII-20/TAFII-15) (TAFII20/TAFII15)
CfaAffx.29414.1.S1_at	2.44E-03	1.41E-02	0.76	PREDICTED: Canis familiaris similar to CG7338-PA (LOC610048); mRNA	XM_847438	LOC610048	similar to CG7338-PA
Cfa.11083.1.A1_s_at	2.17E-03	1.37E-02	0.73	PREDICTED: Canis familiaris similar to Proteasome subunit alpha type 1 (Proteasome component C2) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome nu chain) (30 kDa prosomal protein) (PROS-30) (LOC610188); mRNA	XM_847620	LOC610188	similar to Proteasome subunit alpha type 1 (Proteasome component C2) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome nu chain) (30 kDa prosomal protein) (PROS-30)
Cfa.9169.1.S1_at	3.36E-03	1.56E-02	0.69	PREDICTED: Canis familiaris hypothetical protein LOC610216 (LOC610216); mRNA	XM_847655	LOC610216	hypothetical protein LOC610216
CfaAffx.23970.1.S1_s_at	1.64E-03	1.28E-02	0.74	PREDICTED: Canis familiaris hypothetical protein LOC610216 (LOC610216); mRNA	XM_847655	LOC610216	hypothetical protein LOC610216

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.17653.1.S1_s_at	2.33E-04	9.06E-03	0.69	PREDICTED: Canis familiaris similar to eukaryotic translation initiation factor 4E member 2 (LOC610238); mRNA	XM_847681	LOC610238	similar to eukaryotic translation initiation factor 4E member 2
Cfa.1293.1.A1_at	3.08E-03	1.52E-02	0.69	PREDICTED: Canis familiaris similar to D-3-phosphoglycerate dehydrogenase (3-PGDH) (LOC610301); partial mRNA	XM_847771	LOC610301	similar to D-3-phosphoglycerate dehydrogenase (3-PGDH)
Cfa.4699.1.A1_at	5.39E-03	1.81E-02	0.71	PREDICTED: Canis familiaris similar to Nucleoside diphosphate-linked moiety X motif 8; mitochondrial precursor (Nudix motif 8); transcript variant 1 (LOC610433); mRNA	XM_846618	LOC610433	similar to Nucleoside diphosphate-linked moiety X motif 8, mitochondrial precursor (Nudix motif 8)
CfaAffx.17839.1.S1_at	2.21E-04	9.06E-03	1.32	PREDICTED: Canis familiaris similar to Olfactory receptor 10T2 (LOC610659); mRNA	XM_848198	LOC610659	similar to Olfactory receptor 10T2
Cfa.19552.1.S1_at	4.59E-02	4.85E-02	0.65	PREDICTED: Canis familiaris similar to HCV NS5A-transactivated protein 9 (L5) (LOC610710); mRNA	XM_848253	LOC610710	similar to HCV NS5A-transactivated protein 9 (L5)
CfaAffx.22590.1.S1_s_at	5.96E-03	1.87E-02	0.76	PREDICTED: Canis familiaris similar to Protein C14orf166 (LOC610819); mRNA	XM_848373	LOC610819	similar to Protein C14orf166
Cfa.4223.1.S1_at	2.73E-03	1.47E-02	0.73	PREDICTED: Canis familiaris similar to Leydig cell tumor 10 kDa protein homolog (LOC610870); mRNA	XM_848432	LOC610870	similar to Leydig cell tumor 10 kDa protein homolog
CfaAffx.405.1.S1_x_at	1.96E-04	9.06E-03	0.68	PREDICTED: Canis familiaris similar to 60S ribosomal protein L32 (LOC610983); mRNA	XM_848585	LOC610983	similar to 60S ribosomal protein L32
Cfa.20665.1.S1_at	9.20E-03	2.22E-02	0.72	PREDICTED: Canis familiaris hypothetical protein LOC611035 (LOC611035); mRNA	XM_862772	LOC611035	hypothetical protein LOC611035
CfaAffx.19320.1.S1_s_at	8.30E-03	2.13E-02	0.75	PREDICTED: Canis familiaris hypothetical protein LOC611035 (LOC611035); mRNA	XM_862772	LOC611035	hypothetical protein LOC611035

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

							similar to Eukaryotic translation initiation factor 4E type 3 (eIF4E type 3) (eIF-4E type 3) (mRNA cap-binding protein type 3) (Eukaryotic translation initiation factor 4E-like 3) (Eukaryotic translation initiation factor 4E homologous protein) (mR...
Cfa.11431.1.A1_at	1.55E-03	1.26E-02	0.68	PREDICTED: Canis familiaris similar to Eukaryotic translation initiation factor 4E type 3 (eIF4E type 3) (eIF-4E type 3) (mRNA cap-binding protein type 3) (Eukaryotic translation initiation factor 4E-like 3) (Eukaryotic translation initiation factor 4E homologous protein) (mR... (LOC611215); mRNA	XM_534606	LOC611215	
							similar to Adapter-related protein complex 1 sigma 1B subunit (Sigma-adaptin 1B) (Adaptor protein complex AP-1 sigma-1B subunit) (Golgi adaptor HA1/AP1 adaptin sigma-1B subunit) (Clathrin assembly protein complex 1 sigma-1B small chain) (Sigma 1B s...
CfaAffx.18992.1.S1_s_at	2.89E-02	3.77E-02	0.76	PREDICTED: Canis familiaris similar to Adapter-related protein complex 1 sigma 1B subunit (Sigma-adaptin 1B) (Adaptor protein complex AP-1 sigma-1B subunit) (Golgi adaptor HA1/AP1 adaptin sigma-1B subunit) (Clathrin assembly protein complex 1 sigma-1B small chain) (Sigma 1B s... (LOC611468); mRNA	XM_849137	LOC611468	

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.28021.1.S1_at	6.60E-03	1.94E-02	0.69	PREDICTED: Canis familiaris similar to mast cell-expressed membrane protein 1 (LOC611542); mRNA	XM_849222	LOC611542	similar to mast cell-expressed membrane protein 1
CfaAffx.22588.1.S1_at	1.46E-02	2.72E-02	0.73	PREDICTED: Canis familiaris similar to rab-related GTP-binding protein (LOC611576); mRNA	XM_849260	LOC611576	similar to rab-related GTP-binding protein
CfaAffx.24327.1.S1_at	4.27E-05	7.55E-03	1.36	PREDICTED: Canis familiaris hypothetical protein LOC611848 (LOC611848); mRNA	XM_849569	LOC611848	hypothetical protein LOC611848
Cfa.9152.2.A1_a_at	3.16E-05	7.55E-03	0.75	PREDICTED: Canis familiaris similar to ubiquitin-conjugating enzyme E2N (LOC611865); mRNA	XM_849588	LOC611865	similar to ubiquitin-conjugating enzyme E2N
Cfa.12014.1.A1_a_at	1.31E-03	1.23E-02	0.74	PREDICTED: Canis familiaris similar to Cytoplasmic dynein light chain (T-complex testis-specific protein 1 homolog) (Protein CW-1) (LOC612201); mRNA	XM_849938	LOC612201	similar to Cytoplasmic dynein light chain (T-complex testis-specific protein 1 homolog) (Protein CW-1)
CfaAffx.1907.1.S1_s_at	4.14E-04	9.68E-03	0.66	PREDICTED: Canis familiaris similar to Cytoplasmic dynein light chain (T-complex testis-specific protein 1 homolog) (Protein CW-1) (LOC612201); mRNA	XM_849938	LOC612201	similar to Cytoplasmic dynein light chain (T-complex testis-specific protein 1 homolog) (Protein CW-1)
CfaAffx.30077.1.S1_at	9.96E-02	7.57E-02	1.32	PREDICTED: Canis familiaris hypothetical protein LOC612376 (LOC612376); mRNA	XM_850107	LOC612376	hypothetical protein LOC612376
CfaAffx.23117.1.S1_x_at	1.22E-02	2.50E-02	0.75	PREDICTED: Canis familiaris similar to ATP synthase; H+ transporting; mitochondrial F0 complex; subunit f; isoform 2 (LOC612408); mRNA	XM_850142	LOC612408	similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2
Cfa.11098.1.A1_at	3.71E-03	1.61E-02	0.69	PREDICTED: Canis familiaris hypothetical protein LOC612531 (LOC612531); mRNA	XM_850261	LOC612531	hypothetical protein LOC612531

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.6153.1.S1_s_at	1.20E-03	1.22E-02	0.67	PREDICTED: Canis familiaris similar to Protein C14orf111 (LOC612615); mRNA	XM_850348	LOC612615	similar to Protein C14orf111
Cfa.2516.1.S1_at	4.46E-03	1.70E-02	0.72	PREDICTED: Canis familiaris hypothetical LOC22889; transcript variant 4 (LOC612936); mRNA	XM_859480	LOC612936	hypothetical LOC612936
CfaAffx.13397.1.S1_at	5.53E-03	1.82E-02	0.72	PREDICTED: Canis familiaris similar to CCR4-NOT transcription complex; subunit 1 isoform a (LOC612978); mRNA	XM_848722	LOC612978	similar to CCR4-NOT transcription complex, subunit 1 isoform a
CfaAffx.465.1.S1_s_at	2.34E-03	1.40E-02	0.65	PREDICTED: Canis familiaris similar to Mblk1-related protein-1 isoform 1 (LOC613008); mRNA	XM_849955	LOC613008	similar to Mblk1-related protein-1 isoform 1
Cfa.17983.1.S1_at	2.81E-03	1.48E-02	0.74	PREDICTED: Macaca mulatta similar to CG8009 PA; isoform A (LOC694061); mRNA	XM_001082901	LOC694061	similar to CG8009-PA, isoform A
Cfa.2406.1.A1_at	7.17E-04	1.08E-02	0.7	PREDICTED: Macaca mulatta similar to mitochondrial ribosomal protein S10 (LOC695892); mRNA	XM_001087232	LOC695892	similar to mitochondrial ribosomal protein S10
Cfa.8912.1.A1_at	9.89E-03	2.29E-02	0.69	PREDICTED: Macaca mulatta similar to low density lipoprotein receptor-related protein 11 (LOC697652); mRNA	XR_010332	LOC697652	similar to low density lipoprotein receptor-related protein 11
Cfa.11661.1.A1_s_at	1.44E-04	8.90E-03	0.69	PREDICTED: Macaca mulatta similar to ubiquitin-conjugating enzyme E2; J1 (LOC701100); mRNA	XM_001096217	LOC701100	similar to ubiquitin-conjugating enzyme E2, J1
Cfa.10621.1.S1_at	9.64E-03	2.27E-02	0.74	PREDICTED: Macaca mulatta similar to Zinc finger CCCH-type domain-containing protein 11A; transcript variant 8 (LOC701537); mRNA	XM_001100644	LOC701537	similar to Zinc finger CCCH-type domain-containing protein 11A
CfaAffx.14680.1.S1_at	1.15E-02	2.42E-02	0.73	PREDICTED: Macaca mulatta similar to splicing factor; arginine/serine-rich 2; interacting protein; transcript variant 2 (LOC701894); mRNA	XM_001093433	LOC701894	similar to splicing factor, arginine/serine-rich 2, interacting protein
Cfa.18058.1.S1_at	8.81E-02	7.03E-02	0.73	PREDICTED: Macaca mulatta similar to HBxAg transactivated protein 2; transcript variant 4 (LOC704297); mRNA	XM_001099296	LOC704297	similar to HBxAg transactivated protein 2

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.7602.1.S1_at	9.20E-04	1.15E-02	0.74	PREDICTED: Macaca mulatta hypothetical protein LOC704974 (LOC704974); mRNA	XM_001100756	LOC704974	hypothetical protein LOC704974
Cfa.931.1.A1_at	1.17E-02	2.45E-02	0.74	PREDICTED: Macaca mulatta similar to chromosome 1 open reading frame 9 protein isoform 1 (LOC705776); mRNA	XM_001100732	LOC705776	similar to chromosome 1 open reading frame 9 protein isoform 1
Cfa.11241.1.A1_at	4.55E-03	1.72E-02	0.75	PREDICTED: Macaca mulatta similar to mitochondrial carrier triple repeat 1; transcript variant 1 (LOC706278); mRNA	XM_001099530	LOC706278	similar to mitochondrial carrier triple repeat 1
CfaAffx.21952.1.S1_s_at	1.57E-05	7.55E-03	0.7	PREDICTED: Macaca mulatta similar to Adrenodoxin; mitochondrial precursor (Adrenal ferredoxin) (Ferredoxin-1) (Hepatoredoxin) (LOC709110); mRNA	XM_001105034	LOC709110	similar to Adrenodoxin, mitochondrial precursor (Adrenal ferredoxin) (Ferredoxin-1) (Hepatoredoxin)
CfaAffx.24141.1.S1_at	2.46E-04	9.06E-03	0.73	PREDICTED: Macaca mulatta similar to RCC1-like (LOC712305); mRNA	XR_012607	LOC712305	similar to RCC1-like
Cfa.10226.1.A1_at	4.60E-02	4.86E-02	0.77	PREDICTED: Macaca mulatta similar to egl nine homolog 1; transcript variant 2 (LOC713410); mRNA	XM_001104870	LOC713410	similar to egl nine homolog 1
Cfa.14782.1.S1_a_at	3.16E-02	3.96E-02	0.6	PREDICTED: Macaca mulatta hypothetical protein LOC714586; transcript variant 1 (LOC714586); mRNA	XM_001111772	LOC714586	hypothetical protein LOC714586
Cfa.10431.1.A1_a_at	1.26E-02	2.54E-02	0.72	PREDICTED: Macaca mulatta similar to phosphatidylinositol glycan class V; transcript variant 9 (LOC714898); mRNA	XM_001110112	LOC714898	similar to phosphatidylinositol glycan class V
CfaAffx.26816.1.S1_s_at	2.38E-03	1.40E-02	0.76	PREDICTED: Macaca mulatta similar to Protein C1orf77 homolog; transcript variant 3 (LOC715501); mRNA	XM_001111616	LOC715501	similar to Protein C1orf77 homolog
Cfa.19566.1.S1_at	1.84E-03	1.31E-02	0.75	PREDICTED: Macaca mulatta similar to homolog of yeast MON2 (LOC716872); mRNA	XR_014521	LOC716872	similar to homolog of yeast MON2
Cfa.2344.1.S1_at	2.10E-02	3.21E-02	0.74	PREDICTED: Homo sapiens similar to protein x 013; transcript variant 3 (LOC727778); mRNA	XM_001125757	LOC727778	similar to protein x 013

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.740.1.S1_at	1.62E-03	1.27E-02	0.62	Sus scrofa NADH dehydrogenase 1 beta subcomplex 6 mRNA; complete cds	DQ372077	LOC733605	NADH dehydrogenase 1 beta subcomplex 6
Cfa.2883.1.A1_at	5.63E-03	1.83E-02	0.75	PREDICTED: Pan troglodytes similar to FLJ31818 protein (LOC735339); mRNA	XM_001134676	LOC735339	similar to FLJ31818 protein
Cfa.1695.1.S1_at	2.60E-03	1.44E-02	0.76	PREDICTED: Pan troglodytes similar to Protein EURL homolog; transcript variant 2 (LOC743596); mRNA	XM_001156300	LOC743596	similar to Protein EURL homolog
Cfa.20450.1.S1_at	2.30E-03	1.39E-02	0.72	PREDICTED: Pan troglodytes selenoprotein H (LOC743806); mRNA	XR_020651	LOC743806	selenoprotein H
CfaAffx.24974.1.S1_s_at	3.24E-03	1.55E-02	0.77	PREDICTED: Pan troglodytes similar to Glutamate receptor; ionotropic; N-methyl D-aspartate-like 1A (LOC744063); mRNA	XR_021922	LOC744063	similar to Glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A
CfaAffx.466.1.S1_at	3.94E-04	9.61E-03	1.32	PREDICTED: Bos taurus similar to transmembrane protein 202 (LOC787358); mRNA	XM_001254778	LOC787358	similar to transmembrane protein 202
Cfa.896.1.A1_at	2.84E-03	1.48E-02	0.73	PREDICTED: Bos taurus similar to RIKEN cDNA 4121402D02 gene (LOC787839); mRNA	XM_001254563	LOC787839	similar to RIKEN cDNA 4121402D02 gene
CfaAffx.14833.1.S1_at	4.54E-03	1.71E-02	0.76	PREDICTED: Canis familiaris similar to CG32699-PA (LOC611330); mRNA	XM_848987	LPCAT2	lysophosphatidylcholine acyltransferase 2
Cfa.15317.1.A1_at	8.92E-03	2.19E-02	0.77	PREDICTED: Macaca mulatta lysophosphatidylglycerol acyltransferase 1; transcript variant 2 (LPGAT1); mRNA	XM_001108590	LPGAT1	lysophosphatidylglycerol acyltransferase 1
CfaAffx.22529.1.S1_s_at	5.00E-02	5.10E-02	0.76	PREDICTED: Canis familiaris similar to Alpha-2-macroglobulin receptor-associated protein precursor (Alpha-2-MRAP) (Low density lipoprotein receptor-related protein-associated protein 1) (RAP) (LOC479072); mRNA	XM_536218	LRPAP1	low density lipoprotein receptor-related protein associated protein 1
CfaAffx.4662.1.S1_s_at	3.92E-04	9.61E-03	0.69	PREDICTED: Canis familiaris similar to leucine-rich PPR motif-containing protein (LOC474572); mRNA	XM_531800	LRPPRC	leucine-rich PPR-motif containing

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.21185.1.S1_s_at	1.20E-04	8.90E-03	1.3	PREDICTED: Canis familiaris similar to leucine rich repeat containing 2; transcript variant 2 (LOC476647); mRNA	XM_859331	LRRC2	leucine rich repeat containing 2
Cfa.2068.1.S1_at	5.97E-03	1.87E-02	0.76	PREDICTED: Canis familiaris similar to CG3040-PA (LOC478269); mRNA	XM_535443	LRRC57	leucine rich repeat containing 57
Cfa.11684.1.A1_at	1.41E-03	1.24E-02	0.76	Homo sapiens mRNA for KIAA1437 protein; partial cds	AB037858	LRRC8A	leucine rich repeat containing 8 family, member A
CfaAffx.10169.1.S1_s_at	1.67E-03	1.29E-02	0.72	PREDICTED: Canis familiaris similar to U6 snRNA-associated Sm-like protein LSm1 (Small nuclear ribonuclear CaSm) (Cancer-associated Sm-like) (LOC475587); mRNA	XM_532806	LSM1	LSM1 homolog, U6 small nuclear RNA associated (S. cerevisiae)
Cfa.19032.1.S1_s_at	1.19E-03	1.21E-02	0.73	PREDICTED: Canis familiaris similar to alpha synuclein binding protein (LOC476492); mRNA	XM_533701	LSM14A	LSM14A, SCD6 homolog A (S. cerevisiae)
Cfa.2957.1.A1_s_at	3.79E-03	1.63E-02	0.77	PREDICTED: Canis familiaris similar to alpha synuclein binding protein (LOC476492); mRNA	XM_533701	LSM14A	LSM14A, SCD6 homolog A (S. cerevisiae)
Cfa.3288.1.A1_at	7.92E-04	1.10E-02	0.7	PREDICTED: Canis familiaris similar to alpha synuclein binding protein (LOC476492); mRNA	XM_533701	LSM14A	LSM14A, SCD6 homolog A (S. cerevisiae)
CfaAffx.12446.1.S1_s_at	6.35E-03	1.91E-02	0.75	PREDICTED: Canis familiaris similar to U6 snRNA-associated Sm-like protein LSm6 (LOC612329); mRNA	XM_850069	LSM6	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)
Cfa.8071.2.S1_a_at	1.66E-03	1.28E-02	0.69	PREDICTED: Canis familiaris similar to U6 snRNA-associated Sm-like protein LSm7 (LOC612170); mRNA	XM_849902	LSM7	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.20853.1.S1_s_at	8.81E-03	2.18E-02	0.72	PREDICTED: Canis familiaris similar to U6 snRNA-associated Sm-like protein LSm8; transcript variant 2 (LOC475298); mRNA	XM_861126	LSM8	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae)
Cfa.21629.2.S1_s_at	2.57E-02	3.55E-02	0.72	PREDICTED: Canis familiaris similar to LUC7-like isoform b; transcript variant 2 (LOC479898); mRNA	XM_860439	LUC7L	LUC7-like (S. cerevisiae)
CfaAffx.816.1.S1_at	4.04E-03	1.65E-02	0.72	PREDICTED: Canis familiaris similar to Lymphocyte antigen 96 precursor (MD-2 protein) (ESOP-1) (LOC610524); mRNA	XM_848045	LY96	lymphocyte antigen 96
Cfa.3936.1.A1_at	3.75E-02	4.34E-02	0.76	PREDICTED: Canis familiaris similar to lysozyme-like 6; transcript variant 2 (LOC480492); mRNA	XM_855795	LYZL6	lysozyme-like 6
Cfa.1844.1.S1_at	1.58E-02	2.82E-02	0.73	PREDICTED: Canis familiaris similar to Mitotic spindle assembly checkpoint protein MAD2A (MAD2-like 1) (HsMAD2); transcript variant 1 (LOC476070); mRNA	XM_533278	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)
Cfa.11345.1.A1_s_at	3.44E-03	1.57E-02	0.66	PREDICTED: Canis familiaris similar to Mago nashi protein homolog; transcript variant 1 (LOC479562); mRNA	XM_536702	MAGOH	mago-nashi homolog, proliferation-associated (Drosophila)
CfaAffx.26407.1.S1_at	4.00E-05	7.55E-03	0.67	PREDICTED: Canis familiaris similar to implantation-associated protein; transcript variant 1 (LOC491975); mRNA	XM_549095	MAGT1	magnesium transporter 1
Cfa.9780.1.A1_at	7.21E-03	2.00E-02	0.7	PREDICTED: Canis familiaris similar to corneal wound healing-related protein; transcript variant 4 (LOC476304); mRNA	XM_851202	MAK10	MAK10 homolog, amino-acid N-acetyltransferase subunit (S. cerevisiae)
CfaAffx.1126.1.S1_s_at	7.93E-03	2.08E-02	0.74	PREDICTED: Canis familiaris similar to Mucosa associated lymphoid tissue lymphoma translocation protein 1 (MALT-lymphoma associated translocation) (Paracaspase) (LOC476188); mRNA	XM_533392	MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.10702.1.A1_at	5.96E-04	1.04E-02	0.71	PREDICTED: Canis familiaris similar to mannosidase; alpha; class 1A; member 1 (LOC476275); mRNA	XM_533481	MAN1A1	mannosidase, alpha, class 1A, member 1
Cfa.10702.2.A1_a_at	1.21E-03	1.22E-02	0.75	PREDICTED: Canis familiaris similar to mannosidase; alpha; class 1A; member 1 (LOC476275); mRNA	XM_533481	MAN1A1	mannosidase, alpha, class 1A, member 1
Cfa.9537.1.S1_at	1.81E-03	1.31E-02	0.73	Homo sapiens mRNA; cDNA DKFZp686H1529 (from clone DKFZp686H1529)	AL833486	MAN2A1	mannosidase, alpha, class 2A, member 1
Cfa.16571.1.S1_s_at	4.22E-03	1.67E-02	1.31	PREDICTED: Canis familiaris similar to Microtubule-associated protein 1B (MAP 1B); transcript variant 1 (LOC478092); mRNA	XM_535269	MAP1B	microtubule-associated protein 1B
Cfa.3055.1.A1_at	1.08E-02	2.37E-02	0.73	PREDICTED: Pan troglodytes mitogen-activated protein kinase kinase kinase 2; transcript variant 2 (MAP3K2); mRNA	XM_001137266	MAP3K2	mitogen-activated protein kinase kinase kinase 2
CfaAffx.5642.1.S1_s_at	5.51E-04	1.02E-02	0.69	PREDICTED: Equus caballus mitogen-activated protein kinase kinase kinase 7; transcript variant 4 (MAP3K7); mRNA	XM_001503786	MAP3K7	mitogen-activated protein kinase kinase kinase 7
Cfa.16190.1.A1_at	8.10E-03	2.10E-02	0.73	PREDICTED: Canis familiaris similar to mitogen-activated protein kinase kinase kinase 7 interacting protein 2 isoform 1 (LOC484028); mRNA	XM_541145	MAP3K7IP2	mitogen-activated protein kinase kinase kinase 7 interacting protein 2
CfaAffx.23699.1.S1_at	3.64E-03	1.61E-02	0.69	Canis lupus familiaris mitogen-activated protein kinase 1 (MAPK1); mRNA	NM_001110800	MAPK1	mitogen-activated protein kinase 1
CfaAffx.23699.1.S1_s_at	1.76E-03	1.30E-02	0.76	Canis lupus familiaris mitogen-activated protein kinase 1 (MAPK1); mRNA	NM_001110800	MAPK1	mitogen-activated protein kinase 1
Cfa.1239.1.S1_s_at	1.82E-03	1.31E-02	0.75	Canis familiaris p38 mitogen activated protein kinase mRNA; complete cds	AF003597	MAPK14	mitogen-activated protein kinase 14

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.23968.1.S1_s_at	2.04E-03	1.35E-02	0.7	PREDICTED: Canis familiaris similar to Mitogen-activated protein kinase 6 (Extracellular signal-regulated kinase 3) (ERK-3) (MAP kinase isoform p97) (p97-MAPK); transcript variant 4 (LOC478311); mRNA	XM_858091	MAPK6	mitogen-activated protein kinase 6
CfaAffx.11823.1.S1_s_at	1.34E-03	1.23E-02	0.76	PREDICTED: Canis familiaris similar to Microtubule-associated protein RP/EB family member 1 (APC-binding protein EB1) (End-binding protein 1) (EB1) (LOC608797); mRNA	XM_845932	MAPRE1	microtubule-associated protein, RP/EB family, member 1
Cfa.15713.1.A1_at	4.83E-02	5.00E-02	0.67	PREDICTED: Canis familiaris similar to Macrophage receptor MARCO (Macrophage receptor with collagenous structure) (LOC476117); mRNA	XM_533324	MARCO	macrophage receptor with collagenous structure
Cfa.13953.1.A1_s_at	2.67E-03	1.46E-02	0.72	PREDICTED: Canis familiaris similar to methionine adenosyltransferase II; alpha; transcript variant 7 (LOC475770); mRNA	XM_860499	MAT2A	methionine adenosyltransferase II, alpha
CfaAffx.26280.1.S1_s_at	1.28E-03	1.23E-02	0.71	PREDICTED: Canis familiaris similar to methionine adenosyltransferase II; beta isoform 1 (LOC479301); mRNA	XM_536439	MAT2B	methionine adenosyltransferase II, beta
CfaAffx.18288.1.S1_at	1.74E-04	9.00E-03	0.71	PREDICTED: Canis familiaris similar to methylcrotonoyl-Coenzyme A carboxylase 1 (alpha); transcript variant 1 (LOC478645); mRNA	XM_535817	MCCC1	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)
Cfa.4015.2.A1_s_at	1.82E-02	3.01E-02	0.74	PREDICTED: Canis familiaris similar to Methylmalonyl-CoA epimerase; mitochondrial precursor (DL-methylmalonyl-CoA racemase) (LOC479018); mRNA	XM_536170	MCEE	methylmalonyl CoA epimerase
Cfa.2489.1.S1_at	3.94E-03	1.64E-02	0.69	PREDICTED: Canis familiaris similar to DNA replication licensing factor MCM6 (P105MCM) (LOC476131); mRNA	XM_533338	MCM6	minichromosome maintenance complex component 6
CfaAffx.8672.1.S1_s_at	1.28E-03	1.23E-02	0.7	PREDICTED: Canis familiaris similar to DNA replication licensing factor MCM6 (P105MCM) (LOC476131); mRNA	XM_533338	MCM6	minichromosome maintenance complex component 6

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.2296.1.A1_s_at	2.42E-03	1.41E-02	0.74	PREDICTED: Canis familiaris similar to malignant T cell amplified sequence 1; transcript variant 3 (LOC481038); mRNA	XM_859581	MCTS1	malignant T cell amplified sequence 1
Cfa.3262.1.A1_at	1.84E-03	1.31E-02	0.75	PREDICTED: Canis familiaris similar to Malate dehydrogenase; cytoplasmic; transcript variant 2 (LOC474614); mRNA	XM_860817	MDH1	malate dehydrogenase 1, NAD (soluble)
Cfa.3262.1.A1_s_at	6.81E-04	1.07E-02	0.77	PREDICTED: Canis familiaris similar to Malate dehydrogenase; cytoplasmic; transcript variant 2 (LOC474614); mRNA	XM_860817	MDH1	malate dehydrogenase 1, NAD (soluble)
Cfa.702.2.S1_at	7.06E-03	1.99E-02	0.72	Felis catus mRNA for double minute 2 protein MDM2; complete cds	AB099709	MDM2	Mdm2 p53 binding protein homolog (mouse)
CfaAffx.1587.1.S1_at	1.50E-03	1.25E-02	0.67	Felis catus mRNA for double minute 2 protein MDM2; complete cds	AB099709	MDM2	Mdm2 p53 binding protein homolog (mouse)
CfaAffx.1587.1.S1_s_at	4.33E-02	4.70E-02	0.76	Canis familiaris MDM2 alpha mRNA; complete cds	AF322417	MDM2	Mdm2 p53 binding protein homolog (mouse)
CfaAffx.13482.1.S1_s_at	1.49E-03	1.25E-02	1.39	PREDICTED: Equus caballus mediator complex subunit 12-like (MED12L); mRNA	XM_001917728	MED12L	mediator complex subunit 12-like
CfaAffx.18384.1.S1_s_at	9.33E-04	1.16E-02	0.75	PREDICTED: Canis familiaris similar to mediator of RNA polymerase II transcription; subunit 18 homolog; transcript variant 2 (LOC487334); mRNA	XM_860582	MED18	mediator complex subunit 18
Cfa.4136.1.S1_at	1.48E-02	2.73E-02	0.71	PREDICTED: Canis familiaris similar to SRB7 suppressor of RNA polymerase B homolog; transcript variant 2 (LOC477664); mRNA	XM_847225	MED21	mediator complex subunit 21
CfaAffx.17422.1.S1_s_at	3.54E-03	1.59E-02	0.74	PREDICTED: Canis familiaris similar to SRB7 suppressor of RNA polymerase B homolog; transcript variant 2 (LOC477664); mRNA	XM_847225	MED21	mediator complex subunit 21
Cfa.15341.1.S1_s_at	4.38E-03	1.69E-02	0.73	PREDICTED: Canis familiaris similar to intersex-like (LOC612535); mRNA	XM_850265	MED29	mediator complex subunit 29

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.3244.1.A1_at	7.57E-05	8.57E-03	0.7	familiaris similar to Mediator of RNA polymerase II transcription subunit 31 (Mediator complex subunit SOH1) (hSOH1) (LOC607000); mRNA	XM_843504	MED31	mediator complex subunit 31
Cfa.3124.1.S1_at	1.06E-02	2.35E-02	0.74	Bos taurus mediator complex subunit 6; mRNA (cDNA clone MGC:127713 IMAGE:7955413); complete cds	BC102648	MED6	mediator complex subunit 6
CfaAffx.25501.1.S1_s_at	5.15E-03	1.79E-02	0.76	PREDICTED: Canis familiaris similar to RNA polymerase transcriptional regulation mediator; subunit 6 homolog (Activator-recruited cofactor 33 kDa component) (ARC33) (NY-REN-28 antigen) (LOC490763); mRNA	XM_547885	MED6	mediator complex subunit 6
CfaAffx.26895.1.S1_s_at	3.81E-04	9.61E-03	0.71	Homo sapiens mediator complex subunit 7 (MED7); transcript variant 1; mRNA	NM_001100816	MED7	mediator complex subunit 7
Cfa.9519.1.A1_at	3.42E-05	7.55E-03	0.63	Homo sapiens myocyte enhancer factor 2C (MEF2C); transcript variant 2; mRNA	NM_001131005	MEF2C	myocyte enhancer factor 2C
Cfa.16795.1.S1_at	1.68E-03	1.29E-02	0.71	PREDICTED: Pan troglodytes hypothetical protein LOC461760; transcript variant 4 (LOC461760); mRNA	XM_001142658	MEF2C	myocyte enhancer factor 2C
Cfa.9073.1.A1_s_at	1.34E-04	8.90E-03	0.68	PREDICTED: Canis familiaris similar to MADS box transcription enhancer factor 2; polypeptide C (myocyte enhancer factor 2C); transcript variant 30 (LOC479155); mRNA	XM_853734	MEF2C	myocyte enhancer factor 2C
CfaAffx.13186.1.S1_s_at	1.34E-02	2.61E-02	0.74	PREDICTED: Canis familiaris similar to MADS box transcription enhancer factor 2; polypeptide C (myocyte enhancer factor 2C); transcript variant 30 (LOC479155); mRNA	XM_853734	MEF2C	myocyte enhancer factor 2C
CfaAffx.6283.1.S1_at	2.67E-02	3.62E-02	0.75	familiaris similar to Multiple EGF-like-domain protein 5 precursor (Multiple epidermal growth factor-like domains 9) (LOC481698); mRNA	XM_538819	MEGF9	multiple EGF-like-domains 9

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.10510.1.S1_s_at	1.87E-03	1.32E-02	0.73	familiaris similar to Methionine aminopeptidase 2 (MetAP 2) (Peptidase M 2) (Initiation factor 2 associated 67 kDa glycoprotein) (p67) (p67eIF2); transcript variant 1 (LOC475429); mRNA	XM_847559	METAP2	methionyl aminopeptidase 2
Cfa.10266.1.A1_at	7.08E-04	1.08E-02	0.73	familiaris similar to Hypothetical UPF0049 protein ZK1128.2 in chromosome III; transcript variant 2 (LOC480655); mRNA	XM_863412	METT10D	methyltransferase 10 domain containing
Cfa.2303.1.A1_s_at	2.02E-02	3.16E-02	0.73	PREDICTED: Equus caballus mex-3 homolog C (C. elegans) (MEX3C); mRNA	XM_001916773	MEX3C	mex-3 homolog C (C. elegans)
CfaAffx.20742.1.S1_s_at	3.44E-03	1.57E-02	0.75	familiaris similar to microfibrillar-associated protein 1; transcript variant 2 (LOC478281); mRNA	XM_855367	MFAP1	microfibrillar-associated protein 1
CfaAffx.17646.1.S1_at	6.49E-04	1.05E-02	0.73	PREDICTED: Canis familiaris similar to Transmembrane GTPase MFN1 (Mitofusin-1) (LOC488086); mRNA	XM_545210	MFN1	mitofusin 1
Cfa.5250.1.A1_at	9.15E-04	1.15E-02	0.74	PREDICTED: Canis familiaris similar to CG18549-PA; transcript variant 1 (LOC483336); mRNA	XM_540455	MFSD11	major facilitator superfamily domain containing 11
CfaAffx.21875.1.S1_s_at	2.61E-03	1.44E-02	0.77	familiaris similar to Alpha-1;6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase (Mannoside acetylglucosaminyltransferase 2) (N-glycosyl-oligosaccharide-glycoprotein N-acetylglucosaminyltransferase II) (Beta-1;2-N-acetylglucosaminyltransferase II)... (LOC480312); mRNA	XM_537434	MGAT2	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
Cfa.12884.1.S1_at	4.77E-03	1.74E-02	0.74	PREDICTED: Canis familiaris similar to meningioma expressed antigen 5 (hyaluronidase); transcript variant 12 (LOC477802); mRNA	XM_857266	MGEA5	meningioma expressed antigen 5 (hyaluronidase)
CfaAffx.15618.1.S1_s_at	4.49E-03	1.71E-02	0.75	PREDICTED: Canis familiaris similar to meningioma expressed antigen 5 (hyaluronidase); transcript variant 14 (LOC477802); mRNA	XM_857326	MGEA5	meningioma expressed antigen 5 (hyaluronidase)

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.4313.1.S1_at	1.19E-02	2.47E-02	0.74	PREDICTED: Canis familiaris similar to CG14985-PA (LOC474559); mRNA	XM_531787	MITD1	MIT, microtubule interacting and transport, domain containing 1
Cfa.13251.1.S1_s_at	3.01E-04	9.25E-03	0.74	Homo sapiens cDNA FLJ78507 complete cds	AK291925	MKKS	McKusick-Kaufman syndrome
CfaAffx.14107.1.S1_at	5.99E-04	1.04E-02	1.31	PREDICTED: Canis familiaris similar to matrix metalloproteinase 16 isoform 1 (LOC487036); mRNA	XM_544165	MMP16	matrix metallopeptidase 16 (membrane-inserted)
Cfa.16589.1.S1_at	1.56E-02	2.79E-02	0.76	PREDICTED: Canis familiaris similar to myeloid cell nuclear differentiation antigen (LOC488622); mRNA	XM_545739	MNDA	myeloid cell nuclear differentiation antigen
Cfa.20723.1.S1_at	1.58E-02	2.81E-02	0.72	PREDICTED: Canis familiaris similar to myeloid cell nuclear differentiation antigen (LOC488622); mRNA	XM_545739	MNDA	myeloid cell nuclear differentiation antigen
Cfa.3008.1.A1_at	2.04E-03	1.35E-02	0.7	PREDICTED: Pan troglodytes MOB1; Mps One Binder kinase activator-like 1A; transcript variant 2 (MOBKL1A); mRNA	XM_001159188	MOBKL1A	MOB1, Mps One Binder kinase activator-like 1A (yeast)
Cfa.2714.1.A1_at	7.14E-03	1.99E-02	0.75	PREDICTED: Canis familiaris similar to preimplantation protein 3; transcript variant 1 (LOC478856); mRNA	XM_536018	MOBKL3	MOB1, Mps One Binder kinase activator-like 3 (yeast)
CfaAffx.1442.1.S1_s_at	1.33E-03	1.23E-02	0.69	PREDICTED: Canis familiaris similar to CG31756-PA; transcript variant 3 (LOC481141); mRNA	XM_845015	MON2	MON2 homolog (S. cerevisiae)
CfaAffx.16142.1.S1_at	2.66E-03	1.45E-02	1.37	Homo sapiens MORC family CW-type zinc finger 1 (MORC1); mRNA	NM_014429	MORC1	MORC family CW-type zinc finger 1
Cfa.9449.1.A1_at	6.14E-03	1.89E-02	0.75	Bos taurus MORC family CW-type zinc finger 3; mRNA (cDNA clone IMAGE:8163086); partial cds	BC151785	MORC3	MORC family CW-type zinc finger 3
CfaAffx.18481.1.S1_s_at	4.06E-03	1.65E-02	0.75	PREDICTED: Canis familiaris similar to motile sperm domain containing 2 (LOC491747); mRNA	XM_548867	MOSPD2	motile sperm domain containing 2
CfaAffx.12147.1.S1_s_at	1.01E-03	1.17E-02	0.72	PREDICTED: Canis familiaris similar to M-phase phosphoprotein 9 (LOC477453); mRNA	XM_534651	MPHOSPH9	M-phase phosphoprotein 9

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.19439.1.S1_s_at	3.92E-03	1.64E-02	0.76	PREDICTED: Canis familiaris similar to membrane protein; palmitoylated 6; transcript variant 2 (LOC482362); mRNA	XM_846249	MPP6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)
Cfa.11680.1.A1_at	2.36E-03	1.40E-02	0.76	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L16 (LOC476898); partial mRNA	XM_534101	MRPL16	mitochondrial ribosomal protein L16
CfaAffx.10831.1.S1_at	6.02E-04	1.04E-02	0.77	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L17; transcript variant 1 (LOC610200); mRNA	XM_846034	MRPL17	mitochondrial ribosomal protein L17
Cfa.10307.1.A1_s_at	3.97E-05	7.55E-03	0.68	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L18 (LOC476260); mRNA	XM_533465	MRPL18	mitochondrial ribosomal protein L18
CfaAffx.744.1.S1_at	2.49E-04	9.06E-03	0.75	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L18 (LOC476260); mRNA	XM_533465	MRPL18	mitochondrial ribosomal protein L18
CfaAffx.29394.1.S1_s_at	3.72E-05	7.55E-03	0.71	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L20 (LOC479569); mRNA	XM_536709	MRPL20	mitochondrial ribosomal protein L20
Cfa.5875.3.A1_s_at	5.83E-03	1.85E-02	0.7	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L22 isoform a (LOC479320); mRNA	XM_536458	MRPL22	mitochondrial ribosomal protein L22
Cfa.15082.1.S1_a_at	1.37E-04	8.90E-03	0.73	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L27; transcript variant 4 (LOC491078); mRNA	XM_860518	MRPL27	mitochondrial ribosomal protein L27
CfaAffx.913.1.S1_s_at	1.05E-03	1.19E-02	0.74	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L30 isoform a (LOC474558); mRNA	XM_531786	MRPL30	mitochondrial ribosomal protein L30
CfaAffx.23692.1.S1_s_at	6.59E-03	1.94E-02	0.75	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L34 (LOC610139); mRNA	XM_847552	MRPL34	mitochondrial ribosomal protein L34
Cfa.16020.1.S1_s_at	3.69E-05	7.55E-03	0.71	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L36 (LOC488065); mRNA	XM_545188	MRPL36	mitochondrial ribosomal protein L36
Cfa.11000.1.S1_s_at	8.64E-04	1.13E-02	0.74	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L39 isoform a (LOC487709); mRNA	XM_544833	MRPL39	mitochondrial ribosomal protein L39

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.22522.1.S1_s_at	3.26E-03	1.55E-02	0.75	PREDICTED: Canis familiaris similar to 39S ribosomal protein L40; mitochondrial precursor (L40mt) (MRP-40) (Nuclear localization signal containing protein deleted in velocardiofacial syndrome) (Up-regulated in metastasis) (LOC477567); mRNA	XM_534762	MRPL40	mitochondrial ribosomal protein L40
CfaAffx.29659.1.S1_at	1.59E-04	9.00E-03	0.75	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L41 (predicted) (LOC491225); mRNA	XM_548346	MRPL41	mitochondrial ribosomal protein L41
Cfa.1786.2.S1_a_at	4.46E-02	4.77E-02	0.77	PREDICTED: Canis familiaris similar to Mitochondrial 28S ribosomal protein S32 (S32mt) (MRP-S32); transcript variant 1 (LOC475426); mRNA	XM_532651	MRPL42	mitochondrial ribosomal protein L42
CfaAffx.703.1.S1_s_at	3.83E-03	1.63E-02	0.75	PREDICTED: Canis familiaris similar to Mitochondrial 28S ribosomal protein S32 (S32mt) (MRP-S32); transcript variant 1 (LOC475426); mRNA	XM_532651	MRPL42	mitochondrial ribosomal protein L42
Cfa.2797.1.A1_at	6.15E-04	1.05E-02	0.75	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L46 (LOC479035); mRNA	XM_536185	MRPL46	mitochondrial ribosomal protein L46
Cfa.2797.1.A1_s_at	1.95E-04	9.06E-03	0.75	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L46 (LOC479035); mRNA	XM_536185	MRPL46	mitochondrial ribosomal protein L46
CfaAffx.9326.1.S1_s_at	9.94E-05	8.90E-03	0.74	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L48 isoform 1 (LOC476812); mRNA	XM_534016	MRPL48	mitochondrial ribosomal protein L48
CfaAffx.23288.1.S1_s_at	9.46E-04	1.16E-02	0.77	Homo sapiens CDA09 mRNA; complete cds	AF212248	MRPL51	mitochondrial ribosomal protein L51
Cfa.11655.1.A1_at	1.85E-03	1.31E-02	0.75	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein L9 (LOC609109); mRNA	XM_846311	MRPL9	mitochondrial ribosomal protein L9
Cfa.21309.1.S1_at	2.22E-05	7.55E-03	0.75	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein S10 (LOC474902); mRNA	XM_532137	MRPS10	mitochondrial ribosomal protein S10
Cfa.4020.1.S1_a_at	4.13E-02	4.58E-02	0.72	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein S16 (LOC609906); mRNA	XM_847254	MRPS16	mitochondrial ribosomal protein S16

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.1496.1.A1_at	8.95E-03	2.20E-02	0.74	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein S26 (LOC477175); mRNA	XM_534365	MRPS26	mitochondrial ribosomal protein S26
Cfa.5262.1.A1_at	5.85E-05	8.40E-03	0.67	PREDICTED: Canis familiaris similar to Mitochondrial 28S ribosomal protein S28 (S28mt) (MRP-S28) (MRP-S35) (LOC477919); mRNA	XM_535109	MRPS28	mitochondrial ribosomal protein S28
Cfa.10909.1.A1_s_at	4.68E-03	1.73E-02	0.76	PREDICTED: Canis familiaris similar to Mitochondrial 28S ribosomal protein S30 (S30mt) (MRP-S30) (Programmed cell death protein 9) (LOC479341); mRNA	XM_536480	MRPS30	mitochondrial ribosomal protein S30
CfaAffx.12433.1.S1_s_at	2.33E-03	1.40E-02	0.64	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein S36 (LOC478085); mRNA	XM_535262	MRPS36	mitochondrial ribosomal protein S36
CfaAffx.11447.1.S1_s_at	3.36E-03	1.56E-02	0.76	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein S5 (LOC475746); mRNA	XM_532953	MRPS5	mitochondrial ribosomal protein S5
Cfa.14269.1.S1_a_at	1.36E-03	1.23E-02	0.66	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein S9; transcript variant 2 (LOC474545); mRNA	XM_858101	MRPS9	mitochondrial ribosomal protein S9
CfaAffx.4090.1.S1_s_at	2.28E-03	1.39E-02	0.73	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein S9; transcript variant 2 (LOC474545); mRNA	XM_858101	MRPS9	mitochondrial ribosomal protein S9
CfaAffx.4865.1.S1_s_at	4.30E-03	1.68E-02	0.74	PREDICTED: Canis familiaris similar to mutS homolog 6 (LOC474585); mRNA	XM_531814	MSH6	mutS homolog 6 (E. coli)
CfaAffx.17154.1.S1_at	2.74E-03	1.47E-02	1.31	Canis familiaris tyrosine kinase receptor ron mRNA; partial cds	AY646195	MST1R	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)
Cfa.3664.1.S1_s_at	3.16E-02	3.96E-02	0.58	Canis lupus familiaris mRNA for metallothionein-1; complete cds	D84397	MT1F	metallothionein 1F
Cfa.3542.1.S1_at	5.62E-02	5.43E-02	0.58	Canis lupus familiaris mRNA for metallothionein-II; complete cds	AB028042	MT2A	metallothionein 2A
Cfa.15125.1.S1_at	1.14E-02	2.42E-02	0.76	PREDICTED: Canis familiaris similar to S-methyl-5-thioadenosine phosphorylase (5-methylthioadenosine phosphorylase) (MTA phosphorylase) (MTAPase) (LOC474729); mRNA	XM_531959	MTAP	methylthioadenosine phosphorylase

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.9192.1.A1_at	1.84E-04	9.00E-03	0.73	PREDICTED: Canis familiaris similar to Mitochondrial carrier homolog 2 (Met-induced mitochondrial protein); transcript variant 6 (LOC475977); mRNA	XM_855249	MTCH2	mitochondrial carrier homolog 2 (C. elegans)
Cfa.1889.2.S1_s_at	5.94E-03	1.86E-02	0.76	PREDICTED: Canis familiaris similar to Metal-response element-binding transcription factor 2 (Metal-response element DNA-binding protein M96); transcript variant 1 (LOC479948); mRNA	XM_537073	MTF2	metal response element binding transcription factor 2
CfaAffx.30853.1.S1_at	7.49E-04	1.09E-02	0.74	PREDICTED: Canis familiaris similar to Metal-response element-binding transcription factor 2 (Metal-response element DNA-binding protein M96); transcript variant 3 (LOC479948); mRNA	XM_861836	MTF2	metal response element binding transcription factor 2
Cfa.1889.1.A1_s_at	2.00E-04	9.06E-03	0.75	PREDICTED: Canis familiaris similar to Metal-response element-binding transcription factor 2 (Metal-response element DNA-binding protein M96); transcript variant 8 (LOC479948); mRNA	XM_861899	MTF2	metal response element binding transcription factor 2
CfaAffx.24531.1.S1_s_at	3.38E-03	1.56E-02	0.76	PREDICTED: Canis familiaris similar to C-1-tetrahydrofolate synthase; cytoplasmic (C1-THF synthase) (LOC480352); mRNA	XM_537476	MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase
Cfa.19689.1.S1_at	1.23E-03	1.23E-02	1.36	PREDICTED: Canis familiaris similar to methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like (LOC476245); mRNA	XM_533450	MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like
Cfa.20403.1.S1_a_at	1.66E-02	2.89E-02	1.32	PREDICTED: Canis familiaris similar to C01G5.8; transcript variant 4 (LOC479017); mRNA	XM_851634	MTMR15	myotubularin related protein 15
Cfa.18355.1.S1_at	5.42E-04	1.02E-02	0.66	PREDICTED: Canis familiaris similar to Myotubularin-related protein 6 (LOC477336); mRNA	XM_534530	MTMR6	myotubularin related protein 6

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.18355.1.S1_s_at	1.52E-03	1.25E-02	0.74	PREDICTED: Canis familiaris similar to Myotubularin-related protein 6 (LOC477336); mRNA	XM_534530	MTMR6	myotubularin related protein 6
Cfa.20047.1.S1_s_at	1.03E-03	1.18E-02	0.7	PREDICTED: Canis familiaris similar to Myotubularin-related protein 6 (LOC477336); mRNA	XM_534530	MTMR6	myotubularin related protein 6
CfaAffx.11496.1.S1_at	1.91E-03	1.32E-02	0.71	PREDICTED: Canis familiaris similar to Myotubularin-related protein 6 (LOC477336); mRNA	XM_534530	MTMR6	myotubularin related protein 6
Cfa.19419.1.S1_s_at	1.15E-03	1.21E-02	0.73	PREDICTED: Canis familiaris similar to mitochondrial translational release factor 1-like (LOC484040); mRNA	XM_541157	MTRF1L	mitochondrial translational release factor 1-like
Cfa.11299.1.S1_s_at	2.84E-04	9.15E-03	0.7	PREDICTED: Canis familiaris similar to Metaxin 2 (LOC478811); mRNA	XM_535974	MTX2	metaxin 2
Cfa.19576.1.S1_s_at	4.49E-03	1.71E-02	0.76	familiaris similar to Methylmalonyl-CoA mutase; mitochondrial precursor (MCM) (Methylmalonyl-CoA isomerase) (LOC474930); mRNA	XM_532164	MUT	methylmalonyl Coenzyme A mutase
Cfa.10384.1.S1_at	1.28E-04	8.90E-03	0.73	Bos taurus muted homolog (mouse); mRNA (cDNA clone MGC:159907 IMAGE:8493721); complete cds	BC146091	MUTED	muted homolog (mouse)
Cfa.13565.1.A1_at	2.12E-02	3.24E-02	0.76	Canis familiaris GTP-binding protein Mx2 mRNA; complete cds	AF239824	MX2	myxovirus (influenza virus) resistance 2 (mouse)
CfaAffx.24234.1.S1_s_at	5.01E-03	1.76E-02	0.76	PREDICTED: Canis familiaris similar to Myosin 5A (Myosin Va) (Dilute myosin heavy chain; non-muscle) (LOC478312); mRNA	XM_535487	MYO5A	myosin VA (heavy chain 12, myoxin)
Cfa.11535.1.A1_at	6.24E-03	1.89E-02	0.76	PREDICTED: Canis familiaris similar to Zinc finger protein 42 (Myeloid zinc finger 1) (MZF-1) (Zinc finger and SCAN domain containing protein 6) (LOC484220); mRNA	XM_541336	MZF1	myeloid zinc finger 1
CfaAffx.24408.1.S1_s_at	6.01E-03	1.87E-02	0.71	PREDICTED: Canis familiaris similar to Nedd4 binding protein 2 (LOC479101); mRNA	XM_536248	N4BP2	NEDD4 binding protein 2
CfaAffx.10528.1.S1_at	6.42E-03	1.92E-02	0.71	PREDICTED: Canis familiaris similar to CG7139-PA; isoform A (LOC477316); mRNA	XM_534508	N4BP2L2	NEDD4 binding protein 2-like 2

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.29324.1.S1_at	1.29E-02	2.56E-02	0.73	PREDICTED: Canis familiaris similar to Putative inorganic polyphosphate/ATP-NAD kinase (Poly(P)/ATP NAD kinase); transcript variant 2 (LOC489589); mRNA	XM_843740	NADK	NAD kinase
CfaAffx.31239.1.S1_s_at	2.43E-02	3.45E-02	0.75	familiaris similar to amyloid beta precursor protein-binding protein 1 isoform a; transcript variant 3 (LOC610026); mRNA	XM_859743	NAE1	NEDD8 activating enzyme E1 subunit 1
CfaAffx.6906.1.S1_at	1.60E-02	2.84E-02	0.72	Homo sapiens nicotinamide phosphoribosyltransferase (NAMPT); mRNA	NM_005746	NAMPT	nicotinamide phosphoribosyltransferase
Cfa.604.1.A1_at	1.64E-02	2.87E-02	0.74	PREDICTED: Bos taurus pre-B-cell colony enhancing factor 1; transcript variant 4 (PBEF1); mRNA	XM_878444	NAMPT	nicotinamide phosphoribosyltransferase
Cfa.1585.1.A1_s_at	1.16E-02	2.44E-02	0.74	PREDICTED: Canis familiaris similar to NMDA receptor regulated 1 (LOC483817); mRNA	XM_540937	NARG1	NMDA receptor regulated 1
CfaAffx.16719.1.S1_s_at	5.63E-05	8.24E-03	0.73	acetyltransferase 13; mRNA (cDNA clone MGC:54829 IMAGE:6438976); complete cds	BC046283	Nat13	N-acetyltransferase 13
Cfa.13620.2.A1_s_at	3.04E-04	9.25E-03	0.69	PREDICTED: Canis familiaris similar to N-acetyltransferase 5; transcript variant 1 (LOC477138); mRNA	XM_534329	NAT5	N-acetyltransferase 5
Cfa.13620.1.S1_at	3.13E-03	1.53E-02	0.75	PREDICTED: Canis familiaris similar to N-acetyltransferase 5; transcript variant 2 (LOC477138); mRNA	XM_851508	NAT5	N-acetyltransferase 5
Cfa.861.1.S1_at	5.85E-03	1.85E-02	0.74	PREDICTED: Canis familiaris similar to nibrin isoform 1 (LOC611315); mRNA	XM_848973	NBN	nibrin
CfaAffx.14194.1.S1_s_at	4.16E-03	1.67E-02	0.7	PREDICTED: Canis familiaris similar to nibrin isoform 1 (LOC611315); mRNA	XM_848973	NBN	nibrin
Cfa.6001.1.A1_at	2.48E-04	9.06E-03	0.71	familiaris similar to Nuclear cap binding protein subunit 2 (20 kDa nuclear cap binding protein) (NCBP 20 kDa subunit) (CBP20) (NCBP interacting protein 1) (NIP1) (LOC478603); mRNA	XM_535779	NCBP2	nuclear cap binding protein subunit 2, 20kDa
CfaAffx.17748.1.S1_at	4.62E-02	4.87E-02	0.76	TPA_inf: Canis lupus familiaris ncf1 mRNA for predicted neutrophil cytosolic factor 1; partial cds	BR000287	NCF1	neutrophil cytosolic factor 1

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.17297.1.S1_s_at	8.42E-03	2.14E-02	0.67	PREDICTED: Canis familiaris similar to nucleolin-related protein; transcript variant 4 (LOC608445); mRNA	XM_856520	NCL	nucleolin
Cfa.9842.1.A1_s_at	1.45E-02	2.71E-02	0.74	PREDICTED: Canis familiaris similar to nuclear receptor coactivator 1 isoform 2; transcript variant 3 (LOC475684); mRNA	XM_853439	NCOA1	nuclear receptor coactivator 1
CfaAffx.27681.1.S1_at	6.81E-03	1.96E-02	0.74	PREDICTED: Canis familiaris similar to nuclear receptor co-repressor 1; transcript variant 5 (LOC479515); mRNA	XM_858680	NCOR1	nuclear receptor co-repressor 1
Cfa.3066.1.S1_at	2.46E-02	3.47E-02	0.76	PREDICTED: Canis familiaris similar to kinetochore associated 2 (LOC480190); mRNA	XM_537313	NDC80	NDC80 homolog, kinetochore complex component (S. cerevisiae)
Cfa.865.1.S1_at	2.39E-02	3.42E-02	0.75	PREDICTED: Canis familiaris similar to Nedd4 family interacting protein 2 (LOC476956); mRNA	XM_534156	NDFIP2	Nedd4 family interacting protein 2
Cfa.10289.1.S1_at	4.24E-03	1.68E-02	0.73	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 10; 42kDa precursor (LOC608244); mRNA	XM_845210	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa
CfaAffx.19535.1.S1_s_at	4.09E-04	9.68E-03	0.72	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 10; 42kDa precursor (LOC608244); mRNA	XM_845210	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa
Cfa.4375.1.S1_a_at	9.78E-04	1.16E-02	0.76	PREDICTED: Canis familiaris similar to 13kDa differentiation-associated protein (LOC475428); mRNA	XM_532652	NDUFA12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.18026.1.S1_s_at	1.84E-04	9.00E-03	0.65	PREDICTED: Canis familiaris similar to NADH-ubiquinone oxidoreductase B16.6 subunit (Complex I-B16.6) (CI-B16.6) (Gene associated with retinoic-interferon-induced mortality 19 protein) (GRIM-19) (Cell death-regulatory protein GRIM-19); transcript variant 1 (LOC476659); mRNA	XM_533863	NDUFA13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13
CfaAffx.9746.1.S1_s_at	4.09E-04	9.68E-03	0.71	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 2; 8kDa (LOC478032); mRNA	XM_535211	NDUFA2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa
Cfa.4415.1.S1_at	1.38E-04	8.90E-03	0.76	PREDICTED: Canis familiaris similar to NADH-ubiquinone oxidoreductase MLRQ subunit (Complex I-MLRQ) (CI-MLRQ) (LOC477682); mRNA	XM_534877	NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa
CfaAffx.4275.1.S1_s_at	1.09E-03	1.20E-02	0.69	PREDICTED: Canis familiaris similar to NADH-ubiquinone oxidoreductase MLRQ subunit (Complex I-MLRQ) (CI-MLRQ) (LOC477682); mRNA	XM_534877	NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa
CfaAffx.764.1.S1_at	6.81E-02	6.06E-02	1.33	PREDICTED: Canis familiaris similar to NADH-ubiquinone oxidoreductase MLRQ subunit (Complex I-MLRQ) (CI-MLRQ) (LOC477682); mRNA	XM_534877	NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa
Cfa.11777.1.S1_at	4.67E-05	7.75E-03	1.33	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 6; 14kDa (LOC474483); mRNA	XM_531712	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa
Cfa.11777.2.A1_s_at	2.05E-05	7.55E-03	0.66	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 6; 14kDa (LOC474483); mRNA	XM_531712	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.16755.1.S1_s_at	4.04E-05	7.55E-03	0.74	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 7; 14.5kDa (LOC476722); mRNA	XM_533926	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa
Cfa.714.1.A1_s_at	1.12E-03	1.20E-02	0.74	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 8; 19kDa (LOC480741); mRNA	XM_537861	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa
Cfa.10920.1.S1_s_at	1.51E-03	1.25E-02	0.71	PREDICTED: Canis familiaris similar to Acyl carrier protein; mitochondrial precursor (ACP) (NADH-ubiquinone oxidoreductase 9.6 kDa subunit) (CI-SDAP) (LOC479805); mRNA	XM_536932	NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa
CfaAffx.26929.1.S1_s_at	3.29E-02	4.05E-02	0.75	PREDICTED: Canis familiaris similar to Acyl carrier protein; mitochondrial precursor (ACP) (NADH-ubiquinone oxidoreductase 9.6 kDa subunit) (CI-SDAP) (LOC479805); mRNA	XM_536932	NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa
Cfa.2918.1.S1_s_at	4.01E-03	1.65E-02	0.77	PREDICTED: Canis familiaris similar to Complex I intermediate-associated protein 30; mitochondrial precursor (LOC487505); mRNA	XM_544629	NDUFAF1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1
Cfa.15483.1.A1_s_at	2.10E-04	9.06E-03	0.66	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 3; 12kDa (LOC478869); mRNA	XM_536029	NDUFB3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
Cfa.273.3.A1_s_at	1.26E-06	6.68E-03	0.71	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8; transcript variant 1 (LOC477798); mRNA	XM_534992	NDUFB8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.10947.1.S1_at	4.86E-03	1.75E-02	0.76	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex; 9; 22kDa (LOC475094); mRNA	XM_532326	NDUFB9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa
Cfa.17764.1.S1_s_at	4.13E-03	1.66E-02	0.76	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) Fe-S protein 1; 75kDa precursor; transcript variant 7 (LOC478880); mRNA	XM_854604	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)
Cfa.9529.1.A1_s_at	2.26E-03	1.38E-02	0.67	PREDICTED: Canis familiaris similar to NADH-ubiquinone oxidoreductase 18 kDa subunit; mitochondrial precursor (Complex I-18 kDa) (CI-18 kDa) (Complex I-AQDQ) (CI-AQDQ) (LOC479335); mRNA	XM_536474	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)
CfaAffx.15952.1.S1_s_at	9.10E-04	1.15E-02	0.67	PREDICTED: Canis familiaris similar to NADH-ubiquinone oxidoreductase 18 kDa subunit; mitochondrial precursor (Complex I-18 kDa) (CI-18 kDa) (Complex I-AQDQ) (CI-AQDQ) (LOC479335); mRNA	XM_536474	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)
Cfa.4245.1.S1_s_at	3.88E-05	7.55E-03	0.67	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) Fe-S protein 6; 13kDa (NADH-coenzyme Q reductase) (LOC478629); mRNA	XM_535802	NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)
CfaAffx.28547.1.S1_at	1.87E-03	1.32E-02	0.75	PREDICTED: Canis familiaris similar to NADH dehydrogenase (ubiquinone) flavoprotein 2; 24kDa (LOC480204); mRNA	XM_537328	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.734.1.A1_s_at	2.89E-04	9.23E-03	0.68	PREDICTED: Canis familiaris similar to neural precursor cell expressed; developmentally down-regulated gene 8 (LOC480265); mRNA	XM_537389	NEDD8	neural precursor cell expressed, developmentally down-regulated 8
Cfa.16364.1.A1_at	8.04E-04	1.10E-02	0.45	Bos taurus neuroepithelial cell transforming gene 1; mRNA (cDNA clone MGC:127767 IMAGE:7956312); complete cds	BC102858	NET1	neuroepithelial cell transforming gene 1
Cfa.19790.1.S1_at	6.47E-03	1.93E-02	0.75	PREDICTED: Equus caballus nuclear factor of activated T-cells 5; tonicity-responsive (NFAT5); mRNA	XM_001497295	NFAT5	nuclear factor of activated T-cells 5, tonicity responsive
CfaAffx.31027.1.S1_s_at	2.25E-02	3.32E-02	0.75	PREDICTED: Canis familiaris similar to nuclear factor of activated T-cells 5 isoform b; transcript variant 1 (LOC489734); mRNA	XM_546854	NFAT5	nuclear factor of activated T-cells 5, tonicity responsive
Cfa.2119.1.S1_s_at	8.43E-04	1.12E-02	0.73	PREDICTED: Canis familiaris similar to Protein C14orf120 (LOC490612); mRNA	XM_547734	NGDN	neuroguidin, EIF4E binding protein
CfaAffx.22448.1.S1_s_at	1.93E-02	3.10E-02	0.74	Homo sapiens ninein (GSK3B interacting protein) (NIN); transcript variant 2; mRNA	NM_020921	NIN	ninein (GSK3B interacting protein)
Cfa.466.2.S1_a_at	8.88E-03	2.19E-02	0.76	[illegible] familiaris similar to 60S ribosome subunit biogenesis protein NIP7 homolog (KD93); transcript variant 2 (LOC479673); mRNA	XM_536804	NIP7	nuclear import 7 homolog (S. cerevisiae)
CfaAffx.15298.1.S1_s_at	3.84E-04	9.61E-03	0.74	PREDICTED: Canis familiaris similar to non imprinted in Prader-Willi/Angelman syndrome 2 isoform a (LOC479002); mRNA	XM_536157	NIPA2	non imprinted in Prader-Willi/Angelman syndrome 2
CfaAffx.26479.1.S1_x_at	1.72E-03	1.30E-02	0.71	Canis lupus familiaris nm23-C1 mRNA for NM23-C1; complete cds	AB207044	NME1	non-metastatic cells 1, protein (NM23A) expressed in
Cfa.5818.2.S1_s_at	3.37E-05	7.55E-03	0.73	Sus scrofa mRNA for c-myc transcription factor; complete cds	AB292846	NME2	non-metastatic cells 2, protein (NM23B) expressed in

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.7425.1.S1_x_at	8.76E-02	7.01E-02	1.31	PREDICTED: Canis familiaris similar to Nucleoside diphosphate kinase; mitochondrial precursor (NDP kinase; mitochondrial) (NDK) (nm23-H4) (Nucleoside diphosphate kinase D) (NDPKD) (LOC476911); mRNA	XM_534114	NME4	non-metastatic cells 4, protein expressed in
Cfa.15049.1.S1_s_at	9.37E-02	7.30E-02	0.76	PREDICTED: Canis familiaris similar to N-myc interactor (Nmi) (N-myc and STAT interactor) (LOC476146); mRNA	XM_533353	NMI	N-myc (and STAT) interactor
Cfa.17031.1.S1_at	3.09E-04	9.27E-03	0.76	PREDICTED: Canis familiaris similar to N-myristoyltransferase 1; transcript variant 6 (LOC480494); mRNA	XM_850785	NMT1	N-myristoyltransferase 1
Cfa.377.1.S1_at	2.50E-02	3.50E-02	0.77	PREDICTED: Canis familiaris similar to NAD(P) transhydrogenase; mitochondrial precursor (Pyridine nucleotide transhydrogenase) (Nicotinamide nucleotide transhydrogenase); transcript variant 5 (LOC479342); mRNA	XM_862835	NNT	nicotinamide nucleotide transhydrogenase
CfaAffx.15451.1.S1_s_at	2.12E-03	1.36E-02	0.65	PREDICTED: Canis familiaris similar to nucleolar protein 7; 27kDa (LOC478727); mRNA	XM_535892	NOL7	nucleolar protein 7, 27kDa
Cfa.4420.1.A1_at	1.66E-03	1.28E-02	0.77	PREDICTED: Canis familiaris similar to nucleolar protein family A; member 3 (LOC607299); mRNA	XM_843924	NOLA3	nucleolar protein family A, member 3 (H/ACA small nucleolar RNPs)
CfaAffx.26405.1.S1_at	6.29E-02	5.79E-02	1.32	Mus musculus neurexin III (Nrxn3); mRNA	NM_172544	Nrxn3	neurexin III
CfaAffx.20857.1.S1_s_at	7.07E-04	1.08E-02	0.75	PREDICTED: Canis familiaris similar to N-ethylmaleimide-sensitive factor; transcript variant 1 (LOC490921); mRNA	XM_548044	NSF	N-ethylmaleimide-sensitive factor
CfaAffx.19270.1.S1_at	4.73E-03	1.74E-02	0.65	PREDICTED: Canis familiaris similar to Protein C10orf86 (LOC477849); mRNA	XM_535041	NSMCE4A	non-SMC element 4 homolog A (S. cerevisiae)
CfaAffx.16214.1.S1_s_at	7.55E-03	2.04E-02	0.73	PREDICTED: Canis familiaris similar to Cytosolic purine 5-nucleotidase (5-nucleotidase cytosolic II); transcript variant 1 (LOC477809); mRNA	XM_535002	NT5C2	5'-nucleotidase, cytosolic II

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.7187.1.A1_a_at	7.48E-04	1.09E-02	0.75	PREDICTED: Canis familiaris similar to N-terminal Asn amidase (LOC609485); mRNA	XM_846745	NTAN1	N-terminal asparagine amidase
CfaAffx.28683.1.S1_s_at	9.86E-03	2.29E-02	0.75	PREDICTED: Canis familiaris similar to N-terminal Asn amidase (LOC609485); mRNA	XM_846745	NTAN1	N-terminal asparagine amidase
Cfa.12389.1.A1_at	5.04E-03	1.77E-02	0.73	PREDICTED: Canis familiaris similar to Nucleotide-binding protein 1 (NBP 1); transcript variant 3 (LOC479850); mRNA	XM_858530	NUBP1	nucleotide binding protein 1 (MinD homolog, E. coli)
CfaAffx.13803.1.S1_at	5.15E-03	1.79E-02	0.74	familiaris similar to Nucleobindin 2 precursor (DNA-binding protein NEFA) (Gastric cancer antigen Zg4); transcript variant 7 (LOC476876); mRNA	XM_859996	NUCB2	nucleobindin 2
Cfa.16462.1.S1_s_at	2.68E-04	9.11E-03	0.7	PREDICTED: Canis familiaris similar to nudix-type motif 1 isoform p22 (LOC489894); mRNA	XM_547012	NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1
Cfa.10274.1.S1_s_at	4.39E-04	9.78E-03	0.7	PREDICTED: Canis familiaris similar to ADP-sugar pyrophosphatase (Nucleoside diphosphate-linked moiety X motif 5) (Nudix motif 5) (YSA1H); transcript variant 1 (LOC478006); mRNA	XM_535190	NUDT5	nudix (nucleoside diphosphate linked moiety X)-type motif 5
Cfa.923.1.A1_s_at	1.11E-03	1.20E-02	0.72	familiaris similar to Nuclear pore complex protein Nup107 (Nucleoporin Nup107) (107 kDa nucleoporin); transcript variant 2 (LOC474440); mRNA	XM_855893	NUP107	nucleoporin 107kDa
Cfa.13055.1.S1_at	2.65E-03	1.45E-02	0.75	PREDICTED: Canis familiaris similar to Nucleoporin Nup37 (p37) (LOC475445); mRNA	XM_532669	NUP37	nucleoporin 37kDa
CfaAffx.13595.1.S1_s_at	1.44E-02	2.70E-02	0.74	familiaris similar to Nucleoporin p54 (54 kDa nucleoporin); transcript variant 3 (LOC487813); mRNA	XM_843545	NUP54	nucleoporin 54kDa
CfaAffx.4788.1.S1_at	6.17E-04	1.05E-02	0.72	PREDICTED: Canis familiaris similar to opioid growth factor receptor-like 1 (LOC481876); mRNA	XM_538997	OGFRL1	opioid growth factor receptor-like 1

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.15244.1.S1_at	1.89E-02	3.06E-02	0.76	PREDICTED: Canis familiaris similar to O-linked GlcNAc transferase isoform 1; transcript variant 1 (LOC480955); mRNA	XM_538075	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)
Cfa.874.2.S1_s_at	2.78E-03	1.48E-02	0.72	PREDICTED: Canis familiaris similar to O-linked GlcNAc transferase isoform 1; transcript variant 1 (LOC480955); mRNA	XM_538075	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)
Cfa.18574.1.S1_s_at	1.80E-03	1.30E-02	0.69	PREDICTED: Canis familiaris similar to O-linked GlcNAc transferase isoform 1; transcript variant 3 (LOC480955); mRNA	XM_853469	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)
Cfa.20843.1.S1_s_at	5.51E-04	1.02E-02	0.7	PREDICTED: Canis familiaris similar to O-linked GlcNAc transferase isoform 1; transcript variant 8 (LOC480955); mRNA	XM_853715	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)
Cfa.19273.1.S1_at	9.34E-04	1.16E-02	0.74	PREDICTED: Canis familiaris similar to Putative GTP-binding protein PTD004; transcript variant 2 (LOC478803); mRNA	XM_845227	OLA1	Obg-like ATPase 1

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.1129.1.S1_at	4.45E-03	1.70E-02	0.76	PREDICTED: Canis familiaris similar to optic atrophy 1 isoform 8 (LOC477129); mRNA	XM_534321	OPA1	optic atrophy 1 (autosomal dominant)
Cfa.1129.1.S1_s_at	3.96E-02	4.48E-02	0.76	PREDICTED: Canis familiaris similar to optic atrophy 1 isoform 8 (LOC477129); mRNA	XM_534321	OPA1	optic atrophy 1 (autosomal dominant)
CfaAffx.12889.1.S1_at	4.14E-04	9.68E-03	1.41	PREDICTED: Canis familiaris olfactory receptor (OR04A01); mRNA	XM_540654	OR04A01	olfactory receptor
Cfa.20932.1.S1_s_at	1.27E-04	8.90E-03	0.7	PREDICTED: Canis familiaris similar to origin recognition complex subunit 4 (LOC476141); mRNA	XM_533348	ORC4L	origin recognition complex, subunit 4-like (yeast)
CfaAffx.9239.1.S1_at	1.53E-03	1.26E-02	0.71	PREDICTED: Canis familiaris similar to origin recognition complex subunit 4 (LOC476141); mRNA	XM_533348	ORC4L	origin recognition complex, subunit 4-like (yeast)
Cfa.1563.1.S1_at	1.65E-03	1.28E-02	0.75	PREDICTED: Canis familiaris similar to oxysterol-binding protein-like protein 11; transcript variant 2 (LOC478596); mRNA	XM_844091	OSBPL11	oxysterol binding protein-like 11
Cfa.1061.2.A1_a_at	2.10E-02	3.22E-02	0.76	PREDICTED: Canis familiaris similar to oxysterol binding protein-like 9 isoform b; transcript variant 5 (LOC475355); mRNA	XM_854394	OSBPL9	oxysterol binding protein-like 9
CfaAffx.14794.1.S1_at	3.14E-03	1.53E-02	0.75	Homo sapiens mRNA for putative sialoglycoprotease type 2	AJ295148	OSGEPL1	O-sialoglycoprotein endopeptidase-like 1
Cfa.10153.1.S1_at	2.38E-03	1.40E-02	0.69	Felis catus 3-oxoacid CoA transferase 1 (OXCT1) mRNA; partial cds	EU650370	OXCT1	3-oxoacid CoA transferase 1
Cfa.16830.1.S1_at	5.36E-02	5.30E-02	0.75	PREDICTED: Canis familiaris similar to 3-oxoacid CoA transferase 1 (LOC479347); mRNA	XM_536487	OXCT1	3-oxoacid CoA transferase 1
CfaAffx.28412.1.S1_s_at	1.50E-02	2.75E-02	0.77	PREDICTED: Canis familiaris similar to 3-oxoacid CoA transferase 1 (LOC479347); mRNA	XM_536487	OXCT1	3-oxoacid CoA transferase 1
CfaAffx.28373.1.S1_s_at	1.72E-02	2.93E-02	0.77	PREDICTED: Canis familiaris similar to poly(A) binding protein interacting protein 1; transcript variant 1 (LOC479343); mRNA	XM_536482	PAIP1	poly(A) binding protein interacting protein 1
CfaAffx.15220.1.S1_at	5.48E-02	5.36E-02	0.74	PREDICTED: Canis familiaris similar to PAK1 interacting protein 1 (LOC478719); mRNA	XM_535884	PAK1IP1	PAK1 interacting protein 1

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.11016.1.S1_at	1.06E-02	2.35E-02	0.74	PREDICTED: Canis familiaris similar to PABP1-dependent poly A-specific ribonuclease subunit PAN3 (LOC486024); mRNA	XM_543150	PAN3	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)
CfaAffx.26074.1.S1_at	7.76E-03	2.06E-02	0.65	PREDICTED: Pan troglodytes hypothetical LOC462250 (LOC462250); mRNA	XM_518087	PANK3	pantothenate kinase 3
Cfa.19159.1.A1_at	1.14E-02	2.42E-02	0.74	PREDICTED: Canis familiaris similar to pantothenate kinase 4 (LOC479579); mRNA	XM_536718	PANK4	pantothenate kinase 4
CfaAffx.14274.1.S1_s_at	2.11E-03	1.36E-02	0.68	PREDICTED: Canis familiaris similar to PAP associated domain containing 4; transcript variant 2 (LOC607764); mRNA	XM_844605	PAPD4	PAP associated domain containing 4
CfaAffx.27222.1.S1_at	1.95E-03	1.33E-02	0.75	PREDICTED: Canis familiaris similar to poly(A) polymerase alpha (LOC480430); mRNA	XM_537551	PAPOLA	poly(A) polymerase alpha
CfaAffx.30092.1.S1_s_at	1.05E-04	8.90E-03	0.71	PREDICTED: Canis familiaris similar to DJ-1 protein; transcript variant 6 (LOC479595); mRNA	XM_853938	PARK7	Parkinson disease (autosomal recessive, early onset) 7
CfaAffx.18610.1.S1_s_at	8.08E-03	2.10E-02	0.77	PREDICTED: Canis familiaris similar to presenilin associated; rhomboid-like; transcript variant 2 (LOC488100); mRNA	XM_545224	PARL	presenilin associated, rhomboid-like
CfaAffx.2476.1.S1_at	1.49E-05	7.55E-03	0.76	PREDICTED: Canis familiaris similar to dimerization cofactor of hepatocyte nuclear factor 1 (HNF1) from muscle (LOC609970); mRNA	XM_847332	PCBD2	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2
CfaAffx.2476.1.S1_s_at	2.01E-03	1.35E-02	0.77	PREDICTED: Canis familiaris similar to dimerization cofactor of hepatocyte nuclear factor 1 (HNF1) from muscle (LOC609970); mRNA	XM_847332	PCBD2	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2

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CfaAffx.9732.1.S1_at	3.52E-03	1.59E-02	0.72	familiaris similar to propionyl-Coenzyme A carboxylase; alpha polypeptide precursor; transcript variant 2 (LOC476975); mRNA	XM_534175	PCCA	propionyl Coenzyme A carboxylase, alpha polypeptide
CfaAffx.11739.1.S1_s_at	1.57E-03	1.26E-02	0.77	PREDICTED: Canis familiaris similar to Propionyl-CoA carboxylase beta chain; mitochondrial precursor (PCCase beta subunit) (Propanoyl-CoA:carbon dioxide ligase beta subunit); transcript variant 3 (LOC477076); mRNA	XM_859611	PCCB	propionyl Coenzyme A carboxylase, beta polypeptide
CfaAffx.1550.1.S1_at	5.04E-03	1.77E-02	0.74	PREDICTED: Canis familiaris similar to Protein-L-isoaspartate(D-aspartate) O-methyltransferase (Protein-beta-aspartate methyltransferase) (PIMT) (Protein L-isoaspartyl/D-aspartyl methyltransferase) (L-isoaspartyl protein carboxyl methyltransferase); transcript variant 9 (LOC476242); mRNA	XM_856739	PCMT1	protein-L-isoaspartate (D-aspartate) O-methyltransferase
Cfa.3996.1.A1_s_at	1.01E-03	1.17E-02	0.75	PREDICTED: Canis familiaris similar to Protein-L-isoaspartate(D-aspartate) O-methyltransferase (Protein-beta-aspartate methyltransferase) (PIMT) (Protein L-isoaspartyl/D-aspartyl methyltransferase) (L-isoaspartyl protein carboxyl methyltransferase); transcript variant 10 (LOC476242); mRNA	XM_856769	PCMT1	protein-L-isoaspartate (D-aspartate) O-methyltransferase
Cfa.525.1.S1_at	3.67E-03	1.61E-02	0.67	PREDICTED: Canis familiaris similar to proliferating cell nuclear antigen (LOC477166); mRNA	XM_534355	PCNA	proliferating cell nuclear antigen
Cfa.14096.1.S1_at	7.46E-03	2.03E-02	0.76	PREDICTED: Canis familiaris similar to PEST-containing nuclear protein (PCNP); transcript variant 1 (LOC478546); mRNA	XM_535723	PCNP	PEST proteolytic signal containing nuclear protein
Cfa.14096.2.S1_s_at	1.53E-04	9.00E-03	0.71	PREDICTED: Canis familiaris similar to PEST-containing nuclear protein (PCNP); transcript variant 1 (LOC478546); mRNA	XM_535723	PCNP	PEST proteolytic signal containing nuclear protein

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Cfa.2417.1.S1_at	7.80E-02	6.54E-02	1.31	PREDICTED: Canis familiaris similar to Phosphatidylcholine transfer protein (PC-TP) (StAR-related lipid transfer protein 2) (StARD2) (START domain-containing protein 2) (LOC480563); mRNA	XM_537685	PCTP	phosphatidylcholine transfer protein
Cfa.2830.1.S1_s_at	1.35E-02	2.62E-02	0.77	PREDICTED: Canis familiaris similar to programmed cell death 10; transcript variant 3 (LOC488145); mRNA	XM_856642	PDCD10	programmed cell death 10
Cfa.4486.5.A1_at	1.35E-03	1.23E-02	0.73	PREDICTED: Canis familiaris similar to programmed cell death 2 isoform 1; transcript variant 1 (LOC475041); mRNA	XM_532276	PDCD2	programmed cell death 2
Cfa.20446.1.A1_s_at	1.59E-02	2.82E-02	0.71	PREDICTED: Canis familiaris similar to programmed cell death 5 (LOC476499); mRNA	XM_533708	PDCD5	programmed cell death 5
Cfa.13057.1.A1_s_at	1.17E-03	1.21E-02	0.75	Canis familiaris rod cyclic GMP phosphodiesterase delta subunit mRNA; complete cds	AY029186	PDE6D	phosphodiesterase 6D, cGMP-specific, rod, delta
Cfa.723.1.A1_s_at	3.38E-03	1.56E-02	0.76	Canis familiaris rod cyclic GMP phosphodiesterase delta subunit mRNA; complete cds	AY029186	PDE6D	phosphodiesterase 6D, cGMP-specific, rod, delta
Cfa.10618.1.S1_at	2.02E-03	1.35E-02	0.74	PREDICTED: Canis familiaris similar to Pyruvate dehydrogenase E1 component alpha subunit; somatic form; mitochondrial precursor (PDHE1-A type I); transcript variant 4 (LOC480858); mRNA	XM_853468	PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1
Cfa.10618.1.S2_at	2.05E-03	1.35E-02	0.76	PREDICTED: Canis familiaris similar to Pyruvate dehydrogenase E1 component alpha subunit; somatic form; mitochondrial precursor (PDHE1-A type I); transcript variant 4 (LOC480858); mRNA	XM_853468	PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1
Cfa.21639.1.S1_s_at	2.25E-02	3.32E-02	0.76	PREDICTED: Canis familiaris similar to protein disulfide isomerase-associated 3 precursor (LOC478279); mRNA	XM_535453	PDIA3	protein disulfide isomerase family A, member 3

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Cfa.4275.2.S1_at	1.50E-03	1.25E-02	0.7	familiaris similar to Protein disulfide-isomerase A4 precursor (Protein ERp-72) (ERp72); transcript variant 1 (LOC482715); mRNA	XM_539831	PDIA4	protein disulfide isomerase family A, member 4
CfaAffx.6054.1.S1_s_at	2.44E-03	1.41E-02	0.7	familiaris similar to Protein disulfide-isomerase A4 precursor (Protein ERp-72) (ERp72); transcript variant 3 (LOC482715); mRNA	XM_843145	PDIA4	protein disulfide isomerase family A, member 4
Cfa.20823.1.S1_s_at	1.47E-03	1.25E-02	0.7	PREDICTED: Canis familiaris similar to Protein disulfide-isomerase A6 precursor (Thioredoxin domain containing protein 7) (LOC475668); mRNA	XM_532876	PDIA6	protein disulfide isomerase family A, member 6
CfaAffx.6163.1.S1_s_at	2.52E-03	1.43E-02	0.71	PREDICTED: Canis familiaris similar to Protein disulfide-isomerase A6 precursor (Thioredoxin domain containing protein 7) (LOC475668); mRNA	XM_532876	PDIA6	protein disulfide isomerase family A, member 6
CfaAffx.20244.1.S1_at	5.18E-05	7.92E-03	0.72	PREDICTED: Canis familiaris similar to [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; mitochondrial precursor (Pyruvate dehydrogenase kinase isoform 1) (LOC476828); mRNA	XM_534032	PDK1	pyruvate dehydrogenase kinase, isozyme 1
CfaAffx.25687.1.S1_at	9.52E-03	2.25E-02	0.73	PREDICTED: Canis familiaris similar to PDZ domain containing 11 (LOC491940); mRNA	XM_549060	PDZD11	PDZ domain containing 11
CfaAffx.18596.1.S1_at	1.70E-02	2.91E-02	0.72	PREDICTED: Canis familiaris similar to PDZ domain containing 8 (LOC486909); mRNA	XM_544039	PDZD8	PDZ domain containing 8
CfaAffx.5699.1.S1_s_at	1.33E-03	1.23E-02	0.69	PREDICTED: Canis familiaris similar to pellino protein (LOC481388); mRNA	XM_538508	PELI1	pellino homolog 1 (Drosophila)
CfaAffx.1404.1.S1_at	1.52E-03	1.25E-02	0.72	PREDICTED: Canis familiaris similar to Peroxisomal biogenesis factor 3 (Peroxin-3) (Peroxisomal assembly protein PEX3) (LOC484015); mRNA	XM_541132	PEX3	peroxisomal biogenesis factor 3
Cfa.17565.1.S1_s_at	1.59E-03	1.26E-02	0.75	PREDICTED: Canis familiaris similar to prefoldin 2 (LOC488648); mRNA	XM_545765	PFDN2	prefoldin subunit 2

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Cfa.13766.1.A1_at	1.17E-02	2.45E-02	0.63	Bos taurus 6-phosphofructo-2-kinase/fructose-2;6-biphosphatase 2; mRNA (cDNA clone MGC:152496 IMAGE:8421256); complete cds	BC147889	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2
CfaAffx.9225.1.S1_s_at	1.44E-02	2.70E-02	0.68	PREDICTED: Canis familiaris similar to phosphoglucomutase 2-like 1 (LOC485198); mRNA	XM_542316	PGM2L1	phosphoglucomutase 2-like 1
Cfa.20228.1.S1_at	8.42E-03	2.14E-02	0.75	familiaris similar to Phosphoacetylglucosamine mutase (PAGM) (Acetylglucosamine phosphomutase) (N-acetylglucosamine-phosphate mutase) (Phosphoglucomutase 3); transcript variant 6 (LOC474981); mRNA	XM_862638	PGM3	phosphoglucomutase 3
Cfa.17766.1.S1_s_at	2.39E-02	3.42E-02	0.77	PREDICTED: Canis familiaris similar to pyridoxal (pyridoxine; vitamin B6) phosphatase (LOC610926); mRNA	XM_848509	PGP	phosphoglycolate phosphatase
Cfa.10525.1.A1_s_at	1.85E-03	1.31E-02	0.75	PREDICTED: Canis familiaris hypothetical protein FLJ10975 (PHF10) gene exons 11 12 and; transcript variant 3 (PHF10); mRNA	XM_863444	PHF10	PHD finger protein 10
Cfa.2718.1.A1_at	4.53E-04	9.86E-03	0.73	PREDICTED: Canis familiaris similar to transcription factor INI (LOC474489); mRNA	XM_531718	PHF5A	PHD finger protein 5A
CfaAffx.2508.1.S1_s_at	5.26E-04	1.01E-02	0.69	PREDICTED: Canis familiaris similar to transcription factor INI (LOC474489); mRNA	XM_531718	PHF5A	PHD finger protein 5A
CfaAffx.31211.1.S1_s_at	8.13E-04	1.10E-02	0.71	PREDICTED: Canis familiaris similar to GPI-anchor transamidase precursor (GPI transamidase) (Phosphatidylinositol-glycan biosynthesis; class K protein) (PIG-K) (hGPI8); transcript variant 3 (LOC479985); mRNA	XM_862803	PIGK	phosphatidylinositol glycan anchor biosynthesis, class K
Cfa.1783.1.A1_at	1.19E-02	2.47E-02	0.74	PREDICTED: Pan troglodytes phosphoinositide-3-kinase; class 2; alpha polypeptide; transcript variant 1 (PIK3C2A); mRNA	XM_001172509	PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide
CfaAffx.27145.1.S1_s_at	5.59E-03	1.83E-02	0.72	PREDICTED: Equus caballus phosphoinositide-3-kinase; class 3 (PIK3C3); mRNA	XM_001497768	PIK3C3	phosphoinositide-3-kinase, class 3

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.8254.1.A1_at	3.68E-02	4.30E-02	0.73	PREDICTED: Canis familiaris similar to phosphoinositide-3-kinase; regulatory subunit 4; p150; transcript variant 1 (LOC477064); mRNA	XM_534260	PIK3R4	phosphoinositide-3-kinase, regulatory subunit 4
CfaAffx.7375.1.S1_at	4.47E-03	1.70E-02	0.73	PREDICTED: Canis familiaris similar to CG10739-PA (LOC475903); mRNA	XM_533110	PION	pigeon homolog (Drosophila)
Cfa.871.1.S1_at	8.49E-02	6.88E-02	0.76	PREDICTED: Canis familiaris similar to Pirin (LOC480846); mRNA	XM_537963	PIR	pirin (iron-binding nuclear protein)
Cfa.20719.1.S1_s_at	2.89E-03	1.49E-02	0.77	familiaris similar to Phosphatidylinositol transfer protein beta isoform (PtdIns transfer protein beta) (PtdInsTP) (PI-TP-beta); transcript variant 2 (LOC609712); mRNA	XM_859666	PITPNB	phosphatidylinositol transfer protein, beta
CfaAffx.12014.1.S1_s_at	1.51E-02	2.75E-02	0.72	familiaris similar to praja 2; RING-H2 motif containing; transcript variant 2 (LOC479143); mRNA	XM_850732	PJA2	praja 2, RING-H2 motif containing
Cfa.14230.1.A1_at	5.72E-04	1.03E-02	0.7	PREDICTED: Canis familiaris similar to Transmembrane prostate androgen-induced protein (Solid tumor-associated 1 protein) (LOC485945); mRNA	XM_543070	PMEPA1	prostate transmembrane protein, androgen induced 1
Cfa.290.1.A1_at	2.96E-03	1.51E-02	0.74	PREDICTED: Canis familiaris similar to Mitochondrial processing peptidase beta subunit; mitochondrial precursor (Beta-MPP) (P-52) (LOC475897); mRNA	XM_533104	PMPCB	peptidase (mitochondrial processing) beta
CfaAffx.14811.1.S1_s_at	2.99E-03	1.51E-02	0.76	PREDICTED: Canis familiaris similar to PMS1 protein homolog 1 (DNA mismatch repair protein PMS1); transcript variant 2 (LOC478840); mRNA	XM_850587	PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)
CfaAffx.21428.1.S1_s_at	2.36E-02	3.40E-02	0.75	Canis lupus familiaris pinin; desmosome associated protein (PNN); mRNA	NM_001003231	PNN	pinin, desmosome associated protein
Cfa.9261.1.S1_at	7.96E-04	1.10E-02	0.75	PREDICTED: Canis familiaris similar to DNA polymerase epsilon subunit 4 (LOC483096); mRNA	XM_540212	POLE4	polymerase (DNA-directed), epsilon 4 (p12 subunit)

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.13023.1.S1_s_at	4.70E-05	7.75E-03	0.73	PREDICTED: Canis familiaris similar to DNA polymerase epsilon subunit 4 (LOC483096); mRNA	XM_540212	POLE4	polymerase (DNA-directed), epsilon 4 (p12 subunit)
Cfa.19321.1.S1_at	4.98E-04	1.00E-02	0.76	PREDICTED: Canis familiaris similar to DNA-directed RNA polymerase I 40 kDa polypeptide (RPA40) (RPA39); transcript variant 1 (LOC474912); mRNA	XM_532147	POLR1C	polymerase (RNA) I polypeptide C, 30kDa
CfaAffx.23745.1.S1_s_at	8.87E-04	1.14E-02	0.75	PREDICTED: Canis familiaris similar to polymerase (RNA) II (DNA directed) polypeptide G (LOC476052); mRNA	XM_533260	POLR2G	polymerase (RNA) II (DNA directed) polypeptide G
CfaAffx.30155.1.S1_at	1.11E-03	1.20E-02	1.32	PREDICTED: Canis familiaris similar to DNA-directed RNA polymerase; mitochondrial precursor (MtRPOL) (LOC485102); mRNA	XM_542220	POLRMT	polymerase (RNA) mitochondrial (DNA directed)
CfaAffx.21675.1.S1_s_at	3.27E-03	1.55E-02	0.75	PREDICTED: Canis familiaris similar to inorganic pyrophosphatase (LOC479238); mRNA	XM_536380	PPA1	pyrophosphatase (inorganic) 1
Cfa.20890.1.S1_at	9.14E-03	2.22E-02	0.73	PREDICTED: Canis familiaris similar to inorganic pyrophosphatase 2 isoform 1 (LOC478500); mRNA	XM_535679	PPA2	pyrophosphatase (inorganic) 2
Cfa.9458.1.A1_at	3.09E-03	1.53E-02	0.75	familiaris similar to Phosphopantothenate--cysteine ligase (Phosphopantothenoylcysteine synthetase) (PPC synthetase); transcript variant 1 (LOC475309); mRNA	XM_532539	PPCS	phosphopantothenoylcysteine synthetase
CfaAffx.26086.1.S1_s_at	1.88E-02	3.06E-02	0.76	PREDICTED: Canis familiaris similar to Peptidyl-prolyl cis-trans isomerase B precursor (PPIase) (Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYLP) (CYP-S1); transcript variant 2 (LOC478337); mRNA	XM_847296	PPIB	peptidylprolyl isomerase B (cyclophilin B)
Cfa.7275.1.A1_s_at	3.70E-03	1.61E-02	0.68	PREDICTED: Canis familiaris similar to Peptidyl-prolyl cis-trans isomerase B precursor (PPIase) (Rotamase) (Cyclophilin B) (S-cyclophilin) (SCYLP) (CYP-S1); transcript variant 3 (LOC478337); mRNA	XM_860503	PPIB	peptidylprolyl isomerase B (cyclophilin B)

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CfaAffx.13745.1.S1_s_at	1.35E-04	8.90E-03	0.7	PREDICTED: Canis familiaris similar to peptidylprolyl isomerase D; transcript variant 1 (LOC475481); mRNA	XM_532704	PPID	peptidylprolyl isomerase D (cyclophilin D)
Cfa.16705.1.S1_at	8.39E-04	1.12E-02	0.76	PREDICTED: Canis familiaris similar to Peptidyl-prolyl cis-trans isomerase; mitochondrial precursor (PPIase) (Rotamase) (Cyclophilin F) (LOC610502); mRNA	XM_848021	PPIF	peptidylprolyl isomerase F (cyclophilin F)
CfaAffx.4685.1.S1_s_at	3.24E-03	1.55E-02	0.76	PREDICTED: Canis familiaris similar to peptidyl prolyl isomerase H; transcript variant 1 (LOC606899); mRNA	XM_843144	PPIH	peptidylprolyl isomerase H (cyclophilin H)
CfaAffx.19929.1.S1_s_at	7.02E-03	1.99E-02	0.76	Homo sapiens protein phosphatase 1; regulatory subunit 7 mRNA; complete cds	BT020134	PPP1R7	protein phosphatase 1, regulatory (inhibitor) subunit 7
Cfa.1403.1.S1_s_at	1.15E-03	1.21E-02	0.76	Canis familiaris type 2A protein phosphatase catalytic subunit mRNA; complete cds	AF448499	PPP2CA	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
Cfa.8744.1.A1_s_at	1.51E-03	1.25E-02	0.67	PREDICTED: Canis familiaris similar to beta isoform of regulatory subunit A; protein phosphatase 2 isoform b; transcript variant 1 (LOC479444); mRNA	XM_536579	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform
Cfa.8744.2.S1_at	5.84E-04	1.03E-02	0.76	PREDICTED: Canis familiaris similar to beta isoform of regulatory subunit A; protein phosphatase 2 isoform b; transcript variant 8 (LOC479444); mRNA	XM_857435	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform
Cfa.1163.1.A1_s_at	4.38E-04	9.78E-03	0.76	PREDICTED: Canis familiaris similar to alpha isoform of regulatory subunit B55; protein phosphatase 2; transcript variant 8 (LOC477374); mRNA	XM_853304	PPP2R2A	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform
Cfa.10581.1.S1_s_at	1.09E-02	2.38E-02	0.66	PREDICTED: Canis familiaris similar to peptidylprolyl isomerase domain and WD repeat containing 1; transcript variant 1 (LOC478078); mRNA	XM_535256	PPWD1	peptidylprolyl isomerase domain and WD repeat containing 1

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Cfa.4507.1.A1_at	3.42E-03	1.57E-02	0.74	PREDICTED: Canis familiaris similar to peroxiredoxin 1 (LOC475375); mRNA	XM_532599	PRDX1	peroxiredoxin 1
CfaAffx.7806.1.S1_s_at	8.08E-04	1.10E-02	0.7	PREDICTED: Canis familiaris similar to peroxiredoxin 1 (LOC475375); mRNA	XM_532599	PRDX1	peroxiredoxin 1
Cfa.3121.4.S1_at	3.51E-02	4.20E-02	0.76	PREDICTED: Canis familiaris similar to Peroxiredoxin 6 (Antioxidant protein 2) (1-Cys peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent phospholipase A2) (aiPLA2) (Non-selenium glutathione peroxidase) (NSGPx) (24 kDa protein) (Liver 2D page spot 40) (Red blood cells page... (LOC480069); mRNA	XM_537190	PRDX6	peroxiredoxin 6
Cfa.12159.1.A1_at	7.59E-03	2.04E-02	0.76	PREDICTED: Canis familiaris similar to Px19-like protein (25 kDa protein of relevant evolutionary and lymphoid interest) (PRELI); transcript variant 1 (LOC479276); mRNA	XM_536419	PRELID1	PRELI domain containing 1
CfaAffx.10207.1.S1_s_at	9.84E-03	2.29E-02	0.75	PREDICTED: Canis familiaris similar to Protein kinase C; nu type (nPKC-nu) (Protein kinase EPK2) (LOC483036); mRNA	XM_540151	PRKD3	protein kinase D3
CfaAffx.15427.1.S1_s_at	7.93E-04	1.10E-02	0.68	PREDICTED: Canis familiaris similar to HMT1 hnRNP methyltransferase-like 3; transcript variant 1 (LOC476887); mRNA	XM_534089	PRMT3	protein arginine methyltransferase 3
Cfa.2377.1.S1_at	1.19E-02	2.47E-02	0.73	PREDICTED: Canis familiaris similar to PRP39 pre-mRNA processing factor 39 homolog; transcript variant 1 (LOC480305); mRNA	XM_537427	PRPF39	PRP39 pre-mRNA processing factor 39 homolog (S. cerevisiae)
CfaAffx.5780.1.S1_s_at	1.70E-04	9.00E-03	0.72	PREDICTED: Canis familiaris similar to PRP4 pre-mRNA processing factor 4 homolog (LOC474807); mRNA	XM_532038	PRPF4	PRP4 pre-mRNA processing factor 4 homolog (yeast)
Cfa.3344.1.S1_at	4.54E-04	9.86E-03	0.64	PREDICTED: Canis familiaris similar to Formin binding protein 3 (Huntingtin yeast partner A) (Huntingtin-interacting protein HYPA/FBP11) (Fas ligand associated factor 1) (NY-REN-6 antigen); transcript variant 1 (LOC476152); mRNA	XM_533359	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.9716.1.S1_s_at	9.62E-04	1.16E-02	0.72	PREDICTED: Canis familiaris similar to Formin binding protein 3 (Huntingtin yeast partner A) (Huntingtin-interacting protein HYPA/FBP11) (Fas ligand associated factor 1) (NY-REN-6 antigen); transcript variant 6 (LOC476152); mRNA	XM_852976	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)
Cfa.1509.3.A1_s_at	4.19E-03	1.67E-02	0.74	PREDICTED: Canis familiaris similar to serine/threonine-protein kinase PRP4K; transcript variant 6 (LOC488199); mRNA	XM_851439	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
Cfa.9362.1.S1_at	2.20E-03	1.37E-02	0.67	PREDICTED: Canis familiaris similar to phosphoserine aminotransferase isoform 1 (LOC476318); mRNA	XM_533520	PSAT1	phosphoserine aminotransferase 1
Cfa.4666.1.A1_s_at	7.26E-04	1.08E-02	0.72	PREDICTED: Canis familiaris similar to presenilin enhancer 2 (LOC476479); mRNA	XM_533689	PSENEN	presenilin enhancer 2 homolog (C. elegans)
Cfa.6307.1.A1_s_at	9.21E-06	6.68E-03	0.76	PREDICTED: Canis familiaris similar to presenilin enhancer 2 (LOC476479); mRNA	XM_533689	PSENEN	presenilin enhancer 2 homolog (C. elegans)
Cfa.1804.1.S1_at	1.65E-02	2.88E-02	0.76	PREDICTED: Canis familiaris similar to PC4 and SFRS1 interacting protein 1 isoform 2; transcript variant 1 (LOC474712); mRNA	XM_531939	PSIP1	PC4 and SFRS1 interacting protein 1
Cfa.19196.1.S1_x_at	9.79E-04	1.16E-02	0.67	PREDICTED: Canis familiaris similar to Proteasome subunit alpha type 1 (Proteasome component C2) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome nu chain) (30 kDa prosomal protein) (PROS-30) (LOC476867); mRNA	XM_534070	PSMA1	proteasome (prosome, macropain) subunit, alpha type, 1
CfaAffx.29177.1.S1_s_at	3.17E-04	9.28E-03	0.61	PREDICTED: Canis familiaris similar to Proteasome subunit alpha type 2 (Proteasome component C3) (Macropain subunit C3) (Multicatalytic endopeptidase complex subunit C3); transcript variant 1 (LOC475870); mRNA	XM_533078	PSMA2	proteasome (prosome, macropain) subunit, alpha type, 2

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Cfa.4336.1.S1_s_at	5.83E-04	1.03E-02	0.69	PREDICTED: Canis familiaris similar to proteasome alpha 3 subunit isoform 2; transcript variant 1 (LOC480338); mRNA	XM_537460	PSMA3	proteasome (prosome, macropain) subunit, alpha type, 3
Cfa.10406.1.S1_at	5.71E-03	1.84E-02	0.67	PREDICTED: Canis familiaris similar to Proteasome subunit alpha type 4 (Proteasome component C9) (Macropain subunit C9) (Multicatalytic endopeptidase complex subunit C9) (Proteasome subunit L) (LOC475132); mRNA	XM_532362	PSMA4	proteasome (prosome, macropain) subunit, alpha type, 4
CfaAffx.3522.1.S1_s_at	7.49E-03	2.03E-02	0.72	PREDICTED: Canis familiaris similar to Proteasome subunit alpha type 4 (Proteasome component C9) (Macropain subunit C9) (Multicatalytic endopeptidase complex subunit C9) (Proteasome subunit L) (LOC475132); mRNA	XM_532362	PSMA4	proteasome (prosome, macropain) subunit, alpha type, 4
Cfa.12672.1.A1_s_at	6.93E-03	1.98E-02	0.77	PREDICTED: Canis familiaris similar to Proteasome subunit alpha type 5 (Proteasome zeta chain) (Macropain zeta chain) (Multicatalytic endopeptidase complex zeta chain); transcript variant 2 (LOC490123); mRNA	XM_860992	PSMA5	proteasome (prosome, macropain) subunit, alpha type, 5
Cfa.9709.1.S1_s_at	1.42E-03	1.25E-02	0.75	PREDICTED: Canis familiaris similar to Proteasome subunit alpha type 5 (Proteasome zeta chain) (Macropain zeta chain) (Multicatalytic endopeptidase complex zeta chain); transcript variant 2 (LOC490123); mRNA	XM_860992	PSMA5	proteasome (prosome, macropain) subunit, alpha type, 5
Cfa.9494.1.S1_s_at	3.21E-05	7.55E-03	0.7	PREDICTED: Canis familiaris similar to Proteasome subunit alpha type 6 (Proteasome iota chain) (Macropain iota chain) (Multicatalytic endopeptidase complex iota chain); transcript variant 2 (LOC480290); mRNA	XM_537412	PSMA6	proteasome (prosome, macropain) subunit, alpha type, 6
CfaAffx.7079.1.S1_at	7.93E-06	6.68E-03	0.71	PREDICTED: Canis familiaris TATA-box binding protein (LOC475040); mRNA	XM_532275	PSMB1	proteasome (prosome, macropain) subunit, beta type, 1

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Cfa.4329.1.S1_s_at	2.59E-03	1.44E-02	0.76	familiaris similar to Proteasome subunit beta type 4 precursor (Proteasome beta chain) (Macropain beta chain) (Multicatalytic endopeptidase complex beta chain) (Proteasome chain 3) (LOC475848); mRNA	XM_533057	PSMB4	proteasome (prosome, macropain) subunit, beta type, 4
Cfa.2649.1.S1_s_at	4.63E-04	9.88E-03	0.69	PREDICTED: Canis familiaris similar to Proteasome subunit beta type 6 precursor (Proteasome delta chain) (Macropain delta chain) (Multicatalytic endopeptidase complex delta chain) (Proteasome subunit Y) (LOC607466); mRNA	XM_844148	PSMB6	proteasome (prosome, macropain) subunit, beta type, 6
CfaAffx.26768.1.S1_at	5.68E-02	5.46E-02	0.76	PREDICTED: Canis familiaris similar to peptidase (prosome; macropain) 26S subunit; ATPase 1; transcript variant 2 (LOC478703); mRNA	XM_843431	PSMC1	proteasome (prosome, macropain) 26S subunit, ATPase, 1
Cfa.281.1.S1_s_at	3.83E-04	9.61E-03	0.71	PREDICTED: Canis familiaris similar to proteasome (prosome; macropain) 26S subunit; ATPase 2 (LOC475896); mRNA	XM_533103	PSMC2	proteasome (prosome, macropain) 26S subunit, ATPase, 2
Cfa.3960.1.A1_s_at	9.11E-04	1.15E-02	0.71	PREDICTED: Canis familiaris similar to 26S protease regulatory subunit 6A (TAT-binding protein 1) (TBP-1) (Proteasome subunit P50); transcript variant 2 (LOC475980); mRNA	XM_855582	PSMC3	proteasome (prosome, macropain) 26S subunit, ATPase, 3
CfaAffx.19069.1.S1_s_at	1.84E-03	1.31E-02	0.7	PREDICTED: Canis familiaris similar to proteasome 26S ATPase subunit 6 (LOC478522); mRNA	XM_535701	PSMC6	proteasome (prosome, macropain) 26S subunit, ATPase, 6
CfaAffx.15655.1.S1_s_at	4.12E-04	9.68E-03	0.72	PREDICTED: Canis familiaris similar to proteasome (prosome; macropain) 26S subunit; non-ATPase; 14; transcript variant 2 (LOC478765); mRNA	XM_535931	PSMD14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14

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Cfa.2102.1.A1_s_at	5.98E-04	1.04E-02	0.72	PREDICTED: Canis familiaris similar to Proteasome activator complex subunit 2 (Proteasome activator 28-beta subunit) (PA28beta) (PA28b) (Activator of multicatalytic protease subunit 2) (11S regulator complex beta subunit) (REG-beta); transcript variant 3 (LOC480258); mRNA	XM_855030	PSME2	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)
Cfa.14895.1.A1_s_at	1.43E-02	2.69E-02	0.72	PREDICTED: Canis familiaris similar to Proteasome activator complex subunit 2 (Proteasome activator 28-beta subunit) (PA28beta) (PA28b) (Activator of multicatalytic protease subunit 2) (11S regulator complex beta subunit) (REG-beta); transcript variant 5 (LOC480258); mRNA	XM_855106	PSME2	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)
Cfa.7938.1.A1_s_at	3.48E-05	7.55E-03	0.76	PREDICTED: Canis familiaris similar to proteaseome (prosome; macropain) 28 subunit; 3 (predicted); transcript variant 6 (LOC480512); mRNA	XM_852757	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)
Cfa.552.1.A1_at	6.07E-03	1.87E-02	0.74	PREDICTED: Canis familiaris similar to proteasome (prosome; macropain) activator subunit 4 (LOC474594); mRNA	XM_531823	PSME4	proteasome (prosome, macropain) activator subunit 4
Cfa.16358.1.S1_at	3.65E-02	4.28E-02	0.75	PREDICTED: Canis familiaris similar to tumor necrosis factor superfamily; member 5-induced protein 1 (LOC480215); mRNA	XM_537340	PSMG2	proteasome (prosome, macropain) assembly chaperone 2
CfaAffx.28795.1.S1_s_at	4.16E-02	4.60E-02	0.75	PREDICTED: Canis familiaris similar to tumor necrosis factor superfamily; member 5-induced protein 1 (LOC480215); mRNA	XM_537340	PSMG2	proteasome (prosome, macropain) assembly chaperone 2
Cfa.2529.1.S1_at	3.69E-02	4.31E-02	0.75	PREDICTED: Canis familiaris similar to polypyrimidine tract binding protein 2; transcript variant 4 (LOC490149); mRNA	XM_861727	PTBP2	polypyrimidine tract binding protein 2
Cfa.3452.1.S1_s_at	1.30E-02	2.57E-02	0.74	Canis familiaris prostaglandin E2 receptor EP4 subtype mRNA; complete cds	AF177934	PTGER4	prostaglandin E receptor 4 (subtype EP4)

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CfaAffx.5983.1.S1_at	9.36E-03	2.23E-02	1.39	PREDICTED: Canis familiaris similar to Pleiotrophin precursor (PTN) (Heparin-binding growth-associated molecule) (HB-GAM) (Heparin-binding growth factor 8) (HBGF-8) (Osteoblast specific factor 1) (OSF-1) (Heparin-binding neutrophic factor) (HBNF) (Heparin-binding brain mitoge... (LOC475509); mRNA	XM_532732	PTN	pleiotrophin
Cfa.4403.1.S1_s_at	1.05E-02	2.34E-02	0.73	PREDICTED: Canis familiaris similar to pumilio 1 isoform 1; transcript variant 9 (LOC478158); mRNA	XM_860124	PUM1	pumilio homolog 1 (Drosophila)
Cfa.6493.1.A1_at	8.64E-02	6.96E-02	0.77	PREDICTED: Canis familiaris similar to tRNA pseudouridine synthase A (tRNA-uridine isomerase I) (tRNA pseudouridylate synthase I) (LOC609867); mRNA	XM_847214	PUS1	pseudouridylate synthase 1
Cfa.14845.1.A1_at	1.14E-03	1.20E-02	0.77	PREDICTED: Canis familiaris similar to PWWP domain containing 2; transcript variant 1 (LOC479310); mRNA	XM_536448	PWWP2A	PWWP domain containing 2A
CfaAffx.25782.1.S1_s_at	3.84E-02	4.40E-02	0.73	PREDICTED: Canis familiaris similar to PYD and CARD domain containing isoform a; transcript variant 3 (LOC489925); mRNA	XM_843515	PYCARD	PYD and CARD domain containing
CfaAffx.22488.1.S1_at	6.72E-02	6.02E-02	0.76	PREDICTED: Canis familiaris phosphorylase; glycogen; liver; transcript variant 1 (PYGL); mRNA	XM_537443	PYGL	phosphorylase, glycogen, liver
Cfa.1325.1.S1_s_at	5.97E-03	1.87E-02	0.77	PREDICTED: Canis familiaris similar to glutaminyl-tRNA synthetase; transcript variant 1 (LOC476628); mRNA	XM_533833	QARS	glutaminyl-tRNA synthetase
Cfa.11172.1.A1_at	3.74E-02	4.34E-02	0.76	PREDICTED: Pan troglodytes similar to QKI; transcript variant 2 (LOC472181); mRNA	XM_001154802	QKI	quaking homolog, KH domain RNA binding (mouse)
CfaAffx.6541.1.S1_s_at	2.09E-03	1.35E-02	0.76	PREDICTED: Canis familiaris similar to glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1 (LOC475014); mRNA	XM_532250	QRSL1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1

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Cfa.2882.1.S1_at	7.33E-02	6.32E-02	0.75	PREDICTED: Macaca mulatta RAB11 family interacting protein 2 (class I) (RAB11FIP2); mRNA	XM_001100265	RAB11FIP2	RAB11 family interacting protein 2 (class I)
Cfa.10588.1.A1_at	5.56E-03	1.82E-02	0.71	PREDICTED: Canis familiaris similar to Rab11 family-interacting protein 2 (Rab11-FIP2) (NRip11) (LOC477834); mRNA	XM_535026	RAB11FIP2	RAB11 family interacting protein 2 (class I)
CfaAffx.18629.1.S1_s_at	2.03E-02	3.17E-02	0.77	PREDICTED: Canis familiaris similar to Rab11 family-interacting protein 2 (Rab11-FIP2) (NRip11) (LOC477834); mRNA	XM_535026	RAB11FIP2	RAB11 family interacting protein 2 (class I)
Cfa.1842.1.S1_at	3.89E-03	1.63E-02	0.73	PREDICTED: Canis familiaris similar to Ras-related protein Rab-18; transcript variant 2 (LOC491408); mRNA	XM_843676	RAB18	RAB18, member RAS oncogene family
CfaAffx.21132.1.S1_s_at	2.78E-03	1.48E-02	0.74	PREDICTED: Canis familiaris similar to Ras-related protein Rab-18; transcript variant 6 (LOC491408); mRNA	XM_852130	RAB18	RAB18, member RAS oncogene family
Cfa.5163.1.A1_at	6.67E-02	5.99E-02	0.7	PREDICTED: Canis familiaris similar to Ras-related protein Rab-20 (LOC485549); mRNA	XM_542668	RAB20	RAB20, member RAS oncogene family
Cfa.3880.1.A2_at	3.97E-03	1.64E-02	0.72	PREDICTED: Pan troglodytes similar to GTP-binding protein; transcript variant 2 (LOC464197); mRNA	XM_001158192	RAB2A	RAB2A, member RAS oncogene family
Cfa.3879.1.S1_s_at	5.17E-03	1.79E-02	0.72	C.familiaris GTP-binding protein (rab5) mRNA; complete cds	M35520	RAB5A	RAB5A, member RAS oncogene family
CfaAffx.9333.1.S1_s_at	1.29E-03	1.23E-02	0.73	PREDICTED: Canis familiaris similar to Ras-related protein Rab-6A (Rab-6); transcript variant 2 (LOC608330); mRNA	XM_856012	RAB6A	RAB6A, member RAS oncogene family
Cfa.3637.1.S1_s_at	1.18E-02	2.45E-02	0.72	PREDICTED: Canis familiaris RAB8A; member RAS oncogene family (RAB8A); mRNA	XM_850476	RAB8A	RAB8A, member RAS oncogene family
Cfa.15215.1.A1_at	4.32E-04	9.78E-03	0.73	PREDICTED: Canis familiaris similar to RAB8B; member RAS oncogene family (LOC610601); mRNA	XM_848135	RAB8B	RAB8B, member RAS oncogene family
CfaAffx.18264.1.S1_s_at	1.29E-03	1.23E-02	0.73	PREDICTED: Canis familiaris rab9 GTP-binding protein (RAB9); mRNA	XM_537956	RAB9A	RAB9A, member RAS oncogene family

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CfaAffx.31221.1.S1_at	2.07E-03	1.35E-02	0.69	PREDICTED: Canis familiaris similar to Rab geranylgeranyltransferase; beta subunit (LOC612683); mRNA	XM_850411	RABGGTB	Rab geranylgeranyltransferase, beta subunit
CfaAffx.31221.1.S1_s_at	3.62E-03	1.60E-02	0.68	PREDICTED: Canis familiaris similar to Rab geranylgeranyltransferase; beta subunit (LOC612683); mRNA	XM_850411	RABGGTB	Rab geranylgeranyltransferase, beta subunit
Cfa.12356.1.A1_at	3.00E-03	1.51E-02	0.75	PREDICTED: Canis familiaris similar to RAD17 homolog isoform 2 (LOC478088); mRNA	XM_535265	RAD17	RAD17 homolog (S. pombe)
Cfa.1703.1.A1_at	1.04E-02	2.34E-02	0.77	PREDICTED: Canis familiaris similar to Double-strand-break repair protein rad21 homolog (hHR21) (Nuclear matrix protein 1) (NXP-1) (SCC1 homolog); transcript variant 3 (LOC482021); mRNA	XM_855924	RAD21	RAD21 homolog (S. pombe)
Cfa.507.1.A1_s_at	1.06E-04	8.90E-03	0.69	PREDICTED: Canis familiaris similar to RAD50 homolog isoform 1 (LOC474674); mRNA	XM_531901	RAD50	RAD50 homolog (S. cerevisiae)
CfaAffx.18719.1.S1_s_at	3.10E-03	1.53E-02	0.77	Homo sapiens mRNA export protein (RAE1) mRNA; complete cds	U84720	RAE1	RAE1 RNA export 1 homolog (S. pombe)
Cfa.16557.1.S1_at	9.39E-03	2.24E-02	0.76	PREDICTED: Canis familiaris similar to RNA-binding protein Raly (hnRNP associated with lethal yellow protein) (Maternally expressed hnRNP C-related protein) (LOC485845); mRNA	XM_542969	RALY	RNA binding protein, autoantigenic (hnRNP-associated with lethal yellow homolog (mouse))
Cfa.550.1.S1_s_at	1.96E-02	3.12E-02	0.72	PREDICTED: Canis familiaris similar to RAN-binding protein 2-like 1 isoform 1 (LOC474539); mRNA	XM_531768	RANBP2	RAN binding protein 2
CfaAffx.15465.1.S1_at	1.01E-02	2.31E-02	0.76	PREDICTED: Canis familiaris similar to RAN binding protein 9 (LOC478728); mRNA	XM_535893	RANBP9	RAN binding protein 9
Cfa.1011.1.S1_s_at	1.18E-03	1.21E-02	0.75	PREDICTED: Canis familiaris similar to RAS related protein 1b (LOC608981); mRNA	XM_846157	RAP1B	RAP1B, member of RAS oncogene family
Cfa.21068.1.S1_s_at	2.32E-03	1.39E-02	0.75	PREDICTED: Canis familiaris similar to RAS related protein 1b (LOC608981); mRNA	XM_846157	RAP1B	RAP1B, member of RAS oncogene family

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.28755.1.S1_at	1.48E-02	2.73E-02	0.76	Bos taurus RAP2C; member of RAS oncogene family; mRNA (cDNA clone MGC:143331 IMAGE:8137531); complete cds	BC123730	RAP2C	RAP2C, member of RAS oncogene family
CfaAffx.26106.1.S1_s_at	4.81E-04	1.00E-02	0.67	PREDICTED: Canis familiaris similar to arginyl tRNA synthetase; transcript variant 1 (LOC609803); mRNA	XM_848009	RARS	arginyl-tRNA synthetase
CfaAffx.6591.1.S1_s_at	2.28E-03	1.39E-02	0.76	PREDICTED: Canis familiaris similar to arginyl tRNA synthetase; transcript variant 4 (LOC609803); mRNA	XM_861845	RARS	arginyl-tRNA synthetase
CfaAffx.5556.1.S1_at	1.41E-03	1.24E-02	0.76	PREDICTED: Canis familiaris similar to arginyl tRNA synthetase-like; transcript variant 1 (LOC481911); mRNA	XM_539032	RARS2	arginyl-tRNA synthetase 2, mitochondrial
CfaAffx.11155.1.S1_s_at	3.26E-03	1.55E-02	0.73	PREDICTED: Canis familiaris similar to Rb1-inducible coiled coil protein 1; transcript variant 3 (LOC477876); mRNA	XM_851678	RB1CC1	RB1-inducible coiled-coil 1
CfaAffx.26877.1.S1_at	1.75E-02	2.96E-02	0.67	PREDICTED: Canis familiaris similar to retinoblastoma-binding protein 6 isoform 3; transcript variant 4 (LOC479802); mRNA	XM_855857	RBBP6	retinoblastoma binding protein 6
Cfa.15259.1.A1_at	1.44E-03	1.25E-02	0.72	PREDICTED: Canis familiaris similar to Putative RNA-binding protein 15 (RNA binding motif protein 15) (One-twenty two protein); transcript variant 2 (LOC479909); mRNA	XM_860799	RBM15	RNA binding motif protein 15
Cfa.2814.1.A1_at	3.73E-03	1.62E-02	0.73	PREDICTED: Bos taurus RNA binding motif protein 25; transcript variant 5 (RBM25); mRNA	XM_879644	RBM25	RNA binding motif protein 25
CfaAffx.8829.1.S1_s_at	1.93E-02	3.10E-02	0.76	PREDICTED: Canis familiaris similar to cutaneous T-cell lymphoma tumor antigen se70-2; transcript variant 5 (LOC476955); mRNA	XM_853024	RBM26	RNA binding motif protein 26
CfaAffx.23773.1.S1_at	3.41E-02	4.13E-02	0.77	PREDICTED: Canis familiaris similar to RNA binding motif protein 3 isoform b; transcript variant 3 (LOC609457); mRNA	XM_858097	RBM3	RNA binding motif (RNP1, RRM) protein 3
Cfa.2425.1.S1_s_at	3.27E-03	1.55E-02	0.77	PREDICTED: Canis familiaris similar to RNA binding motif protein 34 (LOC479199); mRNA	XM_536341	RBM34	RNA binding motif protein 34

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Cfa.15731.1.S1_at	4.27E-03	1.68E-02	0.76	PREDICTED: Canis familiaris similar to RNA-binding region containing protein 2 (Hepatocellular carcinoma protein 1) (Splicing factor HCC1); transcript variant 22 (LOC477216); mRNA	XM_860230	RBM39	RNA binding motif protein 39
Cfa.15731.3.S1_s_at	5.26E-03	1.79E-02	0.73	PREDICTED: Canis familiaris similar to RNA-binding region containing protein 2 (Hepatocellular carcinoma protein 1) (Splicing factor HCC1); transcript variant 22 (LOC477216); mRNA	XM_860230	RBM39	RNA binding motif protein 39
CfaAffx.16999.1.S1_s_at	1.00E-02	2.30E-02	0.76	PREDICTED: Canis familiaris similar to RNA-binding protein 5 (RNA binding motif protein 5) (Putative tumor suppressor LUCA15) (G15 protein); transcript variant 1 (LOC476618); mRNA	XM_533821	RBM5	RNA binding motif protein 5
CfaAffx.17487.1.S1_s_at	7.25E-04	1.08E-02	0.72	PREDICTED: Canis familiaris similar to RNA-binding protein 8A (RNA binding motif protein 8A) (Ribonucleoprotein RBM8A) (LOC475827); mRNA	XM_533035	RBM8A	RNA binding motif protein 8A
Cfa.10176.1.A1_at	4.94E-03	1.76E-02	0.76	PREDICTED: Pan troglodytes RCC1-like (RCC2); mRNA	XM_513117	RCC2	regulator of chromosome condensation 2
Cfa.17021.1.S1_at	2.46E-03	1.41E-02	0.75	PREDICTED: Canis familiaris similar to ring finger and CHY zinc finger domain containing 1 isoform 3; transcript variant 3 (LOC612746); mRNA	XM_850688	RCHY1	ring finger and CHY zinc finger domain containing 1
CfaAffx.23665.1.S1_at	1.39E-02	2.66E-02	0.74	PREDICTED: Canis familiaris similar to protein kinase substrate MK2S4 (LOC480089); mRNA	XM_537212	RCSD1	RCSD domain containing 1
Cfa.9131.1.S1_at	2.24E-02	3.32E-02	0.75	PREDICTED: Canis familiaris similar to retinol dehydrogenase 14 (all-trans and 9-cis); transcript variant 4 (LOC482983); mRNA	XM_852489	RDH14	retinol dehydrogenase 14 (all-trans/9-cis/11-cis)
Cfa.1742.1.S1_at	1.97E-02	3.13E-02	1.31	Canis lupus familiaris pap mRNA for pancreatitis-associated protein; complete cds	AB098708	REG3G	regenerating islet-derived 3 gamma
Cfa.18363.1.S1_s_at	4.90E-03	1.75E-02	0.76	PREDICTED: Canis familiaris similar to replication factor C 2 (40kD) isoform 2; transcript variant 1 (LOC489798); mRNA	XM_546916	RFC2	replication factor C (activator 1) 2, 40kDa

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.14188.1.A1_a_at	8.24E-03	2.12E-02	0.76	PREDICTED: Canis familiaris similar to Activator 1 38 kDa subunit (Replication factor C 38 kDa subunit) (A1 38 kDa subunit) (RF-C 38 kDa subunit) (RFC38) (Replication factor C subunit 3) (LOC477308); mRNA	XM_534500	RFC3	replication factor C (activator 1) 3, 38kDa
Cfa.14188.2.A1_s_at	2.05E-03	1.35E-02	0.75	PREDICTED: Canis familiaris similar to Activator 1 38 kDa subunit (Replication factor C 38 kDa subunit) (A1 38 kDa subunit) (RF-C 38 kDa subunit) (RFC38) (Replication factor C subunit 3) (LOC477308); mRNA	XM_534500	RFC3	replication factor C (activator 1) 3, 38kDa
Cfa.17148.1.S1_s_at	6.04E-02	5.66E-02	0.77	PREDICTED: Canis familiaris similar to Activator 1 37 kDa subunit (Replication factor C 37 kDa subunit) (A1 37 kDa subunit) (RF-C 37 kDa subunit) (RFC37) (LOC478667); mRNA	XM_535837	RFC4	replication factor C (activator 1) 4, 37kDa
CfaAffx.22037.1.S1_s_at	1.09E-03	1.20E-02	0.77	PREDICTED: Canis familiaris similar to constitutive photomorphogenic protein 1 (LOC480060); mRNA	XM_537181	RFWD2	ring finger and WD repeat domain 2
Cfa.577.1.A1_at	1.09E-03	1.20E-02	0.73	PREDICTED: Canis familiaris similar to mitochondrial Rho 1; transcript variant 1 (LOC480613); mRNA	XM_537733	RHOT1	ras homolog gene family, member T1
CfaAffx.1320.1.S1_at	1.18E-02	2.46E-02	0.76	PREDICTED: Canis familiaris similar to CG3295-PA (LOC474643); mRNA	XM_531873	RMND5B	required for meiotic nuclear division 5 homolog B (S. cerevisiae)
Cfa.17844.1.A1_at	5.32E-02	5.28E-02	0.75	Canis lupus familiaris ribonuclease L (RNASEL) mRNA; complete cds	DQ497163	RNASEL	ribonuclease L (2',5'-oligoisoadenylate synthetase dependent)
Cfa.1781.1.S1_at	1.41E-02	2.68E-02	0.77	PREDICTED: Canis familiaris similar to ring finger protein 111; transcript variant 5 (LOC478323); mRNA	XM_859256	RNF111	ring finger protein 111
CfaAffx.17475.1.S1_s_at	4.43E-04	9.78E-03	0.76	PREDICTED: Canis familiaris similar to Zinc finger protein 364 (Rabring 7) (LOC612818); mRNA	XM_845209	RNF115	ring finger protein 115

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CfaAffx.2449.1.S1_s_at	2.91E-03	1.49E-02	0.68	PREDICTED: Canis familiaris similar to ring finger protein 139 (LOC609422); mRNA	XM_846679	RNF139	ring finger protein 139
CfaAffx.2480.1.S1_at	1.25E-02	2.53E-02	0.77	PREDICTED: Canis familiaris similar to ring finger protein 146 (LOC476288); mRNA	XM_533493	RNF146	ring finger protein 146
CfaAffx.9057.1.S1_at	1.86E-03	1.32E-02	0.72	PREDICTED: Canis familiaris similar to ring finger protein 170 (LOC475568); mRNA	XM_532788	RNF170	ring finger protein 170
Cfa.10928.1.A1_at	1.22E-02	2.50E-02	0.76	Bos taurus ring finger protein 4; mRNA (cDNA clone MGC:137906 IMAGE:8087140); complete cds	BC114680	RNF4	ring finger protein 4
Cfa.15117.1.S1_at	6.10E-03	1.88E-02	0.76	PREDICTED: Canis familiaris similar to RING-box protein 2 (Rbx2) (RING finger protein 7) (Sensitive to apoptosis gene protein) (LOC477097); mRNA	XM_534291	RNF7	ring finger protein 7
Cfa.15117.1.S1_s_at	1.57E-03	1.26E-02	0.76	PREDICTED: Canis familiaris similar to RING-box protein 2 (Rbx2) (RING finger protein 7) (Sensitive to apoptosis gene protein) (LOC477097); mRNA	XM_534291	RNF7	ring finger protein 7
Cfa.1316.1.S1_at	6.56E-03	1.94E-02	0.74	PREDICTED: Canis familiaris similar to RNA U; small nuclear RNA export adaptor (phosphorylation regulated) (LOC479305); mRNA	XM_846266	RNUXA	RNA U, small nuclear RNA export adaptor (phosphorylation regulated)
CfaAffx.18623.1.S1_s_at	2.41E-03	1.41E-02	0.77	PREDICTED: Canis familiaris similar to Replication protein A 32 kDa subunit (RP-A) (RF-A) (Replication factor-A protein 2) (P34) (LOC487339); mRNA	XM_544465	RPA2	replication protein A2, 32kDa
Cfa.10828.2.S1_a_at	2.12E-02	3.23E-02	0.73	PREDICTED: Canis familiaris similar to ribulose-5-phosphate-3-epimerase; transcript variant 1 (LOC478893); mRNA	XM_536051	RPE	ribulose-5-phosphate-3-epimerase
Cfa.335.1.A1_at	6.38E-04	1.05E-02	0.75	PREDICTED: Pan troglodytes ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase) (RPIA); mRNA	XM_525809	RPIA	ribose 5-phosphate isomerase A
Cfa.10645.1.S1_at	1.36E-02	2.64E-02	0.77	PREDICTED: Canis familiaris similar to ribosomal protein L18a; transcript variant 2 (LOC476672); mRNA	XM_860467	RPL18A	ribosomal protein L18a
CfaAffx.19688.1.S1_s_at	4.05E-04	9.68E-03	0.72	PREDICTED: Canis familiaris similar to ribosomal protein L35a; transcript variant 1 (LOC478597); mRNA	XM_535773	RPL35A	ribosomal protein L35a

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Cfa.3214.1.S1_a_at	4.99E-04	1.00E-02	0.62	PREDICTED: Canis familiaris similar to large subunit ribosomal protein L36a (LOC480311); mRNA	XM_537433	RPL36AL	ribosomal protein L36a-like
Cfa.3214.1.S1_s_at	3.28E-04	9.28E-03	0.64	PREDICTED: Canis familiaris similar to large subunit ribosomal protein L36a (LOC480311); mRNA	XM_537433	RPL36AL	ribosomal protein L36a-like
CfaAffx.30225.1.S1_s_at	1.32E-03	1.23E-02	0.76	PREDICTED: Canis familiaris Ribosomal protein L7a (RPL7A); mRNA	XM_537800	RPL7A	Ribosomal protein L7a
Cfa.9914.1.S1_s_at	2.38E-03	1.40E-02	0.74	familiaris similar to Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precursor (Ribophorin I) (RPN-I); transcript variant 1 (LOC476516); mRNA	XM_533722	RPN1	ribophorin I
Cfa.9914.2.A1_s_at	2.78E-03	1.48E-02	0.74	familiaris similar to Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precursor (Ribophorin I) (RPN-I); transcript variant 3 (LOC476516); mRNA	XM_843737	RPN1	ribophorin I
Cfa.1364.1.A1_at	9.00E-02	7.13E-02	0.75	PREDICTED: Canis familiaris similar to ribophorin II precursor; transcript variant 3 (LOC477223); mRNA	XM_860586	RPN2	ribophorin II
Cfa.21586.1.S1_s_at	4.46E-04	9.79E-03	0.74	PREDICTED: Canis familiaris similar to ribophorin II precursor; transcript variant 3 (LOC477223); mRNA	XM_860586	RPN2	ribophorin II
CfaAffx.27347.1.S1_at	2.50E-02	3.50E-02	0.74	PREDICTED: Pan troglodytes similar to P15RS protein; transcript variant 1 (LOC468522); mRNA	XM_001136295	RPRD1A	Regulation of nuclear pre-mRNA domain containing 1A
Cfa.1201.1.A1_s_at	3.26E-03	1.55E-02	0.73	Canis familiaris mRNA for Ribosomal protein S17 (rpS17 gene)	AJ388523	RPS17	Ribosomal protein S17
Cfa.6966.1.A1_at	1.41E-04	8.90E-03	0.67	PREDICTED: Canis familiaris hypothetical LOC474502 (LOC474502); mRNA	XM_531730	RPS19BP1	ribosomal protein S19 binding protein 1
CfaAffx.2877.1.S1_s_at	2.54E-03	1.44E-02	0.7	PREDICTED: Canis familiaris hypothetical LOC474502 (LOC474502); mRNA	XM_531730	RPS19BP1	ribosomal protein S19 binding protein 1
Cfa.732.1.S1_s_at	2.50E-04	9.06E-03	0.66	PREDICTED: Canis familiaris similar to 40S ribosomal protein S20 (LOC477887); mRNA	XM_535079	RPS20	ribosomal protein S20

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Cfa.732.1.S1_x_at	4.52E-03	1.71E-02	0.76	PREDICTED: Canis familiaris similar to 40S ribosomal protein S20 (LOC477887); mRNA	XM_535079	RPS20	ribosomal protein S20
CfaAffx.386.1.S1_s_at	3.67E-03	1.61E-02	0.54	PREDICTED: Canis familiaris similar to 40S ribosomal protein S20 (LOC477887); mRNA	XM_535079	RPS20	ribosomal protein S20
CfaAffx.8139.1.S1_x_at	1.22E-03	1.22E-02	0.64	PREDICTED: Canis familiaris similar to 40S ribosomal protein S20 (LOC477887); mRNA	XM_535079	RPS20	ribosomal protein S20
Cfa.311.2.A1_x_at	3.06E-04	9.25E-03	0.68	PREDICTED: Canis familiaris similar to ubiquitin and ribosomal protein S27a precursor (LOC474599); mRNA	XM_531829	RPS27A	ribosomal protein S27a
Cfa.311.6.A1_x_at	2.00E-04	9.06E-03	0.69	PREDICTED: Canis familiaris similar to ubiquitin and ribosomal protein S27a precursor (LOC474599); mRNA	XM_531829	RPS27A	ribosomal protein S27a
Cfa.5249.2.S1_a_at	1.35E-04	8.90E-03	0.69	PREDICTED: Canis familiaris similar to 40S ribosomal protein S27-like protein (LOC610569); mRNA	XM_848098	RPS27L	ribosomal protein S27-like
CfaAffx.240.1.S1_s_at	3.58E-03	1.59E-02	0.61	PREDICTED: Canis familiaris similar to 40S ribosomal protein S27-like protein (LOC610569); mRNA	XM_848098	RPS27L	ribosomal protein S27-like
CfaAffx.20420.1.S1_at	1.19E-02	2.47E-02	0.76	PREDICTED: Canis familiaris similar to ribosomal protein S6 kinase polypeptide 3; transcript variant 3 (LOC491768); mRNA	XM_548888	RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3
Cfa.13383.1.A1_s_at	1.17E-03	1.21E-02	0.74	PREDICTED: Canis familiaris similar to ribosomal protein S6 kinase; 70kDa; polypeptide 1; transcript variant 1 (LOC480580); mRNA	XM_537702	RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1
Cfa.297.2.A1_s_at	5.19E-03	1.79E-02	0.75	PREDICTED: Canis familiaris similar to 40S ribosomal protein S9 (LOC476387); mRNA	XM_533590	RPS9	ribosomal protein S9
Cfa.10840.1.S1_s_at	5.49E-03	1.82E-02	0.74	PREDICTED: Canis familiaris similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma laminin-binding protein) (NEM/1CHD4) (Multidrug resistance-associated protein MGr1-Ag); transcript variant 14 (LOC477029); mRNA	XM_855691	RPSA	ribosomal protein SA
Cfa.1831.1.A1_at	1.87E-02	3.05E-02	0.76	PREDICTED: Canis familiaris similar to related RAS viral (r-ras) oncogene homolog 2 (predicted) (LOC476865); mRNA	XM_534068	RRAS2	related RAS viral (r-ras) oncogene homolog 2

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Cfa.3413.1.A1_at	8.95E-03	2.20E-02	0.7	PREDICTED: Canis familiaris similar to Ribonucleoside-diphosphate reductase large subunit (Ribonucleoside-diphosphate reductase M1 subunit) (Ribonucleotide reductase large chain); transcript variant 1 (LOC476823); mRNA	XM_534027	RRM1	ribonucleotide reductase M1
CfaAffx.9942.1.S1_s_at	5.08E-03	1.77E-02	0.72	PREDICTED: Canis familiaris similar to Ribonucleoside-diphosphate reductase large subunit (Ribonucleoside-diphosphate reductase M1 subunit) (Ribonucleotide reductase large chain); transcript variant 5 (LOC476823); mRNA	XM_857130	RRM1	ribonucleotide reductase M1
CfaAffx.6059.1.S1_at	2.32E-02	3.37E-02	0.75	PREDICTED: Canis familiaris similar to Ribonucleoside-diphosphate reductase M2 chain (Ribonucleotide reductase small chain); transcript variant 1 (LOC482963); mRNA	XM_540076	RRM2	ribonucleotide reductase M2 polypeptide
CfaAffx.14564.1.S1_at	2.27E-02	3.33E-02	0.67	PREDICTED: Canis familiaris similar to round spermatid basic protein 1; transcript variant 1 (LOC475802); mRNA	XM_533011	RSBN1	round spermatid basic protein 1
Cfa.13506.1.A1_s_at	3.82E-03	1.63E-02	0.73	PREDICTED: Canis familiaris similar to reticulon 4 interacting protein 1; transcript variant 4 (LOC475013); mRNA	XM_863277	RTN4IP1	reticulon 4 interacting protein 1
Cfa.10177.1.S1_at	6.44E-02	5.87E-02	0.75	PREDICTED: Canis familiaris similar to rap2 interacting protein x; transcript variant 1 (LOC475168); mRNA	XM_532400	RUFY3	RUN and FYVE domain containing 3
Cfa.1681.1.S1_at	3.48E-03	1.58E-02	0.72	PREDICTED: Canis familiaris similar to RuvB-like 1 (49-kDa TATA box-binding protein-interacting protein) (49 kDa TBP-interacting protein) (TIP49a) (Pontin 52) (Nuclear matrix protein 238) (NMP 238) (54 kDa erythrocyte cytosolic protein) (ECP-54) (TIP60-associated protein 54-a...; transcript variant 6 (LOC476512); mRNA	XM_851956	RUVBL1	RuvB-like 1 (E. coli)
CfaAffx.22128.1.S1_at	6.76E-02	6.04E-02	0.77	PREDICTED: Canis familiaris similar to S-100P protein (LOC610295); mRNA	XM_847763	S100P	S100 calcium binding protein P

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CfaAffx.3929.1.S1_at	1.56E-02	2.80E-02	0.76	PREDICTED: Canis familiaris similar to sterile alpha motif domain containing 9-like (LOC482305); mRNA	XM_539422	SAMD9L	sterile alpha motif domain containing 9-like
Cfa.11724.1.A1_s_at	1.81E-04	9.00E-03	0.67	PREDICTED: Canis familiaris similar to SAM50 like protein CGI-51 (LOC474473); mRNA	XM_531702	SAMM50	sorting and assembly machinery component 50 homolog (S. cerevisiae)
CfaAffx.12896.1.S1_s_at	4.70E-03	1.73E-02	0.74	PREDICTED: Macaca mulatta SAM domain; SH3 domain and nuclear localization signals; 1; transcript variant 3 (SAMSN1); mRNA	XM_001082777	SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1
Cfa.4066.1.A1_s_at	1.78E-05	7.55E-03	0.72	PREDICTED: Canis familiaris similar to sin3 associated polypeptide p18 (LOC609404); mRNA	XM_534536	SAP18	Sin3A-associated protein, 18kDa
CfaAffx.12592.1.S1_at	3.99E-02	4.49E-02	0.77	PREDICTED: Canis familiaris similar to sin3 associated polypeptide p30 (LOC607359); mRNA	XM_843990	SAP30	Sin3A-associated protein, 30kDa
Cfa.3394.1.A1_at	5.13E-03	1.78E-02	0.75	PREDICTED: Canis familiaris similar to GTP-binding protein SAR1b (GTBPB) (LOC481509); mRNA	XM_538630	SAR1B	SAR1 gene homolog B (S. cerevisiae)
CfaAffx.2433.1.S1_at	2.46E-03	1.41E-02	0.75	PREDICTED: Canis familiaris similar to GTP-binding protein SAR1b (GTBPB) (LOC481509); mRNA	XM_538630	SAR1B	SAR1 gene homolog B (S. cerevisiae)
CfaAffx.2433.1.S1_s_at	1.08E-03	1.20E-02	0.72	PREDICTED: Canis familiaris similar to GTP-binding protein SAR1b (GTBPB) (LOC481509); mRNA	XM_538630	SAR1B	SAR1 gene homolog B (S. cerevisiae)
Cfa.17197.1.S1_at	5.22E-03	1.79E-02	0.77	PREDICTED: Canis familiaris similar to Shwachman-Bodian-Diamond syndrome protein (LOC607017); mRNA	XM_843539	SBDS	Shwachman-Bodian-Diamond syndrome
CfaAffx.16922.1.S1_at	8.76E-04	1.13E-02	0.7	PREDICTED: Canis familiaris similar to Shwachman-Bodian-Diamond syndrome protein (LOC607017); mRNA	XM_843539	SBDS	Shwachman-Bodian-Diamond syndrome
CfaAffx.12131.1.S1_s_at	3.27E-04	9.28E-03	0.64	PREDICTED: Canis familiaris similar to sno; strawberry notch homolog 1; transcript variant 1 (LOC477451); mRNA	XM_534649	SBNO1	strawberry notch homolog 1 (Drosophila)

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Cfa.18687.1.S1_at	3.64E-03	1.61E-02	1.3	PREDICTED: Canis familiaris similar to Secretory carrier-associated membrane protein 5 (Secretory carrier membrane protein 5); transcript variant 2 (LOC478371); mRNA	XM_862073	SCAMP5	secretory carrier membrane protein 5
CfaAffx.17216.1.S1_s_at	1.69E-02	2.91E-02	1.57	PREDICTED: Canis familiaris similar to Sodium channel protein type III alpha subunit (Voltage-gated sodium channel alpha subunit Nav1.3) (Sodium channel protein; brain III alpha subunit) (Voltage-gated sodium channel subtype III); transcript variant 6 (LOC478772); mRNA	XM_852824	SCN3A	sodium channel, voltage-gated, type III, alpha subunit
Cfa.362.1.A1_at	2.57E-02	3.56E-02	0.76	PREDICTED: Canis familiaris similar to cytochrome oxidase deficient homolog 1 (LOC489505); mRNA	XM_546624	SCO1	SCO cytochrome oxidase deficient homolog 1 (yeast)
Cfa.21262.1.S1_at	1.05E-02	2.34E-02	0.72	PREDICTED: Canis familiaris similar to short coiled-coil protein; transcript variant 1 (LOC606862); mRNA	XM_843274	SCOC	short coiled-coil protein
Cfa.391.1.S1_at	1.06E-03	1.19E-02	0.77	PREDICTED: Canis familiaris similar to SCY1-like 2 protein; transcript variant 1 (LOC482622); mRNA	XM_539739	SCYL2	SCY1-like 2 (S. cerevisiae)
CfaAffx.6509.1.S1_s_at	3.30E-02	4.05E-02	0.75	PREDICTED: Canis familiaris similar to syntenin isoform 3; transcript variant 1 (LOC482977); mRNA	XM_540090	SDCBP	syndecan binding protein (syntenin)
Cfa.10434.1.A1_at	1.44E-03	1.25E-02	0.69	PREDICTED: Canis familiaris similar to Stromal cell-derived factor 2 precursor (SDF-2); transcript variant 1 (LOC480626); mRNA	XM_537746	SDF2	stromal cell-derived factor 2
CfaAffx.28636.1.S1_s_at	1.12E-03	1.20E-02	0.73	PREDICTED: Canis familiaris similar to Stromal cell-derived factor 2 precursor (SDF-2); transcript variant 1 (LOC480626); mRNA	XM_537746	SDF2	stromal cell-derived factor 2
Cfa.8688.1.A1_at	2.35E-03	1.40E-02	0.58	PREDICTED: Canis familiaris similar to Stromal cell-derived factor 2-like protein 1 precursor (SDF2 like protein 1) (PWP1-interacting protein 8) (LOC608633); mRNA	XM_845717	SDF2L1	stromal cell-derived factor 2-like 1

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Cfa.8688.1.A1_s_at	4.89E-03	1.75E-02	0.74	PREDICTED: Canis familiaris similar to Stromal cell-derived factor 2-like protein 1 precursor (SDF2 like protein 1) (PWP1-interacting protein 8) (LOC608633); mRNA	XM_845717	SDF2L1	stromal cell-derived factor 2-like 1
CfaAffx.23546.1.S1_at	1.85E-03	1.31E-02	0.67	PREDICTED: Canis familiaris similar to Stromal cell-derived factor 2-like protein 1 precursor (SDF2 like protein 1) (PWP1-interacting protein 8) (LOC608633); mRNA	XM_845717	SDF2L1	stromal cell-derived factor 2-like 1
Cfa.18281.1.S1_at	4.59E-02	4.86E-02	0.75	PREDICTED: Canis familiaris similar to Succinate dehydrogenase [ubiquinone] flavoprotein subunit; mitochondrial precursor (Fp) (Flavoprotein subunit of complex II); transcript variant 6 (LOC478634); mRNA	XM_851844	SDHA	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)
CfaAffx.24257.1.S1_s_at	7.29E-04	1.08E-02	0.77	PREDICTED: Canis familiaris similar to Succinate dehydrogenase [ubiquinone] iron-sulfur protein; mitochondrial precursor (Ip) (Iron-sulfur subunit of complex II); transcript variant 1 (LOC478217); mRNA	XM_535392	SDHB	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)
CfaAffx.3371.1.S1_s_at	5.52E-04	1.02E-02	0.74	PREDICTED: Canis familiaris similar to Succinate dehydrogenase [ubiquinone] iron-sulfur protein; mitochondrial precursor (Ip) (Iron-sulfur subunit of complex II) (LOC608210); mRNA	XM_845169	SDHB	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)
CfaAffx.16788.1.S1_at	1.88E-03	1.32E-02	0.77	PREDICTED: Canis familiaris similar to SEC22 vesicle trafficking protein-like 1 (LOC475816); mRNA	XM_533025	SEC22B	SEC22 vesicle trafficking protein homolog B (S. cerevisiae)
CfaAffx.16788.1.S1_s_at	3.05E-03	1.51E-02	0.71	PREDICTED: Canis familiaris similar to SEC22 vesicle trafficking protein-like 1 (LOC475816); mRNA	XM_533025	SEC22B	SEC22 vesicle trafficking protein homolog B (S. cerevisiae)

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Cfa.319.1.A1_at	6.51E-03	1.93E-02	0.76	Pongo abelii mRNA; cDNA DKFZp469D0613 (from clone DKFZp469D0613)	CR859634	SEC23IP	SEC23 interacting protein
Cfa.585.1.S1_s_at	2.04E-02	3.17E-02	0.73	PREDICTED: Canis familiaris similar to Protein transport protein Sec24B (SEC24-related protein B) (LOC487898); mRNA	XM_545021	SEC24B	SEC24 related gene family, member B (S. cerevisiae)
Cfa.3895.1.A1_s_at	5.79E-04	1.03E-02	0.71	Canis familiaris protein translocation complex beta subunit mRNA; complete cds	L25052	Sec61b	Sec61 beta subunit
CfaAffx.6574.1.S1_s_at	1.63E-04	9.00E-03	0.61	PREDICTED: Canis familiaris similar to Translocation protein SEC63 homolog (LOC475016); mRNA	XM_532252	SEC63	SEC63 homolog (S. cerevisiae)
Cfa.18769.1.S1_s_at	7.15E-03	1.99E-02	0.76	PREDICTED: Canis familiaris similar to sel-1 suppressor of lin-12-like (LOC480409); mRNA	XM_537530	SEL1L	sel-1 suppressor of lin-12-like (C. elegans)
Cfa.4366.2.A1_at	8.32E-04	1.11E-02	0.68	Canis lupus familiaris selenoprotein K (SELK); mRNA	NM_001114878	SELK	selenoprotein K
CfaAffx.955.1.S1_s_at	3.85E-04	9.61E-03	0.66	Canis lupus familiaris selenoprotein K (SELK); mRNA	NM_001114878	SELK	selenoprotein K
CfaAffx.4164.1.S1_s_at	2.32E-03	1.39E-02	0.76	PREDICTED: Canis familiaris similar to semaphorin 4D (LOC476350); mRNA	XM_533551	SEMA4D	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D
CfaAffx.20279.1.S1_at	7.72E-04	1.10E-02	0.74	PREDICTED: Canis familiaris similar to SUMO1/sentrin specific protease 5 (LOC488033); mRNA	XM_545156	SENP5	SUMO1/sentrin specific peptidase 5
CfaAffx.8046.1.S1_at	1.90E-05	7.55E-03	0.76	PREDICTED: Canis familiaris similar to selenophosphate synthetase; transcript variant 1 (LOC477999); mRNA	XM_535183	SEPHS1	selenophosphate synthetase 1
Cfa.408.1.A1_at	3.46E-04	9.40E-03	0.72	PREDICTED: Canis familiaris similar to selenophosphate synthetase; transcript variant 5 (LOC477999); mRNA	XM_852372	SEPHS1	selenophosphate synthetase 1

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.1706.1.A1_at	3.51E-03	1.59E-02	0.74	Canis lupus familiaris selenophosphate synthetase 2 (SEPHS2); mRNA	NM_001114736	SEPHS2	selenophosphate synthetase 2
Cfa.4458.1.A1_at	1.75E-03	1.30E-02	0.76	Homo sapiens mRNA for KIAA1253 protein; partial cds	AB033079	SERINC1	serine incorporator 1
Cfa.14118.2.A1_s_at	3.70E-04	9.61E-03	0.7	PREDICTED: Canis familiaris similar to tumor differentially expressed 2; transcript variant 2 (LOC476277); mRNA	XM_858663	SERINC1	serine incorporator 1
CfaAffx.2388.1.S1_s_at	1.55E-03	1.26E-02	0.71	PREDICTED: Canis familiaris similar to tumor differentially expressed 2; transcript variant 5 (LOC476277); mRNA	XM_858732	SERINC1	serine incorporator 1
Cfa.6665.1.A1_s_at	7.92E-03	2.08E-02	0.73	PREDICTED: Canis familiaris similar to Splicing factor 3B subunit 2 (Spliceosome associated protein 145) (SAP 145) (SF3b150) (Pre-mRNA splicing factor SF3b 145 kDa subunit); transcript variant 7 (LOC476015); mRNA	XM_860984	SF3B2	splicing factor 3b, subunit 2, 145kDa
Cfa.12208.1.A1_at	4.62E-03	1.72E-02	0.77	PREDICTED: Canis familiaris similar to SF3b10 (LOC611736); mRNA	XM_849442	SF3B5	splicing factor 3b, subunit 5, 10kDa
CfaAffx.1424.1.S1_s_at	3.72E-04	9.61E-03	0.73	PREDICTED: Canis familiaris similar to SF3b10 (LOC611736); mRNA	XM_849442	SF3B5	splicing factor 3b, subunit 5, 10kDa
Cfa.21121.1.S1_at	7.58E-05	8.57E-03	0.73	PREDICTED: Canis familiaris similar to splicing factor; arginine/serine-rich 1 (ASF/SF2); transcript variant 1 (LOC609693); mRNA	XM_847964	SFRS1	splicing factor, arginine/serine-rich 1
Cfa.20238.1.S1_at	9.95E-03	2.30E-02	0.74	PREDICTED: Canis familiaris similar to splicing factor; arginine/serine-rich 1 (ASF/SF2); transcript variant 7 (LOC609693); mRNA	XM_861705	SFRS1	splicing factor, arginine/serine-rich 1
Cfa.21298.1.S1_s_at	1.39E-03	1.24E-02	0.74	PREDICTED: Canis familiaris similar to splicing factor; arginine/serine-rich 10 (transformer 2 homolog; Drosophila) (LOC478663); mRNA	XM_535833	SFRS10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)

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Cfa.4472.1.S1_at	1.60E-03	1.27E-02	0.72	PREDICTED: Canis familiaris similar to splicing factor; arginine/serine-rich 10 (transformer 2 homolog; Drosophila) (LOC478663); mRNA	XM_535833	SFRS10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)
Cfa.4472.1.S1_s_at	1.56E-03	1.26E-02	0.74	PREDICTED: Canis familiaris similar to splicing factor; arginine/serine-rich 10 (transformer 2 homolog; Drosophila) (LOC478663); mRNA	XM_535833	SFRS10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)
Cfa.9497.1.A1_at	9.96E-03	2.30E-02	0.76	PREDICTED: Canis familiaris similar to splicing factor; arginine/serine-rich 11; transcript variant 4 (LOC490216); mRNA	XM_862855	SFRS11	splicing factor, arginine/serine-rich 11
Cfa.15354.1.S1_s_at	1.82E-02	3.01E-02	0.72	PREDICTED: Canis familiaris hypothetical LOC475005; transcript variant 14 (LOC475005); mRNA	XM_863095	SFRS18	splicing factor, arginine/serine-rich 18
CfaAffx.8658.1.S1_s_at	3.31E-04	9.28E-03	0.67	PREDICTED: Canis familiaris similar to Splicing factor; arginine/serine-rich 2 (Splicing factor SC35) (SC-35) (Splicing component; 35 kDa); transcript variant 2 (LOC612817); mRNA	XM_843896	SFRS2	splicing factor, arginine/serine-rich 2
Cfa.10605.1.S1_at	7.69E-04	1.10E-02	0.75	PREDICTED: Canis familiaris similar to Splicing factor; arginine/serine-rich 2 (Splicing factor SC35) (SC-35) (Splicing component; 35 kDa); transcript variant 5 (LOC612817); mRNA	XM_852679	SFRS2	splicing factor, arginine/serine-rich 2
Cfa.2367.1.A1_at	2.93E-03	1.50E-02	0.73	Homo sapiens splicing factor; arginine/serine-rich 2; interacting protein (SFRS2IP); mRNA	NM_004719	SFRS2IP	splicing factor, arginine/serine-rich 2, interacting protein
Cfa.246.1.S1_s_at	1.27E-04	8.90E-03	0.69	PREDICTED: Canis familiaris splicing factor (SRP20); mRNA	XM_532124	SFRS3	splicing factor, arginine/serine-rich 3
CfaAffx.3002.1.S1_at	9.01E-04	1.15E-02	0.76	PREDICTED: Canis familiaris splicing factor (SRP20); mRNA	XM_532124	SFRS3	splicing factor, arginine/serine-rich 3

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Cfa.12115.3.A1_s_at	6.79E-03	1.96E-02	0.76	familiaris similar to Splicing factor; arginine/serine-rich 5 (Pre mRNA splicing factor SRP40) (Insulin-induced growth response protein CL-4) (Delayed-early protein HRS); transcript variant 5 (LOC490754); mRNA	XM_862000	SFRS5	splicing factor, arginine/serine-rich 5
Cfa.11128.2.A1_s_at	1.13E-02	2.41E-02	0.76	PREDICTED: Canis familiaris similar to splicing factor; arginine/serine-rich 7 (LOC475730); mRNA	XM_532939	SFRS7	splicing factor, arginine/serine-rich 7, 35kDa
CfaAffx.10413.1.S1_s_at	1.49E-02	2.74E-02	0.76	PREDICTED: Canis familiaris similar to splicing factor; arginine/serine-rich 7 (LOC475730); mRNA	XM_532939	SFRS7	splicing factor, arginine/serine-rich 7, 35kDa
CfaAffx.26023.1.S1_at	8.31E-03	2.13E-02	1.31	PREDICTED: Canis familiaris similar to Alpha-sarcoglycan precursor (Alpha-SG) (Adhalin) (50 kDa dystrophin-associated glycoprotein) (50DAG) (Dystroglycan 2) (LOC609265); mRNA	XM_846494	SGCA	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)
Cfa.6416.1.A1_at	8.88E-05	8.90E-03	1.32	Canis lupus familiaris sarcoglycan; gamma (35kDa dystrophin-associated glycoprotein) (SGCG); mRNA	NM_001014276	SGCG	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)
Cfa.2341.1.A1_at	1.02E-02	2.32E-02	0.71	PREDICTED: Canis familiaris similar to SH3 domain-binding protein 5 (SH3 domain-binding protein that preferentially associates with BTK) (LOC485657); mRNA	XM_542777	SH3BP5	SH3-domain binding protein 5 (BTK-associated)
CfaAffx.4160.1.S1_s_at	1.61E-02	2.84E-02	0.75	familiaris similar to 26 proteasome complex subunit DSS1 (Deleted in split hand/split foot protein 1) (Split hand/foot deleted protein 1 homolog); transcript variant 1 (LOC608719); mRNA	XM_845285	SHFM1	split hand/foot malformation (ectrodactyly) type 1
Cfa.21077.1.S1_s_at	2.92E-03	1.50E-02	0.77	familiaris similar to Leucine-rich repeat protein SHOC-2 (Ras-binding protein Sur-8); transcript variant 2 (LOC477819); mRNA	XM_859510	SHOC2	soc-2 suppressor of clear homolog (C. elegans)

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Cfa.2346.1.A1_s_at	2.66E-03	1.45E-02	0.66	PREDICTED: Canis familiaris similar to superkiller viralicidic activity 2-like 2; transcript variant 1 (LOC607950); mRNA	XM_844583	SKIV2L2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)
Cfa.14639.1.S1_at	1.32E-02	2.59E-02	0.76	Canis lupus familiaris solute carrier family 11 (proton-coupled divalent metal ion transporters); member 1 (SLC11A1); mRNA	NM_001013851	SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1
CfaAffx.1885.1.S1_s_at	2.04E-02	3.17E-02	0.75	PREDICTED: Canis familiaris similar to Solute carrier family 12; member 2 (Bumetanide-sensitive sodium-(potassium)-chloride cotransporter 1) (Basolateral Na-K-Cl symporter) (LOC481490); mRNA	XM_538611	SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters), member 2
CfaAffx.12315.1.S1_s_at	1.57E-03	1.26E-02	0.72	PREDICTED: Canis familiaris similar to solute carrier family 25; member 36 (LOC477095); mRNA	XM_534289	SLC25A36	solute carrier family 25, member 36
CfaAffx.14394.1.S1_s_at	2.47E-02	3.48E-02	0.77	PREDICTED: Canis familiaris similar to mitochondrial solute carrier-like protein; transcript variant 5 (LOC486115); mRNA	XM_853761	SLC25A37	solute carrier family 25, member 37
Cfa.2658.1.S1_at	5.48E-04	1.02E-02	0.74	PREDICTED: Canis familiaris similar to CG8931-PA (LOC488876); mRNA	XM_545993	SLC25A46	solute carrier family 25, member 46
Cfa.1352.1.S1_s_at	9.84E-04	1.16E-02	0.76	PREDICTED: Canis familiaris similar to solute carrier family 25; member 5; transcript variant 1 (LOC492093); mRNA	XM_549215	SLC25A5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
Cfa.13227.1.A1_s_at	2.22E-02	3.31E-02	0.66	PREDICTED: Canis familiaris similar to Very-long-chain acyl-CoA synthetase (Very-long-chain-fatty-acid-CoA ligase); transcript variant 2 (LOC478298); mRNA	XM_857161	SLC27A2	solute carrier family 27 (fatty acid transporter), member 2
Cfa.593.1.A1_at	1.70E-03	1.29E-02	0.67	PREDICTED: Pan troglodytes acetyl-coenzyme A transporter (SLC33A1); mRNA	XM_516831	SLC33A1	solute carrier family 33 (acetyl-CoA transporter), member 1

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CfaAffx.25900.1.S1_at	7.27E-04	1.08E-02	0.62	PREDICTED: Canis familiaris similar to solute carrier family 35; member B1; transcript variant 5 (LOC480549); mRNA	XM_860061	SLC35B1	solute carrier family 35, member B1
Cfa.17007.1.S1_at	5.28E-03	1.80E-02	0.76	PREDICTED: Canis familiaris similar to solute carrier family 35; member C2; transcript variant 4 (LOC609863); mRNA	XM_861605	SLC35C2	solute carrier family 35, member C2
Cfa.9951.1.A1_at	1.83E-03	1.31E-02	0.73	Homo sapiens mRNA; cDNA DKFZp686H1697 (from clone DKFZp686H1697)	BX647547	SLC38A1	solute carrier family 38, member 1
CfaAffx.16816.1.S1_at	3.51E-04	9.49E-03	1.32	PREDICTED: Canis familiaris similar to System N amino acid transporter 1 (SN1) (N-system amino acid transporter 1) (Solute carrier family 38; member 3) (LOC476617); mRNA	XM_533820	SLC38A3	solute carrier family 38, member 3
Cfa.16809.1.S1_at	2.19E-03	1.37E-02	0.76	PREDICTED: Canis familiaris similar to solute carrier family 41; member 2 (LOC481298); mRNA	XM_538419	SLC41A2	solute carrier family 41, member 2
Cfa.16809.1.S1_s_at	1.06E-03	1.19E-02	0.74	PREDICTED: Canis familiaris similar to solute carrier family 41; member 2 (LOC481298); mRNA	XM_538419	SLC41A2	solute carrier family 41, member 2
CfaAffx.10961.1.S1_at	6.74E-03	1.95E-02	0.72	PREDICTED: Canis familiaris similar to Y4C6B.5 (LOC477324); mRNA	XM_534517	SLC46A3	solute carrier family 46, member 3
CfaAffx.6523.1.S1_at	3.10E-03	1.53E-02	1.31	PREDICTED: Canis familiaris similar to Orphan sodium- and chloride-dependent neurotransmitter transporter NTT5 (Solute carrier family 6 member 16) (LOC484383); mRNA	XM_541498	SLC6A16	solute carrier family 6, member 16
CfaAffx.12404.1.S1_s_at	8.95E-03	2.20E-02	0.75	PREDICTED: Canis familiaris similar to sarcolemma associated protein; transcript variant 17 (LOC476577); mRNA	XM_852570	SLMAP	sarcolemma associated protein
Cfa.660.2.A1_s_at	3.73E-03	1.62E-02	0.72	PREDICTED: Canis familiaris similar to modulator of estrogen induced transcription isoform a; transcript variant 11 (LOC478322); mRNA	XM_859168	SLTM	SAFB-like, transcription modulator
Cfa.15466.1.S1_s_at	6.18E-03	1.89E-02	0.75	PREDICTED: Canis familiaris similar to step II splicing factor SLU7 (LOC479308); mRNA	XM_536446	SLU7	SLU7 splicing factor homolog (S. cerevisiae)

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.936.1.S1_at	1.27E-02	2.54E-02	0.73	PREDICTED: Pan troglodytes SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a5; transcript variant 5 (SMARCA5); mRNA	XM_517459	SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5
CfaAffx.12160.1.S1_s_at	2.27E-02	3.33E-02	0.76	PREDICTED: Canis familiaris similar to SWI/SNF related matrix associated actin dependent regulator of chromatin subfamily A member 5 (SWI/SNF-related matrix-associated actin-dependent regulator of chromatin A5) (Sucrose nonfermenting protein 2 homolog) (hSNF2H)...; transcript variant 1 (LOC475451); mRNA	XM_532676	SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5
Cfa.9379.1.S1_at	5.31E-03	1.80E-02	0.74	PREDICTED: Canis familiaris similar to SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily b; member 1; transcript variant 7 (LOC486407); mRNA	XM_852298	SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1
Cfa.5396.1.A1_s_at	1.59E-02	2.82E-02	0.75	PREDICTED: Canis familiaris similar to SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily e; member 1; transcript variant 1 (LOC608250); mRNA	XM_537645	SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1
Cfa.20347.1.S1_s_at	5.15E-03	1.79E-02	0.76	PREDICTED: Canis familiaris similar to SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily e; member 1; transcript variant 2 (LOC608250); mRNA	XM_845917	SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1

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Cfa.8883.1.A1_at	3.53E-02	4.21E-02	0.75	PREDICTED: Canis familiaris similar to SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily e; member 1; transcript variant 8 (LOC608250); mRNA	XM_857912	SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1
CfaAffx.24592.1.S1_at	5.77E-02	5.52E-02	0.74	PREDICTED: Canis familiaris similar to SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily e; member 1; transcript variant 8 (LOC608250); mRNA	XM_857912	SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1
CfaAffx.22089.1.S1_s_at	8.90E-03	2.19E-02	0.74	PREDICTED: Canis familiaris similar to Structural maintenance of chromosomes 4-like 1 protein (Chromosome-associated polypeptide C) (hCAP-C) (XCAP-C homolog); transcript variant 2 (LOC478679); mRNA	XM_856436	SMC4	structural maintenance of chromosomes 4
Cfa.1060.1.S1_at	7.01E-03	1.98E-02	0.68	PREDICTED: Canis familiaris similar to Structural maintenance of chromosomes 4-like 1 protein (Chromosome-associated polypeptide C) (hCAP-C) (XCAP-C homolog); transcript variant 3 (LOC478679); mRNA	XM_856465	SMC4	structural maintenance of chromosomes 4
CfaAffx.26898.1.S1_at	1.52E-02	2.76E-02	0.76	PREDICTED: Canis familiaris similar to CG9351-PA; isoform A; transcript variant 2 (LOC612974); mRNA	XM_863366	SMEK1	SMEK homolog 1, suppressor of mek1 (Dictyostelium)
Cfa.15673.1.S1_at	1.95E-02	3.11E-02	0.7	PREDICTED: Canis familiaris similar to acid sphingomyelinase-like phosphodiesterase 3A (LOC476279); mRNA	XM_533485	SMPDL3A	sphingomyelin phosphodiesterase, acid-like 3A
CfaAffx.2399.1.S1_s_at	8.61E-03	2.17E-02	0.72	PREDICTED: Canis familiaris similar to acid sphingomyelinase-like phosphodiesterase 3A (LOC476279); mRNA	XM_533485	SMPDL3A	sphingomyelin phosphodiesterase, acid-like 3A

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Cfa.10128.1.A1_at	1.55E-04	9.00E-03	1.34	PREDICTED: Canis familiaris similar to alpha-synuclein isoform NACP140; transcript variant 4 (LOC478478); mRNA	XM_855849	SNCA	synuclein, alpha (non A4 component of amyloid precursor)
CfaAffx.16521.1.S1_at	4.15E-03	1.67E-02	0.77	familiaris similar to U2 small nuclear ribonucleoprotein A (U2 snRNP-A); transcript variant 2 (LOC607102); mRNA	XM_843830	SNRPA1	small nuclear ribonucleoprotein polypeptide A'
Cfa.6238.1.A1_at	2.22E-03	1.37E-02	0.73	PREDICTED: Canis familiaris small nuclear ribonucleoprotein D1 polypeptide (SNRPD1); mRNA	XM_537302	SNRPD1	small nuclear ribonucleoprotein D1 polypeptide 16kDa
Cfa.6238.1.A1_s_at	1.99E-02	3.14E-02	0.75	PREDICTED: Canis familiaris small nuclear ribonucleoprotein D1 polypeptide (SNRPD1); mRNA	XM_537302	SNRPD1	small nuclear ribonucleoprotein D1 polypeptide 16kDa
CfaAffx.27936.1.S1_at	1.45E-02	2.71E-02	0.72	PREDICTED: Canis familiaris small nuclear ribonucleoprotein D1 polypeptide (SNRPD1); mRNA	XM_537302	SNRPD1	small nuclear ribonucleoprotein D1 polypeptide 16kDa
Cfa.11354.1.A1_s_at	1.28E-03	1.23E-02	0.7	PREDICTED: Canis familiaris similar to small nuclear ribonucleoprotein D3 (LOC607772); mRNA	XM_844567	SNRPD3	small nuclear ribonucleoprotein D3 polypeptide 18kDa
Cfa.6533.1.A1_at	6.13E-03	1.88E-02	0.75	PREDICTED: Canis familiaris similar to small nuclear ribonucleoprotein E (LOC478934); mRNA	XM_536093	SNRPE	small nuclear ribonucleoprotein polypeptide E
CfaAffx.26374.1.S1_s_at	6.65E-03	1.94E-02	0.66	PREDICTED: Canis familiaris similar to Nuclear protein SkiP (Ski-interacting protein) (SNW1 protein) (Nuclear receptor coactivator NCoA 62); transcript variant 8 (LOC480405); mRNA	XM_863228	SNW1	SNW domain containing 1
Cfa.1431.1.S1_at	7.47E-03	2.03E-02	0.77	Bos taurus sorting nexin 10; mRNA (cDNA clone MGC:139527 IMAGE:8279999); complete cds	BC122586	SNX10	sorting nexin 10
CfaAffx.5276.1.S1_s_at	1.07E-02	2.36E-02	0.76	PREDICTED: Canis familiaris similar to Sorting nexin-10 (LOC475261); mRNA	XM_532496	SNX10	sorting nexin 10
Cfa.2011.1.S1_s_at	3.77E-03	1.62E-02	0.74	PREDICTED: Canis familiaris similar to sorting nexin 14 isoform a (LOC474985); mRNA	XM_532222	SNX14	sorting nexin 14

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Cfa.19551.1.S1_at	1.30E-02	2.57E-02	0.72	Homo sapiens sorting nexin 18 (SNX18); transcript variant 1; mRNA	NM_001102575	SNX18	sorting nexin 18
CfaAffx.656.1.S1_at	1.62E-03	1.27E-02	1.31	PREDICTED: Canis familiaris similar to Sorting nexin-2; transcript variant 1 (LOC474657); mRNA	XM_531886	SNX2	sorting nexin 2
CfaAffx.5534.1.S1_at	1.06E-02	2.35E-02	0.77	PREDICTED: Canis familiaris similar to sorting nexin 7 (predicted) (LOC481672); mRNA	XM_538794	SNX30	sorting nexin family member 30
CfaAffx.9150.1.S1_s_at	1.26E-03	1.23E-02	0.72	PREDICTED: Canis familiaris similar to Sorting nexin-5 (LOC485754); mRNA	XM_542877	SNX5	sorting nexin 5
Cfa.10850.1.A1_s_at	6.19E-03	1.89E-02	0.7	PREDICTED: Canis familiaris similar to Cytokine inducible SH2-containing protein 5 (Suppressor of cytokine signaling 5) (SOCS-5) (Cytokine-inducible SH2 protein 6) (CIS-6) (LOC474581); mRNA	XM_531810	SOCS5	suppressor of cytokine signaling 5
Cfa.16439.1.A1_at	7.07E-03	1.99E-02	0.73	Homo sapiens suppressor of cytokine signaling 6 (SOCS6); mRNA	NM_004232	SOCS6	suppressor of cytokine signaling 6
CfaAffx.14399.1.S1_s_at	6.60E-03	1.94E-02	0.75	PREDICTED: Canis familiaris similar to SON DNA-binding protein isoform A; transcript variant 13 (LOC478406); mRNA	XM_852050	SON	SON DNA binding protein
Cfa.10358.2.S1_s_at	1.21E-02	2.48E-02	0.76	PREDICTED: Canis familiaris similar to SON DNA-binding protein isoform A; transcript variant 14 (LOC478406); mRNA	XM_852093	SON	SON DNA binding protein
CfaAffx.9541.1.S1_s_at	6.25E-03	1.89E-02	0.72	PREDICTED: Canis familiaris similar to spastin isoform 1; transcript variant 2 (LOC608582); mRNA	XM_857738	SPAST	spastin
Cfa.10316.1.A1_at	1.55E-02	2.79E-02	0.74	PREDICTED: Canis familiaris similar to spermatogenesis associated; serine-rich 2; transcript variant 1 (LOC477617); mRNA	XM_534811	SPATS2	spermatogenesis associated, serine-rich 2
CfaAffx.26814.1.S1_at	1.10E-02	2.39E-02	0.76	PREDICTED: Canis familiaris similar to spindle pole body component 24 homolog (LOC611174); mRNA	XM_848818	SPC24	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.1257.1.A1_s_at	2.77E-03	1.48E-02	0.72	Canis familiaris signal peptidase complex 25 kDa subunit (SPC25) mRNA; complete cds	U12687	SPCS2	signal peptidase complex subunit 2 homolog (S. cerevisiae)
Cfa.3875.1.A1_at	3.86E-03	1.63E-02	0.73	Dog microsomal signal peptidase (SPC22/23) mRNA; complete cds	J04067	SPCS3	signal peptidase complex subunit 3 homolog (S. cerevisiae)
Cfa.6937.1.A1_at	8.59E-03	2.16E-02	0.69	PREDICTED: Canis familiaris similar to SPRY domain-containing SOCS box protein SSB-2 (LOC477710); mRNA	XM_534903	SPSB2	splA/ryanodine receptor domain and SOCS box containing 2
Cfa.1204.2.S1_at	1.33E-03	1.23E-02	0.59	PREDICTED: Canis familiaris beta-spectrin; transcript variant 7 (LOC403743); mRNA	XM_860139	SPTBN1	spectrin, beta, non-erythrocytic 1
Cfa.13084.1.A1_s_at	1.49E-02	2.74E-02	0.74	PREDICTED: Pan troglodytes SLIT-ROBO Rho GTPase activating protein 2; transcript variant 6 (SRGAP2); mRNA	XM_001163967	SRGAP2	SLIT-ROBO Rho GTPase activating protein 2
CfaAffx.20628.1.S1_s_at	1.45E-03	1.25E-02	0.71	Canine mRNA for signal recognition particle 54k protein	X16318	SRP54	signal recognition particle 54kDa
CfaAffx.14631.1.S1_s_at	3.19E-03	1.54E-02	0.75	Canis familiaris mRNA for partial splicing factor SRp55-1 (srp55-1 gene)	AJ388540	SRP55-1	splicing factor SRp55-1
CfaAffx.24803.1.S1_s_at	9.40E-03	2.24E-02	0.75	PREDICTED: Canis familiaris similar to Signal recognition particle 9 kDa protein (SRP9) (LOC611923); mRNA	XM_849646	SRP9	signal recognition particle 9kDa
CfaAffx.19397.1.S1_at	3.38E-02	4.10E-02	1.39	Caenorhabditis elegans Serpentine Receptor; class Z family member (srz-12) (srz-12) mRNA; complete cds	NM_074560	srz-12	Serpentine Receptor, class Z
CfaAffx.27783.1.S1_at	7.38E-03	2.02E-02	0.75	PREDICTED: Canis familiaris similar to SYT; transcript variant 1 (SS18); mRNA	XM_537295	SS18	synovial sarcoma translocation, chromosome 18
CfaAffx.8871.1.S1_at	1.09E-04	8.90E-03	0.67	PREDICTED: Canis familiaris similar to synovial sarcoma translocation gene on chromosome 18-like 2 (LOC609586); mRNA	XM_846873	SS18L2	synovial sarcoma translocation gene on chromosome 18-like 2

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CfaAffx.19266.1.S1_at	1.98E-03	1.34E-02	0.76	PREDICTED: Canis familiaris similar to autoantigen La (LOC478787); mRNA	XM_535952	SSB	Sjogren syndrome antigen B (autoantigen La)
CfaAffx.29787.1.S1_s_at	2.04E-03	1.35E-02	0.74	PREDICTED: Canis familiaris similar to Sjogrens syndrome nuclear autoantigen 1 (LOC480666); mRNA	XM_537785	SSNA1	Sjogren syndrome nuclear autoantigen 1
Cfa.2734.1.S1_s_at	1.07E-02	2.36E-02	0.75	Dog mRNA for signal sequence receptor beta subunit (TRAP-complex beta subunit)	X53529	SSR2	signal sequence receptor, beta (translocon-associated protein beta)
Cfa.6211.1.A1_s_at	6.30E-04	1.05E-02	0.77	PREDICTED: Canis familiaris similar to Translocon-associated protein; delta subunit precursor (TRAP-delta) (Signal sequence receptor delta subunit) (SSR-delta); transcript variant 3 (LOC481082); mRNA	XM_862273	SSR4	signal sequence receptor, delta (translocon-associated protein delta)
Cfa.635.1.A2_at	1.57E-03	1.26E-02	0.77	PREDICTED: Canis familiaris similar to structure specific recognition protein 1; transcript variant 1 (LOC475970); mRNA	XM_533177	SSRP1	structure specific recognition protein 1
Cfa.10782.1.A1_at	5.70E-03	1.84E-02	0.74	Homo sapiens aging-associated protein 14a mRNA; complete cds	AY826824	ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)
Cfa.10575.1.A1_at	4.76E-04	9.98E-03	0.72	PREDICTED: Canis familiaris similar to Lactosylceramide alpha-2;3-sialyltransferase (CMP NeuAc:lactosylceramide alpha-2;3-sialyltransferase) (Ganglioside GM3 synthase) (ST3Gal V) (Sialyltransferase 9) (LOC612022); mRNA	XM_849749	ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.15365.1.A1_at	5.24E-04	1.01E-02	0.71	PREDICTED: Canis familiaris similar to Lactosylceramide alpha-2;3-sialyltransferase (CMP NeuAc:lactosylceramide alpha-2;3-sialyltransferase) (Ganglioside GM3 synthase) (ST3Gal V) (Sialyltransferase 9) (LOC612022); mRNA	XM_849749	ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5
Cfa.18897.1.S1_s_at	1.46E-03	1.25E-02	0.72	PREDICTED: Canis familiaris similar to stromal antigen 2; transcript variant 7 (LOC492111); mRNA	XM_859856	STAG2	stromal antigen 2
CfaAffx.28426.1.S1_at	1.38E-02	2.65E-02	0.72	PREDICTED: Canis familiaris similar to stromal antigen 2; transcript variant 11 (LOC492111); mRNA	XM_859949	STAG2	stromal antigen 2
Cfa.9061.1.S1_at	4.54E-04	9.86E-03	0.75	PREDICTED: Canis familiaris similar to MLN64 N-terminal homolog; transcript variant 1 (LOC483257); mRNA	XM_540376	STARD3NL	STARD3 N-terminal like
Cfa.12403.1.A1_a_at	1.47E-03	1.25E-02	0.67	PREDICTED: Canis familiaris similar to START domain containing 4; sterol regulated (LOC479141); mRNA	XM_536287	STARD4	StAR-related lipid transfer (START) domain containing 4
CfaAffx.23894.1.S1_at	4.65E-03	1.73E-02	0.74	PREDICTED: Canis familiaris similar to Signal transducer and activator of transcription 5B; transcript variant 4 (LOC490969); mRNA	XM_854998	STAT5B	signal transducer and activator of transcription 5B
Cfa.578.1.S1_at	7.23E-03	2.00E-02	0.73	PREDICTED: Pan troglodytes staufen homolog 2; transcript variant 7 (STAU2); mRNA	XM_001165598	STAU2	staufen, RNA binding protein, homolog 2 (Drosophila)
CfaAffx.9883.1.S1_at	3.88E-03	1.63E-02	0.67	PREDICTED: Pan troglodytes striatin; calmodulin binding protein; transcript variant 2 (STRN); mRNA	XM_001166128	STRN	striatin, calmodulin binding protein
Cfa.10858.1.S1_at	4.81E-03	1.75E-02	0.74	PREDICTED: Canis familiaris similar to Oligosaccharyl transferase STT3 subunit homolog (B5) (Integral membrane protein 1); transcript variant 1 (LOC489300); mRNA	XM_546418	STT3A	STT3, subunit of the oligosaccharyl transferase complex, homolog A (S. cerevisiae)

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CfaAffx.16940.1.S1_s_at	1.09E-02	2.38E-02	0.74	PREDICTED: Canis familiaris similar to Oligosaccharyl transferase STT3 subunit homolog (B5) (Integral membrane protein 1); transcript variant 1 (LOC489300); mRNA	XM_546418	STT3A	STT3, subunit of the oligosaccharyl transferase complex, homolog A (S. cerevisiae)
CfaAffx.9075.1.S1_at	2.94E-04	9.25E-03	0.75	PREDICTED: Canis familiaris similar to source of immunodominant MHC-associated peptides; transcript variant 6 (LOC485628); mRNA	XM_856694	STT3B	STT3, subunit of the oligosaccharyl transferase complex, homolog B (S. cerevisiae)
Cfa.19362.1.S1_at	1.36E-03	1.23E-02	0.72	PREDICTED: Canis familiaris similar to syntaxin 12 (LOC478168); mRNA	XM_535342	STX12	syntaxin 12
CfaAffx.18679.1.S1_at	2.70E-03	1.46E-02	0.7	PREDICTED: Canis familiaris similar to syntaxin 12 (LOC478168); mRNA	XM_535342	STX12	syntaxin 12
CfaAffx.1243.1.S1_at	1.51E-03	1.25E-02	0.64	PREDICTED: Canis familiaris similar to Syntaxin-7; transcript variant 4 (LOC483987); mRNA	XM_854052	STX7	syntaxin 7
Cfa.1859.1.S1_at	1.15E-03	1.21E-02	0.72	PREDICTED: Canis familiaris similar to Syntaxin-7; transcript variant 5 (LOC483987); mRNA	XM_854089	STX7	syntaxin 7
CfaAffx.1243.1.S1_s_at	8.64E-04	1.13E-02	0.66	PREDICTED: Canis familiaris similar to Syntaxin-7; transcript variant 5 (LOC483987); mRNA	XM_854089	STX7	syntaxin 7
Cfa.5080.1.S1_at	9.70E-03	2.27E-02	0.75	PREDICTED: Canis familiaris similar to syntaxin 8; transcript variant 1 (LOC479499); mRNA	XM_536638	STX8	syntaxin 8
CfaAffx.1486.1.S1_s_at	3.24E-02	4.01E-02	0.75	PREDICTED: Canis familiaris similar to tomosyn isoform b (LOC476237); mRNA	XM_533442	STXBP5	syntaxin binding protein 5 (tomosyn)
Cfa.20191.1.S1_s_at	2.01E-04	9.06E-03	0.73	PREDICTED: Canis familiaris similar to Succinyl-CoA ligase [ADP-forming] beta-chain; mitochondrial precursor (Succinyl-CoA synthetase; betaA chain) (SCS-betaA) (ATP-specific succinyl-CoA synthetase beta subunit) (LOC485448); mRNA	XM_542566	SUCLA2	succinate-CoA ligase, ADP-forming, beta subunit

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CfaAffx.7625.1.S1_at	7.78E-04	1.10E-02	0.71	PREDICTED: Canis familiaris similar to Succinyl-CoA ligase [ADP-forming] beta-chain; mitochondrial precursor (Succinyl-CoA synthetase; betaA chain) (SCS-betaA) (ATP-specific succinyl-CoA synthetase beta subunit) (LOC485448); mRNA	XM_542566	SUCLA2	succinate-CoA ligase, ADP-forming, beta subunit
Cfa.16185.1.S1_at	9.83E-03	2.29E-02	0.75	PREDICTED: Canis familiaris similar to succinate-CoA ligase; GDP forming; alpha subunit (LOC475775); mRNA	XM_532985	SUCLG1	succinate-CoA ligase, alpha subunit
CfaAffx.10899.1.S1_s_at	4.30E-03	1.68E-02	0.76	PREDICTED: Canis familiaris similar to Succinyl-CoA ligase [GDP-forming] beta-chain; mitochondrial precursor (Succinyl-CoA synthetase; betaG chain) (SCS-betaG) (GTP-specific succinyl-CoA synthetase beta subunit) (LOC476562); mRNA	XM_533767	SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit
Cfa.746.1.S1_s_at	2.61E-03	1.44E-02	0.73	PREDICTED: Canis familiaris similar to SMT3 suppressor of mif two 3 homolog 1 (LOC478874); mRNA	XM_536034	SUMO1	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)
Cfa.20467.1.S1_s_at	1.14E-02	2.42E-02	0.66	PREDICTED: Canis familiaris similar to Transcription initiation protein SPT4 homolog 2; transcript variant 3 (LOC609757); mRNA	XM_861891	SUPT4H1	suppressor of Ty 4 homolog 1 (S. cerevisiae)
CfaAffx.17055.1.S1_s_at	6.34E-03	1.91E-02	0.76	PREDICTED: Canis familiaris similar to suppressor of variegation 4-20 homolog 1 isoform 2; transcript variant 2 (LOC483690); mRNA	XM_846431	SUV420H1	suppressor of variegation 4-20 homolog 1 (Drosophila)
CfaAffx.28292.1.S1_at	2.14E-03	1.36E-02	0.76	PREDICTED: Canis familiaris similar to joined to JAZF1 (LOC491158); mRNA	XM_548278	SUZ12	suppressor of zeste 12 homolog (Drosophila)
Cfa.20926.1.S1_at	6.52E-03	1.93E-02	0.73	PREDICTED: Bos taurus similar to Polycomb protein SUZ12 (Suppressor of zeste 12 protein homolog) (Joined to JAZF1 protein) (Chromatin precipitated E2F target 9 protein) (ChET 9 protein) (SUZ12); mRNA	XM_582605	SUZ12	suppressor of zeste 12 homolog (Drosophila)

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CfaAffx.19115.1.S1_at	2.57E-02	3.55E-02	0.76	familiaris similar to Synaptonemal complex protein 2 (SCP-2 protein) (Synaptonemal complex lateral element protein) (hsSCP2) (LOC477278); mRNA	XM_534470	SYCP2	synaptonemal complex protein 2
CfaAffx.19980.1.S1_s_at	1.55E-02	2.79E-02	0.75	PREDICTED: Canis familiaris similar to CCNDBP1 interactor isoform 1 (LOC478184); mRNA	XM_535357	SYF2	SYF2 homolog, RNA splicing factor (S. cerevisiae)
CfaAffx.6911.1.S1_at	1.10E-03	1.20E-02	0.76	PREDICTED: Canis familiaris similar to synaptophysin-like 1 isoform b (LOC475889); mRNA	XM_533096	SYPL1	synaptophysin-like 1
Cfa.6437.2.A1_s_at	2.69E-03	1.46E-02	0.71	PREDICTED: Canis familiaris similar to transforming acidic coiled-coil containing protein 1 short isoform; transcript variant 2 (LOC475581); mRNA	XM_843572	TACC1	transforming, acidic coiled-coil containing protein 1
CfaAffx.23924.1.S1_at	7.99E-03	2.09E-02	0.76	PREDICTED: Canis familiaris similar to SPT3-associated factor 42 (LOC480090); mRNA	XM_537213	TADA1L	transcriptional adaptor 1 (HFI1 homolog, yeast)-like
CfaAffx.974.1.S1_at	1.49E-02	2.74E-02	0.68	PREDICTED: Canis familiaris similar to TATA box-binding protein-associated factor 2F (LOC487180); mRNA	XM_544308	TAF7	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa
Cfa.2349.1.S1_at	2.83E-02	3.73E-02	0.74	PREDICTED: Pan troglodytes T-cell acute lymphocytic leukemia 1; transcript variant 1 (TAL1); mRNA	XM_001163354	TAL1	T-cell acute lymphocytic leukemia 1
CfaAffx.15620.1.S1_s_at	1.99E-03	1.34E-02	0.74	PREDICTED: Canis familiaris similar to TRAF interacting protein TANK isoform a (LOC608092); mRNA	XM_844996	TANK	TRAF family member-associated NFKB activator
Cfa.20509.1.S1_s_at	3.82E-03	1.63E-02	0.7	PREDICTED: Canis familiaris similar to TAO kinase 3; transcript variant 3 (LOC477502); mRNA	XM_857480	TAOK3	TAO kinase 3
CfaAffx.28814.1.S1_s_at	1.11E-03	1.20E-02	0.75	Bos taurus threonyl-tRNA synthetase; mRNA (cDNA clone MGC:128147 IMAGE:7954199); complete cds	BC103082	TARS	threonyl-tRNA synthetase
Cfa.2825.1.A1_at	2.22E-02	3.31E-02	0.72	PREDICTED: Canis familiaris similar to threonyl-tRNA synthetase (LOC479370); mRNA	XM_536509	TARS	threonyl-tRNA synthetase

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Cfa.18063.1.S1_at	3.93E-02	4.46E-02	0.76	PREDICTED: Canis familiaris similar to CG4552-PA; transcript variant 2 (LOC478539); mRNA	XM_843457	TBC1D23	TBC1 domain family, member 23
CfaAffx.14611.1.S1_s_at	4.37E-02	4.72E-02	0.73	PREDICTED: Canis familiaris similar to CG4552-PA; transcript variant 2 (LOC478539); mRNA	XM_843457	TBC1D23	TBC1 domain family, member 23
Cfa.3145.1.A1_at	1.76E-02	2.96E-02	0.73	PREDICTED: Equus caballus TBC1 domain family; member 9 (with GRAM domain) (TBC1D9); mRNA	XM_001501060	TBC1D9	TBC1 domain family, member 9 (with GRAM domain)
CfaAffx.14521.1.S1_s_at	1.10E-03	1.20E-02	0.74	PREDICTED: Canis familiaris similar to tubulin cofactor a (predicted) (LOC479173); mRNA	XM_536315	TBCA	tubulin folding cofactor A
Cfa.11050.1.S1_s_at	2.43E-03	1.41E-02	0.71	PREDICTED: Canis familiaris similar to transcription elongation factor A (SII) 1 (LOC477879); mRNA	XM_535071	TCEA1	transcription elongation factor A (SII), 1
Cfa.21472.2.S1_s_at	3.88E-03	1.63E-02	0.72	PREDICTED: Canis familiaris similar to Transcription elongation regulator 1 (TATA box-binding protein-associated factor 2S) (Transcription factor CA150) (p144) (Formin-binding protein 28) (FBP 28); transcript variant 5 (LOC478052); mRNA	XM_853724	TCERG1	transcription elongation regulator 1
Cfa.21472.1.S1_s_at	9.76E-03	2.28E-02	0.75	PREDICTED: Canis familiaris similar to Transcription elongation regulator 1 (TATA box-binding protein-associated factor 2S) (Transcription factor CA150) (p144) (Formin-binding protein 28) (FBP 28); transcript variant 8 (LOC478052); mRNA	XM_853836	TCERG1	transcription elongation regulator 1
Cfa.19327.1.A1_at	5.67E-03	1.84E-02	0.75	Homo sapiens cDNA FLJ37747 fis; clone BRHIP2022986	AK095066	TCF4	transcription factor 4
Cfa.2431.1.S1_at	4.13E-03	1.67E-02	0.74	full-length cDNA clone CS0DF023YK14 of Fetal brain of Homo sapiens (human)	CR612521	TCF4	transcription factor 4
Cfa.3808.1.S1_s_at	5.51E-03	1.82E-02	0.77	Dog mRNA for putative transcription factor recognizing thyroglobulin promoter	X51448	TCF4	transcription factor 4

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Cfa.11351.1.A1_at	1.89E-02	3.06E-02	0.74	PREDICTED: Canis familiaris similar to T-cell; immune regulator 1 isoform a; transcript variant 1 (LOC483691); mRNA	XM_540812	TCIRG1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3
Cfa.21272.1.S1_s_at	6.98E-04	1.07E-02	0.74	PREDICTED: Canis familiaris similar to T-complex protein 1; alpha subunit (TCP-1-alpha) (CCT-alpha); transcript variant 6 (LOC484064); mRNA	XM_857632	TCP1	t-complex 1
Cfa.970.1.S1_s_at	4.73E-04	9.95E-03	0.72	PREDICTED: Canis familiaris similar to T-complex protein 1; alpha subunit (TCP-1-alpha) (CCT-alpha); transcript variant 8 (LOC484064); mRNA	XM_857683	TCP1	t-complex 1
Cfa.217.1.S1_s_at	2.21E-02	3.30E-02	0.76	Canis familiaris TCTE1L mRNA; complete cds	AF491301	TCTE1L	t-complex-associated-testis-expressed 1-like
Cfa.10296.1.A1_at	4.96E-05	7.92E-03	0.76	PREDICTED: Canis familiaris similar to Telomeric repeat binding factor 2 interacting protein 1 (TRF2-interacting telomeric protein Rap1) (hRap1) (LOC479643); mRNA	XM_536776	TERF2IP	telomeric repeat binding factor 2, interacting protein
Cfa.11744.1.A1_s_at	1.58E-03	1.26E-02	0.73	PREDICTED: Canis familiaris similar to Testin (TESS); transcript variant 5 (LOC475293); mRNA	XM_860864	TES	testis derived transcript (3 LIM domains)
CfaAffx.19117.1.S1_at	1.74E-03	1.30E-02	0.65	PREDICTED: Canis familiaris similar to Transcription factor A; mitochondrial precursor (mtTFA) (Mitochondrial transcription factor 1) (MtTF1) (Transcription factor 6-like 2) (LOC488989); mRNA	XM_546107	TFAM	transcription factor A, mitochondrial
Cfa.1175.1.A1_s_at	3.03E-02	3.87E-02	0.72	PREDICTED: Canis familiaris similar to transcription factor EC isoform a; transcript variant 1 (LOC475292); mRNA	XM_532523	TFEC	transcription factor EC
Cfa.18602.2.S1_s_at	2.39E-02	3.42E-02	0.67	PREDICTED: Canis familiaris similar to TIA1 protein isoform 2; transcript variant 1 (LOC610625); mRNA	XM_847849	TIA1	TIA1 cytotoxic granule-associated RNA binding protein

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Cfa.5301.1.S1_at	1.85E-04	9.00E-03	1.34	PREDICTED: Canis familiaris similar to tyrosine kinase with immunoglobulin-like and EGF-like domains 1 (LOC482535); mRNA	XM_539652	TIE1	tyrosine kinase with immunoglobulin-like and EGF-like domains 1
Cfa.17788.1.S1_at	1.48E-03	1.25E-02	0.75	PREDICTED: Canis familiaris similar to Mitochondrial import inner membrane translocase subunit Tim23; transcript variant 2 (LOC486776); mRNA	XM_850859	TIMM23	translocase of inner mitochondrial membrane 23 homolog (yeast)
CfaAffx.14014.1.S1_at	8.89E-03	2.19E-02	0.74	Homo sapiens mRNA; cDNA DKFZp686N0351 (from clone DKFZp686N0351); complete cds	BX537965	TIPARP	TCDD-inducible poly(ADP-ribose) polymerase
Cfa.12147.1.A1_s_at	5.58E-02	5.41E-02	1.35	PREDICTED: Canis familiaris similar to talin 1; transcript variant 11 (LOC474759); mRNA	XM_861640	TLN1	talin 1
CfaAffx.601.1.S1_s_at	1.11E-02	2.40E-02	0.75	Canis lupus familiaris TLR4 mRNA for Toll-like receptor 4 protein; complete cds	AB080363	TLR4	toll-like receptor 4
Cfa.10886.1.A1_s_at	1.26E-03	1.23E-02	0.77	PREDICTED: Canis familiaris similar to BBP-like protein 2 isoform a (LOC479020); mRNA	XM_536173	TM2D3	TM2 domain containing 3
CfaAffx.13912.1.S1_s_at	3.91E-04	9.61E-03	0.72	PREDICTED: Canis familiaris similar to Transmembrane 9 superfamily protein member 3 precursor; transcript variant 3 (LOC612786); mRNA	XM_854699	TM9SF3	transmembrane 9 superfamily member 3
CfaAffx.13989.1.S1_s_at	4.70E-04	9.93E-03	0.74	PREDICTED: Canis familiaris similar to Transmembrane 9 superfamily protein member 3 precursor; transcript variant 3 (LOC612786); mRNA	XM_854699	TM9SF3	transmembrane 9 superfamily member 3
CfaAffx.13999.1.S1_s_at	9.85E-06	6.68E-03	0.71	PREDICTED: Canis familiaris similar to Transmembrane 9 superfamily protein member 3 precursor; transcript variant 5 (LOC612786); mRNA	XM_854762	TM9SF3	transmembrane 9 superfamily member 3
CfaAffx.20818.1.S1_s_at	3.21E-02	3.99E-02	0.74	PREDICTED: Canis familiaris similar to putative membrane protein (LOC478992); mRNA	XM_549626	TMCO1	transmembrane and coiled-coil domains 1
CfaAffx.26060.1.S1_s_at	2.34E-03	1.40E-02	0.73	PREDICTED: Canis familiaris similar to transmembrane trafficking protein 21; transcript variant 1 (LOC610559); mRNA	XM_848950	TMED10	transmembrane emp24-like trafficking protein 10 (yeast)

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Cfa.17716.1.S1_s_at	1.38E-02	2.66E-02	0.72	PREDICTED: Canis familiaris similar to Transmembrane emp24 domain containing protein 5 precursor (LOC479947); mRNA	XM_537072	TMED5	transmembrane emp24 protein transport domain containing 5
Cfa.2058.1.A1_at	8.53E-04	1.13E-02	0.74	PREDICTED: Pan troglodytes toll-like receptor adaptor molecule 2; transcript variant 2 (TICAM2); mRNA	XM_001147606	TMED7	transmembrane emp24 protein transport domain containing 7
CfaAffx.7721.1.S1_at	1.79E-04	9.00E-03	0.54	PREDICTED: Canis familiaris hypothetical protein LOC608427 (LOC608427); mRNA	XM_845453	TMEM126A	transmembrane protein 126A
CfaAffx.24003.1.S1_s_at	2.01E-04	9.06E-03	0.76	PREDICTED: Canis familiaris hypothetical LOC479094 (LOC479094); mRNA	XM_536241	TMEM128	transmembrane protein 128
Cfa.10592.1.A1_s_at	1.12E-02	2.40E-02	0.77	PREDICTED: Canis familiaris similar to TPA regulated locus (LOC475144); mRNA	XM_532375	TMEM165	transmembrane protein 165
Cfa.10458.1.S1_at	1.31E-03	1.23E-02	0.76	PREDICTED: Canis familiaris similar to CG14199-PA (LOC610083); mRNA	XM_847481	TMEM167A	transmembrane protein 167A
CfaAffx.10660.1.S1_at	8.09E-02	6.67E-02	1.36	PREDICTED: Canis familiaris hypothetical LOC130733 (LOC475737); mRNA	XM_532944	TMEM178	transmembrane protein 178
Cfa.1619.1.S1_s_at	1.62E-02	2.85E-02	0.76	PREDICTED: Canis familiaris similar to CG12765-PA; transcript variant 3 (LOC479994); mRNA	XM_850617	TMEM183A	transmembrane protein 183A
Cfa.6676.1.S1_s_at	2.26E-03	1.38E-02	0.75	PREDICTED: Canis familiaris similar to HSPC171 protein; transcript variant 1 (LOC489761); mRNA	XM_546881	TMEM208	transmembrane protein 208
CfaAffx.4943.1.S1_s_at	1.01E-02	2.31E-02	0.73	PREDICTED: Canis familiaris similar to transmembrane protein 30A; transcript variant 4 (LOC474973); mRNA	XM_862382	TMEM30A	transmembrane protein 30A
Cfa.838.2.A1_at	6.22E-04	1.05E-02	0.71	Bos taurus cDNA clone IMAGE:8169808; with apparent retained intron	BC114131	TMEM33	transmembrane protein 33
Cfa.1749.1.A1_at	1.57E-02	2.80E-02	0.75	Bos taurus transmembrane protein 41B; mRNA (cDNA clone MGC:143027 IMAGE:8308402); complete cds	BC142213	TMEM41B	transmembrane protein 41B
CfaAffx.14419.1.S1_s_at	4.36E-03	1.69E-02	0.76	PREDICTED: Canis familiaris similar to Transmembrane protein 50B (HCV p7-transregulated protein 3) (LOC478405); mRNA	XM_535582	TMEM50B	transmembrane protein 50B

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.12987.1.S1_s_at	6.14E-03	1.89E-02	0.77	PREDICTED: Canis familiaris similar to CG7506-PA (LOC477915); mRNA	XM_535105	TMEM70	transmembrane protein 70
CfaAffx.28790.1.S1_at	4.22E-02	4.64E-02	0.73	H.sapiens mRNA for BCMA peptide	Z29575	TNFRSF17	tumor necrosis factor receptor superfamily, member 17
CfaAffx.30086.1.S1_at	1.07E-03	1.20E-02	1.3	PREDICTED: Canis familiaris similar to tumor necrosis factor receptor superfamily; member 9 precursor (LOC608274); mRNA	XM_845243	TNFRSF9	tumor necrosis factor receptor superfamily, member 9
Cfa.2395.1.S1_at	1.11E-02	2.39E-02	0.76	Homo sapiens transportin 1 (TNPO1); transcript variant 2; mRNA	NM_153188	TNPO1	transportin 1
Cfa.10462.2.S1_at	1.23E-02	2.52E-02	0.76	PREDICTED: Equus caballus transducer of ERBB2; 1 (TOB1); mRNA	XM_001503158	TOB1	transducer of ERBB2, 1
CfaAffx.26534.1.S1_at	1.25E-03	1.23E-02	1.31	PREDICTED: Canis familiaris similar to TOM1-like 1 protein (Target of myb-like 1 protein) (Src activating and signaling molecule protein); transcript variant 3 (LOC491093); mRNA	XM_847759	TOM1L1	target of myb1 (chicken)-like 1
Cfa.11295.1.S1_at	2.56E-03	1.44E-02	0.73	PREDICTED: Canis familiaris hypothetical protein LOC610171; transcript variant 2 (LOC610171); mRNA	XM_861881	TOMM5	translocase of outer mitochondrial membrane 5 homolog (yeast)
CfaAffx.4435.1.S1_s_at	1.98E-04	9.06E-03	0.67	PREDICTED: Canis familiaris hypothetical protein LOC610171; transcript variant 2 (LOC610171); mRNA	XM_861881	TOMM5	translocase of outer mitochondrial membrane 5 homolog (yeast)
CfaAffx.14675.1.S1_s_at	6.97E-04	1.07E-02	0.76	PREDICTED: Canis familiaris similar to Mitochondrial precursor proteins import receptor (Translocase of outer membrane TOM70) (LOC478541); mRNA	XM_535719	TOMM70A	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)
Cfa.18846.1.S1_at	3.67E-04	9.61E-03	0.72	PREDICTED: Canis familiaris topoisomerase I (TOP); mRNA	XM_534420	TOP1	topoisomerase (DNA) I

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Cfa.11045.1.S1_s_at	4.31E-03	1.68E-02	0.75	PREDICTED: Canis familiaris similar to DNA topoisomerase II; beta isozyme (LOC477044); mRNA	XM_534241	TOP2B	topoisomerase (DNA) II beta 180kDa
Cfa.18453.1.S1_s_at	7.58E-03	2.04E-02	0.69	PREDICTED: Canis familiaris similar to DNA topoisomerase II; beta isozyme (LOC477044); mRNA	XM_534241	TOP2B	topoisomerase (DNA) II beta 180kDa
CfaAffx.10655.1.S1_s_at	3.33E-04	9.28E-03	0.72	familiaris similar to DNA topoisomerase II binding protein 1 (DNA topoisomerase IIbeta-binding protein 1) (TopBP1) (LOC477070); mRNA	XM_534266	TOPBP1	topoisomerase (DNA) II binding protein 1
Cfa.19106.1.S1_at	2.26E-03	1.38E-02	0.69	PREDICTED: Canis familiaris similar to torsin family 3; member A (LOC490326); mRNA	XM_547446	TOR3A	torsin family 3, member A
Cfa.8876.1.A1_at	1.47E-03	1.25E-02	0.76	PREDICTED: Canis familiaris similar to epidermal Langerhans cell protein LCP1; transcript variant 5 (LOC475403); mRNA	XM_859182	TOX4	TOX high mobility group box family member 4
Cfa.13117.1.A1_at	2.84E-03	1.48E-02	1.31	PREDICTED: Canis familiaris similar to epidermal Langerhans cell protein LCP1; transcript variant 6 (LOC475403); mRNA	XM_859203	TOX4	TOX high mobility group box family member 4
Cfa.14202.1.A1_at	2.41E-03	1.40E-02	0.61	PREDICTED: Canis familiaris similar to TP53 regulating kinase (p53-related protein kinase) (Nori-2) (LOC611235); mRNA	XM_848873	TP53RK	TP53 regulating kinase
CfaAffx.25960.1.S1_at	3.83E-04	9.61E-03	1.31	PREDICTED: Canis familiaris tropomyosin; transcript variant 5 (TPM1); mRNA	XM_859795	TPM1	tropomyosin 1 (alpha)
CfaAffx.24216.1.S1_at	1.14E-02	2.42E-02	0.75	PREDICTED: Pan troglodytes hypothetical LOC465115 (LOC465115); partial mRNA	XM_001138061	TPM4	tropomyosin 4
CfaAffx.13954.1.S1_s_at	3.28E-02	4.04E-02	0.73	PREDICTED: Canis familiaris similar to FLN29 gene product (LOC477484); mRNA	XM_534682	TRAFD1	TRAF-type zinc finger domain containing 1
CfaAffx.12600.1.S1_s_at	4.73E-05	7.75E-03	0.73	C.familiaris mRNA for TRAM-protein	X63678	TRAM1	translocation associated membrane protein 1
Cfa.15072.1.A1_s_at	6.87E-04	1.07E-02	0.66	PREDICTED: Canis familiaris similar to hematopoietic stem/progenitor cells 176; transcript variant 2 (LOC479614); mRNA	XM_844929	TRAPPC2L	trafficking protein particle complex 2-like

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Cfa.15072.2.S1_a_at	5.54E-03	1.82E-02	0.72	PREDICTED: Canis familiaris similar to hematopoietic stem/progenitor cells 176; transcript variant 2 (LOC479614); mRNA	XM_844929	TRAPPC2L	trafficking protein particle complex 2-like
CfaAffx.8701.1.S1_s_at	3.56E-03	1.59E-02	0.75	PREDICTED: Canis familiaris similar to p53-inducible cell-survival factor; transcript variant 1 (LOC489217); mRNA	XM_546335	TRIAP1	TP53 regulated inhibitor of apoptosis 1
CfaAffx.1543.1.S1_at	2.49E-05	7.55E-03	1.33	PREDICTED: Canis familiaris similar to tripartite motif-containing 39 isoform 2; transcript variant 2 (LOC481703); mRNA	XM_850566	TRIM39	tripartite motif-containing 39
Cfa.17405.1.S1_s_at	9.21E-03	2.22E-02	0.76	PREDICTED: Canis familiaris similar to 60kD Ro/SSA autoantigen (LOC478957); mRNA	XM_536115	TROVE2	TROVE domain family, member 2
CfaAffx.10082.1.S1_at	2.58E-03	1.44E-02	1.33	Mus musculus 12 days embryo eyeball cDNA; RIKEN full-length enriched library; clone:D230002D19 product:transient receptor protein 4; full insert sequence	AK084139	Trpc4	transient receptor potential cation channel, subfamily C, member 4
Cfa.10978.1.A1_at	3.57E-03	1.59E-02	0.72	PREDICTED: Canis familiaris similar to Elongation factor Ts; mitochondrial precursor (EF-Ts) (EF-TsMt) (LOC481134); mRNA	XM_538255	TSFM	Ts translation elongation factor, mitochondrial
Cfa.832.1.S1_at	5.36E-04	1.02E-02	0.76	PREDICTED: Canis familiaris similar to translin (LOC483876); mRNA	XM_540996	TSN	translin
Cfa.10562.1.S1_at	1.93E-03	1.33E-02	0.7	Bos taurus translin-associated factor X (TSNAX); mRNA	NM_001076006	TSNAX	translin-associated factor X
CfaAffx.9696.1.S1_s_at	2.64E-04	9.11E-03	0.69	PREDICTED: Canis familiaris similar to CG5290-PA (LOC475719); mRNA	XM_532927	TTC27	tetratricopeptide repeat domain 27
CfaAffx.27815.1.S1_s_at	3.88E-03	1.63E-02	0.76	PREDICTED: Canis familiaris hypothetical LOC480172 (LOC480172); mRNA	XM_537296	TTC39C	tetratricopeptide repeat domain 39C
CfaAffx.9012.1.S1_at	6.31E-04	1.05E-02	1.37	PREDICTED: Canis familiaris hypothetical LOC148014 (LOC484503); mRNA	XM_541617	TTC9B	tetratricopeptide repeat domain 9B
Cfa.11081.1.S1_at	5.14E-02	5.18E-02	0.74	PREDICTED: Canis familiaris similar to tubulin; beta 5 (LOC474830); mRNA	XM_532060	TUBB	tubulin, beta
Cfa.19230.1.S1_at	2.51E-02	3.50E-02	0.75	PREDICTED: Canis familiaris similar to tubulin; gamma complex associated protein 2 (LOC480829); mRNA	XM_537946	TUBGCP2	tubulin, gamma complex associated protein 2

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.10170.1.A1_s_at	7.34E-03	2.02E-02	0.76	PREDICTED: Canis familiaris similar to Tu translation elongation factor; mitochondrial (LOC479796); mRNA	XM_536924	TUFM	Tu translation elongation factor, mitochondrial
Cfa.3002.1.S1_at	1.09E-03	1.20E-02	0.72	PREDICTED: Canis familiaris similar to Thioredoxin domain containing protein 1 precursor (Transmembrane Trx-related protein) (Thioredoxin-related transmembrane protein) (LOC610791); mRNA	XM_848339	TXNDC1	thioredoxin domain containing 1
CfaAffx.22542.1.S1_s_at	1.98E-04	9.06E-03	0.74	PREDICTED: Canis familiaris similar to Thioredoxin domain containing protein 1 precursor (Transmembrane Trx-related protein) (Thioredoxin-related transmembrane protein) (LOC610791); mRNA	XM_848339	TXNDC1	thioredoxin domain containing 1
CfaAffx.1033.1.S1_s_at	8.90E-04	1.14E-02	0.68	PREDICTED: Canis familiaris similar to thioredoxin domain containing 10 (LOC476176); mRNA	XM_533381	TXNDC10	thioredoxin domain containing 10
Cfa.20679.1.S1_at	5.01E-03	1.76E-02	0.72	PREDICTED: Canis familiaris similar to disulfide isomerase (LOC609963); mRNA	XM_847320	TXNDC15	thioredoxin domain containing 15
Cfa.19620.1.S1_s_at	1.12E-03	1.20E-02	0.74	PREDICTED: Canis familiaris similar to Thioredoxin domain containing protein 4 precursor (Endoplasmic reticulum resident protein ERp44) (LOC474781); mRNA	XM_532011	TXNDC4	thioredoxin domain containing 4 (endoplasmic reticulum)
Cfa.19939.1.S1_s_at	1.55E-04	9.00E-03	0.73	PREDICTED: Canis familiaris similar to ATP binding protein associated with cell differentiation (LOC474557); mRNA	XM_531785	TXNDC9	thioredoxin domain containing 9
Cfa.11189.1.A1_at	1.73E-04	9.00E-03	0.75	PREDICTED: Canis familiaris similar to dim1; transcript variant 1 (LOC476156); mRNA	XM_533363	TXNL4A	thioredoxin-like 4A
CfaAffx.987.1.S1_s_at	8.35E-05	8.77E-03	0.75	PREDICTED: Canis familiaris similar to dim1; transcript variant 1 (LOC476156); mRNA	XM_533363	TXNL4A	thioredoxin-like 4A
Cfa.10736.1.A1_s_at	5.48E-03	1.82E-02	0.73	PREDICTED: Canis familiaris similar to Splicing factor U2AF 35 kDa subunit (U2 auxiliary factor 35 kDa subunit) (U2 snRNP auxiliary factor small subunit) (LOC478422); mRNA	XM_535599	U2AF1	U2 small nuclear RNA auxiliary factor 1

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Cfa.11590.1.A1_at	2.76E-02	3.68E-02	0.77	PREDICTED: Canis familiaris similar to U2 small nuclear RNA auxiliary factor 1-like 4; transcript variant 3 (LOC476480); mRNA	XM_862681	U2AF1L4	U2 small nuclear RNA auxiliary factor 1-like 4
Cfa.2503.1.S1_at	2.07E-02	3.19E-02	0.75	PREDICTED: Canis familiaris similar to UDP-N acetylhexosamine pyrophosphorylase (Antigen X) (AGX) (Sperm associated antigen 2); transcript variant 1 (LOC488664); mRNA	XM_545781	UAP1	UDP-N-acteylglucosamine pyrophosphorylase 1
Cfa.2503.1.S1_s_at	1.05E-02	2.34E-02	0.77	PREDICTED: Canis familiaris similar to UDP-N acetylhexosamine pyrophosphorylase (Antigen X) (AGX) (Sperm associated antigen 2); transcript variant 1 (LOC488664); mRNA	XM_545781	UAP1	UDP-N-acteylglucosamine pyrophosphorylase 1
Cfa.1092.1.S1_at	4.22E-03	1.68E-02	0.69	PREDICTED: Canis familiaris similar to ubiquitin-activating enzyme E1C isoform 1; transcript variant 3 (LOC476560); mRNA	XM_846697	UBA3	ubiquitin-like modifier activating enzyme 3
CfaAffx.10771.1.S1_s_at	9.84E-04	1.16E-02	0.7	PREDICTED: Canis familiaris similar to ubiquitin-activating enzyme E1C isoform 1; transcript variant 10 (LOC476560); mRNA	XM_859248	UBA3	ubiquitin-like modifier activating enzyme 3
CfaAffx.10573.1.S1_at	5.22E-04	1.01E-02	0.74	PREDICTED: Canis familiaris similar to ubiquitin-activating enzyme E1-domain containing 1 isoform 1 (LOC485664); mRNA	XM_542784	UBA5	ubiquitin-like modifier activating enzyme 5
CfaAffx.28164.1.S1_at	7.47E-05	8.57E-03	0.72	familiaris similar to Ubiquitin-conjugating enzyme E2 A (Ubiquitin-protein ligase A) (Ubiquitin carrier protein A) (HR6A) (mHR6A) (LOC492095); mRNA	XM_549217	UBE2A	ubiquitin-conjugating enzyme E2A (RAD6 homolog)
CfaAffx.9618.1.S1_s_at	4.17E-03	1.67E-02	0.7	familiaris similar to Ubiquitin-conjugating enzyme E2 E1 (Ubiquitin-protein ligase E1) (Ubiquitin carrier protein E1) (UbcM3); transcript variant 1 (LOC477048); mRNA	XM_534245	UBE2E1	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
Cfa.457.1.S1_s_at	7.31E-03	2.01E-02	0.71	familiaris similar to Ubiquitin-conjugating enzyme E2 E3 (Ubiquitin-protein ligase E3) (Ubiquitin carrier protein E3) (Ubiquitin-conjugating enzyme E2-23 kDa) (UbcM2); transcript variant 2 (LOC612823); mRNA	XM_857408	UBE2E3	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)

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Cfa.11340.1.S1_at	2.24E-04	9.06E-03	0.75	PREDICTED: Canis familiaris similar to ubiquitin-conjugating enzyme E2G 2 (LOC611581); mRNA	XM_535603	UBE2G2	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)
CfaAffx.5594.1.S1_at	1.00E-03	1.17E-02	0.6	PREDICTED: Pan troglodytes ubiquitin-conjugating enzyme E2; J1 (UBE2J1); mRNA	XM_518636	UBE2J1	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)
CfaAffx.5595.1.S1_s_at	2.08E-04	9.06E-03	0.66	PREDICTED: Canis familiaris similar to ubiquitin-conjugating enzyme E2; J1; transcript variant 1 (LOC474993); mRNA	XM_532230	UBE2J1	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)
CfaAffx.24469.1.S1_s_at	7.77E-03	2.06E-02	0.69	PREDICTED: Canis familiaris similar to huntingtin interacting protein 2; transcript variant 1 (LOC609531); mRNA	XM_846094	UBE2K	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast)
Cfa.11980.1.A1_s_at	1.62E-03	1.27E-02	0.77	familiaris similar to Ubiquitin-conjugating enzyme E2 L3 (Ubiquitin-protein ligase L3) (Ubiquitin carrier protein L3) (UbcM4); transcript variant 1 (LOC477572); mRNA	XM_534767	UBE2L3	ubiquitin-conjugating enzyme E2L 3
Cfa.17038.1.S1_at	2.46E-02	3.47E-02	0.74	PREDICTED: Canis familiaris similar to ubiquitin-conjugating enzyme E2L 6; transcript variant 1 (LOC475967); mRNA	XM_533174	UBE2L6	ubiquitin-conjugating enzyme E2L 6
Cfa.11552.1.S1_a_at	1.48E-03	1.25E-02	0.75	PREDICTED: Canis familiaris similar to ubiquitin-conjugating enzyme E2 variant 1 (LOC477262); mRNA	XM_534454	UBE2V1	ubiquitin-conjugating enzyme E2 variant 1
Cfa.620.2.S1_s_at	1.26E-03	1.23E-02	0.73	PREDICTED: Canis familiaris similar to ubiquitin protein ligase E3A isoform 3; transcript variant 2 (LOC479010); mRNA	XM_843147	UBE3A	ubiquitin protein ligase E3A
Cfa.620.1.A1_s_at	3.88E-03	1.63E-02	0.74	PREDICTED: Canis familiaris similar to ubiquitin protein ligase E3A isoform 3; transcript variant 5 (LOC479010); mRNA	XM_850686	UBE3A	ubiquitin protein ligase E3A
Cfa.9635.1.A1_at	3.92E-03	1.64E-02	0.77	Homo sapiens mRNA for KIAA0126 gene; partial cds	D50916	UBE4A	ubiquitination factor E4A (UFD2 homolog, yeast)

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Cfa.9708.1.A1_at	1.05E-03	1.19E-02	0.75	Homo sapiens ubiquitin-like 3 (UBL3); mRNA	NM_007106	UBL3	ubiquitin-like 3
CfaAffx.26450.1.S1_s_at	2.52E-03	1.43E-02	0.74	PREDICTED: Canis familiaris similar to ubiquitin-like domain containing CTD phosphatase 1; transcript variant 1 (LOC489153); mRNA	XM_546271	UBLCP1	ubiquitin-like domain containing CTD phosphatase 1
Cfa.18325.1.S1_at	1.28E-03	1.23E-02	0.74	PREDICTED: Canis familiaris similar to ubiquitin-like domain containing CTD phosphatase 1; transcript variant 2 (LOC489153); mRNA	XM_862092	UBLCP1	ubiquitin-like domain containing CTD phosphatase 1
Cfa.3289.1.S1_s_at	3.85E-03	1.63E-02	0.72	PREDICTED: Canis familiaris similar to ubiquilin 1 isoform 1; transcript variant 8 (LOC476312); mRNA	XM_853208	UBQLN1	ubiquilin 1
Cfa.3289.2.S1_s_at	9.83E-03	2.29E-02	0.71	PREDICTED: Canis familiaris similar to ubiquilin 1 isoform 1; transcript variant 8 (LOC476312); mRNA	XM_853208	UBQLN1	ubiquilin 1
Cfa.8225.1.A1_s_at	5.27E-05	7.92E-03	0.76	PREDICTED: Canis familiaris similar to Rep-8 protein (Reproduction 8 protein) (D8S2298E) (LOC475595); mRNA	XM_549449	UBXN8	UBX domain protein 8
Cfa.1152.1.A1_s_at	9.84E-06	6.68E-03	0.69	PREDICTED: Canis familiaris similar to ubiquitin C-terminal hydrolase UCH37 (LOC478958); mRNA	XM_536116	UCHL5	ubiquitin carboxyl-terminal hydrolase L5
CfaAffx.9291.1.S1_s_at	2.63E-02	3.59E-02	1.39	Canis lupus familiaris ucp2 mRNA for uncoupling protein 2; complete cds	AB020887	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)
CfaAffx.9999.1.S1_s_at	2.64E-03	1.45E-02	0.76	PREDICTED: Canis familiaris similar to ubiquitin-fold modifier 1 (LOC477297); mRNA	XM_534489	UFM1	ubiquitin-fold modifier 1
Cfa.20677.2.S1_s_at	5.28E-04	1.01E-02	0.73	PREDICTED: Canis familiaris similar to UDP-glucose pyrophosphorylase 2 isoform a; transcript variant 2 (LOC474615); mRNA	XM_860850	UGP2	UDP-glucose pyrophosphorylase 2
CfaAffx.5656.1.S1_s_at	2.47E-05	7.55E-03	0.67	PREDICTED: Canis familiaris similar to UDP-glucose pyrophosphorylase 2 isoform a; transcript variant 2 (LOC474615); mRNA	XM_860850	UGP2	UDP-glucose pyrophosphorylase 2

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Cfa.2159.1.S1_s_at	7.14E-05	8.52E-03	0.72	PREDICTED: Canis familiaris similar to Serine/threonine-protein kinase Kist (Kinase interacting with stathmin) (U2AF homology motif kinase 1) (PAM COOH-terminal interactor protein 2) (P-CIP2) (LOC478986); mRNA	XM_536143	UHMK1	U2AF homology motif (UHM) kinase 1
Cfa.10244.1.A1_at	1.68E-03	1.29E-02	0.7	PREDICTED: Canis familiaris similar to Uridine 5-monophosphate synthase (UMP synthase) (LOC478593); mRNA	XM_535769	UMPS	uridine monophosphate synthetase
Cfa.10244.1.A1_s_at	9.62E-03	2.26E-02	0.73	PREDICTED: Canis familiaris similar to Uridine 5-monophosphate synthase (UMP synthase) (LOC478593); mRNA	XM_535769	UMPS	uridine monophosphate synthetase
Cfa.10690.1.S1_s_at	5.29E-04	1.01E-02	0.74	PREDICTED: Canis familiaris similar to unc-50 homolog (LOC611651); mRNA	XM_849346	UNC50	unc-50 homolog (C. elegans)
CfaAffx.26344.1.S1_at	2.13E-03	1.36E-02	0.74	PREDICTED: Canis familiaris similar to CG5537-PA; transcript variant 2 (LOC480960); mRNA	XM_538081	UPRT	uracil phosphoribosyltransferase (FUR1) homolog (S. cerevisiae)
Cfa.17017.1.S1_at	1.15E-02	2.42E-02	0.74	PREDICTED: Canis familiaris similar to General vesicular transport factor p115 (Transcytosis associated protein) (TAP) (Vesicle docking protein); transcript variant 1 (LOC478430); mRNA	XM_535607	USO1	USO1 homolog, vesicle docking protein (yeast)
Cfa.18635.1.S1_s_at	5.82E-03	1.85E-02	0.75	PREDICTED: Canis familiaris similar to General vesicular transport factor p115 (Transcytosis associated protein) (TAP) (Vesicle docking protein); transcript variant 1 (LOC478430); mRNA	XM_535607	USO1	USO1 homolog, vesicle docking protein (yeast)
CfaAffx.13431.1.S1_s_at	2.44E-03	1.41E-02	0.64	PREDICTED: Canis familiaris similar to General vesicular transport factor p115 (Transcytosis associated protein) (TAP) (Vesicle docking protein); transcript variant 2 (LOC478430); mRNA	XM_851270	USO1	USO1 homolog, vesicle docking protein (yeast)

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

Cfa.19994.1.S1_s_at	1.51E-04	9.00E-03	0.69	familiaris similar to Ubiquitin carboxyl-terminal hydrolase 1 (Ubiquitin thiolesterase 1) (Ubiquitin-specific processing protease 1) (Deubiquitinating enzyme 1) (hUBP); transcript variant 1 (LOC479549); mRNA	XM_536688	USP1	ubiquitin specific peptidase 1
CfaAffx.28718.1.S1_at	1.27E-02	2.54E-02	0.75	familiaris similar to Ubiquitin carboxyl-terminal hydrolase 1 (Ubiquitin thiolesterase 1) (Ubiquitin-specific processing protease 1) (Deubiquitinating enzyme 1) (hUBP); transcript variant 1 (LOC479549); mRNA	XM_536688	USP1	ubiquitin specific peptidase 1
Cfa.19562.1.S1_at	4.13E-04	9.68E-03	0.68	PREDICTED: Canis familiaris similar to ubiquitin-specific protease 12-like 1 (LOC486033); mRNA	XM_543159	USP12	ubiquitin specific peptidase 12
CfaAffx.11142.1.S1_at	3.20E-03	1.54E-02	0.75	PREDICTED: Canis familiaris similar to ubiquitin-specific protease 12-like 1 (LOC486033); mRNA	XM_543159	USP12	ubiquitin specific peptidase 12
Cfa.2506.1.S1_s_at	1.53E-02	2.77E-02	0.75	PREDICTED: Canis familiaris similar to disrupter of silencing 10 (LOC475167); mRNA	XM_532399	UTP3	UTP3, small subunit (SSU) processome component, homolog (S. cerevisiae)
Cfa.4554.1.S1_s_at	8.75E-03	2.18E-02	0.77	Canis familiaris utrophin mRNA; complete cds	AY095485	UTRN	utrophin
Cfa.1744.1.A1_at	5.06E-04	1.00E-02	0.75	Homo sapiens vesicle-associated membrane protein 7 (VAMP7); transcript variant 1; mRNA	NM_005638	VAMP7	vesicle-associated membrane protein 7
Cfa.2698.1.A1_at	4.06E-03	1.65E-02	0.75	Homo sapiens vav 3 guanine nucleotide exchange factor (VAV3); transcript variant 1; mRNA	NM_006113	VAV3	vav 3 guanine nucleotide exchange factor
Cfa.1590.2.S1_s_at	3.22E-04	9.28E-03	0.74	PREDICTED: Canis familiaris similar to Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial membrane protein porin 1) (Plasmalemmal porin) (Porin 31HL) (Porin 31HM) (LOC474681); mRNA	XM_531907	VDAC1	voltage-dependent anion channel 1

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.23653.1.S1_s_at	3.53E-03	1.59E-02	0.75	PREDICTED: Canis familiaris similar to voltage-dependent anion channel 2; transcript variant 2 (LOC479255); mRNA	XM_846649	VDAC2	voltage-dependent anion channel 2
Cfa.16229.1.S1_at	4.42E-04	9.78E-03	0.75	Canis familiaris von Hippel Lindau disease tumor suppressor (VHL) mRNA; complete cds	AY764285	VHL	von Hippel-Lindau tumor suppressor
Cfa.818.1.A1_s_at	7.73E-03	2.06E-02	0.7	PREDICTED: Canis familiaris similar to vacuolar protein sorting 13A isoform A (LOC476319); mRNA	XM_533522	VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)
CfaAffx.13436.1.S1_s_at	1.36E-03	1.23E-02	0.73	PREDICTED: Canis familiaris similar to Vacuolar protein sorting 29 (Vesicle protein sorting 29); transcript variant 2 (LOC477477); mRNA	XM_856490	VPS29	vacuolar protein sorting 29 homolog (S. cerevisiae)
Cfa.13099.1.S1_s_at	1.78E-03	1.30E-02	0.75	Bos taurus vacuolar protein sorting 35 homolog (S. cerevisiae); mRNA (cDNA clone MGC:128544 IMAGE:7985129); complete cds	BC105430	VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)
Cfa.9366.1.A1_at	5.43E-04	1.02E-02	0.68	PREDICTED: Canis familiaris similar to vacuolar protein sorting 35; transcript variant 1 (LOC475346); mRNA	XM_532570	VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)
Cfa.9366.1.A1_s_at	9.96E-03	2.30E-02	0.73	PREDICTED: Canis familiaris similar to vacuolar protein sorting 35; transcript variant 2 (LOC475346); mRNA	XM_853913	VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)
CfaAffx.1079.1.S1_at	1.65E-03	1.28E-02	0.71	PREDICTED: Canis familiaris similar to vacuolar protein sorting factor 4B; transcript variant 8 (LOC607306); mRNA	XM_852273	VPS4B	vacuolar protein sorting 4 homolog B (S. cerevisiae)
CfaAffx.27241.1.S1_s_at	2.63E-02	3.59E-02	0.77	PREDICTED: Canis familiaris similar to vaccinia related kinase 1 (LOC490848); mRNA	XM_547970	VRK1	vaccinia related kinase 1
CfaAffx.24488.1.S1_s_at	2.36E-04	9.06E-03	0.71	PREDICTED: Canis familiaris similar to KIAA0261; transcript variant 2 (LOC612854); mRNA	XM_859725	WAPAL	wings apart-like homolog (Drosophila)

Table 2:Genes Differentially Expressed in lymphocytes from Fat Animals compared to Lean Animals

CfaAffx.27416.1.S1_s_at	1.24E-02	2.52E-02	0.75	familiaris similar to Tryptophanyl-tRNA synthetase (Tryptophan--tRNA ligase) (TrpRS) (IFP53) (hWRS); transcript variant 1 (LOC480435); mRNA	XM_537554	WARS	tryptophanyl-tRNA synthetase
Cfa.14685.1.A1_at	1.10E-02	2.39E-02	0.75	PREDICTED: Pan troglodytes WD repeat-containing protein 1; transcript variant 2 (WDR1); mRNA	XM_001158182	WDR1	WD repeat domain 1
Cfa.10473.1.S1_s_at	5.98E-03	1.87E-02	0.75	PREDICTED: Canis familiaris similar to WD repeat domain 20 isoform 2; transcript variant 6 (LOC611234); mRNA	XM_863505	WDR20	WD repeat domain 20
Cfa.8901.1.A1_s_at	6.94E-03	1.98E-02	0.72	PREDICTED: Canis familiaris similar to WD repeat domain 36 (LOC488875); mRNA	XM_545992	WDR36	WD repeat domain 36
CfaAffx.11948.1.S1_at	2.50E-03	1.42E-02	0.76	PREDICTED: Canis familiaris similar to WD repeat domain 36 (LOC488875); mRNA	XM_545992	WDR36	WD repeat domain 36
Cfa.2333.1.S1_a_at	2.95E-02	3.81E-02	0.71	PREDICTED: Canis familiaris similar to WD repeat domain 48; transcript variant 8 (LOC477027); mRNA	XM_855010	WDR48	WD repeat domain 48
Cfa.1553.1.A1_at	2.30E-03	1.39E-02	0.73	PREDICTED: Pan troglodytes WD repeat domain 51B; transcript variant 4 (WDR51B); mRNA	XM_001166217	WDR51B	WD repeat domain 51B
CfaAffx.28528.1.S1_at	2.86E-03	1.48E-02	0.76	PREDICTED: Canis familiaris similar to CG5543-PA (LOC489225); mRNA	XM_546343	WDR70	WD repeat domain 70
Cfa.17135.1.S1_s_at	2.85E-03	1.48E-02	0.76	PREDICTED: Canis familiaris similar to WD repeat domain 75 (LOC488443); mRNA	XM_545565	WDR75	WD repeat domain 75
Cfa.15346.1.A1_s_at	7.21E-05	8.52E-03	0.64	PREDICTED: Canis familiaris similar to WD repeats and SOF1 domain containing (LOC475065); mRNA	XM_532299	WDSOF1	WD repeats and SOF1 domain containing
Cfa.847.1.S1_s_at	1.11E-02	2.39E-02	0.75	PREDICTED: Canis familiaris similar to WD repeat; SAM and U-box domain containing 1 (LOC478761); mRNA	XM_535926	WDSUB1	WD repeat, sterile alpha motif and U-box domain containing 1
Cfa.4588.1.A1_at	1.71E-02	2.92E-02	0.76	PREDICTED: Canis familiaris similar to WD40 repeat protein Interacting with phosphoInositides of 49kDa (LOC490899); mRNA	XM_548021	WIPI1	WD repeat domain, phosphoinositide interacting 1
CfaAffx.20768.1.S1_at	1.40E-02	2.67E-02	1.33	PREDICTED: Canis familiaris similar to Wnt-9b protein precursor (Wnt 15) (Wnt-14b) (LOC490919); mRNA	XM_548042	WNT9B	wingless-type MMTV integration site family, member 9B

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CfaAffx.28471.1.S1_at	7.18E-03	2.00E-02	0.69	PREDICTED: Canis familiaris similar to WD SOCS-box protein 1 isoform 1; transcript variant 8 (LOC480619); mRNA	XM_862937	WSB1	WD repeat and SOCS box-containing 1
Cfa.15303.1.S1_at	2.25E-02	3.32E-02	0.75	PREDICTED: Canis familiaris similar to WD SOCS-box protein 1 isoform 1; transcript variant 9 (LOC480619); mRNA	XM_862943	WSB1	WD repeat and SOCS box-containing 1
CfaAffx.272.1.S1_s_at	9.73E-03	2.28E-02	0.73	PREDICTED: Canis familiaris similar to Wilms tumour 1-associating protein isoform 1 (LOC476259); mRNA	XM_533464	WTAP	Wilms tumor 1 associated protein
Cfa.10930.1.S1_s_at	5.47E-03	1.82E-02	0.72	PREDICTED: Canis familiaris similar to WW domain containing E3 ubiquitin protein ligase 1; transcript variant 1 (LOC477930); mRNA	XM_535119	WWP1	WW domain containing E3 ubiquitin protein ligase 1
CfaAffx.5558.1.S1_s_at	1.29E-02	2.56E-02	0.73	PREDICTED: Canis familiaris similar to exportin 1; CRM1 homolog; transcript variant 1 (LOC474609); mRNA	XM_531839	XPO1	exportin 1 (CRM1 homolog, yeast)
Cfa.1421.1.S1_at	4.13E-04	9.68E-03	0.66	PREDICTED: Canis familiaris similar to exportin 1; CRM1 homolog; transcript variant 4 (LOC474609); mRNA	XM_860656	XPO1	exportin 1 (CRM1 homolog, yeast)
CfaAffx.13644.1.S1_at	5.38E-03	1.81E-02	0.76	PREDICTED: Canis familiaris similar to X-ray repair cross complementing protein 4 isoform 1; transcript variant 1 (LOC488923); mRNA	XM_546040	XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4
Cfa.15608.1.A1_at	3.02E-03	1.51E-02	0.74	PREDICTED: Canis familiaris similar to Yip1 domain family; member 1; transcript variant 3 (LOC489581); mRNA	XM_860929	YIPF1	Yip1 domain family, member 1
Cfa.576.1.S1_at	3.79E-04	9.61E-03	0.7	PREDICTED: Canis familiaris similar to smooth muscle cell associated protein 5 (LOC478048); mRNA	XM_535226	YIPF5	Yip1 domain family, member 5
CfaAffx.10465.1.S1_s_at	9.01E-05	8.90E-03	0.73	PREDICTED: Canis familiaris similar to smooth muscle cell associated protein 5 (LOC478048); mRNA	XM_535226	YIPF5	Yip1 domain family, member 5
Cfa.15326.2.S1_at	4.48E-03	1.71E-02	0.45	PREDICTED: Canis familiaris similar to yippee protein homolog; transcript variant 2 (LOC475714); mRNA	XM_857398	YPEL5	yippee-like 5 (Drosophila)
Cfa.1292.1.S1_at	1.48E-03	1.25E-02	0.76	PREDICTED: Canis familiaris similar to ischemia/reperfusion inducible protein (LOC482469); mRNA	XM_539586	YRDC	yrdC domain containing (E. coli)

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Cfa.18982.1.S1_s_at	1.33E-02	2.60E-02	0.75	PREDICTED: Canis familiaris similar to splicing factor YT521-B isoform 2; transcript variant 5 (LOC475161); mRNA	XM_856334	YTHDC1	YTH domain containing 1
Cfa.4461.1.S1_at	1.28E-03	1.23E-02	0.74	PREDICTED: Canis familiaris similar to 14-3-3 protein epsilon (14-3-3E) (Mitochondrial import stimulation factor L subunit) (MSF L); transcript variant 3 (LOC480645); mRNA	XM_863328	YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide
CfaAffx.19065.1.S1_s_at	3.49E-02	4.18E-02	0.71	PREDICTED: Canis familiaris similar to 14-3-3 protein theta (14-3-3 protein tau); transcript variant 1 (LOC607060); mRNA	XM_532871	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide
CfaAffx.6010.1.S1_at	1.57E-03	1.26E-02	0.74	PREDICTED: Canis familiaris similar to 14-3-3 protein theta (14-3-3 protein tau); transcript variant 3 (LOC607060); mRNA	XM_851129	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide
CfaAffx.9531.1.S1_s_at	1.25E-03	1.23E-02	0.74	PREDICTED: Canis familiaris similar to tyrosine 3/tryptophan 5 - monooxygenase activation protein; zeta polypeptide; transcript variant 2 (LOC475864); mRNA	XM_843951	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
Cfa.1579.1.A1_at	2.69E-03	1.46E-02	0.66	Canis lupus familiaris zinc finger; BED-type containing 5 (ZBED5); mRNA	NM_001097982	ZBED5	zinc finger, BED-type containing 5
Cfa.5314.1.A1_at	8.12E-03	2.10E-02	0.75	PREDICTED: Canis familiaris similar to zinc finger and BTB domain containing 20; transcript variant 2 (LOC487987); mRNA	XM_843445	ZBTB20	zinc finger and BTB domain containing 20
Cfa.21382.1.S1_s_at	1.55E-03	1.26E-02	0.71	Canis lupus familiaris zinc finger CCCH-type containing 15 (ZC3H15); mRNA	NM_001114605	ZC3H15	zinc finger CCCH-type containing 15
CfaAffx.2892.1.S1_s_at	2.33E-03	1.39E-02	0.74	PREDICTED: Canis familiaris similar to zinc finger; CCHC domain containing 6; transcript variant 8 (LOC476301); mRNA	XM_851073	ZCCHC6	zinc finger, CCHC domain containing 6

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CfaAffx.2893.1.S1_s_at	3.97E-03	1.64E-02	0.74	PREDICTED: Canis familiaris similar to zinc finger; CCHC domain containing 6; transcript variant 8 (LOC476301); mRNA	XM_851073	ZCCHC6	zinc finger, CCHC domain containing 6
CfaAffx.12605.1.S1_at	4.93E-03	1.75E-02	0.76	PREDICTED: Canis familiaris similar to zinc finger; CCHC domain containing 8 (LOC477460); mRNA	XM_534658	ZCCHC8	zinc finger, CCHC domain containing 8
Cfa.12584.1.A1_at	5.49E-03	1.82E-02	0.76	PREDICTED: Canis familiaris similar to Zinc finger DHHC domain containing protein 7 (Zinc finger protein 370); transcript variant 2 (LOC489676); mRNA	XM_855968	ZDHHC7	zinc finger, DHHC-type containing 7
CfaAffx.6949.1.S1_s_at	1.89E-02	3.06E-02	0.77	familiaris similar to Transcription factor 8 (NIL-2-A zinc finger protein) (Negative regulator of IL2); transcript variant 7 (LOC477966); mRNA	XM_854899	ZEB1	zinc finger E-box binding homeobox 1
Cfa.18913.1.S1_s_at	1.51E-02	2.75E-02	0.74	PREDICTED: Canis familiaris similar to Zinc finger homeobox protein 1b (Smad interacting protein 1) (SMADIP1) (LOC483909); mRNA	XM_541029	ZEB2	zinc finger E-box binding homeobox 2
Cfa.10843.1.A1_at	1.28E-02	2.55E-02	0.74	PREDICTED: Canis familiaris similar to Zinc finger A20 domain containing protein 2 (Zinc finger protein 216); transcript variant 1 (LOC476324); mRNA	XM_533526	ZFAND5	zinc finger, AN1-type domain 5
CfaAffx.28070.1.S1_at	7.04E-04	1.08E-02	1.4	Rattus norvegicus zinc finger protein 830; mRNA (cDNA clone MGC:125001 IMAGE:7381762); complete cds	BC104717	Zfp830	zinc finger protein 830
CfaAffx.12382.1.S1_at	2.85E-04	9.15E-03	0.74	Mus musculus 14 days pregnant adult female placenta cDNA; RIKEN full length enriched library; clone:M5C1055M01 product:zinc finger protein 91; full insert sequence	AK147502	Zfp91	zinc finger protein 91
Cfa.20113.1.S1_s_at	8.20E-04	1.10E-02	0.75	PREDICTED: Canis familiaris similar to zinc finger protein 91 isoform 1; transcript variant 1 (LOC475962); mRNA	XM_533171	ZFP91	zinc finger protein 91 homolog (mouse)
CfaAffx.983.1.S1_s_at	2.06E-03	1.35E-02	0.76	PREDICTED: Canis familiaris similar to zinc finger RNA binding protein; transcript variant 9 (LOC489239); mRNA	XM_863131	ZFR	zinc finger RNA binding protein

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CfaAffx.13975.1.S1_at	2.33E-03	1.39E-02	0.77	familiaris similar to Zinc finger FYVE domain-containing protein 16 (Endofin) (Endosome-associated FYVE domain protein) (LOC479167); mRNA	XM_536310	ZFYVE16	zinc finger, FYVE domain containing 16
CfaAffx.5443.1.S1_at	1.21E-04	8.90E-03	0.76	Pongo abelii mRNA; cDNA DKFZp459I0445 (from clone DKFZp459I0445)	CR860340	ZMPSTE24	zinc metallopeptidase (STE24 homolog, S. cerevisiae)
Cfa.10839.1.A1_at	1.68E-03	1.29E-02	0.76	Homo sapiens zinc metallopeptidase (STE24 homolog; S. cerevisiae) (ZMPSTE24); mRNA	NM_005857	ZMPSTE24	zinc metallopeptidase (STE24 homolog, S. cerevisiae)
CfaAffx.9458.1.S1_s_at	9.09E-04	1.15E-02	0.73	PREDICTED: Canis familiaris similar to Zinc finger MYND domain containing protein 11 (Adenovirus 5 E1A-binding protein) (BS69 protein); transcript variant 1 (LOC478023); mRNA	XM_535205	ZMYND11	zinc finger, MYND domain containing 11
CfaAffx.11973.1.S1_s_at	1.79E-03	1.30E-02	0.75	PREDICTED: Canis familiaris similar to Zinc finger protein 143 (SPH-binding factor); transcript variant 3 (LOC485384); mRNA	XM_858781	ZNF143	zinc finger protein 143
CfaAffx.459.1.S1_s_at	3.29E-03	1.55E-02	0.65	PREDICTED: Canis familiaris similar to zinc finger protein 18 (LOC479505); mRNA	XM_536644	ZNF18	zinc finger protein 18
Cfa.10986.1.A1_s_at	1.01E-03	1.17E-02	0.76	PREDICTED: Canis familiaris similar to zinc finger protein 207 (LOC480611); mRNA	XM_537731	ZNF207	zinc finger protein 207
Cfa.18401.1.S1_s_at	9.11E-04	1.15E-02	0.74	PREDICTED: Canis familiaris similar to zinc finger protein 207 (LOC480611); mRNA	XM_537731	ZNF207	zinc finger protein 207
Cfa.20746.1.S1_at	7.04E-04	1.08E-02	0.75	Homo sapiens zinc finger protein 24 (ZNF24); mRNA	NM_006965	ZNF24	zinc finger protein 24
CfaAffx.20691.1.S1_s_at	5.18E-03	1.79E-02	0.77	PREDICTED: Canis familiaris similar to zinc finger protein 259; transcript variant 2 (LOC479428); mRNA	XM_845219	ZNF259	zinc finger protein 259
Cfa.1662.1.A1_at	3.26E-02	4.02E-02	0.76	PREDICTED: Canis familiaris similar to Zinc finger protein 292 (LOC481908); mRNA	XM_539029	ZNF292	zinc finger protein 292
Cfa.2298.1.A1_at	2.99E-03	1.51E-02	0.77	PREDICTED: Canis familiaris similar to Zinc finger protein 330 (Nucleolar autoantigen 36) (LOC476073); mRNA	XM_533282	ZNF330	zinc finger protein 330

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CfaAffx.30924.1.S1_s_at	9.96E-03	2.30E-02	0.75	PREDICTED: Canis familiaris similar to zinc finger protein 644 isoform 2; transcript variant 7 (LOC479957); mRNA	XM_862032	ZNF644	zinc finger protein 644
CfaAffx.12480.1.S1_at	1.00E-02	2.30E-02	0.75	PREDICTED: Canis familiaris similar to zinc finger protein 654 (LOC487673); mRNA	XM_544797	ZNF654	zinc finger protein 654
CfaAffx.23026.1.S1_at	8.11E-04	1.10E-02	0.73	PREDICTED: Canis familiaris similar to zinc finger protein 655 isoform c; transcript variant 2 (LOC489855); mRNA	XM_546973	ZNF655	zinc finger protein 655
Cfa.1778.1.A1_s_at	4.07E-03	1.65E-02	0.76	PREDICTED: Canis familiaris similar to Zinc finger protein 7 (Zinc finger protein KOX4) (Zinc finger protein HF.16) (LOC475129); mRNA	XM_532359	ZNF7	zinc finger protein 7
Cfa.14593.2.S1_a_at	4.98E-03	1.76E-02	0.77	PREDICTED: Canis familiaris similar to HSPC038 protein (LOC607293); mRNA	XM_843918	ZNF706	zinc finger protein 706
CfaAffx.3501.1.S1_s_at	1.65E-02	2.88E-02	0.76	PREDICTED: Canis familiaris similar to CG10979-PA; transcript variant 5 (LOC475207); mRNA	XM_844414	ZNF800	zinc finger protein 800
CfaAffx.5053.1.S1_x_at	3.10E-02	3.92E-02	1.36	PREDICTED: Canis familiaris similar to zinc finger protein 91 (HPF7; HTF10) (LOC484326); mRNA	XM_541442	ZNF91	zinc finger protein 91
Cfa.6304.1.A1_at	6.80E-04	1.07E-02	0.76	PREDICTED: Canis familiaris similar to Zinc finger HIT domain containing protein 1 (Cyclin G1-binding protein 1) (LOC479729); mRNA	XM_536855	ZNHIT1	zinc finger, HIT type 1
Cfa.9992.1.A1_at	2.81E-03	1.48E-02	0.76	PREDICTED: Pan troglodytes zinc finger; RAN-binding domain containing 1 protein (ZRANB1); mRNA	XM_508099	ZRANB1	zinc finger, RAN-binding domain containing 1
CfaAffx.31255.1.S1_s_at	1.33E-03	1.23E-02	0.7	PREDICTED: Canis familiaris similar to Zinc finger protein 265 (Zinc finger; splicing) (LOC490213); mRNA	XM_547334	ZRANB2	zinc finger, RAN-binding domain containing 2
CfaAffx.21190.1.S1_s_at	3.49E-04	9.46E-03	0.77	PREDICTED: Canis familiaris similar to Centromere/kinetochore protein zw10 homolog; transcript variant 1 (LOC479433); mRNA	XM_536569	ZW10	ZW10, kinetochore associated, homolog (Drosophila)
CfaAffx.31203.1.S1_s_at	4.13E-03	1.66E-02	0.76	PREDICTED: Canis familiaris similar to zinc finger; ZZ domain containing 3; transcript variant 1 (LOC490203); mRNA	XM_547324	ZZZ3	zinc finger, ZZ-type containing 3

Table 3: Key Genes associated with fatty acid metabolism in Fat Animals compared to Lean Animals

Probes identifying Key Genes in Adipose Tissue in fat and lean dogs

Probe	P-Value	Q-Value	Fold-Change	Top BLAST Annot.	Top Hit Accn.	Gene Symbol	Gene Desc.
Cfa.1286.1.A1_at	8.81E-02	1.00E+00	0.56	PREDICTED: Macaca mulatta carnitine palmitoyltransferase 1A (CPT1A); mRNA	XM_001101846	CPT1A	carnitine palmitoyltransferase 1A
Cfa.101.1.S1_s_at	9.54E-02	1.00E+00	0.62	PREDICTED: Canis familiaris carnitine palmitoyl transferase I isoform (CPT1); mRNA	XM_533208	CPT1A	carnitine palmitoyltransferase 1A (liver)
Cfa.17829.1.S1_s_at	7.11E-02	1.00E+00	0.7	PREDICTED: Canis familiaris similar to pyruvate dehydrogenase kinase; isoenzyme 2 (LOC491075); mRNA	XM_548195	PDK2	pyruvate dehydrogenase kinase, isozyme 2
CfaAffx.25948.1.S1_at	7.97E-02	1.00E+00	0.75	PREDICTED: Canis familiaris similar to pyruvate dehydrogenase kinase; isoenzyme 2 (LOC491075); mRNA	XM_548195	PDK2	pyruvate dehydrogenase kinase, isozyme 2
CfaAffx.4097.1.S1_s_at	3.06E-02	1.00E+00	0.36	PREDICTED: Canis familiaris similar to [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; mitochondrial precursor (Pyruvate dehydrogenase kinase isoform 4) (LOC482310); mRNA	XM_539427	PDK4	pyruvate dehydrogenase kinase, isozyme 4
Cfa.16871.1.S1_at	5.07E-02	1.00E+00	0.54	PREDICTED: Canis familiaris similar to solute carrier family 27 (fatty acid transporter); member 6 (LOC474666); mRNA	XM_531894	SLC27A6	solute carrier family 27 (fatty acid transporter), member 6
CfaAffx.2004.1.S1_s_at	1.11E-02	1.00E+00	0.48	PREDICTED: Canis familiaris similar to solute carrier family 27 (fatty acid transporter); member 6 (LOC474666); mRNA	XM_531894	SLC27A6	solute carrier family 27 (fatty acid transporter), member 6

Table 3: Key Genes associated with fatty acid metabolism in Fat Animals compared to Lean Animals

Probes identifying Key Genes in Lymphocytes from fat and lean dogs	P-Value	Q-Value	Fold-Change	Top BLAST Annot.	Top Hit Accn.	Gene Symbol	Gene Desc.
Cfa.15225.1.S1_a_at	1.43E-02	2.69E-02	0.76	familiaris similar to Carnitine O-palmitoyltransferase II; mitochondrial precursor (CPT II) (LOC489585); mRNA	XM_546705	CPT2	carnitine palmitoyltransferase II
CfaAffx.20244.1.S1_at	5.18E-05	7.92E-03	0.72	PREDICTED: Canis familiaris similar to [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; mitochondrial precursor (Pyruvate dehydrogenase kinase isoform 1) (LOC476828); mRNA	XM_534032	PDK1	pyruvate dehydrogenase kinase, isozyme 1
Cfa.13227.1.A1_s_at	2.22E-02	3.31E-02	0.66	familiaris similar to Very-long-chain acyl-CoA synthetase (Very-long-chain-fatty-acid-CoA ligase); transcript variant 2 (LOC478298); mRNA	XM_857161	SLC27A2	solute carrier family 27 (fatty acid transporter), member 2
Cfa.17202.1.S1_at	4.69E-03	1.73E-02	0.74	Bos taurus ELOVL family member 5; elongation of long chain fatty acids (FEN1/Elo2; SUR4/Elo3-like; yeast); mRNA (cDNA clone MGC:128086 IMAGE:7988977); complete cds	BC105391	ELOVL5	ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)
CfaAffx.4290.1.S1_s_at	5.85E-02	5.56E-02	0.74	Pongo abelii mRNA; cDNA DKFZp469M0522 (from clone DKFZp469M0522)	CR857140	ELOVL5	ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)

Example 2

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

[00259] Affymetrix canine GeneChips® Canine-1 and Canine-2 were used (Canine-2 replaced Canine-1) to determine the effect of various test substances or ingredients such as MCTs; TAGs; ALA; EPA; DHA; linoleic acid (LA); Arachidonic Acid (ARA); stearic acid (SA), Myristic acid (MA), 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.

[00260] A sample of the data obtained from these experiments is shown in Table 5. Table 5 shows the probe id, the p-value, the fold change, the annotation of the top BLAST hit, the top BLAST hit accession number, the gene symbol and finally the gene description is given in the last column.

Based upon the physiological condition of the canines (a diagnosis as fat) and a comparison of the information from the Tables1, 2, 3 and 5, i.e, noting genes that are influenced by a test substance or ingredient and are also differentially expressed

in overweight canines compared to lean canines, a nutritional formula useful for selecting and preparing a food composition for overweight 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 1 to 30; EPA - from 1 to 30; EPA/DHA Combo (1.5:1 ratio) - from 4/2 to 30/45; ALA - from 10 to 100; LA - from 30 to 600; ARA - from 5 to 50; SA - from 3 to 60 and MA - from 3 to 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 overweight 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 4: Ingredients Tested in Canine Cell Lines

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

Table 5: Expression Profiling Results From Canine Cell Lines in the Presence of Listed Ingredients

DHA in ETOH (CANINE-1); **5** records FC cutoff: 1.3; P-val cutofff: 0.05

Probe	P-Value	Fold-Change	Top BLAST Annot.	Top Hit Accn.	Gene Symbol	Gene Desc.
1583403_at	4.08E-04	1.56	PREDICTED: Macaca mulatta carnitine palmitoyltransferase 1A (CPT1A); mRNA	XM_001101846	CPT1A	carnitine palmitoyltransferase 1A
1605486_at	2.38E-02	1.79	PREDICTED: Canis familiaris similar to [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; mitochondrial precursor (Pyruvate dehydrogenase kinase isoform 4) (LOC482310); mRNA	XM_539427	PDK4	pyruvate dehydrogenase kinase, isozyme 4
1585355_at	3.63E-02	2.01	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP); transcript variant 1 (LOC474720); mRNA	XM_531946	ADFP	adipose differentiation-related protein
1584951_at	4.00E-02	2.03	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP); transcript variant 4 (LOC474720); mRNA	XM_859697	ADFP	adipose differentiation-related protein
1591083_at	8.66E-04	2.9	PREDICTED: Canis familiaris similar to angiopoietin-like 4 protein (LOC476724); mRNA	XM_533928	ANGPTL4	angiopoietin-like 4

EPA in ETOH (CANINE-1); **8** records FC cutoff: 1.3; P-val cutofff: 0.05

Probe	P-Value	Fold-Change	Top BLAST Annot.	Top Hit Accn.	Gene Symbol	Gene Desc.
1598533_at	2.69E-02	1.32	PREDICTED: Canis familiaris similar to Sorting nexin-10 (LOC475261); mRNA	XM_532496	SNX10	sorting nexin 10
1583403_at	5.32E-03	1.66	PREDICTED: Macaca mulatta carnitine palmitoyltransferase 1A (CPT1A); mRNA	XM_001101846	CPT1A	carnitine palmitoyltransferase 1A
1582824_at	4.05E-03	1.75	PREDICTED: Canis familiaris carnitine palmitoyl transferase I isoform (CPT1); mRNA	XM_533208	CPT1A	carnitine palmitoyltransferase 1A (liver)
1605486_at	4.00E-03	1.84	PREDICTED: Canis familiaris similar to [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; mitochondrial precursor (Pyruvate dehydrogenase kinase isoform 4) (LOC482310); mRNA	XM_539427	PDK4	pyruvate dehydrogenase kinase, isozyme 4
1584951_at	2.21E-02	2.25	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP); transcript variant 4 (LOC474720); mRNA	XM_859697	ADFP	adipose differentiation-related protein
1585355_at	1.38E-02	2.25	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP); transcript variant 1 (LOC474720); mRNA	XM_531946	ADFP	adipose differentiation-related protein
1591083_at	3.86E-06	2.67	PREDICTED: Canis familiaris similar to angiopoietin-like 4 protein (LOC476724); mRNA	XM_533928	ANGPTL4	angiopoietin-like 4

EPA-DHA Combo 1.5-1 ratio (like in fish oil) in ETOH (CANINE-1); **24** records FC cutoff: 1.3; P-val cutofff: 0.05

Probe	P-Value	Fold-Change	Top BLAST Annot.	Top Hit Accn.	Gene Symbol	Gene Desc.
1583403_at	4.45E-03	2.04	PREDICTED: Macaca mulatta carnitine palmitoyltransferase 1A (CPT1A); mRNA	XM_001101846	CPT1A	carnitine palmitoyltransferase 1A
1597510_at	4.84E-02	1.31	PREDICTED: Canis familiaris similar to Sorting nexin-8 (LOC479767); mRNA	XM_536895	SNX8	sorting nexin 8

Table 5: Expression Profiling Results From Canine Cell Lines in the Presence of Listed Ingredients

1588894_at	2.14E-02	1.32	PREDICTED: Canis familiaris similar to O-linked GlcNAc transferase isoform 1; transcript variant 1 (LOC480955); mRNA	XM_538075	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)
1590473_s_at	3.25E-02	-1.53	PREDICTED: Canis familiaris similar to tripartite motif protein TRIM2 (LOC475470); mRNA	XM_532694	LOC475470	similar to tripartite motif protein TRIM2
1591902_at	3.40E-03	1.42	PREDICTED: Canis familiaris similar to electron-transfer-flavoprotein; beta polypeptide isoform 1; transcript variant 2 (LOC476400); mRNA	XM_858214	ETFB	electron-transfer-flavoprotein, beta polypeptide
1584742_at	3.03E-02	3.41	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP); transcript variant 4 (LOC474720); mRNA	XM_859697	ADFP	adipose differentiation-related protein
1588961_at	4.27E-02	1.51	PREDICTED: Canis familiaris similar to WD repeat and SOCS box containing protein 2 (WSB-2) (CS box-containing WD protein); transcript variant 2 (LOC477500); mRNA	XM_857324	WSB2	WD repeat and SOCS box-containing 2
1585479_x_at	2.57E-02	-1.91	PREDICTED: Canis familiaris similar to Translationally controlled tumor protein (TCTP) (p23) (Histamine-releasing factor) (HRF); transcript variant 1 (LOC476924); mRNA	XM_534126	TPT1	tumor protein, translationally-controlled 1
1589063_at	2.83E-02	-1.32	PREDICTED: Canis familiaris hypothetical LOC480214; transcript variant 1 (LOC480214); mRNA	XM_537339	CEP76	centrosomal protein 76kDa
1604059_at	4.31E-02	-1.36	PREDICTED: Canis familiaris similar to radixin; transcript variant 6 (LOC479446); mRNA	XM_857605	RDX	radixin
1585648_x_at	4.29E-02	-1.4	PREDICTED: Canis familiaris similar to 60S ribosomal protein L7; transcript variant 1 (LOC477912); mRNA	XM_535102	RPL7	ribosomal protein L7
1598533_at	2.99E-02	1.6	PREDICTED: Canis familiaris similar to Sorting nexin-10 (LOC475261); mRNA	XM_532496	SNX10	sorting nexin 10
1590911_at	3.60E-02	-1.32	PREDICTED: Canis familiaris similar to mitochondrial ribosomal protein S35 (LOC477660); mRNA	XM_534855	MRPS35	mitochondrial ribosomal protein S35
1591083_at	4.89E-08	4.11	PREDICTED: Canis familiaris similar to angiopoietin-like 4 protein (LOC476724); mRNA	XM_533928	ANGPTL4	angiopoietin-like 4
1585355_at	6.80E-04	4	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP); transcript variant 1 (LOC474720); mRNA	XM_531946	ADFP	adipose differentiation-related protein
1605486_at	4.24E-04	3.62	PREDICTED: Canis familiaris similar to [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; mitochondrial precursor (Pyruvate dehydrogenase kinase isoform 4) (LOC482310); mRNA	XM_539427	PDK4	pyruvate dehydrogenase kinase, isozyme 4
1586154_at	4.87E-02	1.5	PREDICTED: Canis familiaris similar to O-linked GlcNAc transferase isoform 1; transcript variant 11 (LOC480955); mRNA	XM_853825	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)

Table 5: Expression Profiling Results From Canine Cell Lines in the Presence of Listed Ingredients

1585792_at	5.42E-04	1.39	PREDICTED: Canis familiaris similar to electron-transfer-flavoprotein; beta polypeptide isoform 1; transcript variant 1 (LOC476400); mRNA	XM_533603	ETFB	electron-transfer-flavoprotein, beta polypeptide
1584951_at	1.05E-03	3.97	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP); transcript variant 4 (LOC474720); mRNA	XM_859697	ADFP	adipose differentiation-related protein
1584611_at	2.41E-02	-1.47	PREDICTED: Canis familiaris similar to 2-oxoisovalerate dehydrogenase beta subunit; mitochondrial precursor (Branched-chain alpha-keto acid dehydrogenase E1 component beta chain) (BCKDH E1-beta) (LOC474978); mRNA	XM_532213	BCKDHB	branched chain keto acid dehydrogenase E1, beta polypeptide

Alpha-Linolenic acid in ETOH (CANINE-1); **78** records FC cutoff: 1.3; P-val cutofff: 0.05

Probe	P-Value	Fold-Change	Top BLAST Annot.	Top Hit Accn.	Gene Symbol	Gene Desc.
1603697_at	1.88E-02	1.38	PREDICTED: Bos taurus similar to aminopeptidase puromycin sensitive; transcript variant 2 (NPEPPS); mRNA	XM_869645	NPEPPS	aminopeptidase puromycin sensitive
1605401_at	2.73E-02	1.47	Homo sapiens collagen; type IV; alpha 3 (Goodpasture antigen) binding protein (COL4A3BP); transcript variant 1; mRNA	NM_005713	COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein
1603995_at	9.27E-03	1.32	PREDICTED: Canis familiaris similar to heterogeneous nuclear ribonucleoprotein H3 isoform a; transcript variant 1 (LOC479227); mRNA	XM_536369	HNRNPH3	heterogeneous nuclear ribonucleoprotein H3 (2H9)
1596344_at	2.10E-02	1.43	Bos taurus neuroepithelial cell transforming gene 1; mRNA (cDNA clone MGC:127767 IMAGE:7956312); complete cds	BC102858	NET1	neuroepithelial cell transforming gene 1
1590524_at	2.82E-02	-1.4	PREDICTED: Equus caballus similar to engulfment and cell motility 1; transcript variant 1 (LOC100055551); mRNA	XM_001501263	LOC100055551	hypothetical protein LOC100055551
1597449_x_at	3.16E-02	1.49	Synthetic construct DNA; clone: pF1KSDA0016; Homo sapiens TOMM20 gene for translocase of outer mitochondrial membrane 20 homolog; complete cds; without stop codon; in Flexi system	AB383705		
1585402_at	4.17E-02	1.34	Homo sapiens cDNA FLJ36515 fis; clone TRACH2001810	AK093834		
1598681_at	4.86E-02	-1.4	PREDICTED: Canis familiaris similar to CG5038-PA (LOC476977); mRNA	XM_534177	TMTC4	transmembrane and tetratricopeptide repeat containing 4
1604212_at	3.23E-03	1.68	PREDICTED: Macaca mulatta similar to Sorting nexin-10; transcript variant 1 (SNX10); mRNA	XM_001093939	SNX10	sorting nexin 10
1593517_at	4.73E-02	1.31	PREDICTED: Macaca mulatta similar to WD repeat and FYVE domain containing 1 (LOC706913); mRNA	XR_013603	LOC706913	similar to WD repeat and FYVE domain containing 1

Table 5: Expression Profiling Results From Canine Cell Lines in the Presence of Listed Ingredients

1603578_at	2.89E-03	1.35	PREDICTED: Canis familiaris similar to CD63 antigen (Melanoma-associated antigen ME491) (Lysosome-associated membrane glycoprotein 3) (LAMP-3) (Ocular melanoma-associated antigen) (OMA81H) (Granulophysin) (Tetraspanin-30) (Tspan-30) (LOC474391); mRNA	XM_531624	CD63	CD63 molecule
1594326_s_at	1.56E-02	1.46	Bos taurus muted homolog (mouse); mRNA (cDNA clone MGC:159907 IMAGE:8493721); complete cds	BC146091	MUTED	muted homolog (mouse)
1604895_at	4.51E-02	1.54	Macaca fascicularis brain cDNA; clone: QtrA-16528	AB174397		
1592641_at	2.64E-02	1.41	Macaca fascicularis brain cDNA clone: QtrA-16204; similar to human solute carrier family 20 (phosphate transporter); member1 (SLC20A1); mRNA; RefSeq: NM_005415.3	AB174339		
1582469_at	1.72E-02	1.52	Sus scrofa mRNA; clone:AMP010033D02; expressed in alveolar macrophage	AK230731		
1592640_at	3.79E-02	1.53	PREDICTED: Macaca mulatta similar to solute carrier family 20 (phosphate transporter); member 1; transcript variant 4 (LOC699462); mRNA	XM_001089376	LOC699462	similar to solute carrier family 20 (phosphate transporter), member 1
1595929_at	3.38E-02	1.44	PREDICTED: Canis familiaris similar to calreticulin; transcript variant 1 (LOC476694); mRNA	XM_533899	CALR	calreticulin
1592116_at	8.58E-03	2.01	PREDICTED: Canis familiaris similar to crystallin; zeta; transcript variant 1 (LOC611431); mRNA	XM_848704	LOC611431	similar to crystallin, zeta
1592888_at	2.32E-03	1.31	PREDICTED: Canis familiaris similar to suppressor of G2 allele of SKP1 (LOC609605); mRNA	XM_846893	SUGT1	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)
1585238_at	4.17E-02	1.49	PREDICTED: Macaca mulatta cyclin-dependent kinase 5; regulatory subunit 1; transcript variant 2 (CDK5R1); mRNA	XM_001113136	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1
1601402_at	1.71E-02	1.58	PREDICTED: Canis familiaris similar to Canalicular multispecific organic anion transporter 2 (Multidrug resistance-associated protein 3) (Multi-specific organic anion tranporter-D) (MOAT-D) (LOC491084); mRNA	XM_548204	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3
1598427_at	1.50E-02	1.31	Macaca fascicularis brain cDNA clone: QflA-17566; similar to human hypothetical protein LOC284214 (LOC284214); mRNA; RefSeq: XM_378734.1	AB172300		
1605773_at	3.88E-02	1.31	PREDICTED: Canis familiaris hypothetical protein LOC610171; transcript variant 2 (LOC610171); mRNA	XM_861881	TOMM5	translocase of outer mitochondrial membrane 5 homolog (yeast)
1586485_at	1.47E-02	1.61	PREDICTED: Canis familiaris similar to CG1458-PA (LOC610084); mRNA	XM_847482	CISD2	CDGSH iron sulfur domain 2
1604582_s_at	3.45E-02	1.31	PREDICTED: Canis familiaris similar to 5-nucleotidase; cytosolic III isoform 2; transcript variant 3 (LOC475277); mRNA	XM_859990	NT5C3	5'-nucleotidase, cytosolic III
1585056_at	4.99E-02	-1.31	PREDICTED: Canis familiaris similar to cajalin 2 isoform a (LOC482621); mRNA	XM_539738	ANKS1B	ankyrin repeat and sterile alpha motif domain containing 1B
1584435_at	4.62E-02	1.35	PREDICTED: Canis familiaris similar to fused toes homolog; transcript variant 2 (LOC478126); mRNA	XM_858235	AKTIP	AKT interacting protein

Table 5: Expression Profiling Results From Canine Cell Lines in the Presence of Listed Ingredients

1598533_at	8.89E-03	1.65	PREDICTED: Canis familiaris similar to Sorting nexin-10 (LOC475261); mRNA	XM_532496	SNX10	sorting nexin 10
1589037_at	3.90E-02	1.36	PREDICTED: Canis familiaris similar to poly(A) binding protein interacting protein 1; transcript variant 1 (LOC479343); mRNA	XM_536482	PAIP1	poly(A) binding protein interacting protein 1
1585877_at	3.62E-02	1.33	PREDICTED: Canis familiaris similar to SH3 domain-binding protein 5 (SH3 domain-binding protein that preferentially associates with BTK) (LOC485657); mRNA	XM_542777	SH3BP5	SH3-domain binding protein 5 (BTK-associated)
1592753_s_at	3.24E-02	1.81	PREDICTED: Canis familiaris similar to carbonic reductase 4 (LOC477352); mRNA	XM_534547	CBR4	carbonyl reductase 4
1583742_at	2.98E-02	1.63	PREDICTED: Canis familiaris similar to NADP-dependent leukotriene B4 12-hydroxydehydrogenase (15-oxoprostaglandin 13-reductase); transcript variant 4 (LOC474802); mRNA	XM_862485	PTGR1	prostaglandin reductase 1
1586256_at	2.22E-02	-1.39	PREDICTED: Canis familiaris similar to src homology 2 domain-containing transforming protein C; transcript variant 1 (LOC490439); mRNA	XM_547561	SHC1	SHC (Src homology 2 domain containing) transforming protein 1
1591376_s_at	3.92E-02	1.66	PREDICTED: Canis familiaris similar to Protein KIAA0256; transcript variant 1 (LOC487547); mRNA	XM_544672	LOC487547	similar to Protein KIAA0256
1599766_s_at	2.38E-02	1.36	Sus scrofa mRNA; clone:OVRM10110E11; expressed in ovary	AK235738		
1597114_at	2.26E-02	-1.42	PREDICTED: Canis familiaris similar to E1B-55kDa-associated protein 5 isoform d; transcript variant 11 (LOC476452); mRNA	XM_861493	HNRNPUL1	heterogeneous nuclear ribonucleoprotein U-like 1
1588641_at	1.92E-03	-1.47	PREDICTED: Canis familiaris similar to Sorting nexin-9 (LOC476254); mRNA	XM_533460	SNX9	sorting nexin 9
1588829_at	4.80E-02	1.31	PREDICTED: Canis familiaris similar to Tetraspanin-6 (Tspan-6) (Transmembrane 4 superfamily member 6) (T245 protein) (Tetraspanin TM4-D) (A15 homolog); transcript variant 3 (LOC480981); mRNA	XM_856176	TSPAN6	tetraspanin 6
1593131_s_at	2.23E-02	1.39	Canis lupus familiaris CD47 molecule (CD47); mRNA	NM_001080721	CD47	CD47 molecule
1582468_at	4.23E-02	1.46	Canis familiaris CMP-sialic acid transporter gene; complete cds	AY064407	SLC35A1	solute carrier family 35 (CMP-sialic acid transporter), member A1
1591083_at	3.00E-02	2.59	PREDICTED: Canis familiaris similar to angiopoietin-like 4 protein (LOC476724); mRNA	XM_533928	ANGPTL4	angiopoietin-like 4
1583375_x_at	4.75E-02	1.94	PREDICTED: Canis familiaris similar to beta globin (LOC480784); mRNA	XM_537902	LOC480784	similar to beta globin
1588410_at	3.78E-02	1.37	PREDICTED: Canis familiaris malic enzyme 1; NADP(+)-dependent; cytosolic (ME1); mRNA	XM_532217	MÉ1	malic enzyme 1, NADP(+)-dependent, cytosolic
1603290_s_at	2.93E-02	1.35	PREDICTED: Canis familiaris similar to PHD finger protein 22 (LOC487889); mRNA	XM_545012	INTS12	integrator complex subunit 12
1603289_at	9.50E-03	1.32	PREDICTED: Canis familiaris similar to PHD finger protein 22 (LOC487889); mRNA	XM_545012	INTS12	integrator complex subunit 12

Table 5: Expression Profiling Results From Canine Cell Lines in the Presence of Listed Ingredients

1585856_at	3 63E-02	1.33	PREDICTED: Canis familiaris similar to 3(2);5-bisphosphate nucleotidase 1 (Bisphosphate 3-nucleotidase 1) (PAP-inositol-1;4-phosphatase) (PIP) (LOC608525); mRNA	XM_845576	BPNT1	3'(2'), 5'-bisphosphate nucleotidase 1
1593869_s_at	4 26E-02	1.52	PREDICTED: Canis familiaris similar to pleckstrin homology domain containing; family E (with leucine rich repeats) member 1 (LOC477053); mRNA	XM_534250	LOC477053	similar to pleckstrin homology domain containing, family E (with leucine rich repeats) member 1
1583284_at	2 86E-02	1.84	PREDICTED: Canis familiaris beta-spectrin; transcript variant 7 (LOC403743); mRNA	XM_860139	SPTBN1	spectrin, beta, non-erythrocytic 1
1604421_s_at	1 83E-02	1 3	PREDICTED: Canis familiaris similar to mitogen-activated protein kinase kinase 1 interacting protein 1; transcript variant 1 (LOC478492); mRNA	XM_535670	MAP2K1IP1	mitogen-activated protein kinase kinase 1 interacting protein 1
1585792_at	1.47E-02	1.34	PREDICTED: Canis familiaris similar to electron-transfer-flavoprotein; beta polypeptide isoform 1; transcript variant 1 (LOC476400); mRNA	XM_533603	ETFB	electron-transfer-flavoprotein, beta polypeptide
1587615_s_at	1 64E-02	1.54	PREDICTED: Canis familiaris similar to heat shock 70kD protein binding protein; transcript variant 3 (LOC607960); mRNA	XM_844401	LOC607960	similar to heat shock 70kD protein binding protein
1593240_s_at	1.97E-02	1.35	PREDICTED: Canis familiaris similar to heat shock 70kD protein binding protein; transcript variant 4 (LOC607960); mRNA	XM_853827	LOC607960	similar to heat shock 70kD protein binding protein
1605213_at	1 61E-02	1.37	PREDICTED: Canis familiaris similar to preimplantation protein 3; transcript variant 2 (LOC478856); mRNA	XM_852308	MOBKL3	MOB1, Mps One Binder kinase activator-like 3 (yeast)
1605231_at	4 28E-02	1.35	PREDICTED: Canis familiaris similar to heterogeneous nuclear ribonucleoprotein H3 isoform a; transcript variant 1 (LOC479227); mRNA	XM_536369	HNRNPH3	heterogeneous nuclear ribonucleoprotein H3 (2H9)
1589992_s_at	3 32E-02	1 3	PREDICTED: Canis familiaris similar to preimplantation protein 3; transcript variant 1 (LOC478856); mRNA	XM_536018	MOBKL3	MOB1, Mps One Binder kinase activator-like 3 (yeast)
1593901_s_at	4 30E-02	1.35	PREDICTED: Canis familiaris similar to eukaryotic translation initiation factor 2; subunit 3; structural gene X-linked (LOC480866); mRNA	XM_537983	EIF2S3	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa
1592755_s_at	2.94E-02	1.37	PREDICTED: Canis familiaris similar to Electron transfer flavoprotein-ubiquinone oxidoreductase; mitochondrial precursor (ETF-QO) (ETF-ubiquinone oxidoreductase) (ETF dehydrogenase) (Electron-transferring-flavoprotein dehydrogenase); transcript variant 2 (LOC475480); mRNA	XM_848688	ETFDH	electron-transferring-flavoprotein dehydrogenase
1605137_at	4 24E-02	1.4	PREDICTED: Canis familiaris similar to cyclin T2 isoform a; transcript variant 1 (LOC476126); mRNA	XM_533333	CCNT2	cyclin T2
1585757_s_at	3.71E-02	1.42	PREDICTED: Canis familiaris similar to BET1 homolog (Golgi vesicular membrane trafficking protein p18) (hBET1) (LOC475231); mRNA	XM_532463	BET1	blocked early in transport 1 homolog (S. cerevisiae)
1596914_at	1 25E-02	1.44	PREDICTED: Canis familiaris similar to mitogen-activated protein kinase kinase 1 interacting protein 1; transcript variant 1 (LOC478492); mRNA	XM_535670	MAP2K1IP1	mitogen-activated protein kinase kinase 1 interacting protein 1

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1582433_at	1.21E-02	1.5	Canis lupus familiaris BGT1 gene for Betain GABA transporter; complete cds	D42037		
1596207_at	4.32E-03	1.52	PREDICTED: Canis familiaris similar to 5-aminolevulinate synthase; nonspecific; mitochondrial precursor (5-aminolevulinic acid synthase) (Delta-aminolevulinate synthase) (Delta-ALA synthetase) (ALAS-H); transcript variant 4 (LOC476600); mRNA	XM_854753	ALAS1	aminolevulinate, delta-, synthase 1
1583473_s_at	4.58E-02	1.56	PREDICTED: Canis familiaris similar to Beta enolase (2-phospho-D-glycerate hydro-lyase) (Muscle-specific enolase) (MSE) (Skeletal muscle enolase) (Enolase 3); transcript variant 2 (LOC479469); mRNA	XM_851111	ENO3	enolase 3 (beta, muscle)
1585473_s_at	3.38E-02	1.65	PREDICTED: Canis familiaris similar to Aminopeptidase O (AP-O); transcript variant 1 (LOC484139); mRNA	XM_541256	LOC484139	similar to Aminopeptidase O (AP-O)
Linoleic acid in ETOH (CANINE-1); **26** records FC cutoff: 1.3; P-val cutofff: 0.05						
Probe	**P-Value**	**Fold-Change**	**Top BLAST Annot.**	**Top Hit Accn.**	**Gene Symbol**	**Gene Desc.**
1603265_at	3.74E-02	1.42	PREDICTED: Canis familiaris similar to CG15747-PA; transcript variant 4 (LOC610752); mRNA	XM_863270	CCDC55	coiled-coil domain containing 55
1583403_at	2.10E-02	1.85	PREDICTED: Macaca mulatta carnitine palmitoyltransferase 1A (CPT1A); mRNA	XM_001101846	CPT1A	carnitine palmitoyltransferase 1A
1582709_at	4.83E-02	1.73	Canis familiaris immunoglobulin gamma heavy chain B mRNA; complete cds	AF354265		
1588784_at	3.40E-03	-1.31	PREDICTED: Canis familiaris similar to Nuclear factor 1 B-type (Nuclear factor 1/B) (NF1-B) (NFI-B) (NF-I/B) (CCAAT-box binding transcription factor) (CTF) (TGGCA-binding protein); transcript variant 1 (LOC474709); mRNA	XM_531936	LOC474709	similar to Nuclear factor 1 B-type (Nuclear factor 1/B) (NF1-B) (NFI-B) (NF-I/B) (CCAAT-box binding transcription factor) (CTF) (TGGCA-binding protein)
1605570_at	3.26E-02	-1.36	PREDICTED: Equus caballus similar to selenoprotein S (LOC100057595); mRNA	XM_001490893	LOC100057595	similar to selenoprotein S
1588453_at	4.15E-02	-1.38	PREDICTED: Equus caballus myosin; heavy chain 10; non-muscle; transcript variant 1 (MYH10); mRNA	XM_001504825	MYH10	myosin, heavy chain 10, non-muscle
1584742_at	4.77E-02	3.95	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP); transcript variant 4 (LOC474720); mRNA	XM_859697	ADFP	adipose differentiation-related protein
1588378_at	3.50E-02	-1.39	PREDICTED: Canis familiaris similar to Single-stranded DNA-binding protein 2 (Sequence-specific single-stranded-DNA-binding protein 2); transcript variant 1 (LOC479160); mRNA	XM_536304	SSBP2	single-stranded DNA binding protein 2
1598533_at	5.07E-03	1.46	PREDICTED: Canis familiaris similar to Sorting nexin-10 (LOC475261); mRNA	XM_532496	SNX10	sorting nexin 10
1584499_s_at	4.62E-02	1.77	PREDICTED: Canis familiaris similar to smoothelin isoform c; transcript variant 1 (LOC477542); mRNA	XM_534737	SMTN	smoo helin
1591083_at	2.11E-04	4.73	PREDICTED: Canis familiaris similar to angiopoietin-like 4 protein (LOC476724); mRNA	XM_533928	ANGPTL4	angiopoietin-like 4

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1585355_at	3 31E-03	4	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP); transcript variant 1 (LOC474720); mRNA	XM_531946	ADFP	adipose differentiation-related protein
1605486_at	3 29E-04	2.21	PREDICTED: Canis familiaris similar to [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; mitochondrial precursor (Pyruvate dehydrogenase kinase isoform 4) (LOC482310); mRNA	XM_539427	PDK4	pyruvate dehydrogenase kinase, isozyme 4
1605877_at	3 29E-02	-1.34	PREDICTED: Canis familiaris similar to vacuolar protein sorting 28; transcript variant 1 (LOC607677); mRNA	XM_844152	VPS28	vacuolar protein sorting 28 homolog (S. cerevisiae)
1584951_at	6 52E-03	4.23	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP); transcript variant 4 (LOC474720); mRNA	XM_859697	ADFP	adipose differentiation-related protein
1583085_at	4 51E-02	1.43	PREDICTED: Canis familiaris serum/glucocorticoid-regulated kinase 1; transcript variant 7 (SGK1); mRNA	XM_854849	SGK1	serum/glucocorticoid regulated kinase 1
1582824_at	1.42E-02	2.15	PREDICTED: Canis familiaris carnitine palmitoyl transferase I isoform (CPT1); mRNA	XM_533208	CPT1A	carnitine palmitoyltransferase 1A (liver)
Arachidonic acid in ETOH (CANINE-1); **20** records FC cutoff: 1.3; P-val cutofff: 0.05						
Probe	**P-Value**	**old-Change**	**Top BLAST Annot.**	**Top Hit Accn.**	**Gene Symbol**	**Gene Desc.**
1582746_at	4.11E-02	-1.46	PREDICTED: Canis familiaris similar to CD9 antigen (p24) (Leukocyte antigen MIC3) (Motility-related protein) (MRP-1) (Tetraspanin-29) (Tspan-29) (LOC611695); mRNA	XM_849393	CD9	CD9 molecule
1583403_at	6.92E-04	2.06	PREDICTED: Macaca mulatta carnitine palmitoyltransferase 1A (CPT1A); mRNA	XM_001101846	CPT1A	carnitine palmitoyltransferase 1A
1591614_at	2 58E-02	1.35	PREDICTED: Canis familiaris similar to CK2 interacting protein 1; HQ0024c protein; transcript variant 1 (LOC607927); mRNA	XM_844754	PLEKHO1	pleckstrin homology domain containing, family O member 1
1604212_at	8 20E-03	1.48	PREDICTED: Macaca mulatta similar to Sorting nexin-10; transcript variant 1 (SNX10); mRNA	XM_001093939	SNX10	sorting nexin 10
1586816_at	2 50E-02	1.31	PREDICTED: Canis familiaris similar to eukaryotic translation initiation factor 4 gamma; 3 (LOC478202); mRNA	XM_535377	EIF4G3	eukaryotic translation initiation factor 4 gamma, 3
1585704_x_at	2.15E-02	-1.37	PREDICTED: Canis familiaris similar to ribosomal protein S5; transcript variant 5 (LOC476366); mRNA	XM_856770	RPS5	ribosomal protein S5
1584742_at	1 67E-02	4.15	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP); transcript variant 4 (LOC474720); mRNA	XM_859697	ADFP	adipose differentiation-related protein
1598533_at	5.43E-04	1.56	PREDICTED: Canis familiaris similar to Sorting nexin-10 (LOC475261); mRNA	XM_532496	SNX10	sorting nexin 10
1583742_at	1 09E-02	1.49	PREDICTED: Canis familiaris similar to NADP-dependent leukotriene B4 12-hydroxydehydrogenase (15-oxoprostaglandin 13-reductase); transcript variant 4 (LOC474802); mRNA	XM_862485	PTGR1	prostaglandin reductase 1
1591083_at	2 56E-05	4.06	PREDICTED: Canis familiaris similar to angiopoietin-like 4 protein (LOC476724); mRNA	XM_533928	ANGPTL4	angiopoietin-like 4

Table 5: Expression Profiling Results From Canine Cell Lines in the Presence of Listed Ingredients

1585355_at	3 32E-04	4.31	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP); transcript variant 1 (LOC474720); mRNA	XM_531946	ADFP	adipose differentiation-related protein
1605486_at	7 63E-04	2.53	PREDICTED: Canis familiaris similar to [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; mitochondrial precursor (Pyruvate dehydrogenase kinase isoform 4) (LOC482310); mRNA	XM_539427	PDK4	pyruvate dehydrogenase kinase, isozyme 4
1604372_at	3 58E-02	2.08	PREDICTED: Canis familiaris similar to Transforming growth factor-beta-inducible early growth response protein 2 (TGFB-inducible early growth response protein 2) (TIEG-2) (Krueppel-like factor 11) (LOC475665); mRNA	XM_532873	KLF11	Kruppel-like factor 11
1584951_at	4 62E-04	4.29	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP); transcript variant 4 (LOC474720); mRNA	XM_859697	ADFP	adipose differentiation-related protein
1605608_at	3.74E-02	1.44	PREDICTED: Canis familiaris similar to fragile X mental retardation 1; transcript variant 12 (Fmr1); mRNA	XM_861651	FMR1	fragile X mental retardation 1
1584200_at	1.74E-02	-1.32	PREDICTED: Canis familiaris similar to ubiquitin-fold modifier 1 (LOC477297); mRNA	XM_534489	UFM1	ubiquitin-fold modifier 1
1582824_at	3 81E-02	1.75	PREDICTED: Canis familiaris carnitine palmitoyl transferase I isoform (CPT1); mRNA	XM_533208	CPT1A	carnitine palmitoyltransferase 1A (liver)
Stearic acid in ETOH (CANINE-2); **47** records FC cutoff: 1.3; P-val cutofff: 0.05						
Probe	**P-Value**	**Fold-Change**	**Top BLAST Annot.**	**Top Hit Accn.**	**Gene Symbol**	**Gene Desc.**
Cfa.15548.1.A1_at	4 30E-02	-2.38	PREDICTED: Macaca mulatta DNA-crosslink repair gene SNM1 (DCLRE1A); mRNA	XM_001090942	DCLRE1A	DNA cross-link repair 1A (PSO2 homolog, S. cerevisiae)
CfaAffx.24027.1.S1_at	3 03E-02	-1.49	PREDICTED: Canis familiaris similar to heterogeneous nuclear ribonucleoprotein U (LOC476053); mRNA	XM_533261	HNRNPUL2	heterogeneous nuclear ribonucleoprotein U-like 2
Cfa.12280.1.A1_at	2.18E-02	1.31	Sus scrofa mRNA; clone:OVRM10088G09; expressed in ovary	AK235506		
Cfa.1286.1.A1_at	6.47E-03	1.71	PREDICTED: Macaca mulatta carnitine palmitoyltransferase 1A (CPT1A); mRNA	XM_001101846	CPT1A	carnitine palmitoyltransferase 1A
Cfa.15509.2.S1_at	3 09E-02	-1.34	PREDICTED: Macaca mulatta similar to cell division cycle 42; transcript variant 4 (LOC707637); mRNA	XM_001100181	LOC707637	similar to cell division cycle 42
CfaAffx.29294.1.S1_at	3 37E-02	-1.96	PREDICTED: Canis familiaris similar to heterogeneous nuclear ribonucleoprotein A3; transcript variant 4 (LOC609295); mRNA	XM_859193	LOC609295	similar to heterogeneous nuclear ribonucleoprotein A3
Cfa.16629.1.A1_at	1.40E-02	-1.83	Homo sapiens forkhead box P1 (FOXP1); transcript variant 1; mRNA	NM_032682	FOXP1	forkhead box P1
CfaAffx.1280.1.S1_at	3 35E-02	-1.55	PREDICTED: Canis familiaris similar to feminization 1 homolog a; transcript variant 1 (LOC481437); mRNA	XM_538557	FEM1C	fem-1 homolog c (C. elegans)
Cfa.3671.1.A1_s_at	2.40E-02	-1.34	Canis familiaris mRNA for ribosome receptor; p180	X87224	RRBP1	ribosome binding protein 1 homolog 180kDa (dog)

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CfaAffx.3271.1.S1_s_at	3 22E-02	-1.66	PREDICTED: Macaca mulatta similar to Protein C6orf130 homolog; transcript variant 2 (LOC719685); mRNA	XM_001117219	LOC719685	similar to Protein C6orf130 homolog
Cfa.14928.1.S1_s_at	3 64E-02	-1.77	PREDICTED: Canis familiaris similar to heterogeneous nuclear ribonucleoprotein U (LOC476053); mRNA	XM_533261	HNRNPUL2	heterogeneous nuclear ribonucleoprotein U-like 2
CfaAffx.6434.1.S1_x_at	4 36E-02	-1.43	PREDICTED: Canis familiaris similar to Nuclear transport factor 2 (NTF-2); transcript variant 3 (LOC479681); mRNA	XM_859446	NUTF2	nuclear transport factor 2
Cfa.15509.1.S1_at	2 27E-02	-1.48	PREDICTED: Canis familiaris similar to cell division cycle 42; transcript variant 2 (LOC607429); mRNA	XM_844251	LOC607429	similar to cell division cycle 42
Cfa.12323.1.A1_at	4.13E-05	4.09	PREDICTED: Canis familiaris similar to angiopoietin-like 4 protein (LOC476724); mRNA	XM_533928	ANGPTL4	angiopoietin-like 4
Cfa.13103.1.A1_at	3.71E-02	-1.39	PREDICTED: Canis familiaris similar to inositol polyphosphate phosphatase-like 1; transcript variant 2 (LOC485209); mRNA	XM_856340	INPPL1	inositol polyphosphate phosphatase-like 1
CfaAffx.30508.1.S1_at	2.76E-02	-1.34	PREDICTED: Canis familiaris similar to early estrogen-induced gene 1 protein (LOC490130); mRNA	XM_547251	LOC490130	similar to early estrogen-induced gene 1 protein
Cfa.20794.1.S1_s_at	4 58E-02	-2.89	PREDICTED: Canis familiaris similar to fusion (involved in t(12;16) in malignant liposarcoma) (predicted); transcript variant 7 (LOC479778); mRNA	XM_851770	LOC479778	similar to fusion (involved in t(12;16) in malignant liposarcoma) (predicted)
Cfa.18834.1.S1_at	1 39E-05	2.06	PREDICTED: Canis familiaris similar to angiopoietin-like 4 protein (LOC476724); mRNA	XM_533928	ANGPTL4	angiopoietin-like 4
Cfa.17571.1.S1_at	2 22E-02	1.38	PREDICTED: Canis familiaris similar to Mitochondrial carnitine/acylcarnitine carrier protein (Carnitine/acylcarnitine translocase) (CAC); transcript variant 3 (LOC484774); mRNA	XM_858026	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha
CfaAffx.19697.1.S1_at	2 03E-02	-1.31	PREDICTED: Canis familiaris similar to SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily d; member 2; transcript variant 2 (LOC480477); mRNA	XM_845276	SMARCD2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2
CfaAffx.25382.1.S1_s_at	4.40E-02	-1.33	PREDICTED: Canis familiaris similar to Splicing factor; arginine/serine-rich 5 (Pre-mRNA splicing factor SRP40) (Insulin-induced growth response protein CL-4) (Delayed-early protein HRS); transcript variant 20 (LOC490754); mRNA	XM_862155	SFRS5	splicing factor, arginine/serine-rich 5
Cfa.1182.1.S1_s_at	1 38E-02	-1 3	PREDICTED: Canis familiaris similar to forkhead box J3; transcript variant 2 (LOC475310); mRNA	XM_850709	FOXJ3	forkhead box J3
Cfa.21276.1.S1_at	1.44E-02	-2.87	PREDICTED: Canis familiaris similar to protein tyrosine phosphatase 4a1; transcript variant 1 (LOC486655); mRNA	XM_847783	LOC486655	similar to protein tyrosine phosphatase 4a1
CfaAffx.4605.1.S1_s_at	1.48E-02	-2.54	PREDICTED: Canis familiaris similar to protein tyrosine phosphatase 4a1; transcript variant 1 (LOC481863); mRNA	XM_538984	PTP4A1	protein tyrosine phosphatase type IVA, member 1
Cfa.18334.1.S1_s_at	4 57E-02	-1.68	PREDICTED: Canis familiaris similar to heterogeneous nuclear ribonucleoprotein H3 isoform a; transcript variant 2 (LOC479227); mRNA	XM_844897	HNRNPH3	heterogeneous nuclear ribonucleoprotein H3 (2H9)

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Cfa.12953.1.A1_s_at	4 68E-02	-1.62	PREDICTED: Canis familiaris similar to DnaJ (Hsp40) homolog; subfamily C; member 7; transcript variant 8 (LOC480519); mRNA	XM_855672	DNAJC7	DnaJ (Hsp40) homolog, subfamily C, member 7
Cfa.3678.1.S1_s_at	5 00E-02	-1.55	Canis familiaris ras p21 (K-ras) mRNA; partial cds	U62094	K-RAS	ras p21
Cfa.12115.3.A1_s_at	4 39E-02	-1.47	PREDICTED: Canis familiaris similar to Splicing factor; arginine/serine-rich 5 (Pre-mRNA splicing factor SRP40) (Insulin-induced growth response protein CL-4) (Delayed-early protein HRS); transcript variant 5 (LOC490754); mRNA	XM_862000	SFRS5	splicing factor, arginine/serine-rich 5
CfaAffx.24188.1.S1_s_at	4.91E-02	-1.46	PREDICTED: Canis familiaris similar to alpha glucosidase II alpha subunit isoform 2; transcript variant 2 (LOC483784); mRNA	XM_862467	GANAB	glucosidase, alpha; neutral AB
CfaAffx.7822.1.S1_s_at	2 31E-02	-1.45	PREDICTED: Canis familiaris similar to FYVE-finger-containing Rab5 effector protein rabenosyn-5 (LOC484642); mRNA	XM_541756	ZFYVE20	zinc finger, FYVE domain containing 20
CfaAffx.9636.1.S1_at	2.17E-02	-1.45	PREDICTED: Canis familiaris similar to Protein phosphatase 1 regulatory subunit 12A (Myosin phosphatase targeting subunit 1) (Myosin phosphatase target subunit 1) (Protein phosphatase myosin-binding subunit); transcript variant 10 (LOC475411); mRNA	XM_859917	PPP1R12A	protein phosphatase 1, regulatory (inhibitor) subunit 12A
CfaAffx.20356.1.S1_at	3.97E-02	-1.45	PREDICTED: Sus scrofa similar to MLK-related kinase (LOC100152572); mRNA	XM_001925866	LOC100152572	similar to MLK-related kinase
CfaAffx.31073.1.S1_at	3 27E-02	-1.43	PREDICTED: Canis familiaris hypothetical LOC54921; transcript variant 2 (LOC612884); mRNA	XM_858504	LOC612884	hypothetical LOC612884
Cfa.20153.1.S1_s_at	4 39E-02	-1.41	PREDICTED: Canis familiaris similar to H326 (LOC478971); mRNA	XM_536129	WDR42A	WD repeat domain 42A
CfaAffx.25842.1.S1_at	2 01E-02	-1.37	PREDICTED: Canis familiaris similar to aldehyde dehydrogenase family 6; subfamily A1 (LOC490779); mRNA	XM_547901	ALDH6A1	aldehyde dehydrogenase 6 family, member A1
CfaAffx.25251.1.S1_at	3.77E-02	-1.32	PREDICTED: Canis familiaris similar to Butyrate response factor 1 (TIS11B protein); transcript variant 1 (LOC490748); mRNA	XM_547870	ZFP36L1	zinc finger protein 36, C3H type-like 1
CfaAffx.27030.1.S1_s_at	3.49E-02	-1.32	PREDICTED: Canis familiaris similar to dynamin 2 isoform 2; transcript variant 44 (LOC484949); mRNA	XM_863012	DNM2	dynamin 2
CfaAffx.26390.1.S1_at	4.97E-03	-1.31	PREDICTED: Canis familiaris similar to transcriptional regulator ATRX isoform 1; transcript variant 7 (LOC480963); mRNA	XM_855075	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)
CfaAffx.18769.1.S1_s_at	1 64E-02	1.42	PREDICTED: Canis familiaris similar to Mitochondrial carnitine/acylcarnitine carrier protein (Carnitine/acylcarnitine translocase) (CAC); transcript variant 3 (LOC484774); mRNA	XM_858026	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha
CfaAffx.28301.1.S1_s_at	8.45E-05	1.82	PREDICTED: Canis familiaris similar to angiopoietin-like 4 protein (LOC476724); mRNA	XM_533928	ANGPTL4	angiopoietin-like 4
Cfa.431.2.A1_s_at	4.46E-03	1.95	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP); transcript variant 2 (LOC474720); mRNA	XM_859657	ADFP	adipose differentiation-related protein
CfaAffx.3314.1.S1_at	5.75E-03	1.96	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP); transcript variant 1 (LOC474720); mRNA	XM_531946	ADFP	adipose differentiation-related protein

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Cfa.2282.1.S1_at	1 06E-05	2.64	PREDICTED: Canis familiaris similar to [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; mitochondrial precursor (Pyruvate dehydrogenase kinase isoform 4) (LOC482310); mRNA	XM_539427	PDK4	pyruvate dehydrogenase kinase, isozyme 4
Myristic acid in ETOH (CANINE-2); **65** records FC cutoff: 1.3; P-val cutofff: 0.05						
Probe	**P-Value**	**Fold-Change**	**Top BLAST Annot.**	**Top Hit Accn.**	**Gene Symbol**	**Gene Desc.**
CfaAffx.22598.1.S1_at	3 04E-02	-1.35	Zea mays clone 462440 hypothetical protein mRNA; complete cds	EU974992		
CfaAffx.10707.1.S1_at	5 00E-02	1.43	PREDICTED: Canis familiaris similar to Transcription initiation factor TFIID subunit 10 (Transcription initiation factor TFIID 30 kDa subunit) (TAF(II)30) (TAFII-30) (TAFII30) (STAF28); transcript variant 2 (LOC485336); mRNA	XM_858050	TAF10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 30kDa
Cfa.1286.1.A1_at	1 06E-02	1.61	PREDICTED: Macaca mulatta carnitine palmitoyltransferase 1A (CPT1A); mRNA	XM_001101846	CPT1A	carnitine palmitoyltransferase 1A
CfaAffx.10985.1.S1_s_at	2 57E-02	1.41	PREDICTED: Canis familiaris similar to steroid dehydrogenase homolog; transcript variant 1 (LOC475939); mRNA	XM_533148	HSD17B12	hydroxysteroid (17-beta) dehydrogenase 12
CfaAffx.3857.1.S1_at	3.19E-02	-1.34	PREDICTED: Macaca mulatta septin 10; transcript variant 3 (SEPT10); mRNA	XM_001085213	10-Sep	septin 10
Cfa.6309.1.A1_x_at	3 85E-02	1.32	PREDICTED: Ornithorhynchus anatinus hypothetical protein LOC100084338 (LOC100084338); mRNA	XM_001514780	LOC100084338	hypothetical protein LOC100084338
CfaAffx.3196.1.S1_at	3 54E-02	1.31	PREDICTED: Canis familiaris similar to shank-interacting protein-like 1 (LOC475122); mRNA	XM_532352	SHARPIN	SHANK-associated RH domain interactor
CfaAffx.17424.1.S1_at	3.43E-03	-1.37	PREDICTED: Equus caballus similar to PH domain-containing protein C10orf81 (LOC100068233); mRNA	XM_001498104	LOC100068233	hypothetical protein LOC100068233
Cfa.449.1.S1_s_at	4 53E-02	1.33	PREDICTED: Canis familiaris similar to ADAM 9 precursor (A disintegrin and metalloproteinase domain 9) (Metalloprotease/disintegrin/cysteine-rich protein 9) (Myeloma cell metalloproteinase) (Meltrin gamma) (Cellular disintegrin-related protein) (LOC475579); mRNA	XM_532798	ADAM9	ADAM metallopeptidase domain 9 (meltrin gamma)
CfaAffx.18067.1.S1_at	4.77E-02	1.34	Sus scrofa mRNA; clone:OVRM10172B08; expressed in ovary	AK236281	LOC100157814	similar to Splicing factor 3b, subunit 4
CfaAffx.5542.1.S1_x_at	1 09E-02	-1.33	PREDICTED: Canis familiaris similar to eukaryotic translation elongation factor 1 alpha 2; transcript variant 1 (LOC607645); mRNA	XM_537422	LOC607645	similar to eukaryotic translation elongation factor 1 alpha 2
CfaAffx.10306.1.S1_at	1 85E-03	-1.32	PREDICTED: Equus caballus similar to olfactory receptor; family 52; subfamily B; member 6 (predicted) (LOC100069426); mRNA	XM_001499194	LOC100069426	similar to hCG2040517
CfaAffx.29330.1.S1_x_at	8.11E-03	1.64	PREDICTED: Equus caballus similar to magmas-like protein (LOC100069741); mRNA	XM_001499467	LOC100069741	similar to magmas-like protein
Cfa.4113.1.S1_at	7 01E-03	1.52	PREDICTED: Equus caballus similar to macrophage migration inhibitory factor (LOC100053618); mRNA	XM_001489611	LOC100053618	similar to macrophage migration inhibitory factor

Table 5: Expression Profiling Results From Canine Cell Lines in the Presence of Listed Ingredients

Cfa.75.1.S1_at	4.18E-02	1.49	Canis familiaris Cu/Zn superoxide dismutase (SOD1) mRNA; complete cds	AF346417	SOD1	superoxide dismutase 1, soluble
CfaAffx.9675.1.S1_at	1 33E-02	-1.34	Equus caballus myogenic factor 5 gene; partial cds	AF411602		
Cfa.20306.1.S1_s_at	1 88E-03	1.33	PREDICTED: Equus caballus similar to splicing factor; arginine/serine-rich 4 (LOC100070608); mRNA	XM_001500275	LOC100070608	similar to splicing factor, arginine/serine-rich 4
CfaAffx.1293.1.S1_s_at	1.47E-02	1.35	PREDICTED: Canis familiaris similar to R3H domain protein KIAA1002; transcript variant 8 (LOC474412); mRNA	XM_853641	LOC474412	similar to R3H domain protein KIAA1002
Cfa.10309.1.A1_s_at	4.42E-02	1.33	PREDICTED: Canis familiaris similar to Mitochondrial 28S ribosomal protein S25 (S25mt) (MRP-S25) (LOC476523); mRNA	XM_533729	MRPS25	mitochondrial ribosomal protein S25
CfaAffx.15560.1.S1_s_at	4.93E-02	1.52	PREDICTED: Canis familiaris similar to WD repeat and SOCS box containing protein 2 (WSB-2) (CS box-containing WD protein); transcript variant 1 (LOC477500); mRNA	XM_534697	WSB2	WD repeat and SOCS box-containing 2
Cfa.12323.1.A1_at	4 28E-03	3.08	PREDICTED: Canis familiaris similar to angiopoietin-like 4 protein (LOC476724); mRNA	XM_533928	ANGPTL4	angiopoietin-like 4
CfaAffx.14545.1.S1_s_at	7 27E-03	1.33	PREDICTED: Canis familiaris similar to vasopressin-induced protein; 32kDa (LOC608786); mRNA	XM_845909	AVPI1	arginine vasopressin-induced 1
Cfa.10896.2.A1_s_at	2 21E-02	1.32	PREDICTED: Canis familiaris similar to transcription elongation factor B (SIII); polypeptide 2; transcript variant 1 (LOC479873); mRNA	XM_536998	TCEB2	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)
Cfa.101.1.S1_s_at	2 50E-02	1.96	PREDICTED: Canis familiaris carnitine palmitoyl transferase I isoform (CPT1); mRNA	XM_533208	CPT1A	carnitine palmitoyltransferase 1A (liver)
CfaAffx.9670.1.S1_s_at	4.43E-02	1.39	PREDICTED: Canis familiaris similar to 39S ribosomal protein L12; mitochondrial precursor (L12mt) (MRP-L12) (5c5-2) (LOC608030); mRNA	XM_844923	MRPL12	mitochondrial ribosomal protein L12
Cfa.14094.1.A1_at	1 09E-03	-1.47	PREDICTED: Canis familiaris similar to Probable leucyl-tRNA synthetase; mitochondrial precursor (Leucine--tRNA ligase) (LeuRS); transcript variant 2 (LOC476652); mRNA	XM_859540	LARS2	leucyl-tRNA synthetase 2, mitochondrial
Cfa.18834.1.S1_at	3 00E-04	1.7	PREDICTED: Canis familiaris similar to angiopoietin-like 4 protein (LOC476724); mRNA	XM_533928	ANGPTL4	angiopoietin-like 4
Cfa.17571.1.S1_at	8 28E-03	1.87	PREDICTED: Canis familiaris similar to Mitochondrial carnitine/acylcarnitine carrier protein (Carnitine/acylcarnitine translocase) (CAC); transcript variant 3 (LOC484774); mRNA	XM_858026	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha
CfaAffx.27890.1.S1_s_at	1 27E-02	1 3	Canis familiaris multidrug resistance-associated protein 1 (MRP1) mRNA; complete cds	AY363728	ABCC1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1
Cfa.9894.1.A1_s_at	9 33E-03	1.4	PREDICTED: Canis familiaris similar to MHC class II region expressed gene KE2 (LOC609675); mRNA	XM_846463	LOC609675	similar to MHC class II region expressed gene KE2
Cfa.18314.1.S1_s_at	4 65E-02	1.33	PREDICTED: Canis familiaris similar to Golgi autoantigen; golgin subfamily a; 2 (LOC480708); mRNA	XM_537828	GOLGA2	golgi autoantigen, golgin subfamily a, 2
Cfa.349.1.A1_s_at	4.76E-02	-1.31	PREDICTED: Canis familiaris dystonin; transcript variant 16 (DST); mRNA	XM_861720	DST	dystonin

Table 5: Expression Profiling Results From Canine Cell Lines in the Presence of Listed Ingredients

CfaAffx.24152.1.S1_s_at	1.99E-02	1.33	PREDICTED: Canis familiaris similar to 2;3-cyclic-nucleotide 3-phosphodiesterase (CNP) (CNPase) (LOC607694); mRNA	XM_844467	CNP	2',3'-cyclic nucleotide 3' phosphodiesterase
Cfa.1260.1.A1_at	6 52E-03	-1.38	PREDICTED: Canis familiaris similar to Ribonuclease III (RNase III) (Drosha) (p241); transcript variant 4 (LOC479375); mRNA	XM_863142	RNASEN	ribonuclease type III, nuclear
CfaAffx.10828.1.S1_at	1 69E-02	-1.33	PREDICTED: Canis familiaris similar to 5-lipoxygenase activating protein (FLAP) (MK 886-binding protein) (LOC477323); mRNA	XM_534516	ALOX5AP	arachidonate 5-lipoxygenase-activating protein
Cfa.11460.1.A1_at	1 58E-03	-1.31	PREDICTED: Canis familiaris similar to potassium channel tetramerisation domain containing 19 (LOC479689); mRNA	XM_536820	KCTD19	potassium channel tetramerisation domain containing 19
CfaAffx.26483.1.S1_s_at	4 87E-02	1 3	Canis lupus familiaris nm23-C2 mRNA for NM23-C2; complete cds	AB207045	NME2	non-metastatic cells 2, protein (NM23B) expressed in
CfaAffx.27678.1.S1_at	4 61E-02	1.31	PREDICTED: Canis familiaris similar to CG8202-PA (LOC479825); mRNA	XM_536952	LOC479825	similar to CG8202-PA
CfaAffx.22986.1.S1_s_at	2 60E-02	1.31	PREDICTED: Canis familiaris similar to positive cofactor 2; glutamine/Q-rich-associated protein; transcript variant 2 (LOC608008); mRNA	XM_844799	MED15	mediator complex subunit 15
CfaAffx.30749.1.S1_at	2 05E-02	1.31	Canis lupus familiaris prostaglandin E synthase 2 (PTGES2); mRNA	NM_001131050	PTGES2	prostaglandin E synthase 2
Cfa.16771.1.S1_s_at	4.47E-02	1.31	PREDICTED: Canis familiaris similar to Peripheral-type benzodiazepine receptor (PBR) (PKBS) (Mitochondrial benzodiazepine receptor) (LOC474475); mRNA	XM_531704	TSPO	translocator protein (18kDa)
CfaAffx.28507.1.S1_s_at	1 84E-02	1.32	PREDICTED: Canis familiaris similar to intraflagellar transport protein IFT20 (LOC480620); mRNA	XM_537740	LOC480620	similar to intraflagellar transport protein IFT20
CfaAffx.24760.1.S1_s_at	1 23E-02	1.32	PREDICTED: Canis familiaris similar to ilvB (bacterial acetolactate synthase)-like isoform 1 (LOC476683); mRNA	XM_533890	ILVBL	ilvB (bacterial acetolactate synthase)-like
CfaAffx.12244.1.S1_s_at	3 68E-02	1.33	PREDICTED: Canis familiaris similar to solute carrier family 25; member 4 (LOC475630); mRNA	XM_532844	SLC25A4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4
Cfa.12232.1.A1_s_at	1.97E-02	1.34	PREDICTED: Canis familiaris similar to Peripheral-type benzodiazepine receptor (PBR) (PKBS) (Mitochondrial benzodiazepine receptor) (LOC474475); mRNA	XM_531704	TSPO	translocator protein (18kDa)
CfaAffx.18843.1.S1_at	3.15E-02	1.34	PREDICTED: Canis familiaris similar to vacuolar protein sorting 33B (yeast homolog)); transcript variant 3 (LOC479048); mRNA	XM_854985	VPS33B	vacuolar protein sorting 33 homolog B (yeast)
CfaAffx.22419.1.S1_at	4 89E-02	1.35	PREDICTED: Canis familiaris similar to SPRY domain-containing SOCS box protein SSB-2 (LOC477710); mRNA	XM_534903	SPSB2	splA/ryanodine receptor domain and SOCS box containing 2
CfaAffx.30320.1.S1_s_at	4.99E-02	1.36	PREDICTED: Canis familiaris similar to glutathione S-transferase M1 isoform 2; transcript variant 2 (LOC479912); mRNA	XM_860902	GSTM1	glutathione S-transferase M1
CfaAffx.5647.1.S1_at	3.47E-02	1.37	PREDICTED: Canis familiaris similar to purine rich element binding protein B (LOC608031); mRNA	XM_844924	LOC608031	similar to purine rich element binding protein B

Table 5: Expression Profiling Results From Canine Cell Lines in the Presence of Listed Ingredients

Cfa.3226.1.S1_s_at	2 86E-02	1.38	PREDICTED: Canis familiaris similar to BolA-like protein My016 (LOC607859); mRNA	XM_844690	LOC607859	similar to BolA-like protein My016
Cfa.6265.1.A1_s_at	4.17E-02	1.41	PREDICTED: Canis familiaris similar to bolA like 1; transcript variant 1 (LOC475832); mRNA	XM_533041	BOLA1	bolA homolog 1 (E. coli)
CfaAffx.2863.1.S1_at	4.13E-02	1.41	PREDICTED: Canis familiaris similar to Fanconi anemia; complementation group E (LOC608172); mRNA	XM_845108	FANCE	Fanconi anemia, complementation group E
CfaAffx.1478.1.S1_at	3.90E-02	1.41	PREDICTED: Canis familiaris hypothetical LOC144577 (LOC474426); mRNA	XM_531657	LOC474426	hypothetical LOC474426
CfaAffx.26221.1.S1_at	3 30E-02	1.41	Canis lupus familiaris ceroid-lipofuscinosis; neuronal 3 (CLN3); mRNA	NM_001013417	CLN3	ceroid-lipofuscinosis, neuronal 3
Cfa.15994.1.S1_s_at	2.98E-02	1.42	PREDICTED: Canis familiaris similar to Transcription initiation factor TFIID subunit 10 (Transcription initiation factor TFIID 30 kDa subunit) (TAF(II)30) (TAFII-30) (TAFII30) (STAF28); transcript variant 2 (LOC485336); mRNA	XM_858050	TAF10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 30kDa
CfaAffx.28301.1.S1_s_at	5.92E-05	1.67	PREDICTED: Canis familiaris similar to angiopoietin-like 4 protein (LOC476724); mRNA	XM_533928	ANGPTL4	angiopoietin-like 4
Cfa.21036.1.S1_s_at	4.13E-02	1.69	PREDICTED: Canis familiaris similar to aldehyde dehydrogenase 4A1 precursor (LOC612452); mRNA	XM_850179	ALDH4A1	aldehyde dehydrogenase 4 family, member A1
Cfa.449.2.S1_s_at	1 54E-02	1.76	PREDICTED: Canis familiaris similar to ADAM 9 precursor (A disintegrin and metalloproteinase domain 9) (Metalloprotease/disintegrin/cysteine-rich protein 9) (Myeloma cell metalloproteinase) (Meltrin gamma) (Cellular disintegrin-related protein) (LOC475579); mRNA	XM_532798	ADAM9	ADAM metallopeptidase domain 9 (meltrin gamma)
CfaAffx.18769.1.S1_s_at	3 66E-02	1.95	PREDICTED: Canis familiaris similar to Mitochondrial carnitine/acylcarnitine carrier protein (Carnitine/acylcarnitine translocase) (CAC); transcript variant 3 (LOC484774); mRNA	XM_858026	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha
Cfa.2282.1.S1_at	4.77E-02	2.17	PREDICTED: Canis familiaris similar to [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; mitochondrial precursor (Pyruvate dehydrogenase kinase isoform 4) (LOC482310); mRNA	XM_539427	PDK4	pyruvate dehydrogenase kinase, isozyme 4
Cfa.431.2.A1_s_at	1 55E-02	2.19	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP); transcript variant 2 (LOC474720); mRNA	XM_859657	ADFP	adipose differentiation-related protein
CfaAffx.3314.1.S1_at	1 33E-02	2.23	PREDICTED: Canis familiaris similar to Adipophilin (Adipose differentiation-related protein) (ADRP); transcript variant 1 (LOC474720); mRNA	XM_531946	ADFP	adipose differentiation-related protein

Conjugate alpha-linoleic acid in MeOH (CANINE-2); **6** records FC cutoff: 1.3; P-val cutofff: 0.05

Probe	P-Value	Fold-Change	Top BLAST Annot.	Top Hit Accn.	Gene Symbol	Gene Desc.
CfaAffx.31027.1.S1_s_at	4.79E-02	-1.9	PREDICTED: Canis familiaris similar to nuclear factor of activated T-cells 5 isoform b; transcript variant 1 (LOC489734); mRNA	XM_546854	NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive

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CfaAffx.1277.1.S1_s_at	2.05E-02	-1.53	PREDICTED: Pan troglodytes toll-like receptor adaptor molecule 2; transcript variant 3 (TICAM2); mRNA	XM_001147833	TMED7	transmembrane emp24 protein transport domain containing 7
CfaAffx.1277.1.S1_at	2.01E-02	-1.39	PREDICTED: Canis familiaris similar to transmembrane emp24 protein transport domain containing 7; transcript variant 3 (LOC481436); mRNA	XM_853517	TMED7	transmembrane emp24 protein transport domain containing 7
CfaAffx.3039.1.S1_s_at	4.27E-02	1.35	PREDICTED: Canis familiaris similar to Peptidyl-prolyl cis-trans isomerase like 1 (PPIase) (Rotamase); transcript variant 1 (LOC474891); mRNA	XM_532126	PPIL1	peptidylprolyl isomerase (cyclophilin)-like 1
CfaAffx.25112.1.S1_at	4.32E-02	1.35	PREDICTED: Equus caballus vacuolar protein sorting 13 homolog D (S. cerevisiae) (VPS13D); mRNA	XM_001490932	VPS13D	vacuolar protein sorting 13 homolog D (S. cerevisiae)
CfaAffx.29815.1.S1_s_at	4.97E-02	1.35	PREDICTED: Canis familiaris similar to ubiquinol-cytochrome c reductase subunit; transcript variant 1 (LOC611791); mRNA	XM_849498	LOC611791	similar to ubiquinol-cytochrome c reductase subunit

Table 6:Genes Differentially Expressed in lymphocytes from Fat Animals fed on either a high protein diet or the same diet with added fish oil.

diet71341 vs 66934 d113 allgenes FC cutoff: 1.3; P-val cutofff: 0.1; Q-val cutoff: 1								
#samples in group-1 (High protein Diet with Fish Oil): 5 group-2 (High Protein Diet): 4								
Fold change > 1 implies probes are UP regulated in DIET71341 samples.								
Probe	**P-Value**	**Q-Value**	**Fold-Change**	**Top BLAST Annot.**	**Match Perc.**	**Top Hit Accn.**	**Gene Symbol**	**Gene Desc.**
Cfa.5598.1.A1_s_at	7.31E-02	4.54E-01	1.31	PREDICTED: Canis familiaris similar to Septin-2 (NEDD5 protein homolog) (LOC487886); mRNA	98.4	XM_846816	2-Sep	septin 2
Cfa.19142.1.S1_s_at	7.55E-02	4.54E-01	1.59	PREDICTED: Equus caballus septin 7 (SEPT7); mRNA	95.8	XM_001500153	7-Sep	septin 7
Cfa.10334.1.A1_at	7.43E-02	4.54E-01	1.35	Homo sapiens septin 11 (SEPT11); mRNA	79.7	NM_018243	11-Sep	septin 11
Cfa.3030.1.A1_at	1.38E-02	4.46E-01	1.41	Mus musculus adult male hippocampus cDNA; RIKEN full-length enriched library; clone:2900054C01 product:unclassifiable; full insert sequence	79.6	AK013682	2900054C01Rik	RIKEN cDNA 2900054C01 gene
CfaAffx.4198.1.S1_at	1.11E-02	4.46E-01	1.33	PREDICTED: Canis familiaris similar to 2-aminoadipic 6-semialdehyde dehydrogenase; transcript variant 1 (LOC482159); mRNA	100	XM_539278	AASDH	aminoadipate-semialdehyde dehydrogenase
Cfa.2510.1.S1_at	2.00E-02	4.46E-01	1.47	PREDICTED: Pan troglodytes aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase (AASDHPPT); mRNA	36.6	XM_508734	AASDHPPT	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase
CfaAffx.6230.1.S1_at	3.76E-02	4.46E-01	0.73	PREDICTED: Canis familiaris similar to aminoadipate-semialdehyde synthase (LOC482429); mRNA	100	XM_539546	AASS	aminoadipate-semialdehyde synthase
Cfa.4754.1.A1_at	4.28E-03	4.46E-01	1.64	PREDICTED: Canis familiaris similar to ATP-binding cassette; sub-family A; member 6 isoform a; transcript variant 1 (LOC480456); mRNA	100	XM_537574	ABCA6	ATP-binding cassette, sub-family A (ABC1), member 6
Cfa.19800.1.S1_s_at	2.47E-02	4.46E-01	1.57	PREDICTED: Canis familiaris similar to ATP-binding cassette sub-family E member 1 (RNase L inhibitor) (Ribonuclease 4 inhibitor) (RNS4I); transcript variant 1 (LOC475454); mRNA	95.9	XM_532679	ABCE1	ATP-binding cassette, sub-family E (OABP), member 1
CfaAffx.27934.1.S1_s_at	4.27E-02	4.47E-01	1.59	PREDICTED: Canis familiaris similar to alpha/beta hydrolase domain containing protein 3 (LOC480177); mRNA	98.6	XM_537301	ABHD3	abhydrolase domain containing 3

Table 6:Genes Differentially Expressed in lymphocytes from Fat Animals fed on either a high protein diet or the same diet with added fish oil.

Cfa.20999.1.S1_s_at	7.52E-02	4.54E-01	1.42	PREDICTED: Canis familiaris similar to abl-interactor 1 isoform c; transcript variant 20 (LOC607247); mRNA	99.2	XM_853138	ABI1	abl-interactor 1
CfaAffx.7474.1.S1_s_at	3.62E-02	4.46E-01	1.53	PREDICTED: Canis familiaris similar to abl-interactor 1 isoform c; transcript variant 12 (LOC607247); mRNA	100	XM_852773	ABI1	abl-interactor 1
CfaAffx.14971.1.S1_s_at	6.13E-02	4.50E-01	0.76	PREDICTED: Canis familiaris similar to ABI gene family; member 3 (NESH) binding protein isoform 2 (LOC478544); mRNA	71.1	XM_535721	ABI3BP	ABI gene family, member 3 (NESH) binding protein
Cfa.10796.1.S1_at	1.46E-02	4.46E-01	1.32	PREDICTED: Canis familiaris similar to actin-binding LIM protein 1 isoform s; transcript variant 2 (LOC477828); mRNA	100	XM_535022	ABLIM1	actin binding LIM protein 1
Cfa.18661.1.S1_s_at	1.43E-02	4.46E-01	0.75	PREDICTED: Canis familiaris similar to actin-binding LIM protein 1 isoform s; transcript variant 3 (LOC477828); mRNA	100	XM_859794	ABLIM1	actin binding LIM protein 1
CfaAffx.18010.1.S1_s_at	4.98E-02	4.48E-01	1.37	PREDICTED: Canis familiaris similar to actin-binding LIM protein 1 isoform s; transcript variant 4 (LOC477828); mRNA	100	XM_859813	ABLIM1	actin binding LIM protein 1
Cfa.18249.1.S1_s_at	2.52E-02	4.46E-01	0.76	PREDICTED: Canis familiaris similar to striated muscle activator of Rho-dependent signaling (LOC481999); mRNA	98.3	XM_539120	ABRA	actin-binding Rho activating protein
CfaAffx.7032.1.S1_at	2.21E-02	4.46E-01	0.73	PREDICTED: Canis familiaris similar to ankyrin repeat and BTB (POZ) domain containing 1 isoform 2 (LOC609299); mRNA	100	XM_846538	ABTB1	ankyrin repeat and BTB (POZ) domain containing 1
Cfa.1658.1.S1_a_at	1.30E-02	4.46E-01	1.43	PREDICTED: Canis familiaris similar to Acyl-CoA dehydrogenase; medium-chain specific; mitochondrial precursor (MCAD) (LOC490207); mRNA	100	XM_547328	ACADM	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain
CfaAffx.31225.1.S1_s_at	3.89E-02	4.46E-01	1.35	PREDICTED: Canis familiaris similar to Acyl-CoA dehydrogenase; medium-chain specific; mitochondrial precursor (MCAD) (LOC490207); mRNA	100	XM_547328	ACADM	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain

Table 6:Genes Differentially Expressed in lymphocytes from Fat Animals fed on either a high protein diet or the same diet with added fish oil.

Cfa.1502.1.S1_at	2.05E-02	4.46E-01	1.45	PREDICTED: Canis familiaris similar to Acetyl-CoA acetyltransferase; mitochondrial precursor (Acetoacetyl-CoA thiolase) (T2) (LOC489421); mRNA	94.6	XM_546539	ACAT1	acetyl-Coenzyme A acetyltransferase 1
CfaAffx.25757.1.S1_at	2.69E-02	4.46E-01	0.7	PREDICTED: Canis familiaris similar to Peroxisomal acyl-coenzyme A thioester hydrolase 2a (Peroxisomal long-chain acyl-coA thioesterase 2) (ZAP128) (CTE-Ia) (LOC490770); mRNA	100	XM_547892	ACOT2	acyl-CoA thioesterase 2
CfaAffx.11797.1.S1_s_at	2.90E-02	4.46E-01	0.76	PREDICTED: Canis familiaris similar to Acyl-coenzyme A oxidase 2; peroxisomal (Branched-chain acyl-CoA oxidase) (BRCACox) (Trihydroxycoprostanoyl-CoA oxidase) (THCCox) (THCA-CoA oxidase) (LOC484710); mRNA	100	XM_541826	ACOX2	acyl-Coenzyme A oxidase 2, branched chain
CfaAffx.10344.1.S1_at	6.48E-03	4.46E-01	0.56	PREDICTED: Canis familiaris similar to acid phosphatase; prostate isoform 1 (LOC485662); mRNA	99.8	XM_542782	ACPP	acid phosphatase, prostate
CfaAffx.27545.1.S1_at	1.66E-02	4.46E-01	0.73	PREDICTED: Canis familiaris similar to Acetyl-coenzyme A synthetase (Acetate--CoA ligase) (Acyl-activating enzyme) (Acetyl-CoA synthetase) (ACS) (AceCS) (LOC609009); mRNA	100	XM_846187	ACSM5	acyl-CoA synthetase medium-chain family member 5
Cfa.10333.1.A1_at	8.49E-02	4.57E-01	1.6	PREDICTED: Canis familiaris similar to CG6432-PA (LOC475414); mRNA	100	XM_532637	ACSS3	acyl-CoA synthetase short-chain family member 3
CfaAffx.17722.1.S1_s_at	4.28E-03	4.46E-01	1.55	PREDICTED: Canis familiaris similar to Actin-like protein 6A (53 kDa BRG1-associated factor A) (Actin-related protein Baf53a) (ArpNbeta); transcript variant 3 (LOC478637); mRNA	99.6	XM_843131	ACTL6A	actin-like 6A
Cfa.17841.1.S1_s_at	1.04E-02	4.46E-01	0.71	PREDICTED: Canis familiaris similar to actinin; alpha 4; transcript variant 7 (LOC484526); mRNA	96.3	XM_862287	ACTN4	actinin, alpha 4

Table 6:Genes Differentially Expressed in lymphocytes from Fat Animals fed on either a high protein diet or the same diet with added fish oil.

Cfa.10338.1.S1_at	1.22E-02	4.46E-01	1.31	PREDICTED: Canis familiaris similar to Actin-related protein 10 (hARP11); transcript variant 1 (LOC480337); mRNA	99.4	XM_537459	ACTR10	actin-related protein 10 homolog (S. cerevisiae)
CfaAffx.11001.1.S1_at	2.43E-02	4.46E-01	1.45	PREDICTED: Bos taurus ARP6 actin-related protein 6 homolog (yeast); mRNA (cDNA clone MGC:166308 IMAGE:8625002); complete cds	75.6	BC146238	ACTR6	ARP6 actin-related protein 6 homolog (yeast)
Cfa.9426.1.S1_s_at	5.09E-02	4.48E-01	1.33	PREDICTED: Canis familiaris similar to ARP6 actin-related protein 6 homolog; transcript variant 2 (LOC475439); mRNA	81.1	XM_847830	ACTR6	ARP6 actin-related protein 6 homolog (yeast)
CfaAffx.20774.1.S1_at	4.16E-03	4.46E-01	0.7	PREDICTED: Canis familiaris similar to a disintegrin and metalloproteinase domain 8 precursor (LOC491699); mRNA	73.5	XM_548820	ADAM8	ADAM metallopeptidase domain 8
Cfa.2566.1.S1_s_at	6.87E-02	4.53E-01	0.75	PREDICTED: Canis familiaris similar to ADAMTS-like 3 (LOC479060); mRNA	99.6	XM_536209	ADAMTSL3	ADAMTS-like 3
Cfa.1269.1.S1_at	2.35E-02	4.46E-01	1.33	PREDICTED: Canis familiaris similar to adducin 3 (gamma) isoform b; transcript variant 11 (LOC486881); mRNA	94.5	XM_859189	ADD3	adducin 3 (gamma)
CfaAffx.16720.1.S1_s_at	3.07E-02	4.46E-01	1.45	PREDICTED: Canis familiaris similar to adducin 3 (gamma) isoform b; transcript variant 10 (LOC486881); mRNA	98.7	XM_859166	ADD3	adducin 3 (gamma)
CfaAffx.11851.1.S1_at	2.69E-02	4.46E-01	0.74	PREDICTED: Canis familiaris similar to alcohol dehydrogenase; iron containing; 1; transcript variant 3 (LOC477899); mRNA	100	XM_844355	ADHFE1	alcohol dehydrogenase, iron containing, 1
Cfa.19041.1.S1_at	3.78E-02	4.46E-01	1.61	PREDICTED: Canis familiaris similar to adenosine kinase; transcript variant 1 (LOC479253); mRNA	51.5	XM_536396	ADK	adenosine kinase
Cfa.3770.1.S1_at	1.67E-02	4.46E-01	1.33	C.familiaris mRNA for beta2-adrenergic receptor	94.7	X94608	ADRB2	adrenergic, beta-2-, receptor, surface
Cfa.17138.1.S1_at	4.35E-02	4.47E-01	0.75	PREDICTED: Canis familiaris similar to Beta-adrenergic receptor kinase 1 (Beta-ARK-1) (G-protein coupled receptor kinase 2); transcript variant 4 (LOC483701); mRNA	100	XM_859935	ADRBK1	adrenergic, beta, receptor kinase 1

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Cfa.12520.1.A1_s_at	1.64E-02	4.46E-01	1.45	PREDICTED: Canis familiaris similar to adenylosuccinate lyase; transcript variant 1 (LOC474499); mRNA	99.5	XM_531727	ADSL	adenylosuccinate lyase
Cfa.19535.1.S1_at	2.26E-02	4.46E-01	1.38	PREDICTED: Canis familiaris similar to Adenylosuccinate synthetase 2 (IMP--aspartate ligase 2) (AdSS 2) (AMPSase 2) (LOC480098); mRNA	92.6	XM_537220	ADSS	adenylosuccinate synthase
CfaAffx.18582.1.S1_at	1.60E-02	4.46E-01	0.72	Anopheles gambiae str. PEST AGAP004931-PA (AgaP_AGAP004931) mRNA; complete cds	43.8	XM_315018	AgaP_AGAP004931	AGAP004931-PA
CfaAffx.2073.1.S1_at	8.58E-02	4.58E-01	1.41	PREDICTED: Canis familiaris similar to 1-acyl-sn-glycerol-3-phosphate acyltransferase delta (1-AGP acyltransferase 4) (1-AGPAT 4) (Lysophosphatidic acid acyltransferase-delta) (LPAAT-delta) (1-acylglycerol-3-phosphate O-acyltransferase 4) (LOC612306); mRNA	100	XM_850050	AGPAT4	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)
Cfa.13638.1.A1_at	6.47E-02	4.51E-01	1.3	PREDICTED: Pan troglodytes alkyldihydroxyacetone phosphate synthase; transcript variant 3 (AGPS); mRNA	90	XM_001154211	AGPS	alkylglycerone phosphate synthase
Cfa.19737.1.S1_at	6.11E-02	4.50E-01	1.53	PREDICTED: Homo sapiens aryl hydrocarbon receptor; mRNA (cDNA clone MGC:87401 IMAGE:30342582); complete cds	64.8	BC070080	AHR	aryl hydrocarbon receptor
Cfa.2120.2.S1_at	3.55E-02	4.46E-01	1.68	PREDICTED: Canis familiaris similar to androgen-induced 1 (LOC611677); mRNA	53.6	XM_849376	AIG1	androgen-induced 1
Cfa.19796.1.S1_at	2.90E-02	4.46E-01	1.35	PREDICTED: Canis familiaris similar to fused toes homolog; transcript variant 1 (LOC478126); mRNA	98.5	XM_535302	AKTIP	AKT interacting protein
Cfa.21376.1.S1_s_at	7.08E-02	4.54E-01	0.77	PREDICTED: Canis familiaris similar to aldehyde dehydrogenase 4A1 precursor (LOC612452); mRNA	97.9	XM_850179	ALDH4A1	aldehyde dehydrogenase 4 family, member A1
Cfa.21036.1.S1_s_at	6.25E-02	4.50E-01	1.43	PREDICTED: Canis familiaris similar to aldehyde dehydrogenase 4A1 precursor (LOC612452); mRNA	100	XM_850179	ALDH4A1	aldehyde dehydrogenase 4 family, member A1
CfaAffx.1496.1.S1_s_at	1.50E-02	4.46E-01	1.45	PREDICTED: Canis familiaris similar to antiquitin (LOC481486); mRNA	98.9	XM_538607	ALDH7A1	aldehyde dehydrogenase 7 family, member A1

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Cfa.403.1.A1_s_at	1.01E-02	4.46E-01	1.43	PREDICTED: Canis familiaris similar to antiquitin (LOC481486); mRNA	99.3	XM_538607	ALDH7A1	aldehyde dehydrogenase 7 family, member A1
Cfa.403.1.A1_at	3.72E-02	4.46E-01	1.66	PREDICTED: Canis familiaris similar to antiquitin (LOC481486); mRNA	100	XM_538607	ALDH7A1	aldehyde dehydrogenase 7 family, member A1
Cfa.12285.1.A1_s_at	4.31E-02	4.47E-01	1.42	PREDICTED: Canis familiaris similar to alpha 1;3-mannosyltransferase ALG2 isoform 1 (LOC474780); mRNA	99.1	XM_532010	ALG2	asparagine-linked glycosylation 2 homolog (S. cerevisiae, alpha-1,3-mannosyltransferase)
Cfa.12285.1.A1_at	2.08E-02	4.46E-01	1.6	PREDICTED: Canis familiaris similar to alpha 1;3-mannosyltransferase ALG2 isoform 1 (LOC474780); mRNA	100	XM_532010	ALG2	asparagine-linked glycosylation 2 homolog (S. cerevisiae, alpha-1,3-mannosyltransferase)
CfaAffx.4666.1.S1_at	3.41E-02	4.46E-01	1.34	PREDICTED: Canis familiaris similar to alpha 1;3-mannosyltransferase ALG2 isoform 1 (LOC474780); mRNA	100	XM_532010	ALG2	asparagine-linked glycosylation 2 homolog (S. cerevisiae, alpha-1,3-mannosyltransferase)
CfaAffx.28581.1.S1_at	3.86E-02	4.46E-01	1.77	PREDICTED: Canis familiaris similar to Dolichyl pyrophosphate Man9GlcNAc2 alpha-1;3-glucosyltransferase (Dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase) (LOC609974); mRNA	100	XM_847338	ALG6	asparagine-linked glycosylation 6 homolog (S. cerevisiae, alpha-1,3-glucosyltransferase)
Cfa.1139.1.A1_at	3.86E-02	4.46E-01	1.36	PREDICTED: Pan troglodytes hypothetical LOC459598; transcript variant 4 (LOC459598); mRNA	92	XM_515780	AMMECR1L	AMME chromosomal region gene 1-like
Cfa.17250.1.S1_s_at	1.74E-02	4.46E-01	0.74	PREDICTED: Canis familiaris similar to Anaphase promoting complex subunit 2 (APC2) (Cyclosome subunit 2) (LOC491236); mRNA	99.7	XM_548357	ANAPC2	anaphase promoting complex subunit 2

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CfaAffx.9522.1.S1_s_at	8.48E-02	4.57E-01	0.72	PREDICTED: Canis familiaris similar to ankyrin 1 isoform 3 (LOC482842); mRNA	100	XM_539957	ANK1	ankyrin 1, erythrocytic
Cfa.9634.1.A1_at	3.87E-02	4.46E-01	1.48	PREDICTED: Canis familiaris similar to ankyrin repeat; family A (RFXANK-like); 2; transcript variant 2 (LOC478097); mRNA	95.8	XM_857185	ANKRA2	ankyrin repeat, family A (RFXANK-like), 2
CfaAffx.13070.1.S1_at	9.25E-02	4.62E-01	1.37	PREDICTED: Canis familiaris similar to ankyrin repeat; family A (RFXANK-like); 2; transcript variant 1 (LOC478097); mRNA	100	XM_535273	ANKRA2	ankyrin repeat, family A (RFXANK-like), 2
Cfa.17993.1.S1_at	9.77E-02	4.64E-01	1.33	PREDICTED: Canis familiaris similar to ankyrin repeat domain 13C (LOC490215); mRNA	63	XM_547336	ANKRD13C	ankyrin repeat domain 13C
CfaAffx.18265.1.S1_at	7.43E-02	4.54E-01	1.32	PREDICTED: Canis familiaris similar to acidic (leucine-rich) nuclear phosphoprotein 32 family; member E (LOC475834); mRNA	100	XM_533043	ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
Cfa.3774.1.A1_s_at	8.84E-02	4.59E-01	0.66	PREDICTED: Canis familiaris aminopeptidase N; transcript variant 3 (APN); mRNA	100	XM_854733	ANPEP	alanyl (membrane) aminopeptidase
Cfa.3796.1.A1_s_at	1.56E-03	4.46E-01	0.76	C.familiaris mRNA for annexin XIIIb	97.7	X80209	ANXA13	annexin A13
Cfa.229.1.S1_at	7.42E-02	4.54E-01	1.34	PREDICTED: Canis familiaris similar to amine oxidase (flavin containing) domain 2 isoform a; transcript variant 2 (LOC478193); mRNA	100	XM_861517	AOF2	amine oxidase (flavin containing) domain 2
CfaAffx.11074.1.S1_s_at	6.98E-02	4.53E-01	1.35	PREDICTED: Canis familiaris similar to apoptosis inhibitor 5; transcript variant 2 (LOC483413); mRNA	100	XM_851505	API5	apoptosis inhibitor 5
Cfa.11310.1.A1_at	1.86E-02	4.46E-01	1.33	PREDICTED: Canis familiaris similar to APAF1 interacting protein (LOC475943); mRNA	100	XM_533154	APIP	APAF1 interacting protein
Cfa.2457.1.S1_at	4.69E-02	4.48E-01	1.41	PREDICTED: Pan troglodytes amyloid beta precursor protein-binding protein 2 (APPBP2); mRNA	89.2	XM_001136833	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2
Cfa.20988.1.S1_s_at	8.60E-02	4.58E-01	1.48	PREDICTED: Canis familiaris similar to archain; transcript variant 2 (LOC479415); mRNA	96	XM_855468	ARCN1	archain 1

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CfaAffx.17840.1.S1_s_at	9.57E-02	4.63E-01	1.54	PREDICTED: Canis familiaris similar to AT rich interactive domain 4B isoform 1; transcript variant 3 (LOC488959); mRNA	100	XM_843623	ARID4B	AT rich interactive domain 4B (RBP1-like)
Cfa.1032.1.A1_at	8.27E-03	4.46E-01	1.32	PREDICTED: Canis familiaris similar to ADP-ribosylation factor-like 2 binding protein isoform 1 (LOC611248); mRNA	99.8	XM_848889	ARL2BP	ADP-ribosylation factor-like 2 binding protein
CfaAffx.13885.1.S1_at	2.68E-03	4.46E-01	1.42	PREDICTED: Canis familiaris similar to ADP-ribosylation factor-like 2 binding protein isoform 1 (LOC611248); mRNA	100	XM_848889	ARL2BP	ADP-ribosylation factor-like 2 binding protein
Cfa.603.1.S1_at	2.60E-02	4.46E-01	1.65	PREDICTED: Canis familiaris similar to ADP-ribosylation factor-like 6 interacting protein 2; transcript variant 7 (LOC475728); mRNA	97.7	XM_858541	ARL6IP2	ADP-ribosylation factor-like 6 interacting protein 2
Cfa.9452.1.S1_at	3.21E-02	4.46E-01	1.56	PREDICTED: Canis familiaris similar to ADP-ribosylation factor-like 6 interacting protein 5 (LOC476559); mRNA	96	XM_533764	ARL6IP5	ADP-ribosylation-like factor 6 interacting protein 5
Cfa.20059.1.A1_at	9.71E-03	4.46E-01	1.48	PREDICTED: Canis familiaris similar to ADP-ribosylation factor-like 6 interacting protein 5 (LOC476559); mRNA	99.1	XM_533764	ARL6IP5	ADP-ribosylation-like factor 6 interacting protein 5
Cfa.1737.1.A1_at	1.41E-02	4.46E-01	1.63	Bos taurus armadillo repeat containing 1; mRNA (cDNA clone MGC:127965 IMAGE:7954315); complete cds	33.3	BC103407	ARMC1	armadillo repeat containing 1
CfaAffx.22238.1.S1_at	6.76E-02	4.52E-01	0.76	PREDICTED: Canis familiaris similar to armadillo repeat containing 6 (LOC484811); mRNA	93.1	XM_541927	ARMC6	armadillo repeat containing 6
Cfa.18960.1.S1_s_at	3.05E-02	4.46E-01	1.44	PREDICTED: Canis familiaris similar to armadillo repeat containing 8; transcript variant 15 (LOC485684); mRNA	99.2	XM_860147	ARMC8	armadillo repeat containing 8
CfaAffx.12981.1.S1_at	7.52E-03	4.46E-01	1.43	PREDICTED: Canis familiaris similar to Aryl hydrocarbon receptor nuclear translocator-like protein 1 (Brain and muscle ARNT-like 1) (Member of PAS protein 3) (Basic-helix-loop-helix PAS orphan MOP3) (bHLH-PAS protein JAP3); transcript variant 2 (LOC476860); mRNA	98.8	XM_846757	ARNTL	aryl hydrocarbon receptor nuclear translocator-like

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Cfa.1205.1.S1_at	1.45E-02	4.46E-01	1.39	PREDICTED: Canis familiaris similar to Aryl hydrocarbon receptor nuclear translocator-like protein 1 (Brain and muscle ARNT-like 1) (Member of PAS protein 3) (Basic-helix-loop-helix PAS orphan MOP3) (bHLH-PAS protein JAP3); transcript variant 6 (LOC476860); mRNA	99.8	XM_859353	ARNTL	aryl hydrocarbon receptor nuclear translocator-like
CfaAffx.17298.1.S1_at	5.37E-02	4.50E-01	2.01	TPA_inf: Canis familiaris mRNA for arylsulfatase G (arsg gene)	99.7	BN000758	ARSG	arylsulfatase G
CfaAffx.26949.1.S1_s_at	8.35E-02	4.56E-01	0.77	PREDICTED: Canis familiaris similar to ankyrin repeat and SOCS box-containing protein 2 (predicted); transcript variant 2 (LOC490836); mRNA	50	XM_849378	ASB2	ankyrin repeat and SOCS box-containing 2
Cfa.21224.1.S1_s_at	2.40E-02	4.46E-01	1.4	PREDICTED: Canis familiaris similar to Ankyrin repeat and SOCS box protein 3 (ASB-3) (LOC474592); mRNA	100	XM_531821	ASB3	ankyrin repeat and SOCS box-containing 3
Cfa.2140.1.A1_s_at	1.32E-02	4.46E-01	1.37	PREDICTED: Canis familiaris similar to ASF1 anti-silencing function 1 homolog A (LOC476273); mRNA	99.8	XM_533479	ASF1A	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)
Cfa.20089.1.S1_s_at	5.14E-03	4.46E-01	1.42	PREDICTED: Canis familiaris similar to CG17486-PA.3 (LOC478838); mRNA	99.3	XM_536000	ASNSD1	asparagine synthetase domain containing 1
Cfa.10831.1.S1_s_at	2.03E-03	4.46E-01	1.32	PREDICTED: Canis familiaris similar to CG17486-PA.3 (LOC478838); mRNA	100	XM_536000	ASNSD1	asparagine synthetase domain containing 1
Cfa.8442.1.A1_s_at	5.20E-02	4.48E-01	1.37	PREDICTED: Canis familiaris similar to asparaginase-like 1 protein (LOC483789); mRNA	96.9	XM_540910	ASRGL1	asparaginase like 1
Cfa.8442.1.A1_at	7.80E-02	4.55E-01	1.33	PREDICTED: Canis familiaris similar to asparaginase-like 1 protein (LOC483789); mRNA	100	XM_540910	ASRGL1	asparaginase like 1
CfaAffx.2390.1.S1_at	2.17E-02	4.46E-01	1.7	PREDICTED: Canis familiaris similar to two AAA domain containing protein; transcript variant 2 (LOC475090); mRNA	98.3	XM_845427	ATAD2	ATPase family, AAA domain containing 2
CfaAffx.29389.1.S1_s_at	3.16E-02	4.46E-01	1.3	PREDICTED: Canis familiaris similar to AAA-ATPase TOB3 (LOC479568); mRNA	100	XM_536708	ATAD3A	ATPase family, AAA domain containing 3A

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Cfa.15399.1.A1_at	4.56E-02	4.47E-01	1.55	PREDICTED: Canis familiaris similar to arginyltransferase 1 isoform 2; transcript variant 4 (LOC486919); mRNA	100	XM_860764	ATE1	arginyltransferase 1
CfaAffx.28602.1.S1_s_at	3.01E-02	4.46E-01	1.58	PREDICTED: Canis familiaris similar to APG4 autophagy 4 homolog C; transcript variant 1 (LOC489561); mRNA	100	XM_546681	ATG4C	ATG4 autophagy related 4 homolog C (S. cerevisiae)
CfaAffx.10676.1.S1_at	2.86E-02	4.46E-01	0.73	PREDICTED: Canis familiaris similar to CG16965-PA (LOC483395); mRNA	99.8	XM_540514	ATHL1	ATH1, acid trehalase-like 1 (yeast)
CfaAffx.10130.1.S1_s_at	5.91E-02	4.50E-01	1.55	PREDICTED: Canis familiaris similar to calcium-transporting ATPase 2C1 isoform 1a; transcript variant 8 (LOC477066); mRNA	100	XM_858651	ATP2C1	ATPase, Ca++ transporting, type 2C, member 1
CfaAffx.12618.1.S1_at	3.70E-02	4.46E-01	1.48	PREDICTED: Canis familiaris similar to ataxia telangiectasia and Rad3 related protein; transcript variant 4 (LOC477101); mRNA	100	XM_860680	ATR	ataxia telangiectasia and Rad3 related
CfaAffx.26396.1.S1_s_at	5.95E-03	4.46E-01	1.34	PREDICTED: Canis familiaris similar to transcriptional regulator ATRX isoform 1; transcript variant 7 (LOC480963); mRNA	37.7	XM_855075	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)
CfaAffx.26397.1.S1_s_at	5.11E-02	4.48E-01	1.42	PREDICTED: Canis familiaris similar to transcriptional regulator ATRX isoform 1; transcript variant 7 (LOC480963); mRNA	55	XM_855075	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)
CfaAffx.26395.1.S1_s_at	4.32E-02	4.47E-01	1.48	PREDICTED: Canis familiaris similar to transcriptional regulator ATRX isoform 1; transcript variant 2 (LOC480963); mRNA	68.8	XM_854886	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)
Cfa.10959.1.A1_at	1.23E-02	4.46E-01	1.4	PREDICTED: Canis familiaris similar to Ataxin-10 (Spinocerebellar ataxia type 10 protein) (Brain protein E46 homolog); transcript variant 3 (LOC474467); mRNA	100	XM_851945	ATXN10	ataxin 10

Table 6:Genes Differentially Expressed in lymphocytes from Fat Animals fed on either a high protein diet or the same diet with added fish oil.

Cfa.20370.1.S1_s_at	7.75E-02	4.55E-01	1.36	PREDICTED: Canis familiaris similar to Methylglutaconyl-CoA hydratase; mitochondrial precursor (AU-specific RNA-binding enoyl-CoA hydratase) (AU-binding protein/enoyl-CoA hydratase) (LOC476348); mRNA	98.3	XM_533549	AUH	AU RNA binding protein/enoyl-Coenzyme A hydratase
CfaAffx.17580.1.S1_s_at	1.67E-02	4.46E-01	1.31	PREDICTED: Canis familiaris similar to UDP-GalNAc:betaGlcNAc beta 1;3-galactosaminyltransferase; polypeptide 2 (LOC479196); mRNA	100	XM_536338	B3GALNT2	beta-1,3-N-acetylgalactosaminyltransferase 2
CfaAffx.5578.1.S1_s_at	6.05E-02	4.50E-01	1.35	PREDICTED: Canis familiaris similar to UDP-GlcNAc:betaGal beta-1;3 N-acetylglucosaminyltransferase 1 (LOC474611); mRNA	99.8	XM_531841	B3GNT2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2
CfaAffx.12727.1.S1_at	4.14E-02	4.46E-01	0.76	PREDICTED: Canis familiaris similar to beta-1;3-N-acetylglucosaminyltransferase bGnT-4 (LOC486255); mRNA	100	XM_543380	B3GNT4	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4
CfaAffx.1759.1.S1_s_at	2.12E-02	4.46E-01	0.69	PREDICTED: Canis familiaris similar to HLA-B associated transcript 2; transcript variant 2 (LOC481713); mRNA	91.1	XM_844311	BAT2	HLA-B associated transcript 2
Cfa.7385.1.S1_s_at	9.73E-02	4.64E-01	0.77	PREDICTED: Canis familiaris similar to HLA-B associated transcript 2; transcript variant 1 (LOC481713); mRNA	98.1	XM_538834	BAT2	HLA-B associated transcript 2
Cfa.21524.1.S1_s_at	8.54E-03	4.46E-01	0.76	PREDICTED: Canis familiaris similar to HLA-B associated transcript 2; transcript variant 4 (LOC481713); mRNA	98.8	XM_853603	BAT2	HLA-B associated transcript 2
Cfa.18910.1.S1_s_at	2.80E-02	4.46E-01	0.7	PREDICTED: Canis familiaris similar to Bromodomain adjacent to zinc finger domain 2A (Transcription termination factor-I interacting protein 5) (TTF-I interacting protein 5) (Tip5) (hWALp3); transcript variant 1 (LOC481116); mRNA	100	XM_538237	BAZ2A	bromodomain adjacent to zinc finger domain, 2A

Table 6:Genes Differentially Expressed in lymphocytes from Fat Animals fed on either a high protein diet or the same diet with added fish oil.

CfaAffx.7103.1.S1_at	4.26E-02	4.47E-01	1.57	PREDICTED: Canis familiaris similar to Bardet-Biedl syndrome 7 protein isoform b; transcript variant 4 (LOC476092); mRNA	100	XM_852128	BBS7	Bardet-Biedl syndrome 7
Cfa.13280.2.S1_s_at	3.89E-02	4.46E-01	0.72	PREDICTED: Canis familiaris similar to breast cancer anti-estrogen resistance 1 (LOC479648); mRNA	100	XM_847859	BCAR1	breast cancer anti-estrogen resistance 1
Cfa.11286.1.A1_at	1.13E-04	4.46E-01	1.45	PREDICTED: Canis familiaris similar to 2-oxoisovalerate dehydrogenase beta subunit; mitochondrial precursor (Branched-chain alpha-keto acid dehydrogenase E1 component beta chain) (BCKDH E1-beta) (LOC474978); mRNA	93.7	XM_532213	BCKDHB	branched chain keto acid dehydrogenase E1, beta polypeptide
Cfa.18456.1.S1_s_at	1.05E-02	4.46E-01	1.59	PREDICTED: Canis familiaris similar to 2-oxoisovalerate dehydrogenase beta subunit; mitochondrial precursor (Branched-chain alpha-keto acid dehydrogenase E1 component beta chain) (BCKDH E1-beta) (LOC474978); mRNA	99.8	XM_532213	BCKDHB	branched chain keto acid dehydrogenase E1, beta polypeptide
Cfa.21307.1.S1_at	4.62E-02	4.47E-01	1.46	PREDICTED: Canis familiaris similar to B cell lymphoma/leukemia 10 (B-cell CLL/lymphoma 10) (Bcl-10) (CED-3/ICH-1 prodomain homologous E10-like regulator) (CIPER) (CARD-containing molecule enhancing NFkappaB) (Cellular homolog of vCARMEN) (cCARMEN) (Mammalian CARD-containing ... (LOC490183); mRNA	70.4	XM_547304	BCL10	B-cell CLL/lymphoma 10

Table 6:Genes Differentially Expressed in lymphocytes from Fat Animals fed on either a high protein diet or the same diet with added fish oil.

				PREDICTED: Canis familiaris similar to B cell lymphoma/leukemia 10 (B-cell CLL/lymphoma 10) (Bcl-10) (CED-3/ICH-1 prodomain homologous E10-like regulator) (CIPER) (CARD-containing molecule enhancing NFkappaB) (Cellular homolog of vCARMEN) (cCARMEN) (Mammalian CARD-containing ...				
CfaAffx.31062.1.S1_s_at	5.82E-02	4.50E-01	1.37	(LOC490183); mRNA	98.6	XM_547304	BCL10	B-cell CLL/lymphoma 10
CfaAffx.25560.1.S1_at	9.77E-02	4.64E-01	0.68	PREDICTED: Canis familiaris similar to B-cell CLL/lymphoma 7C; transcript variant 3 (LOC479774); mRNA	100	XM_843792	BCL7C	B-cell CLL/lymphoma 7C
Cfa.3934.1.S1_at	9.58E-02	4.63E-01	1.33	PREDICTED: Canis familiaris similar to Bcl-2-associated transcription factor 1 (Btf); transcript variant 10 (LOC483999); mRNA	98.4	XM_855478	BCLAF1	BCL2-associated transcription factor 1
Cfa.21584.1.S1_s_at	1.96E-02	4.46E-01	1.61	PREDICTED: Canis familiaris similar to Bcl-2-associated transcription factor 1 (Btf); transcript variant 7 (LOC483999); mRNA	100	XM_855346	BCLAF1	BCL2-associated transcription factor 1
CfaAffx.1327.1.S1_s_at	8.72E-02	4.59E-01	1.47	PREDICTED: Canis familiaris similar to Bcl-2-associated transcription factor 1 (Btf); transcript variant 10 (LOC483999); mRNA	100	XM_855478	BCLAF1	BCL2-associated transcription factor 1
Cfa.4498.2.A1_at	9.25E-03	4.46E-01	1.4	PREDICTED: Pan troglodytes brain expressed X-linked 2; transcript variant 1 (BEX2); mRNA	84.5	XM_001136246	BEX2	brain expressed X-linked 2
CfaAffx.15522.1.S1_s_at	7.00E-02	4.53E-01	1.35	PREDICTED: Canis familiaris similar to BH3 interacting domain death agonist isoform 1 (LOC486607); mRNA	99.8	XM_543733	BID	BH3 interacting domain death agonist
Cfa.17984.1.S1_at	9.10E-02	4.60E-01	1.56	PREDICTED: Canis familiaris similar to Myc box dependent interacting protein 1 (Bridging integrator 1) (Amphiphysin-like protein) (Amphiphysin II) (Box-dependent myc-interacting protein-1) (LOC483870); mRNA	100	XM_540990	BIN1	bridging integrator 1

Table 6:Genes Differentially Expressed in lymphocytes from Fat Animals fed on either a high protein diet or the same diet with added fish oil.

Cfa.21359.1.S1_s_at	3.60E-02	4.46E-01	1.59	PREDICTED: Canis familiaris similar to Myc box dependent interacting protein 1 (Bridging integrator 1) (Amphiphysin-like protein) (Amphiphysin II) (Box-dependent myc-interacting protein-1) (LOC483870); mRNA	100	XM_540990	BIN1	bridging integrator 1
Cfa.10357.1.A1_at	7.91E-02	4.55E-01	1.38	PREDICTED: Bos taurus similar to Bloom syndrome protein (BLM); mRNA	94.4	XM_613809	BLM	Bloom syndrome
CfaAffx.13430.1.S1_s_at	2.95E-02	4.46E-01	1.62	PREDICTED: Canis familiaris similar to B-cell linker (LOC486814); mRNA	100	XM_543943	BLNK	B-cell linker
Cfa.8257.1.A1_at	7.53E-02	4.54E-01	0.72	Mus musculus biogenesis of lysosome-related organelles complex-1; subunit 1; mRNA (cDNA clone MGC:35972 IMAGE:5359972); complete cds	90.2	BC034662	Bloc1s1	biogenesis of lysosome-related organelles complex-1, subunit 1
CfaAffx.23436.1.S1_at	9.92E-02	4.65E-01	1.4	PREDICTED: Canis familiaris similar to basic leucine zipper nuclear factor 1 (LOC490354); mRNA	98.5	XM_547475	BLZF1	basic leucine zipper nuclear factor 1
Cfa.19858.1.S1_s_at	6.30E-02	4.50E-01	1.31	PREDICTED: Canis familiaris similar to basic leucine zipper nuclear factor 1 (LOC490354); mRNA	99.1	XM_547475	BLZF1	basic leucine zipper nuclear factor 1
CfaAffx.7166.1.S1_s_at	3.49E-02	4.46E-01	1.6	PREDICTED: Canis familiaris similar to Polycomb group ring finger 4 (Polycomb complex protein BMI-1) (RING finger protein 51); transcript variant 2 (LOC487097); mRNA	97.2	XM_844245	BMI1	BMI1 polycomb ring finger oncogene
Cfa.11221.1.A1_at	2.67E-02	4.46E-01	1.71	PREDICTED: Canis familiaris similar to 3(2);5-bisphosphate nucleotidase 1 (Bisphosphate 3-nucleotidase 1) (PAP-inositol-1;4-phosphatase) (PIP) (LOC608525); mRNA	100	XM_845576	BPNT1	3'(2'), 5'-bisphosphate nucleotidase 1
Cfa.11093.1.S1_at	5.40E-02	4.50E-01	1.35	PREDICTED: Canis familiaris similar to Brain protein 44-like protein; transcript variant 5 (LOC609356); mRNA	99.6	XM_858018	BRP44L	brain protein 44-like

Table 6:Genes Differentially Expressed in lymphocytes from Fat Animals fed on either a high protein diet or the same diet with added fish oil.

CfaAffx.11934.1.S1_at	6.55E-02	4.51E-01	1.48	PREDICTED: Canis familiaris similar to TATA binding-protein-associated factor 172 (TBP-associated factor 172) (TAF-172) (TAF(II)170) (B-TFIID transcription factor-associated 170 kDa subunit) (LOC486800); mRNA	100	XM_543929	BTAF1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (Mot1 homolog, S. cerevisiae)
Cfa.16454.1.S1_at	6.30E-02	4.50E-01	1.43	[illegible] familiaris similar to Bruton agammaglobulinemia tyrosine kinase; transcript variant 6 (LOC492019); mRNA	100	XM_856682	BTK	Bruton agammaglobulinemia tyrosine kinase
CfaAffx.19666.1.S1_at	3.79E-02	4.46E-01	1.55	PREDICTED: Canis familiaris similar to BUB3 budding uninhibited by benzimidazoles 3 isoform a; transcript variant 3 (LOC477857); mRNA	92.9	XM_847523	BUB3	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)
Cfa.12011.1.A1_at	1.80E-02	4.46E-01	1.39	PREDICTED: Canis familiaris similar to BUB3 budding uninhibited by benzimidazoles 3 isoform a; transcript variant 1 (LOC477857); mRNA	100	XM_535049	BUB3	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast)
Cfa.673.1.S1_at	1.40E-02	4.46E-01	1.51	PREDICTED: Canis familiaris similar to RNA processing factor 1 (LOC479972); mRNA	100	XM_537096	BXDC5	brix domain containing 5
Cfa.10332.1.S1_at	1.60E-02	4.46E-01	1.49	Pongo abelii mRNA; cDNA DKFZp459K0926 (from clone DKFZp459K0926)	31.3	CR858060	C12orf4	chromosome 12 open reading frame 4
CfaAffx.20797.1.S1_at	4.12E-02	4.46E-01	1.39	Bos taurus chromosome 1 open reading frame 21 ortholog; mRNA (cDNA clone MGC:155149 IMAGE:8483680); complete cds	59.6	BC133418	C16H1ORF21	chromosome 1 open reading frame 21 ortholog
Cfa.13656.1.A1_at	6.76E-02	4.52E-01	1.52	Homo sapiens mRNA; cDNA DKFZp451B077 (from clone DKFZp451B077)	49.3	BX647629	C1orf71	chromosome 1 open reading frame 71
Cfa.1379.1.S1_at	3.40E-02	4.46E-01	0.76	PREDICTED: Canis familiaris similar to Complement C1q subcomponent; A chain precursor (LOC478194); mRNA	98.5	XM_535367	C1QA	complement component 1, q subcomponent, A chain

Table 6:Genes Differentially Expressed in lymphocytes from Fat Animals fed on either a high protein diet or the same diet with added fish oil.

Cfa.16472.2.S1_a_at	6.14E-02	4.50E-01	0.71	PREDICTED: Canis familiaris similar to Complement C1s subcomponent precursor (C1 esterase); transcript variant 2 (LOC486714); mRNA	58.4	XM_848227	C1S	complement component 1, s subcomponent
Cfa.12240.1.A1_at	1.29E-02	4.46E-01	0.68	Sus scrofa complement component C3 (C3) mRNA; complete cds	79.2	AF154933	C3	complement component 3
Cfa.2266.1.S1_at	1.32E-02	4.46E-01	1.64	Bos taurus chromosome 12 open reading frame 23 ortholog; mRNA (cDNA clone MGC:127570 IMAGE:7949219); complete cds	87.4	BC103369	C5H12orf23	chromosome 12 open reading frame 23 ortholog
Cfa.4155.1.A1_at	3.93E-02	4.46E-01	1.72	Homo sapiens chromosome 5 open reading frame 33 (C5orf33); transcript variant 2; mRNA	35.9	NM_153013	C5orf33	chromosome 5 open reading frame 33
Cfa.642.1.S1_at	5.47E-02	4.50E-01	1.4	Homo sapiens cDNA FLJ12910 fis; clone NT2RP2004412	40.2	AK022972	C6orf211	chromosome 6 open reading frame 211
Cfa.18190.1.S1_at	8.77E-02	4.59E-01	1.38	Homo sapiens chromosome 7 open reading frame 23; mRNA (cDNA clone MGC:4175 IMAGE:3634983); complete cds	88	BC002837	C7orf23	chromosome 7 open reading frame 23
Cfa.7840.1.A1_at	5.29E-02	4.49E-01	1.36	PREDICTED: Canis familiaris similar to calcium binding protein 5 (LOC484414); mRNA	99.4	XM_541529	CABP5	calcium binding protein 5
CfaAffx.24377.1.S1_at	2.79E-02	4.46E-01	0.74	PREDICTED: Canis familiaris similar to calcium channel; voltage dependent; alpha 1F subunit (LOC480915); mRNA	100	XM_538035	CACNA1F	calcium channel, voltage-dependent, L type, alpha 1F subunit
Cfa.9932.1.A1_at	9.13E-02	4.61E-01	1.84	troglodytes calcium channel; voltage-dependent; beta 4 subunit; transcript variant 2 (CACNB4); mRNA	86.3	XM_001138685	CACNB4	calcium channel, voltage-dependent, beta 4 subunit
Cfa.4396.1.A1_at	2.20E-02	4.46E-01	1.38	PREDICTED: Canis familiaris similar to calcium/calmodulin-dependent protein kinase ID isoform 2 (LOC607636); mRNA	94.1	XM_844395	CAMK1D	calcium/calmodulin-dependent protein kinase ID

Table 6:Genes Differentially Expressed in lymphocytes from Fat Animals fed on either a high protein diet or the same diet with added fish oil.

CfaAffx.18796.1.S1_at	2.24E-03	4.46E-01	1.65	PREDICTED: Canis familiaris similar to Calcium/calmodulin-dependent protein kinase type II delta chain (CaM-kinase II delta chain) (CaM kinase II delta subunit) (CaMK-II delta subunit) (LOC610764); mRNA	95.5	XM_848313	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta
Cfa.4552.1.S1_s_at	1.23E-02	4.46E-01	0.4	Canis lupus familiaris cathelicidin mRNA; complete cds	95.4	AY392089	CAMP	cathelicidin antimicrobial peptide
CfaAffx.19983.1.S1_at	4.53E-02	4.47E-01	0.57	Canis lupus familiaris cathelicidin mRNA; complete cds	100	AY392089	CAMP	cathelicidin antimicrobial peptide
Cfa.1566.1.A1_at	3.44E-02	4.46E-01	1.51	PREDICTED: Canis familiaris similar to TIP120 protein; transcript variant 5 (LOC474437); mRNA	97.4	XM_531667	CAND1	cullin-associated and neddylation-dissociated 1
CfaAffx.1565.1.S1_s_at	4.12E-02	4.46E-01	1.31	PREDICTED: Canis familiaris similar to TIP120 protein; transcript variant 6 (LOC474437); mRNA	98.6	XM_855867	CAND1	cullin-associated and neddylation-dissociated 1
Cfa.21114.1.S1_s_at	3.05E-02	4.46E-01	0.74	PREDICTED: Canis familiaris similar to Calpain-1 catalytic subunit (Calpain-1 large subunit) (Calcium-activated neutral proteinase 1) (CANP 1) (Calpain mu-type) (muCANP) (Micromolar-calpain); transcript variant 1 (LOC483745); mRNA	100	XM_540866	CAPN1	calpain 1, (mu/l) large subunit
Cfa.2121.1.A1_at	6.05E-02	4.50E-01	1.34	PREDICTED: Canis familiaris similar to membrane component chromosome 11 surface marker 1 isoform 1; transcript variant 1 (LOC607420); mRNA	99.8	XM_844102	CAPRIN1	cell cycle associated protein 1
Cfa.18760.1.S1_s_at	3.56E-03	4.46E-01	0.75	PREDICTED: Canis familiaris similar to cysteinyl-tRNA synthetase isoform c; transcript variant 1 (LOC475998); mRNA	99.4	XM_533205	CARS	cysteinyl-tRNA synthetase
CfaAffx.16071.1.S1_at	4.44E-02	4.47E-01	0.74	PREDICTED: Canis familiaris similar to cysteinyl-tRNA synthetase isoform c; transcript variant 1 (LOC475998); mRNA	100	XM_533205	CARS	cysteinyl-tRNA synthetase
Cfa.6332.1.A1_at	2.61E-02	4.46E-01	1.34	PREDICTED: Canis familiaris similar to CG8257-PA (LOC476983); mRNA	100	XM_534184	CARS2	cysteinyl-tRNA synthetase 2, mitochondrial (putative)

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CfaAffx.12454.1.S1_s_at	2.56E-02	4.46E-01	1.81	Canis lupus familiaris mRNA for caspase-3; complete cds	99.5	AB085580	CASP3	caspase 3, apoptosis-related cysteine peptidase
Cfa.18816.1.S1_at	6.95E-03	4.46E-01	1.63	PREDICTED: Canis familiaris similar to caspase 6 isoform alpha preproprotein (LOC487899); mRNA	94.5	XM_545022	CASP6	caspase 6, apoptosis-related cysteine peptidase
Cfa.18816.1.S1_s_at	4.24E-02	4.47E-01	1.43	PREDICTED: Canis familiaris similar to caspase 6 isoform alpha preproprotein (LOC487899); mRNA	99.3	XM_545022	CASP6	caspase 6, apoptosis-related cysteine peptidase
CfaAffx.17770.1.S1_at	7.30E-02	4.54E-01	1.37	PREDICTED: Canis familiaris similar to caspase 6 isoform alpha preproprotein (LOC487899); mRNA	100	XM_545022	CASP6	caspase 6, apoptosis-related cysteine peptidase
Cfa.20573.1.S1_at	3.43E-02	4.46E-01	0.76	PREDICTED: Canis familiaris similar to carbonic reductase 4 (LOC477352); mRNA	100	XM_534547	CBR4	carbonyl reductase 4
CfaAffx.3836.1.S1_at	4.88E-02	4.48E-01	1.42	PREDICTED: Canis familiaris similar to COBW domain-containing protein 2 (LOC484176); mRNA	100	XM_541292	CBWD2	COBW domain containing 2
CfaAffx.5265.1.S1_x_at	3.48E-02	4.46E-01	1.41	PREDICTED: Canis familiaris similar to chromobox homolog 3; transcript variant 5 (LOC482015); mRNA	99.3	XM_859382	CBX3	chromobox homolog 3 (HP1 gamma homolog, Drosophila)
Cfa.296.1.S1_at	2.24E-03	4.46E-01	1.44	PREDICTED: Canis familiaris similar to chromobox homolog 3; transcript variant 4 (LOC482015); mRNA	100	XM_859368	CBX3	chromobox homolog 3 (HP1 gamma homolog, Drosophila)
CfaAffx.2035.1.S1_s_at	6.60E-02	4.51E-01	1.33	PREDICTED: Canis familiaris similar to chromobox homolog 3; transcript variant 5 (LOC482015); mRNA	100	XM_859382	CBX3	chromobox homolog 3 (HP1 gamma homolog, Drosophila)
CfaAffx.25366.1.S1_s_at	6.67E-02	4.51E-01	0.77	PREDICTED: Canis familiaris similar to putative NFkB activating protein; transcript variant 1 (LOC484911); mRNA	100	XM_542027	CC2D1A	coiled-coil and C2 domain containing 1A
CfaAffx.21274.1.S1_at	3.21E-02	4.46E-01	1.6	PREDICTED: Canis familiaris similar to cell-cycle and apoptosis regulatory protein 1; transcript variant 5 (LOC479230); mRNA	100	XM_855565	CCAR1	cell division cycle and apoptosis regulator 1

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Cfa.10456.1.A1_at	7.93E-02	4.55E-01	1.33	PREDICTED: Canis familiaris similar to kynurenine aminotransferase III isoform 1; transcript variant 1 (LOC479959); mRNA	94.7	XM_537084	CCBL2	cysteine conjugate-beta lyase 2
CfaAffx.3956.1.S1_at	1.87E-03	4.46E-01	1.35	PREDICTED: Canis familiaris similar to CG4996-PA (LOC475228); mRNA	100	XM_532460	CCDC132	coiled-coil domain containing 132
Cfa.9084.1.A1_at	3.70E-02	4.46E-01	1.53	PREDICTED: Canis familiaris similar to Coiled-coil domain containing protein 3 precursor (LOC607593); mRNA	100	XM_844332	CCDC3	coiled-coil domain containing 3
Cfa.10335.1.S1_at	1.09E-02	4.46E-01	1.41	PREDICTED: Canis familiaris similar to CG32662-PA (LOC480471); mRNA	95.6	XM_537590	CCDC45	coiled-coil domain containing 45
Cfa.18528.1.S1_at	9.04E-02	4.60E-01	1.3	PREDICTED: Canis familiaris similar to CG3493-PA (LOC480462); mRNA	97.2	XM_537580	CCDC46	coiled-coil domain containing 46
Cfa.20277.1.S1_at	4.74E-02	4.48E-01	1.45	domain containing 5 (spindle associated); mRNA (cDNA clone MGC:134225 IMAGE:8043019); complete cds	61.7	BC110011	CCDC5	coiled-coil domain containing 5 (spindle associated)
Cfa.9835.1.A1_at	7.97E-02	4.55E-01	1.42	Bos taurus coiled-coil domain containing 88C; mRNA (cDNA clone MGC:160122 IMAGE:8520598); complete cds	47.2	BC149856	CCDC88C	coiled-coil domain containing 88C
CfaAffx.17112.1.S1_s_at	2.35E-02	4.46E-01	1.32	PREDICTED: Canis familiaris similar to GGA-binding partner (p56 accessory protein) (HSD8); transcript variant 2 (LOC486622); mRNA	54.9	XM_860231	CCDC91	coiled-coil domain containing 91
Cfa.3424.1.S1_at	9.38E-02	4.62E-01	1.62	PREDICTED: Canis familiaris similar to GGA-binding partner (p56 accessory protein) (HSD8); transcript variant 4 (LOC486622); mRNA	95.5	XM_860280	CCDC91	coiled-coil domain containing 91
Cfa.389.1.S1_at	3.73E-02	4.46E-01	1.36	PREDICTED: Canis familiaris similar to Cyclin C; transcript variant 7 (LOC475007); mRNA	96.1	XM_863125	CCNC	cyclin C
CfaAffx.26324.1.S1_s_at	3.67E-02	4.46E-01	1.3	PREDICTED: Canis familiaris similar to Cyclin G1 (Cyclin G); transcript variant 4 (LOC479303); mRNA	98.8	XM_861898	CCNG1	cyclin G1
CfaAffx.13729.1.S1_at	8.90E-02	4.59E-01	1.32	PREDICTED: Canis familiaris similar to cyclin G2 (LOC478442); mRNA	100	XM_535619	CCNG2	cyclin G2
CfaAffx.24405.1.S1_at	3.55E-02	4.46E-01	1.32	PREDICTED: Canis familiaris similar to cell cycle progression 1 isoform 2; transcript variant 3 (LOC487566); mRNA	79.5	XM_858478	CCPG1	cell cycle progression 1

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CfaAffx.24597.1.S1_at	1.44E-03	4.46E-01	1.66	PREDICTED: Canis familiaris similar to C-C chemokine receptor type 7 precursor (C-C CKR-7) (CC-CKR-7) (CCR-7) (MIP-3 beta receptor) (EBV-induced G-protein coupled receptor 1) (EBI1) (BLR2) (LOC491011); mRNA	100	XM_548131	CCR7	chemokine (C-C motif) receptor 7
Cfa.18704.1.S1_s_at	7.42E-02	4.54E-01	1.37	PREDICTED: Canis familiaris similar to chaperonin containing TCP1; subunit 2; transcript variant 1 (LOC474445); mRNA	100	XM_531675	CCT2	chaperonin containing TCP1, subunit 2 (beta)
Cfa.5626.1.A1_at	6.68E-02	4.51E-01	1.32	PREDICTED: Canis familiaris similar to chaperonin containing TCP1; subunit 3 isoform c; transcript variant 2 (LOC480123); mRNA	100	XM_859150	CCT3	chaperonin containing TCP1, subunit 3 (gamma)
Cfa.1285.1.A1_at	2.61E-02	4.46E-01	1.31	Homo sapiens partial mRNA for chaperonin subunit 6A (CCT6A gene)	91.5	AM295155	CCT6A	chaperonin containing TCP1, subunit 6A (zeta 1)
Cfa.1034.1.S1_at	4.85E-03	4.46E-01	1.38	PREDICTED: Canis familiaris similar to T-complex protein 1; theta subunit (TCP-1-theta) (CCT-theta); transcript variant 3 (LOC478399); mRNA	100	XM_850938	CCT8	chaperonin containing TCP1, subunit 8 (theta)
Cfa.8311.1.S1_at	8.62E-02	4.58E-01	1.54	PREDICTED: Canis familiaris similar to CD164 antigen; sialomucin; transcript variant 2 (LOC475020); mRNA	85	XM_863346	CD164	CD164 molecule, sialomucin
CfaAffx.8078.1.S1_at	4.79E-02	4.48E-01	0.75	PREDICTED: Canis familiaris similar to polycythemia rubra vera 1 (LOC612424); mRNA	95.9	XM_850154	CD177	CD177 molecule
CfaAffx.1028.1.S1_s_at	7.85E-02	4.55E-01	1.52	PREDICTED: Canis familiaris similar to CD226 antigen precursor (DNAX accessory molecule-1) (DNAM-1) (LOC609196); mRNA	100	XM_846412	CD226	CD226 molecule
Cfa.3508.1.S1_s_at	6.85E-02	4.53E-01	1.52	Canis familiaris T-cell costimulatory molecule CD28 (CD28) mRNA; complete cds	99	AF259962	CD28	CD28 molecule
Cfa.822.1.S1_at	7.08E-02	4.54E-01	1.41	Homo sapiens CD2-associated protein (CD2AP); mRNA	83.8	NM_012120	CD2AP	CD2-associated protein
CfaAffx.22280.1.S1_s_at	3.57E-02	4.46E-01	0.75	PREDICTED: Pan troglodytes similar to TREM4 alpha; transcript variant 1 (LOC740064); mRNA	67.2	XM_001153114	CD300LG	CD300 molecule-like family member g

Table 6:Genes Differentially Expressed in lymphocytes from Fat Animals fed on either a high protein diet or the same diet with added fish oil.

Cfa.3619.1.S1_s_at	1.22E-02	4.46E-01	1.57	Canis familiaris hematopoietic antigen CD38 mRNA; complete cds	99.8	AF117714	CD38	CD38 molecule
Cfa.3890.1.S1_at	7.92E-03	4.46E-01	1.4	Dog CD3 epsilon subunit mRNA; complete cds	65.7	M55410	CD3E	CD3e molecule, epsilon (CD3-TCR complex)
Cfa.179.1.S2_s_at	3.39E-02	4.46E-01	1.32	Canis familiaris CD154 (CD154) mRNA; complete cds	97.2	AY333790	CD40LG	CD40 ligand
Cfa.179.1.S1_s_at	9.15E-02	4.61E-01	1.48	Canis familiaris CD154 (CD154) mRNA; complete cds	100	AY333790	CD40LG	CD40 ligand
Cfa.1961.1.S1_at	3.60E-02	4.46E-01	1.34	Homo sapiens cDNA FLJ39351 fis; clone PEBLM2001072	62.7	AK096670	CD47	CD47 molecule
Cfa.21011.1.S1_at	2.08E-02	4.46E-01	1.55	PREDICTED: Canis familiaris similar to T-cell surface glycoprotein CD8 beta chain precursor (Antigen CD8B); transcript variant 2 (LOC483076); mRNA	100	XM_859954	CD8B	CD8b molecule
CfaAffx.12060.1.S1_s_at	7.44E-02	4.54E-01	1.48	PREDICTED: Canis familiaris similar to T-cell surface glycoprotein CD8 beta chain precursor (Antigen CD8B); transcript variant 2 (LOC483076); mRNA	100	XM_859954	CD8B	CD8b molecule
Cfa.20663.1.A1_at	9.90E-02	4.65E-01	1.53	familiaris similar to Cell division control protein 2 homolog (p34 protein kinase) (Cyclin-dependent kinase 1) (CDK1); transcript variant 1 (LOC488997); mRNA	58	XM_546115	CDC2	cell division cycle 2, G1 to S and G2 to M
CfaAffx.7716.1.S1_at	4.45E-02	4.47E-01	0.76	PREDICTED: Canis familiaris similar to Cdc42 effector protein 4 (LOC475907); mRNA	58.9	XM_533114	CDC42EP4	CDC42 effector protein (Rho GTPase binding) 4
Cfa.8928.1.A1_at	4.74E-03	4.46E-01	1.47	Pongo abelii mRNA; cDNA DKFZp459I233 (from clone DKFZp459I233)	59.7	CR861291	CDC42SE2	CDC42 small effector 2
CfaAffx.2024.1.S1_at	1.01E-02	4.46E-01	1.61	PREDICTED: Canis familiaris similar to CDC42 small effector 2 (LOC609492); mRNA	100	XM_846751	CDC42SE2	CDC42 small effector 2
CfaAffx.16477.1.S1_at	7.13E-02	4.54E-01	1.4	PREDICTED: Equus caballus cell division cycle 73; Paf1/RNA polymerase II complex component; homolog (S. cerevisiae) (CDC73); mRNA	92.1	XM_001492217	CDC73	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)

Table 6:Genes Differentially Expressed in lymphocytes from Fat Animals fed on either a high protein diet or the same diet with added fish oil.

Cfa.18970.1.S1_at	3.38E-02	4.46E-01	1.43	PREDICTED: Canis familiaris similar to transcription factor RAM2 (LOC482347); mRNA	100	XM_539464	CDCA7L	cell division cycle associated 7-like
CfaAffx.30575.1.S1_at	3.56E-02	4.46E-01	1.38	Bos taurus cadherin 13, H-cadherin (heart); mRNA (cDNA clone MGC:128634 IMAGE:7986572); complete cds	80	BC107535	CDH13	cadherin 13, H-cadherin (heart)
Cfa.10960.1.S1_at	6.52E-02	4.51E-01	1.55	PREDICTED: Canis familiaris similar to CDK2-associated protein 1 (LOC475806); mRNA	64.2	XM_533015	CDK2AP1	CDK2-associated protein 1
CfaAffx.11224.1.S1_at	7.82E-02	4.55E-01	1.43	PREDICTED: Canis familiaris similar to Cell division protein kinase 8 (Protein kinase K35); transcript variant 3 (LOC486035); mRNA	63.7	XM_854727	CDK8	cyclin-dependent kinase 8
CfaAffx.12648.1.S1_s_at	2.25E-02	4.46E-01	1.47	PREDICTED: Canis familiaris similar to collaborates/cooperates with ARF (alternate reading frame) protein (LOC607991); mRNA	98.1	XM_844869	CDKN2AIP	CDKN2A interacting protein
CfaAffx.12648.1.S1_at	1.75E-02	4.46E-01	1.48	PREDICTED: Canis familiaris similar to collaborates/cooperates with ARF (alternate reading frame) protein (LOC607991); mRNA	100	XM_844869	CDKN2AIP	CDKN2A interacting protein
CfaAffx.12649.1.S1_s_at	1.84E-02	4.46E-01	1.53	PREDICTED: Canis familiaris similar to collaborates/cooperates with ARF (alternate reading frame) protein (LOC607991); mRNA	100	XM_844869	CDKN2AIP	CDKN2A interacting protein
CfaAffx.8108.1.S1_at	1.69E-02	4.46E-01	0.59	Canis lupus familiaris carcinoembryonic antigen-related cell adhesion molecule 23 isoform 4L (CEACAM23) mRNA; complete cds	90.7	EF137906	CEACAM23	carcinoembryonic antigen-related cell adhesion molecule 23
CfaAffx.17785.1.S1_at	7.62E-02	4.54E-01	0.74	PREDICTED: Canis familiaris similar to CCAAT/enhancer binding protein epsilon (LOC490607); mRNA	47.4	XM_547729	CEBPE	CCAAT/enhancer binding protein (C/EBP), epsilon
CfaAffx.10125.1.S1_at	2.53E-02	4.46E-01	1.47	PREDICTED: Canis familiaris similar to CCAAT/enhancer binding protein zeta; transcript variant 1 (LOC483035); mRNA	88.9	XM_540150	CEBPZ	CCAAT/enhancer binding protein zeta
Cfa.1767.1.A1_s_at	5.41E-02	4.50E-01	1.37	PREDICTED: Canis familiaris similar to centromere protein C 1 (LOC475158); mRNA	95.8	XM_532388	CENPC1	centromere protein C 1

Table 6:Genes Differentially Expressed in lymphocytes from Fat Animals fed on either a high protein diet or the same diet with added fish oil.

Cfa.18979.1.S1_s_at	5.87E-02	4.50E-01	0.74	PREDICTED: Canis familiaris similar to centaurin delta 2 isoform a (LOC485207); mRNA	99.8	XM_542325	CENTD2	centaurin, delta 2
CfaAffx.10305.1.S1_at	8.22E-02	4.56E-01	0.7	PREDICTED: Canis familiaris similar to centaurin; delta 3 (LOC487188); mRNA	100	XM_544316	CENTD3	centaurin, delta 3
CfaAffx.24199.1.S1_s_at	7.36E-02	4.54E-01	1.5	PREDICTED: Canis familiaris similar to KARP 1-binding protein; transcript variant 1 (LOC480096); mRNA	100	XM_537218	CEP170	centrosomal protein 170kDa
Cfa.8966.1.A1_s_at	6.09E-02	4.50E-01	1.47	PREDICTED: Canis familiaris hypothetical LOC480216 (LOC480216); mRNA	98.4	XM_537341	CEP192	centrosomal protein 192kDa
Cfa.844.1.S1_at	9.99E-02	4.65E-01	1.35	PREDICTED: Equus caballus centrosomal protein 63kDa; transcript variant 2 (CEP63); mRNA	40	XM_001498444	CEP63	centrosomal protein 63kDa
Cfa.4072.1.A1_at	2.47E-02	4.46E-01	1.75	Homo sapiens centrosomal protein 68kDa (CEP68); mRNA	42.9	NM_015147	CEP68	centrosomal protein 68kDa
CfaAffx.12215.1.S1_at	1.70E-02	4.46E-01	1.43	PREDICTED: Canis familiaris similar to centrosomal protein 70 kDa (LOC477084); mRNA	100	XM_534279	CEP70	centrosomal protein 70kDa
CfaAffx.30235.1.S1_s_at	6.10E-02	4.50E-01	1.31	PREDICTED: Canis familiaris similar to choline/ethanolaminephosphotransferase; transcript variant 4 (LOC612948); mRNA	98.3	XM_860637	CEPT1	choline/ethanolamine phosphotransferase 1
CfaAffx.13146.1.S1_at	6.79E-02	4.52E-01	1.41	PREDICTED: Canis familiaris similar to centrin 3 (LOC488915); mRNA	90.6	XM_546032	CETN3	centrin, EF-hand protein, 3 (CDC31 homolog, yeast)
CfaAffx.13146.1.S1_s_at	7.55E-02	4.54E-01	1.42	PREDICTED: Canis familiaris similar to centrin 3 (LOC488915); mRNA	100	XM_546032	CETN3	centrin, EF-hand protein, 3 (CDC31 homolog, yeast)
Cfa.14267.1.S1_at	2.52E-02	4.46E-01	0.76	PREDICTED: Canis familiaris similar to complement component 2 precursor; transcript variant 4 (LOC474853); mRNA	99.5	XM_855278	CFB	complement factor B
CfaAffx.1961.1.S1_s_at	2.62E-02	4.46E-01	0.75	PREDICTED: Canis familiaris similar to complement component 2 precursor; transcript variant 5 (LOC474853); mRNA	100	XM_855317	CFB	complement factor B
Cfa.3541.1.A1_at	1.00E-02	4.46E-01	1.38	PREDICTED: Canis familiaris p97 homologous protein (P97); mRNA	95.9	XM_546829	CFDP1	craniofacial development protein 1

Table 6:Genes Differentially Expressed in lymphocytes from Fat Animals fed on either a high protein diet or the same diet with added fish oil.

CfaAffx.30731.1.S1_s_at	4.03E-02	4.46E-01	1.34	PREDICTED: Canis familiaris p97 homologous protein (P97); mRNA	99.8	XM_546829	CFDP1	craniofacial development protein 1
Cfa.10261.1.S1_at	7.68E-02	4.55E-01	1.46	PREDICTED: Canis familiaris similar to cofilin 2 (LOC490649); mRNA	98.8	XM_547771	CFL2	cofilin 2 (muscle)
Cfa.18930.1.S1_s_at	6.15E-02	4.50E-01	0.74	PREDICTED: Canis familiaris similar to properdin P factor; complement (LOC491859); mRNA	97.2	XM_548978	CFP	complement factor properdin
CfaAffx.9394.1.S1_s_at	5.01E-02	4.48E-01	0.76	PREDICTED: Canis familiaris similar to chromodomain helicase DNA binding protein 8; transcript variant 1 (LOC475401); mRNA	100	XM_532624	CHD8	chromodomain helicase DNA binding protein 8
CfaAffx.13243.1.S1_s_at	5.08E-02	4.48E-01	0.74	PREDICTED: Canis familiaris similar to choline dehydrogenase (LOC484723); mRNA	100	XM_541839	CHDH	choline dehydrogenase
Cfa.447.1.S1_at	1.00E-02	4.46E-01	2	PREDICTED: Pan troglodytes cysteine-rich hydrophobic domain 2; transcript variant 2 (CHIC2); mRNA	84.1	XM_001145791	CHIC2	cysteine-rich hydrophobic domain 2
CfaAffx.3999.1.S1_at	3.00E-02	4.46E-01	1.49	familiaris similar to Cysteine-rich hydrophobic domain 2 protein (BrX-like translocated in leukemia) (LOC611250); mRNA	100	XM_848892	CHIC2	cysteine-rich hydrophobic domain 2
CfaAffx.15079.1.S1_s_at	7.45E-02	4.54E-01	1.31	Mus musculus chitinase domain containing 1 (Chid1); transcript variant 2; mRNA	83.5	NM_026522	Chid1	chitinase domain containing 1
Cfa.18535.1.S1_s_at	7.53E-02	4.54E-01	1.48	PREDICTED: Canis familiaris similar to chromatin modifying protein 2B (LOC487675); mRNA	99.4	XM_544799	CHMP2B	chromatin modifying protein 2B
Cfa.17691.1.S1_at	7.60E-03	4.46E-01	1.43	familiaris similar to cysteine and histidine-rich domain (CHORD)-containing; zinc-binding protein 1 (LOC476773); mRNA	68.1	XM_533979	CHORDC1	cysteine and histidine-rich domain (CHORD)-containing 1
CfaAffx.7350.1.S1_s_at	2.08E-03	4.46E-01	1.51	familiaris similar to cysteine and histidine-rich domain (CHORD)-containing; zinc-binding protein 1 (LOC476773); mRNA	100	XM_533979	CHORDC1	cysteine and histidine-rich domain (CHORD)-containing 1
CfaAffx.12805.1.S1_at	6.07E-02	4.50E-01	1.43	PREDICTED: Canis familiaris similar to carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2 (LOC485701); mRNA	100	XM_542821	CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2

Table 6:Genes Differentially Expressed in lymphocytes from Fat Animals fed on either a high protein diet or the same diet with added fish oil.

CfaAffx.7706.1.S1_s_at	2.72E-02	4.46E-01	0.73	PREDICTED: Canis familiaris similar to Creatine kinase M-type (Creatine kinase; M chain) (M-CK) (LOC476435); mRNA	100	XM_533641	CKM	creatine kinase, muscle
Cfa.13608.1.A1_at	2.62E-02	4.46E-01	1.35	Mus musculus mammary gland RCB-0526 Jyg-MC(A) cDNA; RIKEN full-length enriched library; clone:G830017A10 product:B-cell stimulating factor 3; full insert sequence	37.5	AK166218	Clcf1	cardiotrophin-like cytokine factor 1
Cfa.1328.1.A1_at	5.30E-02	4.49E-01	1.45	Canis familiaris mRNA for chloride channel 3 (clcn3 gene)	56.5	AM048629	clcn3	chloride channel 3
CfaAffx.19424.1.S1_at	3.33E-02	4.46E-01	0.77	PREDICTED: Canis familiaris similar to claudin 4 (LOC489802); mRNA	100	XM_546920	CLDN4	claudin 4
Cfa.18933.2.S1_at	6.63E-02	4.51E-01	1.38	PREDICTED: Canis familiaris similar to osteoclast inhibitory lectin isoform 1 (LOC611449); mRNA	53.8	XM_849116	CLEC2D	C-type lectin domain family 2, member D
Cfa.18933.1.S1_at	3.82E-02	4.46E-01	1.54	PREDICTED: Canis familiaris similar to osteoclast inhibitory lectin isoform 1 (LOC611449); mRNA	59.9	XM_849116	CLEC2D	C-type lectin domain family 2, member D
Cfa.18933.2.S1_s_at	9.51E-02	4.63E-01	1.4	PREDICTED: Canis familiaris similar to osteoclast inhibitory lectin isoform 1 (LOC611449); mRNA	100	XM_849116	CLEC2D	C-type lectin domain family 2, member D
Cfa.2567.2.S1_at	3.22E-02	4.46E-01	1.72	PREDICTED: Canis familiaris similar to UMP-CMP kinase (Cytidylate kinase) (Deoxycytidylate kinase) (Cytidine monophosphate kinase) (Uridine monophosphate/cytidine monophosphate kinase) (UMP/CMP kinase) (UMP/CMPK) (Uridine monophosphate kinase) (LOC610291); mRNA	87.5	XM_847756	CMPK1	cytidine monophosphate (UMP-CMP) kinase 1, cytosolic
Cfa.2956.1.S1_s_at	1.75E-02	4.46E-01	1.6	PREDICTED: Canis familiaris similar to cornichon-like isoform 1; transcript variant 4 (LOC609358); mRNA	100	XM_859302	CNIH	cornichon homolog (Drosophila)
Cfa.20110.1.S1_at	6.39E-03	4.46E-01	1.32	PREDICTED: Pan troglodytes CNKSR family member 3 (CNKSR3); mRNA	50.9	XM_518820	CNKSR3	CNKSR family member 3
CfaAffx.4925.1.S1_s_at	2.24E-03	4.46E-01	0.76	PREDICTED: Canis familiaris similar to CCR4 NOT transcription complex; subunit 3; transcript variant 4 (LOC484312); mRNA	65.5	XM_857708	CNOT3	CCR4-NOT transcription complex, subunit 3

DEMANDE OU BREVET VOLUMINEUX

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CECI EST LE TOME 1 DE 2
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JUMBO APPLICATIONS/PATENTS

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THIS IS VOLUME 1 OF 2
CONTAINING PAGES 1 TO 329

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NOM DU FICHIER / FILE NAME :

NOTE POUR LE TOME / VOLUME NOTE:

75852-115

CLAIMS:

1. A composition for canine consumption comprising:

(a) 26 wt. % to 35 wt. % of crude protein on a dry matter basis;

(b) 7.5 wt. % to 8.5 wt. % of crude fat on a dry matter basis;

(c) 20 wt. % to 30 wt. % of total dietary fiber on a dry matter basis; and

(d) 10 wt. % to 20 wt. % of crude fiber on a dry matter basis.

2. The composition of claim 1, wherein the protein is present in 28 wt. % to 33 wt. %, and/or

wherein the crude fat is present in 7.6 wt. % to 8.0 wt. %.

3. The composition of claim 1 or 2, wherein the protein is present in 30 wt. % to 31 wt. %.

4. The composition of claim 1, wherein the total dietary fiber is present in 22 wt. % to 28 wt. %, and optionally,

wherein the crude fiber is present in 12 wt. % to 18 wt. %.

5. The composition of claim 4, wherein the total dietary fiber is present in 24 wt. % to 26%.

6. The composition of claim 4 or 5, wherein the crude fiber is present in 14 wt. % to 16%.

7. The composition of claim 1, wherein the total dietary fiber is present in an amount of 31 wt. % to 34 wt. %.

8. The composition of claim 1, wherein the crude fiber is present in an amount of 21 wt. % to 24 wt. %.

9. The composition of claim 1, wherein the composition further comprises at least 0.02% omega-3 polyunsaturated fatty acid.

10. The composition of claim 1, further comprising 0.05% to 10% omega-3 polyunsaturated fatty acid.

11. The composition of claim 1, further comprising 0.1% to 6% omega-3 polyunsaturated fatty acid.

12. The composition of claim 9, 10, or 11 wherein the omega-3 polyunsaturated fatty acid is Docosahexaenoic acid (DHA) and/or Eicosapentaenoic acid (EPA).

13. The composition of any one of claims 1 to 12, wherein the composition is for use in medicine.

14. The composition of any one of claims 1 to 12, wherein the composition is for use in preventing or treating obesity.

15. The composition of any one of claims 1 to 5 for use in preventing or treating one or more of:

insulin resistance, pancreatitis, hypothyroidism, osteoarthritis, dyslipidemia, hypertension, ocular disorders, altered kidney function, respiratory diseases, artherosclerosis, diabetes mellitus, urinary tract disease, hepatic lipdosis, hepatic dyslipidemia, hepatic lipidosis, neoplasia, oral/dental disease, dermatopathy, lameness, hyperlipidemia, glucose metabolism disorders, and coronary disease.

FIGURE 1

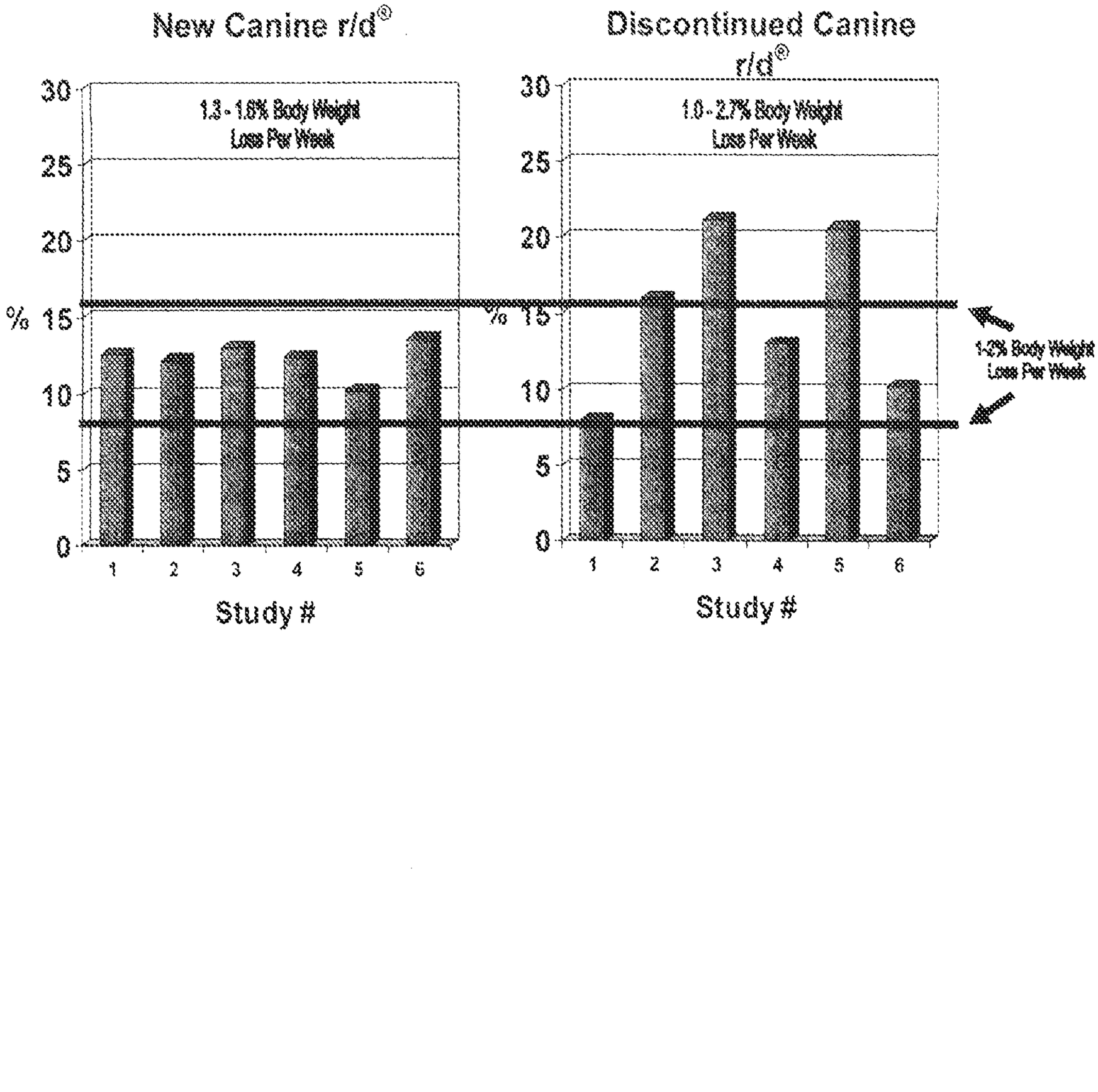
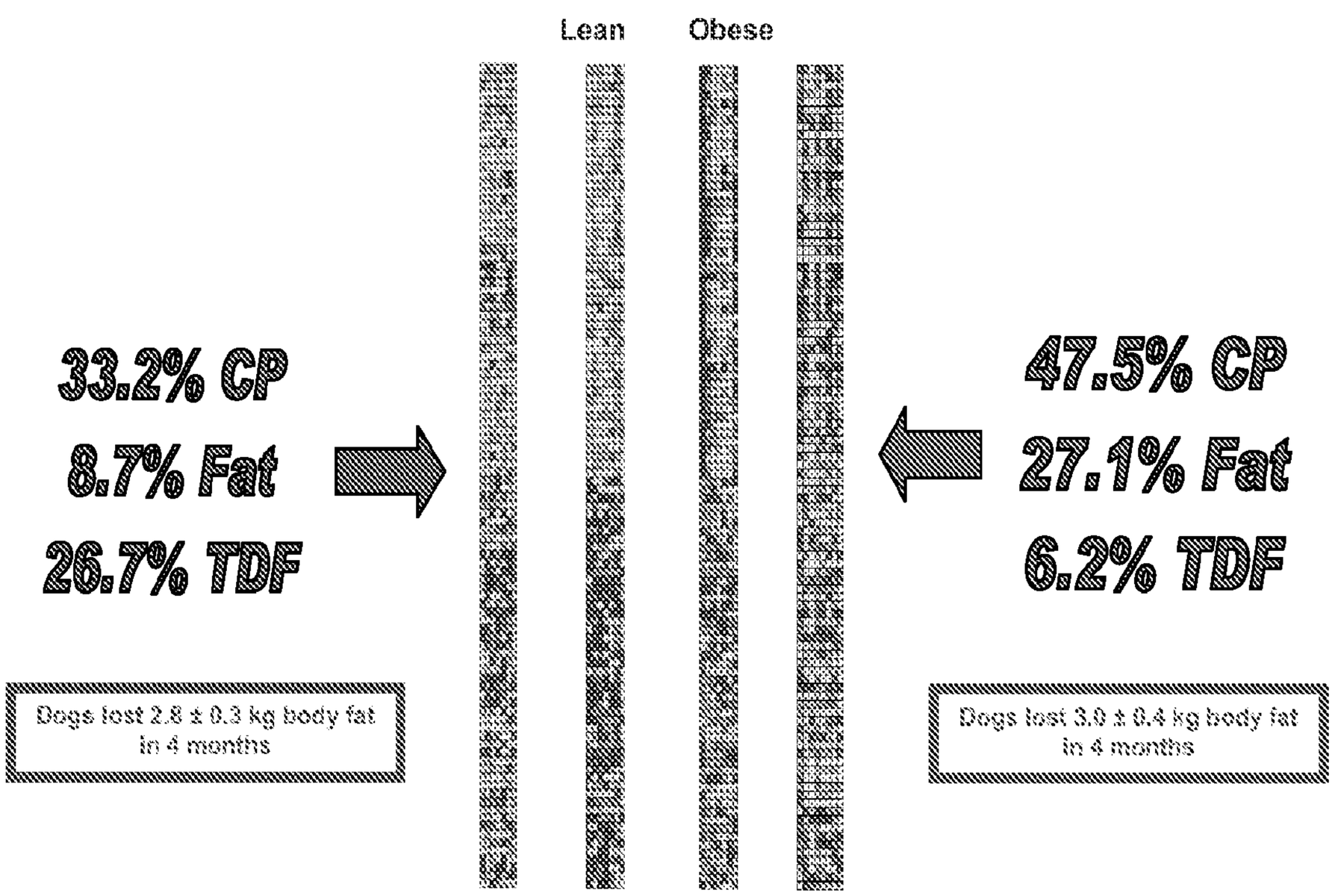
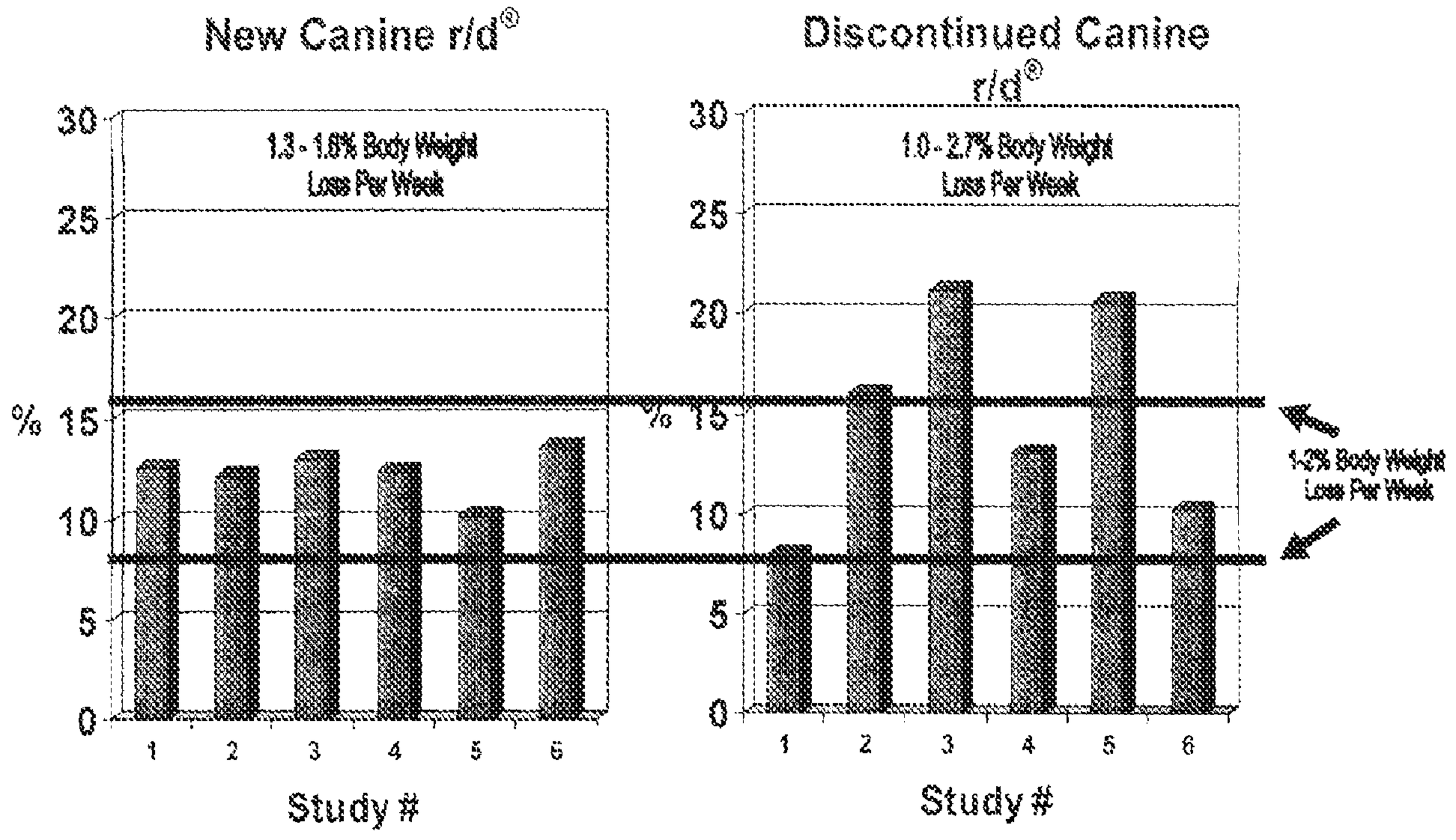

New Canine r/d®
Discontinued Canine r/d®
1.3 - 1.6% Body Weight Loss Per Week
1.0 - 2.7% Body Weight Loss Per Week
1-2% Body Weight Loss Per Week
%
30
25
20
15
10
5
0
1
2
3
4
5
6
Study #

FIGURE 2



Gene Expression Profiles


New Canine r/d®
Discontinued Canine r/d®
1.3 - 1.8% Body Weight Loss Per Week
1.0 - 2.7% Body Weight Loss Per Week
1.3% Body Weight Loss Per Week
%
30
25
20
15
10
5
0
1
2
3
4
5
6
Study #