USE OF DHA AND ARA IN THE PREPARATION OF A COMPOSITION FOR REGULATING GENE EXPRESSION

BACKGROUND OF THE INVENTION

(1) Field of the Invention.

[0001] The present invention relates generally to a method for modulating gene expression in subjects.

(2) Description of the Related Art

[0002] Every gene contains the information required to make a protein or a non-coding ribonucleic acid (RNA). In order to produce functional RNA and protein molecules in a cell, however, a gene must be expressed. Gene expression occurs in two major stages, transcription and protein synthesis. During transcription, the gene is copied to produce an RNA molecule (a primary transcript) with essentially the same sequence as the gene. Most human genes are divided into exons and introns, and only the exons carry information required for protein synthesis. Most primary transcripts are therefore processed by splicing to remove intron sequences and generate a mature transcript or messenger RNA (mRNA) that only contains exons.

[0003] The second stage of gene expression, protein synthesis, is also known as translation. During this stage there is no direct correspondence between the nucleotide sequence in deoxyribonucleic acid (DNA) and RNA and the sequence of amino acids in the protein. In fact, three nucleotides are required to specify one amino acid.

[0004] All genes in the human genome are not expressed in the same manner. Some genes are expressed in all cells all of the time. These so-called housekeeping genes are essential for very basic cellular functions. Other genes are expressed in particular cell types or at particular stages of development. For example, the genes that encode muscle proteins such as actin and myosin are expressed only in muscle cells, not in the cells of

the brain. Still other genes can be activated or inhibited by signals circulating in the body, such as hormones.

[0005] This differential gene expression is achieved by regulating transcription and translation. All genes are surrounded by DNA sequences that control their expression. Proteins called transcription factors bind to these sequences and can switch the genes on or off. Gene expression is therefore controlled by the availability and activity of different transcription factors.

[0006] As transcription factors are proteins themselves, they must also be produced by genes, and these genes must be regulated by other transcription factors. In this way, all genes and proteins can be linked into a regulatory hierarchy starting with the transcription factors present in the egg at the beginning of development. A number of human diseases are known to result from the absence or malfunction of transcription factors and the disruption of gene expression thus caused.

[0007] If genes are not expressed in the right time, place and amount, disease may occur. Thus, it would be beneficial to provide a composition that can regulate or modulate the expression of certain genes in subjects and thereby prevent the onset of or treat various diseases and disorders.

SUMMARY OF THE INVENTION

[0008] Briefly, the present invention is directed to a novel method for modulating the expression of one or more genes in a subject, wherein the gene is selected from the group consisting of those genes listed in Tables 4 – 9 herein under the "Gene Symbol" column, the method comprising administering to the subject DHA and ARA, alone or in combination with one another. The subject can be an infant or a child. The subject can be one that is in need of such modulation. In particular situations, ARA and DHA can be administered in a ratio of ARA:DHA of between about 1:10 to about 10:1 by weight.

[0009] The present invention is also directed to a novel method for upregulating the expression of one or more genes in a subject, wherein the gene is selected from the group consisting of those genes listed in Tables 4 and 6 herein under the "Gene Symbol" column, the method comprising administering to the subject DHA or ARA, alone or in combination with one another.

[00010] The present invention is additionally directed to a novel method for downregulating the expression of one or more genes in a subject, wherein the gene is selected from the group consisting of those genes listed in Tables 5 and 7 under the "Gene Symbol" column, the method comprising administering to the subject DHA or ARA, alone or in combination with one another.

[00011] The present invention is also directed to a novel method for upregulating the expression of one or more genes in a subject, wherein the gene is selected from the group consisting of TIMM8A, TIMM23, NF1, SFTPB, ACADSB, SOD, PDE3A, NSMAF, OSBP2, FTH1, SPTLC2, FOXP2, LUM, BRCA1, ADAM17, ADAM33, TOB1, XCL1, XCL2, RNASE2, RNASE3, SULT1C1, HSPCA, CD44, CD24, OSBPL9, FCER1G, FXD3, NRF1, STK3, and KIR2DS1, the method comprising administering to the subject DHA or ARA, alone or in combination with one another.

[00012] The invention is further directed, in an embodiment, to a method for modulating the expression of one or more genes in a subject, wherein the gene is selected from the group consisting of TIMM8A, TIMM23, NF1, LUM, BRCA1, ADAM17, TOB1, RNASE2, RNASE3, NRF1, STK3, FZD3, ADAM8, PERP, COL4A6, PLA2G6, MSRA, CTSD, CTSB, LMX1B, BHMT, TNNC1, PDE3A, PPARD, NPY1R, LEP, and any combination thereof.

[00013] The present invention is also, in an embodiment, directed to a method for treating or preventing tumors in a subject, the method

comprising modulating a gene selected from the group consisting of TOB1, NF1, FZD3, STK3, BRCA1, NRF1, PERP, and COL4A6 in the subject by administering to the subject an effective amount of DHA or ARA, alone or in combination with one another.

[00014] The invention is directed to a method for treating or preventing neurodegeneration in a subject, the method comprising modulating a gene selected from the group consisting of PLA2G6, TIMM8A, ADAM17, TIMM23, MSRA, CTSD, CTSB, LMX1B, and BHMT in the subject by administering to the subject an effective amount of DHA or ARA, alone or in combination with one another. The invention is also directed to a method for improving vision in a subject, the method comprising modulating the LUM gene in the subject by administering to the subject an effective amount of DHA or ARA, alone or in combination with one another. The invention is further directed to a method for treating or preventing macular degeneration in a subject, the method comprising modulating the LUM gene in the subject by administering to the subject an effective amount of DHA or ARA, alone or in combination with one another.

[00015] In other embodiments, the invention is directed to a method for stimulating an immune response in a subject, the method comprising modulating a gene selected from the group consisting of RNASE2, RNASE3, and ADAM8 in the subject by administering to the subject an effective amount of DHA or ARA, alone or in combination with one another. The invention is directed to a method for improving lung function in a subject, the method comprising modulating the ADAM33 gene in the subject by administering to the subject an effective amount of DHA or ARA, alone or in combination with one another. The invention is also directed to a method for improving cardiac function in a subject, the method comprising modulating a gene selected from the group consisting of TNNC1 and PDE3A in the subject by administering to the subject an

effective amount of DHA or ARA, alone or in combination with one another.

[00016] Still further, the invention is directed to a method for treating or preventing obesity in a subject, the method comprising modulating a gene selected from the group consisting of PPARD, NPY1R, and LEP in the subject by administering to the subject an effective amount of DHA or ARA, alone or in combination with one another.

[00017] Among the several advantages found to be achieved by the present invention, is that it provides a useful method for the modulation of selected genes in a subject. It also provides a method to upregulate or downregulate certain genes by easily administered compounds. It also provides a method for the prevention and/or treatment of various diseases and disorders in infancy, childhood, adolescence or adulthood.

BRIEF DESCRIPTION OF THE DRAWINGS

[00018] For a more complete understanding of the present invention, reference is now made to the following descriptions taken in conjunction with the accompanying drawings.

[00019] Figure 1 illustrates the ingenuity network analysis generated from L3/C comparisons. The network is graphically represented as nodes (genes) and edges (the biological relationship between genes).

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

[00020] Reference now will be made in detail to the embodiments of the invention, one or more examples of which are set forth below. Each example is provided by way of explanation of the invention, not a limitation of the invention. In fact, it will be apparent to those skilled in the art that various modifications and variations can be made in the present invention without departing from the scope or spirit of the invention. For instance, features illustrated or described as part of one embodiment, can be used on another embodiment to yield a still further embodiment.

[00021] Thus, it is intended that the present invention covers such modifications and variations as come within the scope of the appended claims and their equivalents. Other objects, features and aspects of the present invention are disclosed in or are obvious from the following detailed description. It is to be understood by one of ordinary skill in the art that the present discussion is a description of exemplary embodiments only, and is not intended as limiting the broader aspects of the present invention.

[00022] The term "modulation", as used herein, means a positive or negative regulatory effect on the expression of a gene.

[00023] As used herein, the term "upregulate" means a positive regulatory effect on the expression of a gene.

[00024] The term "downregulate" means a negative regulatory effect on the expression of a gene.

[00025] As used herein the term "expression" means the conversion of genetic information encoded in a gene into mRNA, transfer RNA (tRNA) or ribosomal RNA (rRNA) through transcription.

[00026] The term "infant" means a postnatal human that is less than about 1 year of age.

[00027] The term "child" means a human that is between about 1 year and 12 years of age. In some embodiments, a child is between the ages of about 1 and 6 years. In other embodiments, a child is between the ages of about 7 and 12 years.

[00028] The term "subject" means any animal. Exemplary subjects can be domestic animals, farm or zoo animals, wild animals, non-human animals, or humans. Non-humans subjects can include dogs, cats, horses, pigs, cattle, chickens, turkeys, and the like. Human subjects can be infants, children, and/or adults.

[00029] The terms "in need of", when used to describe a subject, mean that the subject belongs to a class of subjects that would benefit from the

gene modulation resulting from the administration of ARA and DHA. In some cases, a subject is in need of such modulation due to genetic factors, and in other cases the subject may be in need of such modulation due to nutritional factors, disease, trauma, or physical disorder.

[00030] As used herein, the term "infant formula" means a composition that satisfies the nutrient requirements of an infant by being a substitute for human milk. In the United States, the contents of an infant formula are dictated by the federal regulations set forth at 21 C.F.R. Sections 100, 106, and 107. These regulations define macronutrient, vitamin, mineral, and other ingredient levels in an effort to stimulate the nutritional and other properties of human breast milk.

[00031] In accordance with the present invention, the inventors have discovered a novel method for modulating the expression of one or more genes in a subject by administering docosahexaenoic acid (DHA) and arachidonic acid (ARA) to the subject. In some embodiments, certain genes are upregulated and in other embodiments certain genes are downregulated via the method of the present invention. In some embodiments, the method comprises administering docosahexaenoic acid (DHA) and arachidonic acid (ARA) to the subject in a ratio of ARA:DHA of between about 1:10 to about 10:1 by weight. In some embodiments, a ratio of about 1:5 to about 5:1 can be used, and in other embodiments a ratio of about 1:2 to about 2:1 can be used.

[00032] In fact, the present inventors have shown that the administration of DHA or ARA, alone or in combination with one another, can modulate the expression of genes across diverse biological processes. They have also shown that DHA or ARA, alone or in combination with one another, modulate the expression of genes involved in learning, memory, speech development, lung function, iron storage and transport, oxygenation, immune function, anti-cancer effects, tumor suppression, adiposity, weight gain, obesity, atherosclerosis and many other biological functions and disorders.

[00033] DHA and ARA are long chain polyunsaturated fatty acids (LCPUFA) which have previously been shown to contribute to the health and growth of infants. Specifically, DHA and ARA have been shown to support the development and maintenance of the brain, eyes and nerves of infants. Birch, E., *et al.*, *A Randomized Controlled Trial of Long-Chain Polyunsaturated Fatty Acid Supplementation of Formula in Term Infants after Weaning at 6 Weeks of Age*, Am. J. Clin. Nutr. 75:570-580 (2002). Clandinin, M., *et al.*, *Formulas with Docosahexaenoic Acid (DHA) and Arachidonic Acid (ARA) Promote Better Growth and Development Scores in Very-Low-Birth-Weight Infants (VLBW)*, Pediatr. Res. 51:187A-188A (2002). DHA and ARA are typically obtained through breast milk in infants that are breast-fed. In infants that are formula-fed, however, DHA and ARA must be supplemented into the diet.

[00034] While it is known that DHA and ARA are beneficial to the development of brain, eyes and nerves in infants, DHA and ARA previously have not been shown to have any effect on the modulation of genetic expression in a subject – in particular in an infant. The effects of DHA or ARA, alone or in combination with one another, on the modulation of genetic expression in the present invention were surprising and unexpected.

[00035] In the present invention, the subject can be an infant. Furthermore, the subject can be in need of the modulation of the expression of one or more genes. Such modulation could be upregulation or downregulation of one or more genes. The subject can be at risk for developing a disease or disorder related to the increased or reduced expression of a particular gene. The subject can be at risk due to genetic predisposition, lifestyle, diet, or inherited syndromes, diseases, or disorders.

[00036] In the present invention, the form of administration of DHA and ARA is not critical, as long as a therapeutically effective amount is

administered to the subject. In some embodiments, the DHA and ARA are administered to a subject via tablets, pills, encapsulations, caplets, gelcaps, capsules, oil drops, or sachets. In another embodiment, the DHA and ARA are added to a food or drink product and consumed. The food or drink product may be a children's nutritional product such as a follow-on formula, growing up milk, or a milk powder or the product may be an infant's nutritional product, such as an infant formula.

[00037] When the subject is an infant, it is convenient to provide DHA and ARA as supplements into an infant formula which can then be fed to the infant. The DHA and the ARA can be administered to the subject separately or in combination.

[00038] In an embodiment, the infant formula for use in the present invention is nutritionally complete and contains suitable types and amounts of lipid, carbohydrate, protein, vitamins and minerals. The amount of lipid or fat typically can vary from about 3 to about 7 g/100 kcal. The amount of protein typically can vary from about 1 to about 5 g/100 kcal. The amount of carbohydrate typically can vary from about 8 to about 12 g/100 kcal. Protein sources can be any used in the art, *e.g.*, nonfat milk, whey protein, casein, soy protein, hydrolyzed protein, amino acids, and the like. Carbohydrate sources can be any used in the art, *e.g.*, lactose, glucose, corn syrup solids, maltodextrins, sucrose, starch, rice syrup solids, and the like. Lipid sources can be any used in the art, *e.g.*, vegetable oils such as palm oil, canola oil, corn oil, soybean oil, palmolein, coconut oil, medium chain triglyceride oil, high oleic sunflower oil, high oleic safflower oil, and the like.

[00039] Conveniently, commercially available infant formula can be used. For example, Enfalac, Enfamil®, Enfamil® Premature Formula, Enfamil® with Iron, Lactofree®, Nutramigen®, Pregestimil®, and ProSobee® (available from Mead Johnson & Company, Evansville, IN, U.S.A.) may be supplemented with suitable levels of DHA or ARA, alone or in combination with one another, and used in practice of the method of

the invention. Additionally, Enfamil® LIPIL®, which contains effective levels of DHA and ARA, is commercially available and may be utilized in the present invention.

[00040] The method of the invention requires the administration of a DHA or ARA, alone or in combination with one another. In this embodiment, the weight ratio of ARA:DHA is typically from about 1:3 to about 9:1. In one embodiment of the present invention, this ratio is from about 1:2 to about 4:1. In yet another embodiment, the ratio is from about 2:3 to about 2:1. In one particular embodiment the ratio is about 2:1. In another particular embodiment of the invention, the ratio is about 1:1.5. In other embodiments, the ratio is about 1:1.3. In still other embodiments, the ratio is about 1:1.9. In a particular embodiment, the ratio is about 1.5:1. In a further embodiment, the ratio is about 1.47:1.

[00041] In certain embodiments of the invention, the level of DHA is between about 0.0% and 1.00% of fatty acids, by weight. Thus, in certain embodiments, ARA alone may treat or reduce obesity.

[00042] The level of DHA may be about 0.32% by weight. In some embodiments, the level of DHA may be about 0.33% by weight. In another embodiment, the level of DHA may be about 0.64% by weight. In another embodiment, the level of DHA may be about 0.67% by weight. In yet another embodiment, the level of DHA may be about 0.96% by weight. In a further embodiment, the level of DHA may be about 1.00% by weight.

[00043] In embodiments of the invention, the level of ARA is between 0.0% and 0.67% of fatty acids, by weight. Thus, in certain embodiments of the invention, DHA alone can moderate gene expression in a subject. In another embodiment, the level of ARA may be about 0.67% by weight. In another embodiment, the level of ARA may be about 0.5% by weight. In yet another embodiment, the level of DHA may be between about 0.47% and 0.48% by weight.

[00044] The amount of DHA in an embodiment of the present invention is typically from about 3 mg per kg of body weight per day to about 150 mg per kg of body weight per day. In one embodiment of the invention, the amount is from about 6 mg per kg of body weight per day to about 100 mg per kg of body weight per day. In another embodiment the amount is from about 15 mg per kg of body weight per day to about 60 mg per kg of body weight per day.

[00045] The amount of ARA in an embodiment of the present invention is typically from about 5 mg per kg of body weight per day to about 150 mg per kg of body weight per day. In one embodiment of this invention, the amount varies from about 10 mg per kg of body weight per day to about 120 mg per kg of body weight per day. In another embodiment, the amount varies from about 15 mg per kg of body weight per day to about 90 mg per kg of body weight per day. In yet another embodiment, the amount varies from about 20 mg per kg of body weight per day to about 60 mg per kg of body weight per day.

[00046] The amount of DHA in infant formulas for use in the present invention typically varies from about 2 mg/100 kilocalories (kcal) to about 100 mg/100 kcal. In another embodiment, the amount of DHA varies from about 5 mg/100 kcal to about 75 mg/100 kcal. In yet another embodiment, the amount of DHA varies from about 15 mg/100 kcal to about 60 mg/100 kcal.

[00047] The amount of ARA in infant formulas for use in the present invention typically varies from about 4 mg/100 kcal to about 100 mg/100 kcal. In another embodiment, the amount of ARA varies from about 10 mg/100 kcal to about 67 mg/100 kcal. In yet another embodiment, the amount of ARA varies from about 20 mg/100 kcal to about 50 mg/100 kcal. In a particular embodiment, the amount of ARA varies from about 25 mg/100 kcal to about 40 mg/100 kcal. In a particular embodiment, the amount of ARA is about 30 mg/100kcal.

[00048] The infant formula supplemented with oils containing DHA or ARA, alone or in combination with one another, for use in the present invention can be made using standard techniques known in the art. For example, an equivalent amount of an oil which is normally present in infant formula, such as high oleic sunflower oil, may be replaced with DHA or ARA.

[00049] The source of the ARA and DHA can be any source known in the art such as marine oil, fish oil, single cell oil, egg yolk lipid, brain lipid, and the like. The DHA and ARA can be in natural form, provided that the remainder of the LCPUFA source does not result in any substantial deleterious effect on the infant. Alternatively, the DHA and ARA can be used in refined form. The LCPUFA source may or may not contain eicosapentaenoic acid (EPA). In some embodiments, the LCPUFA used in the invention contains little or no EPA. For example, in certain embodiments, the infant formulas used herein contain less than about 20 mg/100 kcal EPA; in some embodiments less than about 10 mg/100 kcal EPA; in other embodiments less than about 5 mg/100 kcal EPA; and in still other embodiments substantially no EPA.

[00050] Sources of DHA and ARA may be single cell oils as taught in U.S. Pat. Nos. 5,374,657, 5,550,156, and 5,397,591, the disclosures of which are incorporated herein by reference in their entirety.

[00051] In an embodiment of the present invention, DHA or ARA, alone or in combination with one another, may be supplemented into the diet of an infant from birth until the infant reaches about one year of age. In a particular embodiment, the infant may be a preterm infant. In another embodiment of the invention, DHA or ARA, alone or in combination with one another, may be supplemented into the diet of a subject from birth until the subject reaches about two years of age. In other embodiments, DHA or ARA, alone or in combination with one another, may be supplemented into the diet of a subject for the lifetime of the subject.

Thus, in particular embodiments, the subject may be a child, adolescent, or adult.

[00052] In an embodiment, the subject of the invention is a child between the ages of one and six years old. In another embodiment the subject of the invention is a child between the ages of seven and twelve years old. In particular embodiments, the administration of DHA to children between the ages of one and twelve years of age is effective in modulating the expression of various genes, such as those listed in Tables 4-9. In other embodiments, the administration of DHA and ARA to children between the ages of one and twelve years of age is effective in modulating the expression of various genes, such as those listed in Tables 4-9.

[00053] In certain embodiments of the invention, DHA or ARA, alone or in combination with one another, are effective in modulating the expression of certain genes in an animal subject. The animal subject can be one that is in need of such regulation. The animal subject is typically a mammal, which can be domestic, farm, zoo, sports, or pet animals, such as dogs, horses, cats, cattle, and the like.

[00054] The present invention is also directed to the use of DHA or ARA, alone or in combination with one another, for the preparation of a medicament for modulating the expression of one or more genes in a subject, wherein the gene is selected from the group consisting of those genes listed in Tables 4-7 under the "Gene Symbol" column. In this embodiment, the DHA or ARA, alone or in combination with one another, may be used to prepare a medicament for the regulation of gene expression in any human or animal neonate. For example, the medicament could be used to regulate gene expression in domestic, farm, zoo, sports, or pet animals, such as dogs, horses, cats, cattle, and the like. In some embodiments, the animal is in need of the regulation of gene expression.

[00055] The following examples describe various embodiments of the present invention. Other embodiments within the scope of the claims herein will be apparent to one skilled in the art from consideration of the specification or practice of the invention as disclosed herein. It is intended that the specification, together with the examples, be considered to be exemplary only, with the scope and spirit of the invention being indicated by the claims which follow the examples. In the examples, all percentages are given on a weight basis (w/w) unless otherwise indicated.

Example 1

[00056] This example describes the results of DHA and ARA supplementation in modulating gene expression.

Methods

Animals

All animal work took place at the Southwest Foundation for Biomedical Research (SFBR) located in San Antonio, TX. Animal protocols were approved by the SFBR and Cornell University Institutional Animal Care and Use Committee (IACUC). Animal characteristics are summarized in Table 1.

Table 1. Baboon Neonate Characteristics

Number of animals	14
Gender	10 female, 4 male
Conceptional age at delivery (days)	181.8 ± 6.2
Birth weight (g)	860.3 ± 150.8
Weight at 12 weeks (g)	1519.1 ± 280.7
Weight gain (g)	658.8 ± 190.4

[00057] Fourteen pregnant baboons delivered spontaneously around 182 days gestation. Neonates were transferred to the nursery within 24 hours of birth and randomized to one of three diet groups. Animals were housed in enclosed incubators until 2 weeks of age and then moved to individual stainless steel cages in a controlled access nursery. Room temperatures were maintained at temperatures between 76°F to 82°F,

with a 12 hour light/dark cycle.. They were fed experimental formulas until 12 weeks of life.

Diets

[00058] Animals were assigned to one of the three experimental formulas, with LCPUFA concentrations presented in Table 2.

Table 2. Formula LCPUFA composition

	C	L	L3
DHA (%, w/w)	0	0.42±0.02	1.13±0.04
DHA (mg/100 kcal)	0	21.3±1.0	62.8±1.9
ARA (%, w/w)	0	0.77±0.02	0.71±0.01
ARA (mg/100 kcal)	0	39.4±0.9	39.2±0.7

[00059] Target concentrations were set as shown in brackets and diets were formulated with excess to account for analytical and manufacturing variability and/or possible losses during storage. Control (C) and L, moderate DHA formula, are the commercially available human infant formulas Enfamil® and Enfamil LIPIL®, respectively. Formula L3 had an equivalent concentration of ARA and was targeted at three-fold the concentration of DHA.

[00060] Formulas were provided by Mead Johnson & Company (Evansville, IN) in ready-to-feed form. Each diet was sealed in cans assigned two different color-codes to mask investigators. Animals were offered 1 ounce of formula four times daily at 07:00, 10:00, 13:00 and 16:00 with an additional feed during the first 2 nights. On day 3 and beyond, neonates were offered 4 ounces total; when they consumed the entire amount, the amount offered was increased in daily 2 ounce increments. Neonates were hand fed for the first 7-10 days until independent feeding was established.

Growth

[00061] Neonatal growth was assessed using body weight measurements, recorded two or three times weekly. Head circumference and crown-rump length data were obtained weekly for each animal. Organ weights were recorded at necropsy at 12 weeks.

Sampling & Array Hybridization

[00062] Twelve week old baboon neonates were anesthetized and euthanized at 84.4 ± 1.1 days. RNA from the precentral gyrus of the cerebral cortex was placed in RNALater according to vendor instructions and was used for the microarray analysis and validation of microarray results.

[00063] Microarray studies utilizing baboon samples with human oligonucleotide arrays have been successfully carried out previously. Cerebral cortex global messenger RNA in the three groups was analyzed using Affymetrix Genechip™ HG-U133 Plus 2.0 arrays. See http://www.affymetrix.com/products/arrays/specific/hgu133plus.affx. The HG-U133 Plus 2.0 has >54,000 probe sets representing 47,000 transcripts and variants, including 38,500 well-characterized human genes. One hybridization was performed for each animal (12 chips total). RNA preparations and array hybridizations were processed at Genome Explorations, Memphis, TN <http://www.genome-explorations.com>. The completed raw data sets were downloaded from the Genome Explorations secure ftp servers.

Statistics

[00064] Data are expressed as mean±SD. Statistical analysis was conducted using analysis of variance (ANOVA) to test the hypothesis of equivalent means for measures taken at 12 weeks, and Tukey's correction was used to control for multiple comparisons. Formula consumption, body weight, head circumference, and crown-rump length changes over time were tested with a random coefficient regression model to compare LCPUFA groups (L, L3) to control (C). Analysis were performed using SAS for Windows 9.1 (SAS Institute, Cary, NC) with significance declared at $p<0.05$.

Microarray Data Analysis

[00065] Raw data (.CEL files) were uploaded into Iobion's Gene Traffic MULTI 3.2 (Iobion Informatics, La Jolla, CA, USA) and analyzed by using the robust multi-array analysis (RMA) method. In general, RMA performs three operations specific to Affymetrix GeneChip arrays: global background normalization, normalization across all of the selected hybridizations, and log2 transformation of "perfect match" oligonucleotide probe values. Statistical analysis using the significance analysis tool set in Gene Traffic was utilized to perform Multiclass ANOVA on all probe level normalized data. Pairwise comparisons were made between C versus L and C versus L3 and all probe set comparisons reaching $P < 0.05$ were included in the analysis. Gene lists of differentially expressed probe sets were generated from this output for functional analysis.

Bioinformatics Analysis

[00066] Expression data was annotated using NIH DAVID <http://apps1.niaid.nih.gov/david> and NetAffx <http://www.affymetrix.com/analysis/index.affx>. Genes were grouped into functional categories and pathways based on the Gene Ontology Consortium <http://www.geneontology.org>, Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway Database <http://www.genome.jp/kegg/pathway.html> and <BioCarta <http://www.biocarta.com/>.

RNA Isolation and RT PCR

[00067] Real-Time Polymerase Chain Reaction (RT PCR) was conducted on nine genes to confirm the results of the array analysis. Total RNA from 30 mg samples of baboon cerebral cortex brain tissue homogenates was extracted using the RNeasy Mini kit (Qiagen, Valencia, CA). Each RNA preparation was treated with DNase I according to the manufacturer's instructions. The yield of total RNA was assessed by 260 nm UV absorption. The quality of RNA was analyzed by 260/280 nm

ratios of the samples and by agarose gel electrophoresis to verify RNA integrity.

[00068] One microgram total RNA from each group (C, L, L3) was reverse-transcribed into first strand cDNA using the iScript cDNA synthesis kit (Bio-Rad, Hercules, CA). The iScript reverse transcriptase was a modified MMLV-derived reverse transcriptase and the iScript reaction mix contains both oligo(dT) and random primers. The generated first strand cDNA was stored at -20^{0}C until used.

[00069] Quantitative real-time PCR using SYBR green and TaqMan assay methods was used to verify the differential expression of selected genes that were upregulated in the L3/C comparison. All the primers were gene-specific and generated from human sequences <www.ensembl.org>. PCR primers were designed with PrimerQuest software (IDT, Coralville, IA) and ordered from Integrated DNA Technologies (IDT, Coralville, IA). Initially primers were tested by polymerase chain reactions with baboon cerebral cortex brain cDNA as template in a 30 μl reaction volume using Eppendorf gradient thermal cycler (Eppendorf), with 1 μm of each primer, 0.25 mm each of dNTPs, 3 μl of 10× PCR buffer (Perkin-Elmer Life Sciences, Foster City, CA, USA), 1.5 mM $MgCl_2$ and 1.5 U *Taq* polymerase (Ampli *Taq* II; Perkin-Elmer Life Sciences). Thermal cycling conditions were: initial denaturation at 95°C for 5 minutes followed by 25-35 cycles of denaturation at 95°C for 30 seconds, annealing at 60°C for 1 minute and extension at 72°C for 1 minute, with a final extension at 72°C for 2 minutes. PCR products were separated by electrophoresis on 2% agarose gel stained with ethidium bromide and bands of appropriate sizes were obtained. The PCR products of LUM, TIMM8A, UCP2, ß-ACTIN, ADAM17 and ATP8B1 were sequenced and deposited with GenBank (Acc Numbers: DQ779570, DQ779571, DQ779572, DQ779573, DQ779574 and DQ779575, respectively).

[00070] Initially standardized primers for genes (ATP8B1, ADAM17, NF1, FZD3, ZNF611, UCP2, EGFR and control ß-ACTIN) were used for SYBR green real time PCR assay (Power SYBR Green PCR Master Mix, Applied Biosystems, Foster City, CA). The baboon LUM, TIMM8A and ß-ACTIN sequences were used to design TaqMan Assay (Assay by Design; <www.appliedbiosystems.com>). The selected gene symbols, primer pairs and probe details are depicted in Table 3.

Table 3. Real Time PCR Primers and Probes TaqMan Assay and SYBR Green Real Time PCR Primers

Real Time PCR Primers and Probes TaqMan Assay			
Gene Symbol	**Forward Primer**	**Reverse Primer**	**TaqMan Probe**
LUM	TGGGCAATCATCACCAAACTGT	ACATGGCACTTGGGTAGCTTT	CAGGGCAGTTACATTCT
TIMM8A	TGCACCAGATGACTGAACTTTGTT	AGCCCGACTGTCCAACTTTG	TCCATGCACTTCTCCC
β-ACTIN	CCAGCACGATGAAGATCAAGATC A	GCCGCCGATCCACACA	CCTGAGCGCAAGTACT
SYBR Green Real Time-PCR Primers			
Gene Symbol	**Forward Primer**	**Reverse Primer**	
ATP8B1	ACCATTGCCTCTGCTCTTGT	TTCAACCGCTTGCGATGCTT	
ADAM17	TGCTACTTGCAAAGGCGTGT	ACCCAACGATGTTGTCTGCT	
NF1	TGCTGCAATTGCCTGTGTCA	TCCACAACCTTGCACTGCTT	
FZD3	ACAGCAGCTTTGGCAATGGA	AATGTGGCCGAGAGGCAAAT	
ZNF611	TTGTCAACAGGGCAAGGCAA	TGGGTGCTTCAAGGCCATTT	
UCP2	AGCACCGTCAATGCCTACAA	AGGCAGAAGTGAAGTGGCAA	
EGFR	TGCCAAGGCACGAGTAACAA	AGGAATTCGCTCCACTGTGT	
β-ACTIN	ATTGCCGACAGGATGCAGAA	AAGCATTTGCGGTGGACGAT	

[00071] Quantitative real time PCR reactions were done with the Applied Biosystems Prism 7300/7500 real time PCR system (Applied Biosystems, Foster City, CA). After 2 minutes of UNG activation at 50°C, initial denaturation at 95°C was carried out for 10 minutes, the cycling conditions of 40 cycles consisted of denaturation at 95°C for 15 seconds, annealing at 60°C for 30 seconds, and elongation at 72°C for 1 minute. For SYBR green method UNG activation step was eliminated. All reactions were done in triplicate and ß-ACTIN was used as the reference gene. Relative quantification was performed by using comparative CT method (ABI Relative Quantification Chemistry guide # 4347824).

Network Analysis

[00072] A web-delivered bioinformatics tool set, Ingenuity pathway analysis (IPA 3.0) <http://www.ingenuity.com>, was used to identify functional networks influenced by the dietary treatments. IPA is a knowledge database generated from the peer-reviewed scientific publications that enables discovery, visualization and exploration of functional biological networks in gene expression data and delineates the functions most significant to those networks. The 1108 differentially expressed probe sets identified by microarray data, as discussed below, were used for network analyses. Affymetrix probe set ID's were uploaded into IPA and queried against all other genes stored in the IPA knowledge database to generate a set of networks having up to 35 genes. Each Affymetrix probe set ID was mapped to its corresponding gene identifier in the IPA knowledge database. Probe sets representing genes having direct interactions with genes in the IPA knowledge database are called "focus" genes, which were then used as a starting point for generating functional networks. Each generated network was assigned a score according to the number of differentially regulated focus genes in the dataset. These scores are derived from negative logarithm of the *P* indicative of the likelihood that focus genes found together in a network

due to random chance. Scores of 4 or higher have 99.9% confidence level of significance.

Results and Discussion

[00073] Of the 38,000 well-characterized genes analyzed, significance analysis ($P < 0.05$) identified changes in expression levels of approximately 1108 probe sets (ps) in at least one of the brain, spleen, thymus and liver. This represents 2.05% of the total > 54,000 ps on the oligoarray. Most ps showed < 2-fold change and some genes were modulated differently in different organs.

[00074] For the L/C comparisons, 534 ps were upregulated and 574 ps were downregulated, while for the L3/C comparisons, 666 ps were upregulated and 442 ps were downregulated. This illustrates that more genes were overexpressed in the cerebral cortex in response to increasing formula ARA and DHA.

[00075] Of the approximately 1108 genes that were modulated, approximately 700 of them have names and known functions. The remaining genes are known only by their license plate (i.e., some ill-described property).

[00076] Table 4 illustrates genes that were shown to be upregulated in the brain by DHA and ARA supplementation that have a known biological function. The first column shows the Affymetrix Probe ID No., a number given to the gene during the study. The second column, entitled "Gene Symbol" describes the commonly recognized name of the genes. The third column shows the expression change of the gene. Positive values indicate an upregulation and negative values indicate a downregulation. The expression change is provided as a "log2 value", or a log base 2 value. For purposes of discussion herein, some of these values were converted to linear percentages.

[00077] The fifth column in Table 4, entitled "Organ", lists an abbreviation for the organ in which the gene was modulated. The

abbreviations are as follows: liver (L), brain (B), and thymus (T). The sixth, seventh, eighth and ninth columns, entitled "biological function", "molecular function", "cellular component" and "pathway", provide any known information about that gene related to those functions.

[00078] Tables 5 through 7 contain the same categories as those discussed in Table 4. Table 5 illustrates genes that were shown to be downregulated by DHA and ARA supplementation at either 0.33% DHA or 1.00% DHA that have a known biological function. Table 6 illustrates genes that were shown to be upregulated by DHA and ARA supplementation at either 0.33% DHA or 1.00% DHA that have no known biological function. Table 7 illustrates genes that were shown to be downregulated by DHA and ARA supplementation at either 0.33% DHA or 1.00% DHA that have no known biological function.

[00079] Table 8 illustrates spleen genes that were either upregulated or downregulated as a result of 1.00% DHA and 0.67% ARA supplementation. The first column shows the Affymetrix Probe ID No., the second column describes the commonly recognized name of the genes, and the third column shows the expression change of the gene. The fourth, fifth, and sixth columns provide any known information about those genes. Table 9 illustrates spleen genes that were either upregulated or down regulated as a result of 0.33% DHA and 0.67% ARA supplementation. The columns are organized in the same manner as those in Table 8.

Table 4. Genes with known function upregulated by 3x LCPUFA (L3, 1.00% DHA-0.67% ARA) supplementation in Brain (B), Liver (L) and Thymus (T).

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
228834_at	TOB1	1.36	2.216	L	negative regulation of cell proliferation	SH3/SH2 adaptor protein activity /// protein binding	---	Circadian Exercise
231628_s_at	SERPINB6	-0.536	2.198	B	---	serine-type endopeptidase inhibitor activity /// protein binding	cytosol	---
228834_at	TOB1	0.382	1.07	T	negative regulation of cell proliferation	SH3/SH2 adaptor activity /// protein binding	---	Circadian Exercise
231591_at	BHMT	-0.306	0.957	L	protein amino acid methylation// regulation of homocysteine metabolism	betaine-homocysteine S-methyltransferase activity	---	Glycine, serine and threonine metabolism/// Methionine metabolism
231655_x_at	SERPINB6	-0.232	0.857	B	---	serine-type endopeptidase inhibitor activity /// protein binding	cytosol	---
1564654_at	COL4A6	0.165	0.69	B	phosphate transport /// cell adhesion /// extracellular matrix organization and biogenesis	extracellular matrix structural constituent /// protein binding	collagen /// collagen type IV /// cytoplasm	ECM-receptor interaction
208137_x_at	ZNF611	0.14	0.659	B	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
210800_at	TIMM8A	0.06	0.646	B	mitochondrial inner membrane protein import/// neurogenesis/// perception of sound /// protein transport	---	mitochondrial inner membrane protein insertion complex	---
238895_at	TEBP/// PTGI	0.021	0.604	B	telomere maintenance /// prostaglandin biosynthesis /// protein folding /// signal transduction	telomerase activity /// prostaglandin-E synthase activity /// unfolded protein binding	chromosome, telomeric region /// telomerase holoenzyme complex	---
230867_at	LOC131873	0.056	0.581	B	phosphate transport	---	cytoplasm	---
206844_at	FBP2	-0.432	0.58	T	carbohydrate metabolism /// fructose metabolism /// gluconeogenesis	fructose-2,6-bisphosphate 2-phosphatase activity /// hydrolase activity /// fructose-bisphosphatase activity /// phosphoric ester hydrolase activity	---	Glycolysis and Gluconeogenesis /// Glycolysis / Gluconeogenesis /// Pentose phosphate pathway /// Fructose and mannose metabolism /// Carbon fixation
205745_x_at	ADAM17	0.448	0.576	B	proteolysis and peptidolysis /// cell-cell signaling	metalloendopeptidase activity /// zinc ion binding /// hydrolase activity	integral to plasma membrane	Notch Signaling

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
233808_at	STK3	0.038	0.566	B	protein amino acid phosphorylation /// apoptosis /// signal transduction /// protein kinase cascade /// positive regulation of apoptosis	magnesium ion binding /// protein kinase activity /// protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity /// protein dimerization activity	nucleus /// cytoplasm	MAPK signaling pathway
215208_x_at	RPL35A	0.132	0.541	B	protein biosynthesis	tRNA binding /// structural constituent of ribosome	intracellular /// ribosome /// cytosolic large ribosomal subunit (sensu Eukaryota)	Ribosomal Proteins
231201_at	PTGER1	0.184	0.527	L	G-protein coupled receptor protein signaling pathway	prostaglandin E receptor activity/// rhodopsin like-receptor activity	Integral to plasma membrane	Calcium signaling pathway/// Neuroactive ligand-receptor interaction
238269_at	FBXL7	0.03	0.519	B	ubiquitin cycle	---	---	---
206851_at	RNASE3	0.693	0.512	T	RNA catabolism /// defense response to bacteria	nucleic acid binding /// endonuclease activity /// pancreatic ribonuclease activity /// ribonuclease activity /// hydrolase activity	extracellular region /// soluble fraction	---
208844_at	VDAC3	-0.018	0.512	B	Adenine transport	voltage-gated anion channel porin activity	integral to plasma membrane	Calcium signaling pathway
221304_at	UGT1A10	-0.058	0.507	B	metabolism	glucuronosyltransferase activity	integral to membrane/// endoplasmic reticulum	Starch and sucrose metabolism/// Androgen and estrogen metabolism/// Porphyrin and chlorophyll metabolism/// Pentose and glucuronate interconversions
1554583_a_at	MGC50559	-0.035	0.495	B	---	S-adenosylmethionine-dependent methyltransferase activity /// transferase activity	---	---
213102_at	ACTR3	0.196	0.493	T	cell motility	structural molecule activity /// Arp2/3 protein complex protein binding	---	---
216600_x_at	ALDOB	-0.016	0.492	B	fructose metabolism /// glycolysis	fructose-bisphosphate aldolase activity /// lyase activity	cytoplasm	Glycolysis and Gluconeogenesis /// Glycolysis / Gluconeogenesis /// Pentose phosphate pathway /// Inositol metabolism /// Fructose and mannose metabolism /// Carbon fixation
236165_at	MSL3L1	0.13	0.487	L	chromatin assembly or disassembly /// regulation of transcription, DNA-dependent /// chromatin modification	chromatin binding	chromatin /// nucleus	---

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values):	Expression change (log2 Values):		Geneontology	Geneontology	Geneontology	
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
216202_s_at	SPTLC2	0.338	0.486	B	biosynthesis	serine C-palmitoyltransferase activity /// acyltransferase activity /// transferase activity, transferring nitrogenous groups	endoplasmic reticulum /// integral to membrane	Glycosphingolipid metabolism
231710_at	CAPS	-0.283	0.483	L	intracellular signaling cascade	calcium ion binding	---	---
238991_at	ASB1	0.191	0.482	L	intracellular signaling cascade /// negative regulation of cytokine biosynthesis	---	intracellular	---
209904_at	TNNC1	0.194	0.481	L	muscle development	calcium ion binding	---	---
233868_x_at	ADAM33	0.124	0.481	B	proteolysis and peptidolysis /// integrin-mediated signaling pathway /// regulation of cytokine biosynthesis /// regulation of cell proliferation	metalloendopeptidase activity /// metallopeptidase activity /// zinc ion binding /// hydrolase activity	integral to membrane	---
215387_x_at	GPC6	-0.159	0.472	L	---	---	extracellular matrix (sensu Metazoa) /// integral to plasma membrane /// membrane	---
232597_x_at	SFRS2IP	-0.102	0.472	B	mRNA processing /// RNA splicing	pre-mRNA splicing factor activity	DNA-directed RNA polymerase II, core complex	Apoptosis
213575_at	TRA2A	0.044	0.47	L	nuclear mRNA splicing, via spliceosome	RNA binding /// pre-mRNA splicing factor activity	nucleus	---
1555516_at	FOXP2	-0.105	0.463	B	regulation of transcription, DNA-dependent	nucleic acid binding /// transcription factor activity /// zinc ion binding	nucleus	---
215949_x_at	IGHM	-0.015	0.461	L	immune response	antigen binding	membrane fraction	---
205355_at	ACADSB	-0.15	0.46	B	electron transport /// fatty acid metabolism	acyl-CoA dehydrogenase activity /// oxidoreductase activity	mitochondrion	Fatty Acid Degradation
227803_at	ENPP5	0.194	0.457	T	nucleotide metabolism	hydrolase activity	integral to membrane	---
221418_s_at	THRAP5	0.401	0.457	L	regulation of transcription from Pol II promoter /// transcription from Pol II promoter /// transcription initiation from Pol II promoter /// androgen receptor signaling pathway	transcription cofactor activity /// transcription coactivator activity /// receptor activity /// RNA polymerase II transcription mediator activity /// transcriptional activator activity /// thyroid hormone receptor coactivator activity /// vitamin D receptor binding /// thyroid hormone receptor binding	mediator complex /// nucleus	---
216844_at	RoXaN	-0.248	0.455	B	---	nucleic acid binding /// zinc ion binding	nucleus	---

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values):	Expression change (log2 Values):		Geneontology	Geneontology	Geneontology	
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
214211_at	FTH1	-0.113	0.451	B	iron ion transport /// intracellular sequestering of iron ion /// immune response /// cell proliferation /// negative regulation of cell proliferation	binding /// ferric iron binding /// kinase binding	plasma membrane /// ferritin complex	---
214594_x_at	ATP8B1	0.357	0.447	B	lipid metabolism /// cation transport /// digestion /// bile acid transport	magnesium ion binding /// phospholipid-translocating ATPase activity /// ATP binding /// hydrolase activity /// ATPase activity	integral to plasma membrane	Folate biosynthesis/// Starch and sucrose metabolism
244357_at	LOC64744	-0.073	0.446	B	regulation of GTPase activity	---	---	---
241093_at	38601	0.496	0.444	T	cytokinesis /// cell cycle	protein binding /// GTP binding	---	---
221305_s_at	UGT1A8 /// U	0.127	0.442	B	metabolism /// metabolism	UDP-glycosyltransferase activity /// glucuronosyltransferase activity /// transferase activity, transferring hexosyl groups	microsome /// integral to membrane	Pentose and glucuronate interconversions /// Androgen and estrogen metabolism /// Starch and sucrose metabolism /// Porphyrin and chlorophyll metabolism
242364_x_at	EVER1	0.003	0.442	B	---	---	integral to membrane	---
205542_at	STEAP	0.087	0.442	B	---	channel or pore class transporter activity	early endosome /// integral to plasma membrane /// intercellular junction /// integral to Golgi membrane /// vesicular fraction	---
242725_at	KDELR2	0.256	0.439	L	intracellular protein transport	receptor activity /// KDEL sequence binding	endoplasmic reticulum /// Golgi apparatus /// integral to membrane	---
233815_at	NAALAD2	0.093	0.438	B	proteolysis and peptidolysis	carboxypeptidase activity /// dipeptidyl-peptidase IV activity /// peptidase activity /// metallopeptidase activity /// dipeptidase activity /// glutamate carboxypeptidase II activity	integral to membrane	---
233041_x_at	BTBD9	0.104	0.436	B	cell adhesion	protein binding	---	---
205342_s_at	SULT1C1	0.438	0.435	T	amine metabolism	sulfotransferase activity /// transferase activity	cytoplasm	cysteine metabolism
205852_at	CDK5R2	-0.014	0.435	L	regulation of cyclin dependent protein kinase activity	cyclin-dependent protein kinase 5 activator activity	cyclin-dependent protein kinase 5 activator complex	---
208141_s_at	MGC4293	-0.217	0.435	L	---	binding	---	---
213027_at	SSA2	0.098	0.434	B	transcription from Pol III promoter	RNA binding	ribonucleoprotein complex	---

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
208107_s_at	LOC81691	-0.004	0.432	B	nuclear mRNA splicing, via spliceosome	nucleic acid binding /// exonuclease activity	nucleus	---
214507_s_at	EXOSC2	0.402	0.431	B	rRNA processing	3'-5'-exoribonuclease activity /// exonuclease activity /// 7S RNA binding /// hydrolase activity	exosome (RNase complex) /// nucleus /// cytoplasm	---
220411_x_at	FLJ23447	-0.032	0.43	B	---	---	integral to membrane	---
211851_x_at	BRCA1	0.061	0.43	B	cell cycle checkpoint /// DNA repair /// regulation of transcription from Pol II promoter /// regulation of transcription from Pol III promoter /// DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator /// protein ubiquitination /// regulation of cell proliferation /// regulation of apoptosis /// positive regulation of DNA repair /// negative regulation of cell cycle /// negative regulation of centriole replication	DNA binding /// damaged DNA binding /// transcription coactivator activity /// ubiquitin-protein ligase activity /// protein binding /// zinc ion binding /// tubulin binding /// transcriptional activator activity	ubiquitin ligase complex /// extracellular space /// intracellular /// nucleus /// transcription factor complex /// gamma-tubulin ring complex	DNA Repair
211051_s_at	EXTL3	-0.012	0.429	L	---	glucuronyl-galactosyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase activity /// transferase activity, transferring glycosyl groups	endoplasmic reticulum /// integral to membrane	Chondroitin / Heparan sulfate biosynthesis
213936_x_at	SFTPB	0.047	0.429	B	lipid metabolism /// sphingolipid metabolism /// respiratory gaseous exchange /// organogenesis /// regulation of liquid surface tension	---	extracellular space /// lysosome	---
211094_s_at	NF1	-0.015	0.428	B	Ras protein signal transduction /// negative regulation of cell proliferation /// negative regulation of cell cycle	enzyme inhibitor activity /// Ras GTPase activator activity	cytoplasm	MAPK signaling pathway
1569617_at	OSBP2	-0.22	0.428	B	lipid transport /// steroid metabolism	---	---	---
242567_at	ABTB1	-0.1	0.426	B	---	translation elongation factor activity /// protein binding	---	---
226145_s_at	FRAS1	-0.063	0.423	T	cell communication	---	extracellular matrix (sensu Metazoa) /// integral to membrane	---
223088_x_at	ECHDC1	-0.488	0.421	L	metabolism	catalytic activity	mitochondrion	---

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Geneontology Pathway
1557953_at	ZKSCAN1	0.098	0.42	L	*regulation of transcription, DNA-dependent*	*nucleic acid binding /// transcription factor activity /// zinc ion binding*	*nucleus*	---
237399_at	MTA3	-0.03	0.42	B	regulation of transcription, DNA-*dependent*	transcription factor activity	nucleus	---
211638_at	IGHA2	-0.064	0.419	L	*immune response*	antigen binding	membrane fraction	---
203165_s_at	SLC33A1	0.08	0.418	L	transport	acetyl-CoA transporter activity	*membrane fraction /// endoplasmic reticulum membrane /// integral to plasma membrane*	ganglioside biosynthesis
220581_at	C6orf97	-0.043	0.416	B	muscle development	actin binding	cytoskeleton	---
1557925_at	MSRA	0.095	0.416	B	response to oxidative stress/// sulfur amino acid metabolism/// *response to external stimulus*/// physiological process/// response to biotic stimulus/// protein modification/// oxygen and reactive oxygen species metabolism	oxidoreductase activity, acting on sulfur group of *donors, disulfide as acceptor*/// oxidoreductase activity/// protein-methionine-S-*oxide reductase activity*/// catalytic activity	---	---
241572_at	MGC50721	0.288	0.415	B	---	protein binding	---	---
222935_x_at	SLC39A8	0.063	0.413	L	transport /// metal ion transport	metal ion transporter activity	integral to membrane	---
208082_x_at	MKRN4	0.393	0.412	B	*protein ubiquitination*	*nucleic acid binding///* ubiquitin-protein ligase activity/// zinc ion binding	*ubiquitin ligase complex*	---
209278_s_at	TFPI2	0.006	0.409	L	blood coagulation	serine-type endopeptidase inhibitor activity /// extracellular matrix structural constituent /// protease *inhibitor activity*	extracellular matrix (sensu *Metazoa*)	---
230253_at	SCUBE3	0.06	0.401	B	*Coagulation/// physiological* process/// blood coagulation/// regulation of body fluids/// *organismal physiological* process/// hemostasis	signal *transducer activity///* receptor activity/// calcium ion binding	---	---
231902_at	LOC152485	0.026	0.401	B	---	nucleic acid binding /// zinc ion binding	nucleus	---
201630_s_at	ACP1	0.251	0.4	T	protein amino acid *dephosphorylation*	acid phosphatase activity /// protein tyrosine phosphatase activity /// non-membrane spanning protein tyrosine phosphatase activity /// hydrolase activity	soluble fraction /// cytoplasm	gamma-*hexachlorocyclohexane degradation/// riboflavin metabolism*

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values):	Expression change (log2 Values):		Geneontology	Geneontology	Geneontology	
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
217046_s_at	AGER	-0.11	0.399	L	inflammatory response /// cell surface receptor linked signal transduction	transmembrane receptor activity	integral to plasma membrane	---
232665_x_at	SMURF1	0.197	0.399	B	ubiquitin cycle /// ectoderm development /// cell differentiation /// negative regulation of BMP signaling pathway /// protein ubiquitination during ubiquitin-dependent protein catabolism	ubiquitin-protein ligase activity /// ligase activity	intracellular	Tryptophan metabolism/// TGF-beta signaling pathway/// Ubiquitin mediated proteolysis
208439_s_at	FCN2	-0.08	0.398	L	phosphate transport /// opsonization /// antimicrobial humoral response (sensu Vertebrata)	antigen binding /// calcium ion binding /// sugar binding	cytoplasm	---
243209_at	KCNQ4	0.108	0.396	T	cation transport /// potassium ion transport /// perception of sound	voltage-gated potassium channel activity	membrane fraction /// voltage-gated potassium channel complex /// membrane	---
214567_s_at	XCL1 /// XCL2	0.49	0.396	T	calcium ion homeostasis /// chemotaxis /// immune response /// signal transduction /// cell-cell signaling /// sensory perception /// antimicrobial humoral response (sensu Vertebrata) /// chemotaxis /// signal transduction /// cell-cell signaling /// circulation	chemokine activity /// chemokine activity	extracellular region /// soluble fraction	cytokine-cytokine receptor interaction
227863_at	CTSD	0.181	0.394	L	proteolysis and peptidolysis	cathepsin D activity /// pepsin A activity /// hydrolase activity	extracellular region /// lysosome	---
1555943_at	MGC5352	0.088	0.391	B	metabolism	catalytic activity	---	---
1553072_at	BNIPL	-0.044	0.39	L	apoptosis	---	---	---
229714_at	HS6ST3	-0.072	0.39	L	---	transferase activity	---	---
242293_at	ING3	0.019	0.388	L	regulation of transcription, DNA-dependent	DNA binding	---	---
208079_s_at	STK6	-0.331	0.387	B	protein amino acid phosphorylation /// cell cycle /// mitosis	protein serine/threonine kinase activity /// protein binding /// ATP binding /// transferase activity	nucleus /// spindle	---
220705_s_at	ADAMTS7	0.042	0.386	L	proteolysis and peptidolysis /// integrin-mediated signaling pathway	metalloendopeptidase activity /// zinc ion binding /// hydrolase activity	extracellular matrix (sensu Metazoa) /// extracellular matrix	---
232148_at	NSMAF	-0.054	0.386	B	ceramide metabolism /// signal transduction	receptor signaling protein activity	soluble fraction /// cytoplasm	---
220480_at	HAND2	0.072	0.384	L	angiogenesis /// regulation of transcription, DNA-dependent /// development	DNA binding	nucleus	---

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values):	Expression change (log2 Values):		Geneontology	Geneontology	Geneontology	
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
213275_x_at	CTSB	0.051	0.384	B	proteolysis and peptidolysis	cathepsin B activity /// hydrolase activity	intracellular /// lysosome	---
204652_s_at	NRF1	0.189	0.383	L	generation of precursor metabolites and energy /// regulation of transcription, DNA-dependent /// regulation of transcription from Pol II promoter	transcription factor activity	nucleus	---
200027_at	NARS	-0.054	0.382	T	protein biosynthesis /// asparaginyl-tRNA aminoacylation /// aspartyl-tRNA aminoacylation	nucleic acid binding /// aspartate-tRNA ligase activity /// asparagine-tRNA ligase activity /// ATP binding /// ligase activity	soluble fraction /// cytoplasm	Alanine and aspartate metabolism /// Aminoacyl-tRNA biosynthesis
1555082_a_at	NEK11	0.156	0.381	L	protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding	---	---
226533_at	HINT3	0.036	0.381	B	---	kinase activity/// catalytic activity	---	---
234563_at	PDE3A	0.105	0.379	B	lipid metabolism /// signal transduction	cGMP-inhibited cyclic-nucleotide phosphodiesterase activity /// hydrolase activity	membrane	Purine metabolism
228148_at	ZNF584	0.099	0.379	B	regulation of transcription, DNA-dependent	nucleic acid binding /// DNA binding /// zinc ion binding	intracellular /// nucleus	---
213631_x_at	DHODH	0.015	0.378	B	pyrimidine nucleotide biosynthesis	dihydroorotate dehydrogenase activity/// dihydroorotate oxidase activity/// oxidoreductase activity	mitochondrial inner membrane	Pyrimidine metabolism
223257_at	KIAA1333	0.112	0.378	B	regulation of transcription, DNA-dependent /// ubiquitin cycle /// protein ubiquitination	DNA binding /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex /// intracellular	---
229191_at	TBCD	-0.179	0.377	L	protein folding /// beta-tubulin folding	binding /// chaperone binding	microtubule	---
205766_at	TCAP	-0.087	0.376	L	protein complex assembly /// sarcomere alignment	structural constituent of muscle	cytoplasm	Striated muscle contraction
229554_at	LUM	0.038	0.375	B	visual perception /// collagen fibril organization	extracellular matrix structural constituent /// collagen binding	extracellular matrix (sensu Metazoa) /// fibrillar collagen	---
202312_s_at	COL1A1	-0.07	0.374	L	skeletal development /// phosphate transport /// perception of sound /// epidermis development	extracellular matrix structural constituent /// structural constituent of bone	collagen /// collagen type I /// cytoplasm	Inflammatory Response Pathway
1555538_s_at	FAM9B	-0.003	0.373	B	---	---	nucleus	---

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values):	Expression change (log2 Values):		Geneontology	Geneontology	Geneontology	
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
214724_at	DIXDC1	0.398	0.373	B	frizzled signaling pathway /// development	actin binding /// signal transducer activity	intracellular	---
230416_at	SLC18A2	0.115	0.373	B	monoamine transport	transporter activity	integral to plasma membrane	---
212063_at	CD44	0.453	0.372	T	cell adhesion /// cell-matrix adhesion /// cell-cell adhesion	receptor activity /// protein binding /// collagen binding /// hyaluronic acid binding /// hyaluronic acid binding	integral to plasma membrane /// membrane /// integral to membrane	ECM-receptor interaction
240262_at	CTNNA1	-0.047	0.372	L	cell adhesion	structural molecule activity /// protein binding /// cadherin binding	actin cytoskeleton	---
238908_at	CALU	-0.248	0.372	L	---	calcium ion binding	endoplasmic reticulum /// Golgi apparatus	---
222392_x_at	PERP	0.058	0.372	B	---	---	integral to membrane	---
230736_at	SVIL	0.416	0.371	T	cytoskeletal anchoring /// myogenesis	actin filament binding /// actin filament binding	nucleus /// cytoplasm /// plasma membrane /// actin cytoskeleton /// costamere	---
1563187_at	KCNH7	-0.149	0.368	B	regulation of transcription, DNA-dependent /// cation transport /// potassium ion transport /// signal transduction	signal transducer activity /// voltage-gated potassium channel activity	membrane /// integral to membrane	---
1566342_at	SOD2	-0.095	0.368	B	age-dependent response to reactive oxygen species/// cellular defense response (sensu Vertebrata)/// regulation of transcription from RNA polymerase II promoter/// response to oxidative stress/// response to superoxide/// superoxide metabolism	manganese superoxide dismutase activity/// manganese ion binding/// oxidoreductase activity/// superoxide dismutase activity	mitochondrion	---
201102_s_at	PFKL	-0.056	0.367	L	fructose 6-phosphate metabolism /// glycolysis	magnesium ion binding /// 6-phosphofructokinase activity /// ATP binding /// kinase activity /// transferase activity	cytoplasm /// 6-phosphofructokinase complex	Glycolysis and Gluconeogenesis/// pentose phosphate pathway
241015_at	SESN3	0.045	0.366	B	cell cycle arrest	---	nucleus	---
214372_x_at	ERN2	-0.03	0.365	L	electron transport /// mRNA processing /// protein amino acid phosphorylation /// metabolism	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// oxidoreductase activity /// endoribonuclease activity, producing 5'-phosphomonoesters	---	---

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
215960_at	SLC5A4	-0.167	0.365	B	transport /// sodium ion transport	transporter activity /// sugar porter activity /// symporter activity	integral to membrane	---
230125_at	GUSB	0.004	0.364	L	carbohydrate metabolism/// glycosaminoglycan catabolism	beta-glucuronidase activity	lysosome	Glycosaminoglycan degradation/// Pentose and glucuronate interconversions/// Porphyrin and chlorophyll metabolism/// Starch and sucrose metabolism
243124_at	BANP	0.064	0.363	B	---	---	nucleus	---
205640_at	ALDH3B1	-0.213	0.362	L	alcohol metabolism /// lipid metabolism /// metabolism	aldehyde dehydrogenase (NAD(P)+) activity /// oxidoreductase activity	---	Glycolysis / Gluconeogenesis /// Histidine metabolism /// Tyrosine metabolism /// Phenylalanine metabolism
240535_at	LOC124245	-0.157	0.362	L	---	nucleic acid binding	---	---
216667_at	RNASE2	0.335	0.361	T	RNA catabolism /// chemotaxis /// sensory perception	nucleic acid binding /// endonuclease activity /// pancreatic ribonuclease activity /// ribonuclease activity /// hydrolase activity	extracellular region	---
214250_at	NUMA1	0.004	0.361	L	mitotic anaphase /// nuclear organization and biogenesis	structural molecule activity	nucleus /// spindle microtubule	---
213426_s_at	CAV2	-0.033	0.361	L	---	---	caveolar membrane/// integral to membrane	Focal adhesion/// Integrin mediated cell adhesion
206055_s_at	SNRPA1	0.151	0.359	T	RNA splicing	RNA binding	snRNP U2	mRNA processing
242982_x_at	ITGB8	0.067	0.359	L	cell-matrix adhesion /// integrin-mediated signaling pathway	receptor activity /// protein binding	integrin complex /// integral to membrane	Integrin-mediated cell adhesion
1565778_at	ABCA8	-0.159	0.359	L	---	nucleotide binding /// ATP binding /// ATPase activity	---	---
238324_at	p66alpha	-0.002	0.358	L	DNA methylation /// regulation of transcription, DNA-dependent /// negative regulation of transcription, DNA-dependent	transcription factor activity /// transcriptional repressor activity /// protein binding, bridging	nucleus /// NuRD complex	---
215181_at	CDH22	-0.174	0.358	L	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	integral to membrane	---
210706_s_at	RNF24	0.174	0.358	L	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
218827_s_at	Cep192	0.247	0.358	B	---	---	integral to membrane	---
211969_at	HSPCA	-0.225	0.357	T	protein folding /// response to unfolded protein	ATP binding /// unfolded protein binding	---	---
1565698_at	HECTD2	-0.097	0.357	B	ubiquitin cycle	Ubiquitin-protein ligase activity	intracellular	---

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		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
201867_s_at	TBL1X	0.029	0.356	B	regulation of transcription, DNA-dependent /// ubiquitin cycle /// signal transduction /// visual perception /// perception of sound	---	nucleus	Wnt signaling
227562_at	MAP2K1IP1	0.111	0.355	T	---	kinase activity	---	MAPK signaling pathway
222272_x_at	SCIN	0.05	0.354	B	---	actin binding	cytoskeleton	---
216379_x_at	CD24	0.515	0.353	T	humoral immune response	---	plasma membrane	---
218430_s_at	FLJ12994	-0.052	0.353	L	regulation of transcription, DNA-dependent	DNA binding	---	---
240935_at	TCF2	0.081	0.353	B	regulation of transcription, DNA-dependent /// positive regulation of transcription	transcription factor activity /// transcriptional activator activity	nucleus	---
242756_at	WASL	0.003	0.353	B	protein complex assembly /// cell motility /// actin polymerization and/or depolymerization	actin binding /// small GTPase regulatory/interacting protein activity	actin cytoskeleton	Adherens junction/// Regulation of actin cytoskeleton
201829_at	NET1	-0.441	0.352	L	---	---	nucleus	---
202191_s_at	GAS7	-0.015	0.351	L	cell cycle arrest /// development /// neurogenesis	transcription factor activity	---	---
1561039_a_at	ZNF81	0.135	0.35	B	regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	nucleus	---
208998_at	UCP2	0.217	0.35	B	transport /// mitochondrial transport /// proton transport	transporter activity /// binding	membrane fraction /// mitochondrion /// mitochondrial inner membrane /// integral to membrane	Electron Transport Chain
225783_at	NCE2	0.271	0.348	T	ubiquitin cycle	ubiquitin conjugating enzyme activity /// ligase activity	---	---
211904_x_at	RAD52	0.032	0.348	L	DNA repair /// double-strand break repair /// DNA recombination /// mitotic recombination /// meiotic recombination	DNA binding	nucleus	---
218724_s_at	TGIF2	0.019	0.347	B	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
226090_x_at	RABL3	0.113	0.347	B	protein transport/// small GTPase mediated signal transduction	GTP binding	---	---
1556294_at	FXYD2	-0.176	0.345	L	ion transport	ion channel activity /// potassium ion binding/// sodium ion binding	integral to membrane	---
217281_x_at	IGHG1 /// IGH	0.137	0.345	L	immune response	antigen binding	membrane fraction	---
235946_at	RIBC1	-0.058	0.345	L	---	---	flagellum	---

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215045_at	TNRC4	-0.307	0.344	L	nuclear mRNA splicing, via spliceosome /// neurogenesis	nucleic acid binding /// transcription factor activity /// mRNA binding	nucleus	---
205916_at	S100A7	-0.082	0.344	B	epidermis development	calcium ion binding	---	---
212014_x_at	CD44	0.054	0.344	B	cell adhesion /// cell-matrix adhesion /// cell-cell adhesion	receptor activity /// protein binding /// collagen binding /// hyaluronic acid binding	integral to plasma membrane /// membrane /// integral to membrane	---
235450_at	FBXL4	0.027	0.343	B	ubiquitin cycle	---	nucleus	---
214016_s_at	SFPQ	-0.121	0.342	B	nuclear mRNA splicing, via spliceosome /// RNA splicing	DNA binding /// RNA binding /// pre-mRNA splicing factor activity	nucleus	---
210889_s_at	FCGR2B	0.044	0.342	B	immune response /// signal transduction	receptor activity /// IgG binding	plasma membrane /// integral to membrane	---
205180_s_at	ADAM8	0.077	0.339	L	proteolysis and peptidolysis	metalloendopeptidase activity /// zinc ion binding /// hydrolase activity	integral to plasma membrane	---
214510_at	GPR20	-0.092	0.339	B	G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity	integral to plasma membrane	---
214148_at	FOXM1	-0.25	0.338	L	response to oxidative stress/// transcription from RNA polymerase II promoter	transcription factor activity	nucleus	---
215239_x_at	ZNF273	0.31	0.338	B	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
208446_s_at	ZFYVE9	-0.187	0.337	B	endocytosis /// transforming growth factor beta receptor complex assembly /// SMAD protein heteromerization /// SMAD protein nuclear translocation	receptor activity /// protein binding /// serine-type peptidase activity /// zinc ion binding	cytoplasm /// early endosome	TGF Beta Signaling Pathway
218470_at	CGI-04	0.078	0.337	B	protein biosynthesis /// tyrosyl-tRNA aminoacylation	tyrosine-tRNA ligase activity /// ATP binding /// ligase activity	mitochondrion	---
241104_at	ARGBP2	-0.098	0.336	L	---	nucleic acid binding /// structural constituent of cytoskeleton /// protein binding /// cytoskeletal adaptor activity /// zinc ion binding /// structural constituent of muscle	nucleus /// cytoskeleton /// actin cytoskeleton /// Z disc	---
1558995_at	ZNF547	-0.054	0.336	B	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
202833_s_at	SERPINA1	-0.027	0.335	B	acute-phase response	serine-type endopeptidase inhibitor activity /// protein binding	extracellular region	Complement and coagulation cascades

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		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
244485_at	HLA-DPB1	0.068	0.335	B	detection of pest, pathogen or parasite/// antigen processing, exogenous antigen via MHC class II /// immune response/// pathogenesis	MHC class II receptor activity/// antigen binding	integral to membrane	---
235212_at	C14orf102	-0.076	0.334	L	---	binding	---	---
222083_at	GLYAT	0.007	0.333	B	acyl-CoA metabolism /// response to toxin		mitochondrion	---
210538_s_at	BIRC3	-0.018	0.332	T	anti-apoptosis /// cell surface receptor linked signal transduction /// protein ubiquitination /// regulation of apoptosis	ubiquitin-protein ligase activity /// protein binding /// protein binding /// zinc ion binding	ubiquitin ligase complex	Apoptosis
1566363_at	DNTT	0.168	0.331	B	DNA replication /// DNA modification /// antimicrobial humoral response (sensu Vertebrata)	magnesium ion binding /// DNA binding /// DNA-directed DNA polymerase activity /// DNA nucleotidylexotransferase activity /// transferase activity	nucleus	---
236549_x_at	SLIC1	0.101	0.329	L	intracellular signaling cascade	sugar binding	---	---
212587_s_at	PTPRC	-0.602	0.328	L	protein amino acid dephosphorylation /// cell surface receptor linked signal transduction	receptor activity /// transmembrane receptor protein tyrosine phosphatase activity /// hydrolase activity	integral to plasma membrane	---
243346_at	LMOD3	0.011	0.328	L	---	tropomyosin binding	cytoskeleton	---
217409_at	MYO5A	-0.198	0.328	B	transport/// actin filament-based movement	ATP binding/// ATPase activity, coupled/// actin binding/// microfilament motor activity	myosin	---
210211_s_at	HSPCA	-0.031	0.327	T	protein folding /// response to unfolded protein	ATP binding /// unfolded protein binding	---	---
227147_s_at	EGLN2	0.025	0.327	L	protein metabolism/// estrogen receptor signaling pathway/// regulation of cell growth/// response to hypoxia	ferrous iron binding/// oxidoreductase activity	nucleus	---
1553037_a_at	SYN2	0.077	0.327	L	synaptic transmission /// neurotransmitter secretion	---	synaptic vesicle /// synapse	---
235136_at	ORMDL3	-0.155	0.327	B	---	---	integral to membrane	---
242849_at	SASH1	0.097	0.325	L	negative regulation of cell cycle	---	---	---
220258_s_at	FLJ10385	0.277	0.325	L	---	kinase activity	---	---
201295_s_at	WSB1	0.175	0.325	B	intracellular signaling cascade	---	---	---
232497_at	ZNF3	-0.2	0.324	L	regulation of transcription, DNA-dependent /// cell differentiation /// immune cell activation	nucleic acid binding /// transcription factor activity /// zinc ion binding	nucleus	---
229202_at	PCNXL2	-0.142	0.323	T	---	---	integral to membrane	---

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		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
213042_s_at	ATP2A3	-0.243	0.323	L	transport /// cation transport /// calcium ion transport /// metabolism /// proton transport	magnesium ion binding /// calcium-transporting ATPase activity /// calcium ion binding /// ATP binding /// hydrolase activity /// hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	endoplasmic reticulum /// integral to plasma membrane	Calcium regulation in cardiac cells /// Smooth muscle contraction
1556963_at	MGC39900	-0.012	0.323	L	cytoskeleton organization and biogenesis	actin binding	cytoplasm	---
211188_at	CD84	0.164	0.323	B	defense response /// homophilic cell adhesion	---	integral to plasma membrane	---
241642_x_at	TLK1	0.027	0.322	B	regulation of chromatin assembly or disassembly /// protein amino acid phosphorylation /// intracellular protein transport /// response to DNA damage stimulus /// cell cycle /// intracellular signaling cascade /// chromatin modification	protein serine/threonine kinase activity /// ATP binding /// transferase activity	nucleus	---
234770_at	OR51A1P	0.059	0.321	L	G-protein coupled receptor protein signaling pathway/// perception of smell	olfactory receptor activity	integral to membrane	---
223068_at	EML4	-0.305	0.321	L	microtubule-based process /// mitosis	---	cytoplasm	---
228370_at	SNRPN	-0.019	0.321	B	mRNA processing	RNA binding /// pre-mRNA splicing factor activity	nucleus /// small nucleolar ribonucleoprotein complex	mRNA processing
232457_at	KIAA1102	-0.148	0.32	L	smooth muscle contraction	actin binding /// zinc ion binding	---	---
236908_at	ACPL2	0.037	0.319	B	---	acid phosphatase activity	---	---
206529_x_at	SLC26A4	0.062	0.317	B	transport /// perception of sound /// sulfate transport	sulfate porter activity /// chloride transporter activity /// iodide transporter activity	integral to membrane	---
241249_at	PSMD5	-0.039	0.316	L	---	---	proteasome complex (sensu Eukaryota)	Proteasome Degradation
207832_at	BAIAP2	-0.052	0.315	L	axonogenesis /// insulin receptor signaling pathway	receptor activity /// protein C-terminus binding /// growth factor activity /// cytoskeletal adaptor activity	cytoplasm /// plasma membrane	Dentatorubropallidoluysian atrophy/// Regulation of actin cytoskeleton/// Adherens junction
218751_s_at	FBXW7	-0.14	0.315	L	ubiquitin cycle	---	nucleus	Ubiquitin mediated proteolysis
204994_at	MX2	0.019	0.315	B	immune response	GTPase activity /// GTP binding	nucleus /// cytoplasm	---

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213387_at	KIAA1240	-0.258	0.315	B	---	ATP binding /// nucleoside-triphosphatase activity	---	---
216725_at	MGC45428	-0.03	0.314	L	protein amino acid phosphorylation /// intracellular signaling cascade	protein serine/threonine kinase activity /// ATP binding /// transferase activity	---	---
236190_at	XYLT1	-0.087	0.314	B	carbohydrate metabolism///glycosaminoglycan biosynthesis/// physiological process	transferase activity, transferring hexosyl groups/// protein xylosyltransferase activity///acetylglucosaminyltransferase activity/// catalytic activity	---	Chondroitin/ Heparan sulfate biosynthesis
240805_at	RPL15	0.298	0.313	T	protein biosynthesis	structural constituent of ribosome	intracellular /// ribosome	ribosome
211647_x_at	IGHG1	-0.034	0.313	B	immune response	antigen binding	membrane fraction	---
1555378_at	DRF1	0.016	0.313	B	---	nucleic acid binding /// zinc ion binding /// kinase activity	---	---
217762_s_at	RAB31	0.215	0.312	T	small GTPase mediated signal transduction	GTPase activity /// GTP binding	---	---
235857_at	KCTD11	-0.159	0.312	L	potassium ion transport	ion channel activity /// voltage-gated potassium channel activity	voltage-gated potassium channel complex /// membrane	---
204361_s_at	SCAP2	-0.139	0.312	L	protein complex assembly /// signal transduction	SH3/SH2 adaptor protein activity /// kinase activity	---	---
218605_at	TFB2M	0.282	0.311	T	rRNA modification	rRNA (adenine-N6,N6-)-dimethyltransferase activity /// rRNA methyltransferase activity	---	---
220109_at	TF	-0.028	0.31	L	transport /// iron ion transport /// iron ion homeostasis	ferric iron binding	extracellular region	---
1566109_at	MYNN	-0.021	0.31	B	transcription, DNA-dependent	nucleic acid binding /// transcription factor activity /// protein binding /// zinc ion binding	nucleus	---
215967_s_at	LY9	0.471	0.309	T	cell adhesion /// humoral defense mechanism (sensu Vertebrata)	protein binding	integral to plasma membrane	---
244466_at	ZNF544	-0.061	0.309	L	regulation of transcription, DNA-dependent	nucleic acid binding /// zinc ion binding	intracellular /// nucleus	---
242433_at	ZBTB11	-0.159	0.309	B	regulation of transcription, DNA-dependent	DNA binding /// protein binding /// zinc ion binding	nucleus	---

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		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)		Biological Function	Molecular Function	Cellular Component	
228219_s_at	UPB1	-0.155	0.308	L	nitrogen compound metabolism	beta-ureidopropionase activity /// hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	---	Pyrimidine metabolism/// Pantothenate and CoA biosynthesis/// beta-Alanine metabolism///
238687_x_at	FLJ20582	-0.049	0.307	L	---	nucleic acid binding /// zinc ion binding	nucleus	---
222004_s_at	DOCK6	0.135	0.307	B	---	guanyl-nucleotide exchange factor activity /// GTP binding /// GTPase binding	---	---
222128_at	CACNB2	0.242	0.306	L	calcium ion transport/// neuromuscular junction development	calcium ion binding	voltage-gated calcium channel complex /// membrane fraction	MAPK signaling pathway
213740_s_at	ZFPL1	-0.166	0.306	L	---	---	integral to membrane	---
224414_s_at	CARD6	0.113	0.306	B	regulation of apoptosis	protein binding	intracellular	---
1552724_at	OTEX	0.121	0.305	B	regulation of transcription, DNA-dependent /// development /// gametogenesis /// steroid hormone receptor signaling pathway	transcription factor activity	nucleus	---
210636_at	PPARD	0.022	0.304	L	generation of precursor metabolites and energy /// regulation of transcription from Pol II promoter /// lipid metabolism	transcription factor activity /// steroid hormone receptor activity	nucleus	Wnt signaling pathway
241607_at	RGPR	0.079	0.304	B	---	phosphopantetheine binding	---	---
202419_at	FVT1	0.026	0.303	T	metabolism	oxidoreductase activity /// 3-dehydrosphinganine reductase activity	extracellular space /// endoplasmic reticulum /// integral to membrane	---
220234_at	CA8	0.423	0.301	T	one-carbon compound metabolism	carbonate dehydratase activity /// zinc ion binding	---	Nitrogen metabolism
241344_at	GLB1	-0.085	0.301	L	carbohydrate metabolism	beta-galactosidase activity /// hydrolase activity, acting on glycosyl bonds	lysosome /// beta-galactosidase complex	Galactose metabolism /// N-Glycan degradation /// Glycosaminoglycan degradation /// Glycerolipid metabolism /// Glycosphingolipid metabolism
214387_x_at	SFTPC	-0.009	0.301	B	regulation of liquid surface tension/// respiratory gaseous exchange	---	extracellular	---
206610_s_at	F11	-0.148	0.3	L	proteolysis and peptidolysis /// blood coagulation	coagulation factor IXa activity /// coagulation factor XIa activity /// chymotrypsin activity /// trypsin activity /// hydrolase activity	extracellular region /// membrane	complement and coagulation cascades

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204232_at	FCER1G	0.524	0.299	T	immune response /// cell surface receptor linked signal transduction	transmembrane receptor activity /// receptor signaling protein activity /// IgE binding	plasma membrane /// integral to plasma membrane	Hemostasis
201200_at	CREG1	0.207	0.299	T	regulation of cell growth /// regulation of transcription from RNA polymerase II promoter /// development /// cell proliferation	RNA polymerase II transcription factor activity /// transcription corepressor activity	---	---
221368_at	NEU2	-0.054	0.299	L	carbohydrate metabolism	exo-alpha-sialidase activity /// hydrolase activity, acting on glycosyl bonds	cytoplasm	N-Glycan degradation /// Glycosphingolipid metabolism
211260_at	BMP7	-0.254	0.299	L	skeletal development /// growth	cytokine activity /// growth factor activity	---	cytokine-cytokine receptor interaction
221077_at	ARMC4	0.062	0.299	B	cell adhesion	structural molecule activity /// protein binding	cytoskeleton	---
239504_at	BCLAF1	-0.142	0.299	B	regulation of transcription, DNA-dependent /// induction of apoptosis	DNA binding /// transcriptional repressor activity	nucleus	---
1556595_at	WWOX	-0.021	0.298	L	metabolism /// steroid metabolism	electron transporter activity /// protein binding /// oxidoreductase activity	---	---
203997_at	PTPN3	0.4	0.296	T	protein amino acid dephosphorylation /// protein amino acid dephosphorylation	protein tyrosine phosphatase activity /// protein tyrosine phosphatase activity /// receptor activity /// structural molecule activity /// structural molecule activity /// cytoskeletal protein binding /// hydrolase activity	nucleus /// cytoplasm /// cytoplasm /// cytoskeleton /// membrane	---
234013_at	TRA@	-0.067	0.296	B	cellular defense response	receptor activity /// MHC protein binding /// peptide antigen binding	integral to plasma membrane	---
224882_at	ACAS2L	-0.15	0.294	L	metabolism	catalytic activity /// acetate-CoA ligase activity /// ligase activity	mitochondrion	---
229046_s_at	PLEKHB1	-0.113	0.294	L	phototransduction	signal transducer activity	integral to membrane	---
219921_s_at	DOCK5	0.648	0.292	T	---	guanyl-nucleotide exchange factor activity /// GTP binding /// GTPase binding	---	---
215764_x_at	AP2A2	0.092	0.291	L	protein complex assembly /// intracellular protein transport /// endocytosis	structural molecule activity /// lipid binding	Golgi apparatus /// coated pit /// AP-2 adaptor complex /// clathrin coat of trans-Golgi network vesicle	---

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		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
203129_s_at	KIF5C	-0.158	0.291	L	organelle organization and biogenesis /// microtubule-based movement	microtubule motor activity /// ATP binding	kinesin complex	---
212175_s_at	AK2	0.305	0.29	T	nucleobase, nucleoside, nucleotide and nucleic acid metabolism	adenylate kinase activity /// ATP binding /// kinase activity /// transferase activity	mitochondrion	Purine metabolism
235697_at	ZNF544	-0.139	0.29	L	regulation of transcription, DNA-dependent	nucleic acid binding /// zinc ion binding	intracellular /// nucleus	---
232969_at	CARD8	-0.042	0.29	L	regulation of apoptosis	protein binding	nucleus	---
244276_at	LOC152831	0.038	0.29	B	carbohydrate metabolism	hydrolase activity, hydrolyzing O-glycosyl compounds	integral to membrane	---
233132_at	LOC96610	0.092	0.29	B	---	antigen binding	---	---
242454_at	AMBP	0.095	0.29	B	transport /// cell adhesion /// pregnancy /// anti-inflammatory response /// heme catabolism /// negative regulation of JNK cascade /// negative regulation of immune response	transporter activity /// calcium channel inhibitor activity /// IgA binding /// heme binding /// trypsin inhibitor activity /// plasmin inhibitor activity /// protein homodimerization activity /// calcium oxalate binding	extracellular region /// plasma membrane	---
212128_s_at	DAG1	-0.188	0.289	L	protein complex assembly /// muscle contraction	laminin receptor activity /// calcium ion binding /// protein binding	extracellular matrix (sensu Metazoa) /// membrane fraction /// integral to plasma membrane /// actin cytoskeleton	---
222520_s_at	ESRRBL1	0.377	0.289	B	---	Signal transducer activity/// receptor activity	---	Huntington's disease
236610_at	PDE4D	-0.016	0.288	B	signal transduction /// cyclic nucleotide metabolism	3',5'-cyclic-nucleotide phosphodiesterase activity /// cAMP-specific phosphodiesterase activity /// hydrolase activity	soluble fraction /// insoluble fraction	G Protein Signaling /// Smooth muscle contraction /// Purine metabolism
224247_s_at	MRPS10	0.463	0.287	T	protein biosynthesis	structural constituent of ribosome	mitochondrion /// mitochondrial ribosome /// ribosome	---
232660_at	BAD	-0.056	0.286	L	induction of apoptosis /// apoptotic program	protein binding	cytoplasm /// mitochondrial outer membrane	Apoptosis /// amyotrophic lateral sclerosis/// focal adhesion
230855_at	GATA4	-0.029	0.285	B	heart development/// positive regulation of transcription, DNA-dependent/// transcription from RNA polymerase II promoter	DNA binding/// RNA polymerase II transcription factor activity/// zinc ion binding/// transcriptional activator activity	nucleus	---

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
214490_at	ARSF	0.026	0.284	L	metabolism	arylsulfatase activity /// calcium ion binding /// sulfuric ester hydrolase activity /// hydrolase activity	---	---
203375_s_at	TPP2	-0.39	0.284	L	*proteolysis and peptidolysis*	*aminopeptidase activity /// subtilase activity /// tripeptidyl-peptidase II activity /// D-alanyl-D-alanine endopeptidase activity /// hydrolase activity*	*cytoplasm*	---
242796_x_at	PPP2R3A	-0.015	0.284	B	*protein amino acid dephosphorylation*	*phosphoprotein phosphatase activity /// calcium ion binding /// protein binding /// protein phosphatase type 2A regulator activity*	*protein phosphatase type 2A complex*	*Glycogen Metabolism*
224228_s_at	PRDM7	-0.152	0.284	B	*regulation of transcription, DNA-dependent*	*DNA binding /// zinc ion*	*nucleus*	---
215681_at	MAST2	-0.112	0.283	L	*protein amino acid phosphorylation*	*protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// protein binding /// ATP binding*	---	---
210005_at	GART	-0.043	0.283	B	*purine nucleotide biosynthesis /// 'de novo' IMP biosynthesis /// purine base biosynthesis*	*catalytic activity /// phosphoribosylamine-glycine ligase activity /// phosphoribosylformylglycinamidine cyclo-ligase activity /// phosphoribosylglycinamide formyltransferase activity /// transferase activity /// ligase activity*	*cytoplasm*	*Purine metabolism*
1552792_at	SOCS4	0.068	0.283	B	*cell growth and/or maintenance/// regulation of cell size/// cellular morphogenesis/// cell communication/// intracellular signaling cascade*	---	---	*JAK-STAT signaling pathway*
231510_at	GLI2	-0.19	0.281	L	*regulation of transcription, DNA-dependent /// transcription from Pol II promoter /// signal transduction /// organogenesis*	*transcription factor activity /// transcription coactivator activity /// zinc ion binding*	*nucleus*	---
211648_at	IGHG1	-0.014	0.281	L	*immune response*	*antigen binding*	*membrane fraction*	---

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209848_at	ADH5	0.039	0.281	B	*ethanol oxidation*	alcohol dehydrogenase activity, zinc-dependent /// formaldehyde dehydrogenase (glutathione) activity /// electron transporter activity /// fatty acid binding /// zinc ion binding /// oxidoreductase activity	---	Fatty acid metabolism/// glycolysis / gluconeogenesis/// pyruvate metabolism/// glycerolipid metabolism/// tyrosine metabolism/// bile acid biosynthesis/// methane metabolism
218699_at	RAB7L1	0.214	0.278	T	*intracellular protein transport* /// small GTPase mediated signal transduction	GTPase activity /// GTP binding	---	---
244381_at	LGALS8	0.397	0.278	T	---	sugar binding /// sugar binding	extracellular space	---
208231_at	NRG1	0.041	0.278	B	neurogenesis /// embryonic development /// cell differentiation	receptor binding /// growth factor activity /// transmembrane receptor protein tyrosine kinase activator activity /// receptor tyrosine kinase binding	extracellular region /// integral to membrane	---
218911_at	YEATS4	0.097	0.278	B	regulation of cell growth /// *regulation of transcription, DNA-dependent* /// chromatin modification	transcription factor activity	nucleus	---
206504_at	CYP24A1	0.041	0.278	B	electron transport	monooxygenase activity /// electron transporter activity /// oxygen binding	mitochondrion	Ascorbate and aldarate metabolism/// gamma-*hexachlorocyclohexane* degradation/// flavonoids, stilbene and lignin biosynthesis/// *fluorene* degradation/// limonene and pinene degradation
202416_at	DNAJC7	0.08	0.277	T	protein folding	heat shock protein binding /// *unfolded protein binding*	---	---
207314_x_at	KIR3DL2	0.604	0.277	T	*cellular defense response*	*receptor activity*	*integral to plasma membrane*	---
223561_at	NEK6	0.445	0.277	T	protein amino acid *phosphorylation /// positive* regulation of I-kappaB kinase/NF-kappaB cascade	magnesium ion binding /// *protein serine/threonine* kinase activity /// protein-tyrosine kinase activity /// *signal transducer activity* /// ATP binding /// transferase activity	nucleus	Proteasome Degradation

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217175_at	UGT2B15	0.052	0.277	B	*lipid metabolism /// response to* external stimulus/// physiological process	Transferase activity, transferring hexosyl groups/// catalytic activity/// glucuronosyltransferase activity	---	starch and sucrose metabolism/// porphyrin and chlorophyll metabolism/// pentose and glucuronate interconversions/// androgen and estrogen metabolism
205389_s_at	ANK1	0.133	0.277	B	exocytosis /// cytoskeleton *organization and biogenesis* /// signal transduction /// maintenance of epithelial cell polarity	structural molecule activity /// *structural constituent of* cytoskeleton /// protein binding /// cytoskeletal adaptor activity /// *enzyme* binding /// spectrin binding	cytoskeleton /// plasma *membrane* /// *actin* cytoskeleton /// basolateral plasma membrane	---
209628_at	NXT2	0.182	0.277	B	mRNA processing /// mRNA-nucleus export /// protein-nucleus *import* /// *protein transport*	protein transporter activity	nucleus	---
230193_at	MGC33630	-0.035	0.277	B	---	calcium ion binding	---	---
239446_x_at	DCBLD2	-0.358	0.276	L	cell adhesion /// negative regulation of cell growth /// intracellular receptor-mediated signaling pathway /// wound healing	protein binding	integral to plasma membrane /// cell surface /// integral to membrane	---
205372_at	PLAG1	0.02	0.276	B	---	nucleic acid binding /// transcription factor activity /// zinc ion binding	nucleus	---
243519_at	UBE3C	-0.036	0.274	L	protein polyubiquitination /// ubiquitin cycle	ubiquitin-protein ligase activity /// protein binding	intracellular	---
236243_at	ZCCHC6	-0.169	0.274	L	---	nucleic acid binding /// zinc ion binding /// nucleotidyltransferase activity	nucleus	---
226877_at	LOC132241	0.056	0.274	L	protein biosynthesis	structural constituent of ribosome	intracellular /// ribosome	---
201261_x_at	BGN	-0.416	0.274	L	---	extracellular matrix structural constituent	extracellular matrix (sensu Metazoa)	---
1564630_at	EDN1	-0.014	0.273	L	signal transduction /// cell-cell *signaling* /// *regulation of blood* pressure /// positive regulation of cell proliferation /// pathogenesis /// *regulation of vasoconstriction*	hormone activity	extracellular space /// *soluble fraction*	Prostaglandin synthesis *regulation*
206366_x_at	XCL2	0.412	0.273	L	*chemotaxis* /// immune response /// signal transduction /// cell-cell signaling /// circulation	chemokine activity	extracellular region /// soluble fraction	cytokine-cytokine receptor interaction

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224113_at	CARD14	-0.084	0.273	L	*activation of NF-kappaB-inducing* kinase /// regulation of apoptosis	protein binding	intracellular /// plasma membrane	---
1557553_at	PPP1R12B	0.144	0.273	B	*regulation of muscle contraction* /// signal transduction	enzyme activator activity	---	Regulation of actin cytoskeleton/// focal adhesion
208638_at	PDIA6	0.163	0.272	T	electron transport /// protein folding	protein disulfide isomerase activity /// electron transporter activity /// isomerase activity	endoplasmic reticulum	---
235644_at	PHTF1	-0.08	0.272	B	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
207734_at	LAX	-0.002	0.271	L	cation transport	ATP binding /// ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	membrane	---
232505_at	DCTN2	-0.085	0.271	B	microtubule-based process /// mitosis /// cell proliferation	motor activity	kinetochore /// centrosome /// cytoskeleton /// dynactin complex /// membrane /// dynein complex	---
240614_at	KCNC2	-0.073	0.27	L	cation transport /// potassium ion transport	voltage-gated potassium channel activity /// protein binding	voltage-gated potassium channel complex /// membrane	---
230946_at	FMN2	-0.27	0.27	L	cell organization and biogenesis/// intracellular signaling cascade	actin binding	nucleus	---
237485_at	SFRS3	0.351	0.269	T	nuclear mRNA splicing, via spliceosome	nucleic acid binding /// RNA binding	nucleus	mRNA Processing, Transcription, Gene Expression
202506_at	SSFA2	0.094	0.269	B	---	---	plasma membrane	---
211245_x_at	KIR2DL4	0.384	0.268	T	cellular defense response /// signal transduction	*receptor activity* /// transmembrane receptor activity	integral to plasma membrane	---
229489_at	SLC19A1	-0.221	0.268	L	transport /// folic acid transport	folic acid binding /// folic acid transporter activity /// reduced folate carrier activity /// methotrexate transporter activity	membrane fraction /// integral to plasma membrane /// membrane	---
205465_x_at	HS3ST1	0.279	0.268	L	---	sulfotransferase activity /// transferase activity	Golgi lumen /// integral to membrane	Chondroitin / Heparan sulfate biosynthesis
219256_s_at	SH3TC1	0.866	0.268	L	---	binding	---	---
219425_at	SULT4A1	-0.083	0.267	L	steroid metabolism	sulfotransferase activity /// transferase activity	cytosol	cysteine metabolism

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1552578_a_at	MYO3B	0.134	0.267	L	*protein amino acid* phosphorylation /// visual perception	*motor activity* /// actin binding /// protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	*cytoskeleton* /// *myosin*	---
1560274_at	WTAP	-0.12	0.267	B	---	---	nucleus	---
237831_x_at	MMAA	-0.033	0.267	B	---	ATP binding	*mitochondrion*	---
238462_at	STS-1	0.104	0.265	T	metabolism	catalytic activity	---	---
220822_at	Mageh1	-0.179	0.265	L	apoptosis	---	---	---
224726_at	MIB1	-0.169	0.264	L	protein ubiquitination	ubiquitin-protein ligase activity/// *zinc ion binding*	ubiquitin ligase complex/// *membrane*/// *mitochondrion*	notch signaling pathway
223835_x_at	OTP	0.042	0.264	B	regulation of transcription, DNA-dependent /// *development*	transcription factor activity	nucleus	---
1565653_at	KIAA1833	-0.01	0.264	B	---	binding	---	---
215591_at	SATB2	0.138	0.263	B	regulation of transcription, DNA-dependent	DNA binding /// transcription factor activity	nucleus	---
221923_s_at	NPM1	0.388	0.262	T	intracellular protein transport /// nucleocytoplasmic transport /// response to stress /// centrosome cycle /// cell aging /// negative *regulation of cell proliferation* /// ribosome assembly /// activation of NF-kappaB transcription factor	nucleic acid binding /// *transcription coactivator* activity /// RNA binding /// Tat protein binding /// protein *homodimerization activity* /// protein heterodimerization activity /// NF-kappaB binding /// *unfolded protein binding*	nucleus /// nucleolus /// *cytoplasm* /// *centrosome*	Nuclear Receptors
229093_at	NOS3	0.036	0.262	L	electron transport /// amino acid metabolism /// nitric oxide biosynthesis /// cell motility	nitric-oxide synthase activity /// electron transporter activity /// calcium ion binding /// calmodulin binding /// FMN binding /// *oxidoreductase* activity	*cytoplasm*	Arginine and proline metabolism
234495_at	KLK15	-0.303	0.262	L	*proteolysis and peptidolysis*	*chymotrypsin activity* /// trypsin activity /// peptidase activity /// hydrolase activity	*extracellular region*	---
1569114_at	TRIM37	-0.033	0.262	L	protein ubiquitination	ubiquitin-protein ligase activity /// *zinc ion binding*	ubiquitin ligase complex	---
1561386_at	SPFH2	-0.083	0.262	L	---	---	integral to membrane	---
1569121_at	SLC25A24	-0.149	0.262	B	transport /// mitochondrial transport	transporter activity /// binding /// calcium ion binding	mitochondrion /// mitochondrial inner membrane /// membrane	---
213352_at	TMCC1	0.332	0.261	T	---	---	integral to membrane	---

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219111_s_at	DDX54	-0.125	0.261	L	regulation of transcription, DNA-dependent /// RNA processing /// ribosome biogenesis /// estrogen receptor signaling pathway	transcription corepressor activity /// RNA binding /// ATP-dependent RNA helicase activity /// receptor binding /// ATP binding /// hydrolase activity /// estrogen receptor binding	nucleolus	---
223122_s_at	SFRP2	-0.013	0.261	B	Development	signal transducer activity/// receptor activity	---	Wnt signaling
210077_s_at	SFRS6	-0.069	0.261	B	nuclear mRNA splicing, via spliceosome /// mRNA splice site selection	RNA binding /// pre-mRNA splicing factor activity	nucleus	mRNA processing
204010_s_at	KRAS	-0.06	0.261	B	regulation of cell cycle /// small GTPase mediated signal transduction	GTPase activity /// GTP binding	---	MAPK signaling pathway/// focal adhesion/// tight junction/// regulation of actin cytoskeleton
232632_at	TM4SF8	-0.14	0.26	B	cell motility /// cell proliferation	---	integral to membrane	---
1570085_at	TTLL1	-0.082	0.26	B	protein modification	ligase activity	---	---
1568878_s_at	FGFR1OP	0.093	0.259	B	positive regulation of cell proliferation	---	---	---
217021_at	CYB5	-0.077	0.259	B	electron transport	cytochrome-c oxidase activity	mitochondrion /// microsome /// integral to membrane	---
230687_at	SLC13A3	0.089	0.259	B	transport /// sodium ion transport	transporter activity /// symporter activity	membrane /// integral to membrane	---
215151_at	DOCK10	-0.023	0.259	B	---	guanyl-nucleotide exchange factor activity /// GTP binding /// GTPase binding	---	---
210530_s_at	NR2C1	0.397	0.258	T	transcription /// regulation of transcription, DNA-dependent	transcription factor activity /// steroid hormone receptor activity /// steroid hormone receptor activity	nucleus	---
243463_s_at	RIT1	0.086	0.258	B	signal transduction/// small GTPase mediated signal transduction	GTP binding/// calmodulin binding	plasma membrane	---
213444_at	KIAA0543	0.386	0.257	L	regulation of transcription, DNA-dependent /// cell adhesion	nucleic acid binding /// protein dimerization activity	intracellular	---
220735_s_at	SENP7	0.036	0.257	L	proteolysis and peptidolysis /// ubiquitin cycle /// protein sumoylation	cysteine-type peptidase activity	nucleus	---
228129_at	PAI-RBP1	-0.097	0.257	L	---	RNA binding	nucleus	---
218906_x_at	KLC2	-0.07	0.257	L	---	microtubule motor activity /// binding	kinesin complex	---
1566191_at	JJAZ1	0.116	0.257	B	regulation of transcription, DNA-dependent /// chromatin modification	nucleic acid binding /// zinc ion binding	nucleus	---

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210165_at	DNASE1	0.47	0.256	L	DNA catabolism /// apoptosis	actin binding /// endonuclease activity /// deoxyribonuclease I activity /// deoxyribonuclease activity /// hydrolase activity	extracellular region	---
241602_at	ZNF582	0.069	0.256	B	regulation of transcription, DNA-dependent	nucleic acid binding /// zinc ion binding	nucleus	---
208487_at	LMX1B	0.344	0.255	T	embryonic development (sensu Mammalia) /// regulation of transcription, DNA-dependent /// development /// dorsal/ventral pattern formation /// neuron cell differentiation /// embryonic limb morphogenesis	transcription factor activity /// protein binding /// zinc ion binding	nucleus /// nucleus	---
239206_at	CR1L	0.073	0.255	T	---	receptor activity	---	---
228586_at	ENG	-0.065	0.255	L	circulation /// organogenesis /// cell adhesion	protein binding	integral to plasma membrane	---
206312_at	GUCY2C	0.16	0.255	B	cGMP biosynthesis /// protein amino acid phosphorylation /// receptor guanylyl cyclase signaling pathway /// intracellular signaling cascade	guanylate cyclase activity /// protein-tyrosine kinase activity /// receptor activity /// ATP binding /// lyase activity	integral to plasma membrane /// brush border	Purine metabolism
201460_s_at	TIA1	-0.015	0.255	B	apoptosis /// induction of apoptosis	RNA binding /// poly(A) binding	---	---
242915_at	LOC91120	-0.007	0.255	B	regulation of transcription, DNA-dependent	nucleic acid binding /// DNA binding /// zinc ion binding	nucleus	---
235293_at	HRASLS3	-0.048	0.254	L	cell cycle	---	integral to membrane	---
242337_at	IGBP1	-0.17	0.253	L	response to biotic stimulus /// regulation of signal transduction /// B-cell activation	protein phosphatase type 2A regulator activity	cytoplasm	---
220634_at	TBX4	-0.267	0.253	L	regulation of transcription, DNA-dependent /// development	transcription factor activity	nucleus	---
210631_at	NF1	0.047	0.253	B	Ras protein signal transduction /// negative regulation of cell proliferation /// negative regulation of cell cycle	enzyme inhibitor activity /// Ras GTPase activator activity	cytoplasm	MAPK signaling pathway
241725_at	E2F7	0.364	0.252	T	regulation of cell cycle /// regulation of transcription, DNA-dependent	transcription factor activity	transcription factor complex	---
236645_at	HBP1	-0.101	0.252	B	regulation of transcription, DNA-dependent	DNA binding	---	---
218047_at	OSBPL9	0.047	0.251	T	lipid transport /// steroid metabolism	---	---	---
221638_s_at	STX16	-0.167	0.251	L	intracellular protein transport /// intra-Golgi transport	t-SNARE activity /// protein transporter activity	microsome /// Golgi apparatus /// Golgi stack /// membrane /// integral to membrane	---

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228772_at	HNMT	0.076	0.251	L	respiratory gaseous exchange	methyltransferase activity /// S-adenosylmethionine-dependent methyltransferase activity /// transferase activity /// histamine N-methyltransferase activity	---	Histidine metabolism
208128_x_at	KIF25	-0.108	0.251	L	microtubule-based movement	microtubule motor activity /// ATP binding	microtubule associated complex	---
216509_x_at	MLLT10	0.108	0.251	B	regulation of transcription, DNA-dependent	DNA binding/// transcription factor activity	nucleus	---
211302_s_at	PDE4B	0.382	0.25	T	signal transduction	cAMP-specific phosphodiesterase activity /// hydrolase activity	soluble fraction /// insoluble fraction	G Protein Signaling /// Smooth muscle contraction /// Purine metabolism
235958_at	PLA2G4F	-0.536	0.25	L	phospholipid catabolism	phospholipase activity	---	---
210329_s_at	SGCD	-0.095	0.25	L	cytoskeleton organization and biogenesis /// muscle development	---	cytoskeleton /// plasma membrane /// sarcoglycan complex /// integral to membrane	---
1556730_at	PHLDA1	0.101	0.249	B	---	---	nucleus	---
204840_s_at	EEA1	0.182	0.249	B	vesicle fusion /// synaptic vesicle to endosome fusion /// early endosome to late endosome transport	nucleic acid binding /// calmodulin binding /// phosphatidylinositol binding /// zinc ion binding /// GTP-dependent protein binding /// protein homodimerization activity	nucleus /// early endosome /// cytosol /// extrinsic to plasma membrane	---
231242_at	BHLHB3	-0.074	0.248	L	regulation of transcription, DNA-dependent /// cell proliferation /// organogenesis /// cell differentiation	transcription factor activity	nucleus	circadian rhythm
231234_at	CTSC	-0.001	0.248	B	proteolysis and peptidolysis /// immune response	cysteine-type endopeptidase activity /// dipeptidyl-peptidase I activity /// hydrolase activity	lysosome	---
202114_at	SNX2	0.079	0.247	T	intracellular protein transport /// endocytosis /// intracellular signaling cascade	protein transporter activity	---	---
220438_at	QPCTL	-0.124	0.247	B	proteolysis and peptidolysis	peptidase activity	---	---
209710_at	GATA2	-0.091	0.246	L	regulation of transcription, DNA-dependent /// transcription from Pol II promoter	transcription factor activity	nucleus	---
215742_at	SHFM3	-0.103	0.246	B	ubiquitin-dependent protein catabolism /// ubiquitin cycle /// development /// Wnt receptor signaling pathway /// embryonic limb morphogenesis	---	---	ubiquitin ligase complex
235648_at	ZNF567	0.101	0.245	B	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---

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205401_at	AGPS	-0.24	0.244	L	*electron transport /// lipid* metabolism /// lipid biosynthesis	alkylglycerone-phosphate synthase activity /// transferase activity	*peroxisome*	Glycerophospholipid metabolism
229511_at	SMARCE1	0.009	0.244	B	DNA metabolism/// *chromosome* organization and biogenesis (sensu eukarya)/// metabolism/// nucleobase, nucleoside, nucleotide and nucleic acid metabolism/// regulation of *transcription from pol ii promoter*/// nuclear organization and biogenesis/// cellular physiological *process*/// *cell growth and/or* maintenance/// cell organization and biogenesis	transcription cofactor activity/// DNA binding/// transcription regulator activity/// transcription coactivator activity/// chromatin binding/// *transcription factor binding*/// protein binding	---	Control of Gene Expression by Vitamin D Receptor/// Chromatin Remodeling by hSWI/SNF ATP-dependent Complexes
219683_at	FZD3	0.178	0.244	B	G-protein coupled receptor protein signaling pathway /// frizzled signaling pathway /// development /// cell proliferation	G-protein coupled receptor activity /// Wnt receptor activity	Integral to plasma membrane	Wnt signaling
216002_at	FNTB	0.113	0.244	B	protein amino acid farnesylation	prenyltransferase activity /// protein farnesyltransferase activity /// transferase activity	cytoplasm	N-Glycans biosynthesis/// Ubiquinone biosynthesis/// Porphyrin and chlorophyll metabolism
207629_s_at	ARHGEF2	-0.029	0.243	L	*cellular morphogenesis* /// intracellular protein transport /// actin filament organization /// *negative regulation of microtubule* depolymerization /// cell surface receptor linked signal transduction /// intracellular signaling *cascade* /// regulation of Rho protein signal transduction /// regulation of cell *proliferation*	*Rho guanyl-nucleotide* exchange factor activity /// microtubule binding /// zinc ion binding /// *Rho GTPase* binding /// diacylglycerol binding /// Rac guanyl-*nucleotide exchange factor* activity /// Rac GTPase binding	*microtubule*	---
219736_at	TRIM36	0.09	0.243	B	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
211916_s_at	MYO1A	-0.17	0.243	B	perception of sound /// actin filament-based movement	microfilament motor activity /// actin binding /// calmodulin binding /// ATP binding /// ATPase activity, coupled	muscle myosin /// brush border /// myosin	---
207688_s_at	INHBC	0.069	0.242	B	cell growth and/or maintenance/// cellular physiological process	signal transducer activity/// transforming growth factor beta receptor binding/// hormone activity/// growth factor activity	---	Cytokine-cytokine receptor interaction/// TGF-beta signaling pathway

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		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
1555464_at	IFIH1	0.066	0.242	B	DNA restriction	nucleic acid binding /// ATP binding /// ATP-dependent helicase activity /// type III site-specific deoxyribonuclease activity	---	---
219671_at	HPCAL4	0.416	0.241	T	central nervous system development	calcium ion binding	---	---
228434_at	BTNL9	-0.248	0.241	L	---	---	integral to membrane	---
241043_at	ORC5L	-0.012	0.241	L	DNA replication /// DNA replication initiation	nucleotide binding /// DNA replication origin binding /// ATP binding	nucleus /// nuclear origin of replication recognition complex	cell cycle
237905_at	KRT25A	0.416	0.24	T	---	structural molecule activity	intermediate filament	---
242511_at	ST3GAL3	-0.045	0.24	L	protein amino acid glycosylation	N-acetyllactosaminide alpha-2,3-sialyltransferase activity	Golgi apparatus /// integral to membrane	Keratan sulfate biosynthesis /// Blood group glycolipid biosynthesis-lactoseries
218687_s_at	MUC13	-0.26	0.239	L	---	---	integral to membrane	---
1566087_at	B3GTL	0.066	0.239	B	---	transferase activity, transferring glycosyl groups	membrane	---
206810_at	ZNF44	0.052	0.239	B	regulation of transcription, DNA-dependent	nucleic acid binding /// DNA binding /// zinc ion binding	nucleus	---
214225_at	PIN4	0.329	0.238	T	protein folding	peptidyl-prolyl cis-trans isomerase activity /// isomerase activity	mitochondrial matrix	---
242591_at	XLHSRF-1	0.168	0.238	B	cytoplasm organization and biogenesis/// cytoskeleton-dependent intracellular transport/// intracellular transport/// physiological process/// microtubule-based movement /// microtubule-based process/// cytoskeleton organization and biogenesis/// cellular physiological process/// cell growth and/or maintenance/// cell organization and biogenesis	motor activity/// microtubule motor activity/// heat shock protein activity	---	---
1555265_at	ABCC13	-0.007	0.238	B	transport	ATP binding /// ATPase activity, coupled to transmembrane movement of substances	nucleus /// integral to membrane	---
219659_at	ATP8A2	0.421	0.237	T	cation transport /// negative regulation of cell proliferation	magnesium ion binding /// phospholipid-translocating ATPase activity /// ATP binding /// hydrolase activity /// hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances /// ATPase activity	membrane /// integral to membrane	---

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values):	Expression change (log2 Values):		Geneontology	Geneontology	Geneontology	
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
233704_at	RANBP17	0.274	0.237	T	protein-nucleus import, docking /// protein transport	GTP binding /// protein transporter activity	nucleus /// nuclear pore /// cytoplasm	---
228823_at	POLR2J2	-0.241	0.237	L	transcription	DNA binding	---	---
225999_at	KIAA1238	0.001	0.237	L	protein modification /// ribosome biogenesis	---	mitochondrion	---
211514_at	RIPK5	0.057	0.237	L	protein amino acid phosphorylation	protein kinase activity /// protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// receptor activity /// ATP binding	---	---
236625_at	PARVG	-0.132	0.237	L	cell-matrix adhesion	actin binding /// protein binding	cytoskeleton	---
226316_at	C13orf10	-0.103	0.237	B	---	nucleic acid binding		
212317_at	TNPO3	0.32	0.236	T	protein transport	receptor activity /// binding	nucleus	---
205543_at	HSPA4L	-0.12	0.236	L	protein folding /// response to unfolded protein	ATP binding /// unfolded protein binding	nucleus /// cytoplasm	---
239898_x_at	ZNF286	-0.11	0.236	B	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
1569323_at	PTPRG	0.163	0.235	B	protein amino acid dephosphorylation /// one-carbon compound metabolism /// transmembrane receptor protein tyrosine kinase signaling pathway	carbonate dehydratase activity /// transmembrane receptor protein tyrosine phosphatase activity /// zinc ion binding /// hydrolase activity	integral to plasma membrane	Phosphatidylinositol signaling system
213331_s_at	NEK1	-0.086	0.235	B	cytokinesis /// protein amino acid phosphorylation /// cell cycle /// mitosis	magnesium ion binding /// protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	nucleus	
201685_s_at	C14orf92	-0.196	0.234	L	regulation of transcription, DNA-dependent	DNA binding	chromatin /// nucleus	---
214664_at	PAICS	0.095	0.233	T	purine nucleotide biosynthesis /// 'de novo' IMP biosynthesis /// purine base biosynthesis	phosphoribosylaminoimidazole carboxylase activity /// phosphoribosylaminoimidazolesuccinocarboxamide synthase activity /// lyase activity /// ligase activity	phosphoribosylaminoimidazole carboxylase complex	Purine metabolism
210909_x_at	LPAL2	0.014	0.233	B	---	---	integral to membrane	---
1565588_at	SP140	0.128	0.232	T	regulation of transcription, DNA-dependent /// defense response	transcription factor activity	nucleus /// nuclear membrane /// nucleoplasm	---
218705_s_at	SNX24	0.245	0.232	L	intracellular signaling cascade /// protein transport	---	---	---
221653_x_at	APOL2	-0.182	0.232	L	lipid metabolism /// lipid transport /// acute-phase response /// development /// cholesterol metabolism /// lipoprotein metabolism	receptor binding /// high-density lipoprotein binding /// lipid binding	extracellular region /// intracellular	---

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		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
243633_at	LYN	-0.031	0.231	L	protein amino acid phosphorylation /// intracellular signaling cascade	receptor signaling protein tyrosine kinase activity /// ATP binding /// transferase activity	---	---
239226_at	RTKN	0.006	0.23	L	signal transduction	protein binding	intracellular	G13 Signaling Pathway
204253_s_at	VDR	-0.131	0.23	L	regulation of transcription, DNA-dependent /// signal transduction	transcription factor activity /// steroid hormone receptor activity /// vitamin D3 receptor activity	nucleus	Ovarian Infertility Genes /// Nuclear Receptors
227770_at	VPS4A	-0.127	0.23	L	---	nucleotide binding /// ATP binding /// nucleoside-triphosphatase activity	cytosol	---
225264_at	RARSL	-0.36	0.23	L	arginyl-tRNA aminoacylation	arginine-tRNA ligase activity /// ATP binding	---	---
218102_at	DERA	-0.038	0.23	B	---	deoxyribose-phosphate aldolase activity/// lyase activity/// catalytic activity/// aldolase activity	---	---
231270_at	CA13	-0.156	0.229	L	one-carbon compound metabolism	carbonate dehydratase activity /// zinc ion binding /// lyase activity	---	---
225194_at	PLRG1	-0.462	0.229	L	nuclear mRNA splicing, via spliceosome	transcription corepressor activity /// signal transducer activity	spliceosome complex	---
237789_at	DHCR24	-0.234	0.229	B	lipid metabolism/// macromolecule metabolism/// electron transport/// cholesterol metabolism	oxidoreductase activity/// catalytic activity	---	tryptophan metabolism/// 1,1,1-trichloro-2,2-bis(4-chlorophenyl)ethane/// propanoate metabolism/// fatty acid biosynthesis
214302_x_at	GJA12	-0.146	0.229	B	cell communication	connexon channel activity	connexon complex/// integral to membrane	---
207054_at	IMPG1	-0.039	0.229	B	visual perception	receptor activity /// extracellular matrix structural constituent	extracellular matrix (sensu Metazoa)	---
220667_at	MGC20741	-0.185	0.229	B	ubiquitin-dependent protein catabolism /// ubiquitin cycle	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity /// hydrolase activity	---	---
1554623_x_at	DGKE	-0.148	0.229	B	protein kinase C activation /// intracellular signaling cascade /// phospholipid biosynthesis	diacylglycerol kinase activity /// ATP binding /// transferase activity /// diacylglycerol binding	integral to membrane	Glycerolipid metabolism /// Glycerophospholipid metabolism /// Phosphatidylinositol signaling system
242859_at	TFCP2	0.03	0.229	B	regulation of transcription from Pol II promoter	transcription factor activity	---	---
235521_at	HOXA3	-0.036	0.228	L	regulation of transcription, DNA-dependent /// development	transcription factor activity	nucleus	---

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233044_at	EGFR	-0.103	0.228	B	protein amino acid phosphorylation /// epidermal growth factor receptor signaling pathway /// cell proliferation /// negative regulation of cell cycle	receptor activity /// epidermal growth factor receptor activity /// ATP binding /// transferase activity	endosome /// cytoskeleton /// integral to plasma membrane	MAPK signaling pathway//// calcium signaling pathway/// cadherin-mediated cell adhesion/// regulation of actin cytoskeleton/// cytokine-cytokine receptor interaction/// adherens junction /// focal adhesion
226134_s_at	MSI2	0.619	0.228	B	---	RNA binding	---	---
225535_s_at	TIMM23	0.145	0.226	T	protein-mitochondrial targeting	protein translocase activity	mitochondrion /// mitochondrial inner membrane presequence translocase complex /// integral to plasma membrane /// outer membrane	---
1559393_at	FLJ38508	0.089	0.226	B	one-carbon compound metabolism /// biosynthesis	oxidoreductase activity /// hydroxymethyl-, formyl- and related transferase activity /// cofactor binding	---	---
205488_at	GZMA	-0.002	0.226	B	proteolysis and peptidolysis /// apoptosis /// cleavage of lamin /// immune response /// cytolysis	chymotrypsin activity /// granzyme A activity /// trypsin activity /// protein binding /// hydrolase activity /// protein homodimerization activity	immunological synapse /// nucleus	Neuroactive ligand-receptor interaction
1555982_at	ZFYVE16	0.002	0.226	B	endosome transport/// protein-lysosome targeting/// regulation of endocytosis/// signal transduction/// vesicle organization and biogenesis	phosphatidylinositol binding/// protein binding/// protein transporter activity/// zinc ion binding	membrane	TGF-beta signaling pathway
215938_s_at	PLA2G6	0.274	0.225	T	phospholipid metabolism /// lipid catabolism	phospholipase A2 activity /// hydrolase activity	cytoplasm /// membrane	phospholipid degradation//// prostaglandin and leukotriene metabolism/// mapk signaling pathway/// glycerolipid metabolism
221227_x_at	COQ3	0.112	0.225	T	ubiquinone biosynthesis	hexaprenyldihydroxybenzoate methyltransferase activity /// O-methyltransferase activity /// 2-polyprenyl-6-methoxy-1,4-benzoquinone methyltransferase activity /// transferase activity	mitochondrion	Ubiquinone biosynthesis
244260_at	WHSC2	-0.277	0.225	L	development//// regulation of transcription, DNA-dependent	---	nucleus	---
226017_at	CKLFSF7	0.424	0.225	L	chemotaxis	cytokine activity	integral to membrane	---

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207092_at	LEP	-0.009	0.225	B	energy reserve metabolism /// signal transduction /// cell-cell signaling	hormone activity	extracellular space	Neuroactive ligand-receptor interaction /// cytokine-cytokine receptor interaction
1554014_at	CHD2	0.111	0.225	B	chromatin assembly or disassembly /// regulation of transcription from Pol II promoter /// chromosome organization and biogenesis (sensu Eukaryota)	chromatin binding /// ATP-dependent DNA helicase activity /// helicase activity /// ATP binding /// hydrolase activity	chromatin /// nucleus	---
222793_at	DDX58	0.008	0.225	B	---	nucleotide binding /// nucleic acid binding /// helicase activity /// ATP binding /// nucleoside-triphosphatase activity	---	---
236219_at	TMEM20	0.135	0.225	B	---	---	---	---
217681_at	WNT7B	0.178	0.224	L	frizzled-2 signaling pathway /// cell-cell signaling /// development	signal transducer activity /// extracellular matrix structural constituent	extracellular region	Wnt signaling pathway
206983_at	CCR6	-0.022	0.224	L	cell motility /// chemotaxis /// humoral immune response /// cellular defense response /// signal transduction /// G-protein coupled receptor protein signaling pathway /// positive regulation of cytosolic calcium ion concentration /// antimicrobial humoral response (sensu Vertebrata)	rhodopsin-like receptor activity /// receptor activity /// C-C chemokine receptor activity	integral to plasma membrane	cytokine-cytokine receptor interaction
219218_at	KIAA1447	-0.091	0.224	L	---	DNA binding	nucleus	---
241574_s_at	IMP-1	-0.035	0.224	L	---	RNA binding	---	---
223078_s_at	TMOD3	-0.075	0.224	L	---	actin binding /// tropomyosin binding	cytoskeleton	---
1555431_a_at	IL31RA	0.03	0.224	B	MAPKKK cascade /// anti-apoptosis /// defense response /// transmembrane receptor protein tyrosine kinase signaling pathway /// JAK-STAT cascade /// positive regulation of cell proliferation /// cytokine and chemokine mediated signaling pathway /// macrophage differentiation /// positive regulation of tyrosine phosphorylation of Stat3 protein /// positive regulation of tyrosine phosphorylation of Stat5 protein /// homeostasis /// negative regulation of macrophage activation /// positive regulation of transcription, DNA-dependent	transcription coactivator activity /// receptor activity /// hematopoietin/interferon-class (D200-domain) cytokine receptor activity /// protein kinase binding /// cytokine binding	integral to membrane	---

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215392_at	USP3	0.094	0.224	B	ubiquitin-dependent protein catabolism /// ubiquitin cycle	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity /// hydrolase activity	---	---
236417_at	MFN1	-0.012	0.224	B	---	GTPase activity /// GTP binding /// hydrolase activity	mitochondrion /// integral to membrane /// outer membrane	---
235706_at	CPM	0.306	0.223	T	proteolysis and peptidolysis /// aromatic compound metabolism /// morphogenesis	carboxypeptidase A activity /// ferric iron binding /// metallopeptidase activity	plasma membrane	---
236904_x_at	TECTA	-0.115	0.223	L	cell-matrix adhesion /// perception of sound	extracellular matrix structural constituent	extracellular matrix (sensu Metazoa) /// extracellular space /// membrane	---
1560108_at	NYREN18	-0.112	0.223	L	---	---	nucleus	---
204930_s_at	BNIP1	-0.028	0.223	B	apoptosis /// anti-apoptosis	---	integral to membrane	---
214532_x_at	POU5F1	-0.13	0.222	L	regulation of transcription, DNA-dependent /// morphogenesis	transcription factor activity	nucleus	---
207243_s_at	CALM2	-0.439	0.222	L	---	---	---	Phosphatidylinositol signaling system/// Huntington's disease/// Calcium signaling pathway
240307_at	FUBP1	0.053	0.222	B	regulation of transcription, DNA-dependent /// phosphate transport	transcription factor activity	nucleus /// cytoplasm	---
236243_at	ZCCHC6	-0.099	0.222	B	---	nucleic acid binding /// zinc ion binding /// nucleotidyltransferase activity	nucleus	---
1558815_at	ARGBP2	0.023	0.221	L	---	nucleic acid binding /// structural constituent of cytoskeleton /// protein binding /// cytoskeletal adaptor activity /// zinc ion binding /// structural constituent of muscle	nucleus /// cytoskeleton /// actin cytoskeleton /// Z disc	---
210205_at	B3GALT4	-0.237	0.221	L	protein amino acid glycosylation	galactosyltransferase activity /// UDP-galactose beta-N-acetylglucosamine beta-1,3-galactosyltransferase activity /// transferase activity, transferring glycosyl groups /// ganglioside galactosyltransferase activity	Golgi apparatus /// membrane /// integral to membrane	Ganglioside biosynthesis
208252_s_at	CHST3	0.274	0.22	T	carbohydrate metabolism /// sulfur metabolism /// chondroitin sulfate biosynthesis	chondroitin 6-sulfotransferase activity /// transferase activity	Golgi apparatus /// integral to membrane /// intrinsic to Golgi membrane	chondroitin/ heparan sulfate biosynthesis

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244212_at	CCNC	-0.15	0.22	L	regulation of transcription, DNA-dependent/// regulation of progression through cell cycle	---	nucleus	---
232408_at	ZFYVE28	-0.19	0.22	L	---	zinc ion binding	---	---
205869_at	PRSS1	0.524	0.219	T	proteolysis and peptidolysis /// proteolysis and peptidolysis /// digestion /// negative regulation of blood coagulation	chymotrypsin activity /// trypsin activity /// trypsin activity /// calcium ion binding /// peptidase activity	extracellular region	neuroactive ligand-receptor interaction
227628_at	LOC493869	0.246	0.219	T	response to oxidative stress	glutathione peroxidase activity /// oxidoreductase activity	---	---
216706_x_at	IGHD /// IGHG	-0.031	0.219	L	immune response	antigen binding /// antigen binding	membrane fraction	---
1570114_at	MAMDC1	0.315	0.217	T	---	---	membrane /// integral to membrane	---
238329_at	M-RIP	-0.174	0.217	L	lipid transport /// lipoprotein metabolism	lipid binding	extracellular region	---
218793_s_at	SCML1	0.101	0.217	B	regulation of transcription, DNA-dependent /// morphogenesis	transcription factor activity	nucleus	---
232563_at	MGC27466	0.033	0.217	B	regulation of transcription, DNA-dependent	nucleic acid binding /// zinc ion binding	nucleus	---
236436_at	LOC283130	0.153	0.216	T	transport	transporter activity /// binding	mitochondrial inner membrane /// membrane	---
244285_at	C6orf102	0.083	0.216	B	microtubule-based movement	microtubule motor activity /// ATP binding	microtubule associated complex	---
244788_at	MRC2	0.075	0.216	B	endocytosis	receptor activity /// sugar binding	integral to membrane	---
237310_at	EXT1	-0.079	0.215	L	skeletal development /// glycosaminoglycan biosynthesis /// signal transduction /// negative regulation of cell cycle	transferase activity, transferring glycosyl groups /// N-acetylglucosaminyl-proteoglycan 4-beta-glucuronosyltransferase activity	endoplasmic reticulum membrane /// Golgi apparatus /// integral to membrane	---
235839_at	LOC348645	-0.124	0.215	L	---	DNA binding	nucleus	---
222578_s_at	UBE1DC1	0.022	0.215	B	L-serine biosynthesis	catalytic activity /// oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	---	---
220146_at	TLR7	0.093	0.215	B	inflammatory response	transmembrane receptor activity	integral to membrane	TOLL-like receptor signaling pathway
232842_at	DOCK8	0.304	0.213	T	---	guanyl-nucleotide exchange factor activity /// GTP binding /// GTPase binding	---	---
228552_s_at	ISYNA1	-0.259	0.213	L	myo-inositol biosynthesis /// phospholipid biosynthesis	inositol-3-phosphate synthase activity /// isomerase activity	---	Inositol phosphate metabolism/// Streptomycin biosynthesis
218986_s_at	FLJ20035	0.029	0.213	L	---	nucleic acid binding /// helicase activity /// ATP binding /// hydrolase activity	---	---

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237069_s_at	TRPM1	-0.073	0.213	B	cation transport	calcium channel activity	membrane fraction /// integral to plasma membrane /// membrane	---
224285_at	GPR174	-0.07	0.212	L	G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity /// purinergic nucleotide receptor activity, G-protein coupled	integral to membrane	GPCRDB Class A Rhodopsin like
207944_at	OCM	0.274	0.211	T	---	calcium ion binding /// calcium ion binding	---	---
1566086_at	B3GTL	0.179	0.211	T	---	transferase activity, transferring glycosyl groups	membrane	---
215547_at	TSC22D2	-0.284	0.211	L	regulation of transcription, DNA-dependent	transcription factor activity	---	---
204446_s_at	ALOX5	0.037	0.21	L	electron transport /// inflammatory response /// leukotriene biosynthesis	arachidonate 5-lipoxygenase activity /// iron ion binding /// lipoxygenase activity /// oxidoreductase activity	---	Prostaglandin and leukotriene metabolism
230369_at	GPR161	-0.101	0.21	L	G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity /// receptor activity	integral to membrane	GPCRDB Class A Rhodopsin like2
234671_at	KRTAP4-2	0.597	0.209	T	---	---	keratin filament	---
224668_at	C20orf35	0.112	0.209	L	protein transport	protein binding	cytoplasm /// Golgi apparatus /// integral to membrane	---
234746_at	IL1RAPL1	-0.14	0.209	L	signal transduction /// learning and/or memory	transmembrane receptor activity	integral to membrane	---
207657_x_at	TNPO1	-0.676	0.208	L	protein-nucleus import, docking /// protein-nucleus import, translocation /// protein transport	binding /// nuclear localization sequence binding /// protein transporter activity	nucleus /// nuclear pore /// cytoplasm	---
239026_x_at	CENTG3	0.012	0.208	L	small GTPase mediated signal transduction /// regulation of GTPase activity	GTPase activator activity /// GTP binding	---	---
205991_s_at	PRRX1	0.227	0.208	L	regulation of transcription, DNA-dependent /// development	transcription factor activity /// transcription coactivator activity	nucleus	---
33850_at	MAP4	-0.151	0.208	L	negative regulation of microtubule depolymerization	structural molecule activity	microtubule associated complex	---
206375_s_at	HSPB3	0.343	0.208	B	protein folding /// response to unfolded protein	---	---	---
1567056_at	OR8G2	-0.166	0.207	B	G-protein coupled receptor protein signaling pathway/// perception of smell	olfactory receptor activity/// receptor activity	integral to membrane	---
221365_at	MLNR	0.158	0.206	L	smooth muscle contraction /// G-protein coupled receptor protein signaling pathway /// digestion	rhodopsin-like receptor activity /// growth hormone-releasing hormone receptor activity	integral to plasma membrane	Neuroactive ligand-receptor interaction
221447_s_at	GLT8D2	-0.066	0.206	B	carbohydrate biosynthesis	transferase activity /// transferase activity, transferring hexosyl groups	---	---

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231192_at	EDG7	-0.046	0.206	B	G-protein signaling, coupled to cyclic nucleotide second messenger /// positive regulation of cytosolic calcium ion concentration /// synaptic transmission	lysosphingolipid and lysophosphatidic acid receptor activity /// lipid binding	integral to plasma membrane	Neuroactive ligand-receptor interaction
205242_at	CXCL13	0.472	0.205	T	chemotaxis /// inflammatory response /// positive regulation of cytosolic calcium ion concentration /// cell-cell signaling /// sensory perception	chemokine activity	extracellular region /// soluble fraction	Cytokine-cytokine receptor interaction
201548_s_at	JARID1B	-0.287	0.205	L	regulation of transcription, DNA-dependent	DNA binding /// transcription factor activity	nucleus	---
208300_at	PTPRH	-0.183	0.205	L	protein amino acid dephosphorylation	transmembrane receptor protein tyrosine phosphatase activity /// hydrolase activity	integral to plasma membrane	---
204471_at	GAP43	-0.104	0.205	L	regulation of cell growth /// protein kinase C activation /// neurogenesis /// response to wounding	calmodulin binding	membrane	---
239557_at	LRRFIP2	-0.058	0.205	L	---	LRR domain binding	---	---
212362_at	ATP2A2	-0.015	0.204	L	transport /// cation transport /// calcium ion transport /// cell adhesion /// metabolism /// epidermis development /// proton transport	magnesium ion binding /// calcium-transporting ATPase activity /// calcium ion binding /// ATP binding /// hydrolase activity /// hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	membrane fraction /// endoplasmic reticulum /// microsome /// integral to plasma membrane	Calcium regulation in cardiac cells /// Smooth muscle contraction
217596_at	UPF3A	-0.051	0.204	L	mRNA catabolism, nonsense-mediated decay	nucleocytoplasmic transporter activity	nucleus /// cytoplasm	---
244041_at	STX6	-0.066	0.204	B	transport /// intracellular protein transport /// vesicle fusion /// trans-Golgi to endosome transport	protein binding /// protein transporter activity	early endosome /// Golgi apparatus /// integral to plasma membrane /// clathrin-coated vesicle /// perinuclear region	---
219710_at	SH3TC2	-0.018	0.203	B	cyclic-nucleotide-mediated signaling/// G-protein coupled receptor protein signaling pathway/// cell communication	signal transducer activity/// serotonin receptor activity/// G-protein coupled receptor activity/// rhodopsin-like receptor activity	---	Neuroactive ligand-receptor interaction
204399_s_at	EML2	0.091	0.203	B	visual perception /// perception of sound	---	microtubule associated complex	---
217176_s_at	ZFX	-0.027	0.203	B	regulation of transcription, DNA-dependent /// regulation of transcription	DNA binding /// transcription coactivator activity /// zinc ion binding /// transcription regulator activity /// metal ion binding	nucleus	---

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244090_at	ITPR1	-0.069	0.202	L	cation transport /// calcium ion transport /// signal transduction	inositol 1,4,5-triphosphate-sensitive calcium-release channel activity /// calcium channel activity /// inositol-1,4,5-triphosphate receptor activity	endoplasmic reticulum membrane /// integral to membrane	Phosphatidylinositol signaling system/// Calcium signaling pathway
227149_at	TNRC6C	0.481	0.202	B	---	nucleic acid binding	---	---
226984_at	FGD5	-0.098	0.202	B	---	zinc ion binding	---	---
212830_at	EGFL5	0.25	0.201	T	---	structural molecule activity /// calcium ion binding	integral to membrane	---
1558183_at	ZNF17	-0.058	0.201	L	regulation of transcription, DNA-dependent	nucleic acid binding /// DNA binding /// zinc ion binding	nucleus	---
231599_x_at	DPF1	-0.124	0.201	L	regulation of transcription, DNA-dependent /// induction of apoptosis /// protein ubiquitination	DNA binding /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex /// nucleus	---
203377_s_at	CDC40	-0.177	0.201	L	nuclear mRNA splicing, via spliceosome /// RNA splicing	---	spliceosome complex	mRNA processing Reactome
201549_x_at	JARID1B	0.35	0.2	T	regulation of transcription, DNA-dependent	DNA binding /// transcription factor activity	nucleus /// nucleus	---
208473_s_at	GP2	0.384	0.2	T	---	---	membrane fraction /// membrane	---
217054_at	MUC3A	-0.189	0.2	L	maintenance of gastrointestinal epithelium	extracellular matrix constituent, lubricant activity	extracellular region	---
203348_s_at	ETV5	0.271	0.199	T	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
231276_at	PDE3B	-0.245	0.199	L	signal transduction	cGMP-inhibited cyclic-nucleotide phosphodiesterase activity/// catalytic activity/// hydrolase activity	membrane	Purine metabolism
223118_s_at	USP47	-0.356	0.199	L	ubiquitin-dependent protein catabolism /// ubiquitin cycle	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity	---	---
239169_at	RAD52B	0.21	0.199	L	nuclear mRNA splicing, via spliceosome	nucleic acid binding	---	---
235039_x_at	LIN9	-0.255	0.198	T	---	receptor activity	---	---
216687_x_at	UGT2B15 ///	0.049	0.198	L	xenobiotic metabolism /// metabolism /// steroid metabolism	glucuronosyltransferase activity	microsome /// integral to membrane /// membrane fraction	Pentose and glucuronate interconversions /// Androgen and estrogen metabolism /// Starch and sucrose metabolism /// Porphyrin and chlorophyll metabolism
242436_at	PLEKHH2	-0.247	0.197	L	---	binding	cytoskeleton	---
241915_at	LOC123876 //	0.077	0.197	B	metabolism	catalytic activity /// ligase activity	---	---
37079_at	C6orf68	0.098	0.197	B	metabolism	transferase activity	---	---

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
204461_x_at	RAD1	0.053	0.197	B	cell cycle checkpoint /// DNA repair	damaged DNA binding /// 3'-5' exonuclease activity	nucleus	---
226310_at	AVO3	-0.102	0.196	L	---	binding	---	---
1560712_at	DKFZp686L1	-0.114	0.196	B	proteolysis and peptidolysis	chymotrypsin activity /// trypsin activity /// peptidase activity	---	---
240709_at	SEZ6L	-0.178	0.196	B	---	---	integral to membrane	---
232469_x_at	SSBP3	0.009	0.196	B	regulation of transcription, DNA-dependent	single-stranded DNA binding /// transcription regulator activity	nucleus	---
1559909_a_at	TIMM17B	0.234	0.195	T	protein-mitochondrial targeting	protein translocase activity	mitochondrion /// mitochondrial inner membrane presequence translocase complex /// integral to membrane	---
208567_s_at	KCNJ12	0.204	0.195	L	ion transport /// potassium ion transport /// muscle contraction /// regulation of heart contraction rate	inward rectifier potassium channel activity /// voltage-gated ion channel activity /// potassium channel inhibitor activity /// potassium channel regulator activity	membrane fraction /// integral to plasma membrane /// integral to membrane	---
235624_at	HDLBP	-0.147	0.195	L	lipid transport /// cholesterol metabolism	nucleic acid binding /// RNA binding /// lipid transporter activity /// lipid binding	nucleus /// plasma membrane	---
228187_at	GAS1	-0.229	0.195	L	cell cycle arrest/// negative regulation of cell proliferation/// negative regulation of S phase of mitotic cell cycle	---	anchored to plasma membrane	Hedgehog signaling pathway
204416_x_at	APOC1	0.33	0.194	L	lipid metabolism /// lipid transport /// lipoprotein metabolism	lipid transporter activity	extracellular region	Statin Pathway
219441_s_at	LRRK1	-0.226	0.194	L	protein amino acid phosphorylation	protein kinase activity /// ATP binding	---	---
211213_at	ORC5L	0.058	0.194	L	DNA replication /// DNA replication initiation	nucleotide binding /// DNA replication origin binding /// ATP binding	nucleus /// nuclear origin of replication recognition complex	Cell cycle /// DNA replication Reactome /// G1 to S cell cycle Reactome
207284_s_at	ASPH	0.01	0.194	L	muscle contraction /// peptidyl-amino acid modification	peptide-aspartate beta-dioxygenase activity /// binding /// electron transporter activity /// iron ion binding /// calcium ion binding /// structural constituent of muscle /// oxidoreductase activity /// oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	integral to endoplasmic reticulum membrane	---

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		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
205978_at	KL	0.022	0.194	B	carbohydrate metabolism	hydrolase activity, hydrolyzing O-glycosyl compounds /// signal transducer activity /// beta-glucosidase activity	extracellular space /// membrane fraction /// soluble fraction /// integral to plasma membrane /// integral to membrane	---
226198_at	VAPA	0.283	0.193	T	protein complex assembly /// exocytosis /// membrane fusion /// positive regulation of I-kappaB kinase/NF-kappaB cascade	signal transducer activity /// structural molecule activity	integral to membrane	Circadian Exercise/// Tight junction
214741_at	ZNF131	-0.084	0.193	T	transcription /// regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	nucleus	---
204751_x_at	DSC2	-0.39	0.193	L	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	cytoskeleton /// intercellular junction /// integral to membrane	---
1559739_at	CHPT1	0.02	0.193	L	regulation of cell growth /// CDP-choline pathway /// platelet activating factor biosynthesis	diacylglycerol cholinephosphotransferase activity /// transferase activity /// diacylglycerol binding	microsome /// integral to membrane	---
1553183_at	UMODL1	0.043	0.193	B	---	calcium ion binding	---	---
216799_at	CORO2B	-0.151	0.193	B	actin cytoskeleton organization and biogenesis	actin binding	actin cytoskeleton /// membrane	---
222171_s_at	PKNOX2	0.266	0.192	T	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
205857_at	SLC18A2	-0.106	0.192	L	monoamine transport	transporter activity /// monoamine transporter activity	membrane fraction /// integral to plasma membrane	---
1557637_at	PPP3CA	0.117	0.192	B	protein amino acid dephosphorylation	protein serine/threonine phosphatase activity /// calcium ion binding /// calmodulin binding /// hydrolase activity	calcineurin complex	MAPK signaling pathway/// Wnt signaling pathway/// Apoptosis/// Calcium signaling pathway/// Amyotrophic lateral sclerosis
203127_s_at	SPTLC2	0.278	0.191	T	biosynthesis	serine C-palmitoyltransferase activity /// acyltransferase activity /// transferase activity, transferring nitrogenous groups	endoplasmic reticulum /// integral to membrane	Glycosphingolipid metabolism
1555457_at	DBC1	0.17	0.191	T	cell cycle /// cell death	protein binding	---	---
236867_at	TRPV1	-0.172	0.191	L	cation transport /// cell surface receptor linked signal transduction /// chemosensory behavior	receptor activity /// calcium channel activity	integral to plasma membrane	Neuroactive ligand-receptor interaction
241010_x_at	DKFZP564K0	-0.289	0.191	L	positive regulation of I-kappaB kinase/NF-kappaB cascade	signal transducer activity	---	---
202638_s_at	ICAM1	0.37	0.191	L	cell-cell adhesion	transmembrane receptor activity /// protein binding	integral to plasma membrane	---
1558522_at	MPP6	0.079	0.191	B	protein complex assembly	protein binding	membrane	---

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212292_at	SLC7A1	-0.251	0.19	L	*amino acid metabolism* /// transport /// amino acid transport	*receptor activity* /// basic amino acid transporter activity /// amino acid permease activity	*integral to plasma* membrane	---
243373_at	SEMA3D	0.141	0.19	B	development /// neurogenesis	receptor activity	membrane	---
241403_at	CLK4	0.258	0.19	B	protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	nucleus	mRNA processing
220436_at	LOC389722	0.209	0.19	B	cell adhesion	structural molecule activity	---	---
240444_x_at	RSN	0.012	0.19	B	---	nucleic acid binding /// microtubule binding	endosome /// intermediate filament /// microtubule cytoskeleton	---
1555131_a_at	PER3	0.158	0.189	T	transcription /// regulation of transcription, DNA-dependent /// signal transduction /// rhythmic process	signal transducer activity	nucleus	Circadian rhythm
1552623_at	HSH2D	-0.169	0.189	L	intracellular signaling cascade	---	---	---
236030_at	RCOR2	-0.353	0.189	L	regulation of transcription, DNA-dependent /// regulation of transcription	DNA binding	nucleus	---
1555425_x_at	SSH2	-0.056	0.189	L	protein amino acid dephosphorylation	protein tyrosine/serine/threonine phosphatase activity	---	---
227151_at	MGC32065	-0.038	0.188	L	intracellular signaling cascade	---	---	---
217247_at	RBM3	0.147	0.188	L	RNA processing	RNA binding /// nucleic acid binding	---	---
220108_at	GNA14	0.259	0.188	B	G-protein coupled receptor protein signaling pathway /// protein amino acid ADP-ribosylation /// signal transduction	GTP binding /// GTPase activity /// signal transducer activity	heterotrimeric G-protein complex /// plasma membrane	*Calcium signaling pathway*
205525_at	CALD1	0.124	0.187	B	muscle contraction /// muscle development	actin binding /// calmodulin binding /// tropomyosin binding /// myosin binding	cytoskeleton	---
203078_at	CUL2	0.056	0.187	B	G1/S transition of mitotic cell cycle /// ubiquitin cycle /// cell cycle /// cell cycle arrest /// negative regulation of cell proliferation /// induction of apoptosis by intracellular signals	---	---	Ubiquitin mediated *proteolysis*
229644_at	PREP	-0.11	0.186	L	*proteolysis and peptidolysis*	*prolyl oligopeptidase activity* /// hydrolase activity	*cytoplasm*	---
1569383_s_at	ZFYVE28	0.332	0.186	B	---	zinc ion binding	---	---

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		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
207557_s_at	RYR2	0.156	0.185	T	cation transport /// calcium ion transport /// calcium ion homeostasis /// muscle contraction /// signal transduction /// regulation of heart contraction rate	receptor activity /// ryanodine-sensitive calcium-release channel activity /// calcium ion binding /// calmodulin binding /// calcium-release channel activity	plasma membrane /// integral to plasma membrane	Calcium regulation in cardiac cells /// Smooth muscle contraction
215717_s_at	FBN2	0.172	0.185	T	morphogenesis	extracellular matrix structural constituent /// calcium ion binding	extracellular matrix (sensu Metazoa)	---
226909_at	KIAA1729	0.095	0.185	T	---	nucleic acid binding /// zinc ion binding	nucleus	---
225412_at	FLJ14681	0.095	0.185	L	---	---	integral to membrane	---
244360_at	FBXL17	-0.155	0.185	B	ubiquitin cycle	---	---	---
1564631_at	FLJ25818	0.094	0.185	B	---	calcium ion binding	---	---
234971_x_at	PLCD3	-0.159	0.184	L	lipid metabolism /// intracellular signaling cascade	phosphoinositide phospholipase C activity /// calcium ion binding	---	Wnt signaling pathway
203561_at	FCGR2A	0.005	0.184	B	immune response	receptor activity /// receptor signaling protein activity /// IgG binding	plasma membrane /// integral to membrane	---
228698_at	SOX7	-0.004	0.184	B	regulation of transcription, DNA-dependent	DNA binding	nucleus	---
218459_at	TOR3A	-0.34	0.183	L	chaperone cofactor dependent protein folding	ATP binding	endoplasmic reticulum	---
227314_at	ITGA2	-0.008	0.183	B	cell-matrix adhesion /// integrin-mediated signaling pathway /// blood coagulation /// organogenesis	magnesium ion binding /// receptor activity /// collagen binding	plasma membrane /// integrin complex /// integral to membrane	ECM-receptor interaction/// focal adhesion/// regulation of actin cytoskeleton/// hemostasis
218621_at	HEMK1	-0.09	0.183	B	DNA methylation /// protein amino acid methylation	DNA binding /// N-methyltransferase activity /// protein methyltransferase activity /// S-adenosylmethionine-dependent methyltransferase activity /// transferase activity	---	Selenoamino acid metabolism/// tryptophan metabolism/// histidine metabolism/// tyrosine metabolism/// ubiquinone biosynthesis/// nitrobenzene degradation/// aminophosphonate metabolism/// androgen and estrogen metabolism
242612_at	NPEPPS	-0.057	0.182	L	proteolysis and peptidolysis	aminopeptidase activity/// zinc ion binding	cytosol/// nucleus	---
207857_at	LILRA2	-0.149	0.182	L	immune response	receptor activity	integral to membrane	---
232988_at	KIAA0182	-0.178	0.182	L	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
223365_at	DHX37	-0.283	0.182	L	---	nucleic acid binding /// ATP binding /// ATP-dependent helicase activity /// hydrolase activity	---	---

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237077_at	ACPP	0.217	0.181	T	regulation of cell cycle	acid phosphatase activity /// protein tyrosine phosphatase activity /// hydrolase activity	extracellular region	gamma-Hexachlorocyclohexane degradation /// Riboflavin metabolism
1560330_at	PCDH15	0.095	0.181	T	cell adhesion /// homophilic cell adhesion /// sensory perception /// visual perception /// perception of sound	calcium ion binding /// protein binding	membrane /// integral to membrane	—
238235_at	CRK7	0.306	0.181	T	autophosphorylation	RNA polymerase II transcription factor activity /// protein serine/threonine kinase activity /// ATP binding /// transferase activity	nucleus	—
59999_at	HIF1AN	-0.118	0.181	L	regulation of transcription, DNA-dependent	peptide-aspartate beta-dioxygenase activity /// oxidoreductase activity /// oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	nucleus	—
222522_x_at	MRPS10	-0.064	0.181	B	protein biosynthesis	structural constituent of ribosome	intracellular /// mitochondrion /// mitochondrial ribosome /// ribosome	—
1557053_s_at	UBE2G2	-0.257	0.181	B	ubiquitin cycle	ubiquitin conjugating enzyme activity /// ubiquitin-protein ligase activity /// ligase activity	—	Parkinson's disease
220911_s_at	KIAA1305	-0.003	0.181	B	DNA recombination	DNA binding	—	—
220034_at	IRAK3	0.237	0.18	T	protein amino acid phosphorylation /// signal transduction /// cytokine and chemokine mediated signaling pathway /// regulation of protein complex disassembly	magnesium ion binding /// protein serine/threonine kinase activity /// protein binding /// ATP binding /// transferase activity	—	Apoptosis
242716_at	SLC30A1	0.012	0.18	L	zinc ion transport/// cation transport	cation transporter activity	integral to membrane	—
1558103_a_at	TM6SF1	0.246	0.18	B	—	—	integral to membrane	—
240953_at	ACPP	0.024	0.179	B	regulation of cell cycle	acid phosphatase activity /// protein tyrosine phosphatase activity /// hydrolase activity	extracellular region	gamma-Hexachlorocyclohexane degradation /// Riboflavin metabolism
217493_x_at	NCR2	-0.166	0.179	B	cellular defense response /// signal transduction	transmembrane receptor activity	integral to plasma membrane	—
226444_at	SLC39A10	0.216	0.178	T	transport /// metal ion transport	nucleic acid binding /// zinc ion binding /// metal ion transporter activity	nucleus /// membrane /// integral to membrane	—

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227748_at	RP11-82K18.	-0.148	0.178	T	metabolism/// physiological process/// biosynthesis	carbon-sulfur lyase activity/// transferase activity, transferring nitrogenous groups/// lyase activity/// transferase activity/// transaminase activity/// catalytic activity/// 1-aminocyclopropane-1-carboxylate synthase activity	---	---
208560_at	KCNA10	-0.037	0.178	L	cation transport /// potassium ion transport	intracellular cyclic nucleotide activated cation channel activity /// voltage-gated potassium channel activity /// protein binding	membrane fraction /// voltage-gated potassium channel complex /// membrane	---
204582_s_at	KLK3	0.065	0.178	L	proteolysis and peptidolysis /// negative regulation of angiogenesis	chymotrypsin activity /// trypsin activity /// peptidase activity /// hydrolase activity	extracellular region	---
208153_s_at	FAT2	-0.155	0.178	B	cell adhesion /// homophilic cell adhesion	structural molecule activity /// calcium ion binding /// protein binding	membrane /// integral to membrane	---
223315_at	NTN4	-0.013	0.176	L	---	structural molecule activity	extracellular matrix (sensu Metazoa)	---
216734_s_at	BLR1	-0.152	0.176	B	cell motility /// G-protein coupled receptor protein signaling pathway /// B-cell activation	rhodopsin-like receptor activity /// angiotensin type II receptor activity /// C-X-C chemokine receptor activity	integral to plasma membrane	Cytokine-cytokine receptor interaction
244145_at	FYCO1	0.02	0.176	B	intracellular protein transport	zinc ion binding /// protein carrier activity	membrane	---
220015_at	FLJ20321	-0.053	0.175	L	---	nucleic acid binding /// zinc ion binding	nucleus	---
237817_at	SSR3	-0.074	0.175	L	cotranslational protein-membrane targeting	signal sequence binding	endoplasmic reticulum /// translocon complex /// microsome /// integral to endoplasmic reticulum membrane	---
231686_at	GATM	-0.116	0.175	B	carboxylic acid metabolism/// creatine biosynthesis	transferase activity, transferring one-carbon groups/// catalytic activity	---	arginine and proline metabolism/// glycine, serine and threonine metabolism/// urea cycle and metabolism of amino groups
211522_s_at	GNRHR	-0.021	0.175	B	G-protein coupled receptor protein signaling pathway /// development	rhodopsin-like receptor activity /// gonadotropin-releasing hormone receptor activity	plasma membrane /// integral to membrane	Neuroactive ligand-receptor interaction
241262_at	FLJ10504	-0.06	0.175	B	proteolysis and peptidolysis	subtilase activity	---	---
230243_at	RG9MTD2	0.261	0.175	B	---	methyltransferase activity /// transferase activity	---	---
226175_at	MGC29649	0.274	0.174	L	---	binding	---	---

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244517_x_at	RNF146	0.018	0.174	B	*protein ubiquitination*	*ubiquitin-protein ligase activity /// zinc ion binding*	*ubiquitin ligase complex*	---
234985_at	LOC143458	0.252	0.173	T	---	receptor activity	---	---
1569078_at	C17orf27	0.035	0.173	L	*protein ubiquitination*	*ubiquitin-protein ligase activity /// zinc ion binding*	*ubiquitin ligase complex*	---
1552935_at	ZCCHC5	0.143	0.173	B	---	nucleic acid binding	---	---
209370_s_at	SH3BP2	-0.009	0.172	T	*intracellular signaling cascade*	SH3/SH2 adaptor activity	---	---
231762_at	FGF10	0.002	0.172	T	protein-nucleus import, *translocation /// regulation of cell cycle /// response to stress /// signal transduction /// cell-cell signaling /// fibroblast growth factor receptor signaling pathway /// organogenesis /// embryonic limb morphogenesis /// regulation of transcription /// positive regulation of receptor mediated endocytosis /// urothelial cell proliferation /// positive regulation of urothelial cell proliferation*	fibroblast growth factor receptor binding /// growth *factor activity /// heparin* binding	extracellular space /// nucleus /// cell surface	*MAPK signaling pathway/// Regulation of actin cytoskeleton*
237788_at	GRIA4	-0.036	0.172	L	ion transport /// potassium ion transport /// glutamate signaling pathway /// synaptic transmission	receptor activity /// ionotropic glutamate receptor activity /// transporter activity /// ion channel activity /// glutamate-gated ion channel activity /// potassium channel activity	plasma membrane /// integral to membrane	---
232415_at	PCDHB13	0.045	0.172	B	cell adhesion /// homophilic cell adhesion /// synaptic transmission /// synaptogenesis /// calcium-dependent cell-cell adhesion	calcium ion binding /// protein binding	integral to membrane	---

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1563860_at	LOC400965	-0.087	0.172	B	transmembrane receptor protein tyrosine kinase signaling pathway/// response to external stimulus/// lymphocyte activation/// T-cell activation/// physiological process/// immune cell activation/// enzyme linked receptor protein signaling pathway/// cellular physiological process/// cell surface receptor linked signal transduction/// immune response/// response to biotic stimulus/// response to stimulus/// defense response/// signal transduction/// cell communication/// cell activation/// organismal physiological process	MHC class I protein binding/// signal transducer activity/// receptor binding		---
1562406_at	TRHDE	0.11	0.171	T	proteolysis and peptidolysis /// sterol depletion response, sterol regulatory element binding-protein cleavage /// signal transduction /// cell-cell signaling	aminopeptidase activity /// membrane alanyl aminopeptidase activity /// zinc ion binding /// pyroglutamyl-peptidase II activity	integral to plasma membrane	---
220921_at	SPANXB1 ///	-0.011	0.171	L	spermatid cell development	---	nucleus	---
202683_s_at	RNMT	0.382	0.171	L	mRNA capping	RNA binding /// mRNA (guanine-N7-)-methyltransferase activity /// methyltransferase activity /// transferase activity	nucleus	mRNA processing Reactome
232938_at	SFMBT2	-0.182	0.171	B	regulation of transcription	---	nucleus	---
222722_at	OGN	0.343	0.171	B	---	growth factor activity	---	---
224365_s_at	TIGD7	-0.184	0.17	T	---	DNA binding	chromosome, pericentric region /// nucleus	---
237089_at	ADAMTS16	0.003	0.17	B	proteolysis and peptidolysis	metalloendopeptidase activity	extracellular matrix (sensu Metazoa)	---
221089_at	NOX3	0.32	0.169	T	electron transport	oxidoreductase activity	membrane	---
207848_at	AVP	-0.209	0.169	L	generation of precursor metabolites and energy /// water transport /// signal transduction /// cell-cell signaling /// regulation of blood pressure	neurohypophyseal hormone activity	extracellular region /// soluble fraction	Neuroactive ligand-receptor interaction
244097_at	CR2	-0.023	0.169	B	immune response /// complement activation, classical pathway	receptor activity /// complement receptor activity	plasma membrane /// integral to membrane	Complement and coagulation cascades
1562161_at	MGC9850	-0.053	0.168	B	---	---	---	RNA transcription
209384_at	PROSC	0.17	0.167	T	---	---	cytoplasm	---
221650_x_at	CTGLF1	-0.092	0.167	L	regulation of GTPase activity	GTPase activator activity	---	---
1564351_at	POU2F1	0.166	0.167	B	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	Transcription, RNA Polymerase III

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216749_at	TRERF1	0.013	0.166	L	steroid biosynthesis /// cholesterol catabolism /// development /// homeostasis /// positive regulation of transcription, DNA-dependent /// regulation of hormone biosynthesis	DNA binding /// transcription factor activity /// transcription factor binding /// zinc ion binding /// DNA bending activity /// RNA polymerase II transcription mediator activity /// ligand-dependent nuclear receptor transcription coactivator activity	nucleus	---
209704_at	M96	-0.054	0.166	L	regulation of transcription, DNA-dependent	DNA binding	nucleus	---
211627_x_at	ESR1	-0.159	0.166	L	transcription /// regulation of transcription, DNA-dependent /// signal transduction /// cell growth /// estrogen receptor signaling pathway /// negative regulation of mitosis	DNA binding /// transcription factor activity /// steroid hormone receptor activity /// receptor activity /// steroid binding /// nitric-oxide synthase regulator activity /// estrogen receptor activity	nucleus /// membrane /// chromatin remodeling complex	Nuclear Receptors
206477_s_at	NOVA2	-0.1	0.166	L	---	---	---	---
236733_at	FAF1	-0.127	0.166	B	apoptosis	RNA binding	nucleus	---
240716_at	CASC1	0.102	0.166	B	secretory pathway/// vesicle-mediated transport/// vesicle targeting/// hemopoiesis/// membrane fusion/// exocytosis/// cellular physiological process/// vesicle fusion/// cell growth and/or maintenance/// organogenesis/// morphogenesis/// hemocyte differentiation (sensu arthropoda)/// hemocyte development/// cellular process/// cell differentiation	protein binding	nucleus	---
1554240_a_at	ITGAL	0.842	0.165	L	cell motility /// cell-matrix adhesion /// integrin-mediated signaling pathway	magnesium ion binding /// receptor activity /// protein binding	integrin complex /// integral to membrane	integrin-mediated cell adhesion
201822_at	TIMM17A	-0.29	0.165	L	protein-mitochondrial targeting	protein translocase activity	mitochondrion /// mitochondrial inner membrane presequence translocase complex /// integral to plasma membrane	---

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		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
234149_at	THRAP3	0.17	0.165	B	regulation of transcription, DNA-dependent /// transcription initiation from Pol II promoter /// androgen receptor signaling pathway	receptor activity /// ATP binding /// RNA polymerase II transcription mediator activity /// transcriptional activator activity /// ligand-dependent nuclear receptor transcription coactivator activity /// vitamin D receptor binding /// thyroid hormone receptor binding	mediator complex /// nucleus	—
242690_at	ATP11C	0.015	0.165	B	cation transport	magnesium ion binding /// phospholipid-translocating ATPase activity /// ATP binding /// ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism /// hydrolase activity /// ATPase activity	membrane /// integral to membrane	—
1555626_a_at	SLAMF1	-0.101	0.164	B	positive regulation of cell proliferation /// antimicrobial humoral response (sensu Vertebrata) /// lymphocyte activation	antigen binding /// transmembrane receptor activity	cell surface /// integral to membrane	—
1560648_s_at	TSPYL1	-0.08	0.164	B	nucleosome assembly	—	nucleus	—
244098_at	ADAMTS3	-0.064	0.163	L	collagen fibril organization /// collagen catabolism	metalloendopeptidase activity /// heparin binding /// zinc ion binding	extracellular matrix (sensu Metazoa)	—
231769_at	FBXO6	0.482	0.163	L	ubiquitin cycle /// protein catabolism	protein binding	—	—
1552489_s_at	MPP4	0.042	0.163	L	—	protein binding	—	—
209863_s_at	TP73L	-0.14	0.163	B	regulation of transcription, DNA-dependent /// apoptosis /// development	transcription factor activity	nucleus	—
226864_at	PKIA	-0.061	0.162	T	negative regulation of protein kinase activity	cAMP-dependent protein kinase inhibitor activity	—	Calcium regulation in cardiac cells /// Smooth muscle contraction
1564344_at	ATP9B	0.087	0.162	L	cation transport /// metabolism /// aminophospholipid transport	magnesium ion binding /// catalytic activity /// phospholipid-translocating ATPase activity /// ATP binding /// ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism /// hydrolase activity /// ATPase activity /// cation-transporting ATPase activity	membrane /// integral to membrane	—

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values):	Expression change (log2 Values):		Geneontology	Geneontology	Geneontology	
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
235897_at	COPZ2	0.206	0.161	T	intracellular protein transport	---	Golgi cis-face /// membrane /// clathrin vesicle coat /// COPI vesicle coat	---
207873_x_at	SEZ6L	0.274	0.161	T	---	---	integral to membrane	---
243353_at	PDCD8	-0.179	0.161	L	electron transport /// DNA fragmentation during apoptosis /// apoptosis /// DNA damage response, signal transduction resulting in induction of apoptosis	electron carrier activity /// disulfide oxidoreductase activity /// FAD binding	nucleus /// mitochondrion	Apoptosis
201076_at	NHP2L1	-0.235	0.161	L	regulation of cell cycle /// protein biosynthesis	RNA binding /// structural constituent of ribosome	spliceosome complex /// nucleolus /// ribosome	---
227539_at	GNA13	0.187	0.161	B	cell motility /// signal transduction /// G-protein coupled receptor protein signaling pathway	GTPase activity /// receptor signaling protein activity /// protein binding /// GTP binding	membrane	G Protein Signaling /// G13 Signaling Pathway
226833_at	FLJ32499	0.468	0.16	T	electron transport /// transport	---	---	---
230081_at	PLCXD3	-0.139	0.16	B	intracellular signaling cascade	phospholipase C activity	---	---
41856_at	UNC5B	-0.105	0.159	L	apoptosis /// signal transduction /// development	receptor activity /// protein binding	integral to membrane	---
213849_s_at	PPP2R2B	0.359	0.158	T	signal transduction	phosphoprotein phosphatase activity /// protein phosphatase type 2A regulator activity /// protein phosphatase type 2A regulator activity /// hydrolase activity	protein phosphatase type 2A complex	Glycogen Metabolism
241162_at	FARP1	0.363	0.158	T	---	Rho guanyl-nucleotide exchange factor activity /// binding /// cytoskeletal protein binding	cytoplasm /// cytoskeleton /// cytoskeleton /// membrane	---
225659_at	LOC339745	-0.224	0.158	L	---	protein binding	---	---
1557257_at	BCL10	0.283	0.157	T	induction of apoptosis /// cell cycle /// regulation of apoptosis /// positive regulation of I-kappaB kinase/NF-kappaB cascade /// negative regulation of cell cycle	signal transducer activity /// protein binding	intracellular	---
222440_s_at	THRAP3	-0.228	0.157	L	regulation of transcription, DNA-dependent /// transcription initiation from Pol II promoter /// androgen receptor signaling pathway	receptor activity /// ATP binding /// RNA polymerase II transcription mediator activity /// transcriptional activator activity /// ligand-dependent nuclear receptor transcription coactivator activity /// vitamin D receptor binding /// thyroid hormone receptor binding	mediator complex /// nucleus	---
229648_at	RICS	-0.184	0.157	B	---	GTPase activator activity	---	---

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		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
206308_at	DNMT2	0.132	0.156	T	DNA methylation	DNA binding /// DNA (cytosine-5-)- methyltransferase activity	nucleus /// nucleus	---
65493_at	ABC1	-0.015	0.156	L	---	binding	---	---
240295_at	PAPPA	-0.01	0.156	B	proteolysis and peptidolysis /// pregnancy /// cell differentiation	metallopeptidase activity /// zinc ion binding /// hydrolase activity	extracellular space /// membrane	---
1554736_at	PARG1	0.304	0.155	T	intracellular signaling cascade /// Rho protein signal transduction	Rho GTPase activator activity /// diacylglycerol binding	---	---
228237_at	PAPPA2	0.315	0.155	T	regulation of cell growth /// regulation of cell growth /// proteolysis and peptidolysis /// proteolysis and peptidolysis /// cell differentiation	metallopeptidase activity /// metallopeptidase activity /// zinc ion binding /// zinc ion binding	intracellular /// intracellular /// membrane	---
222838_at	SLAMF7	0.3	0.155	T	---	receptor activity	---	---
207017_at	RAB27B	-0.065	0.155	L	small GTPase mediated signal transduction	GTPase activity /// GTP binding	---	---
215332_s_at	CD8B1	0.072	0.155	B	immune response /// transmembrane receptor protein tyrosine kinase signaling pathway /// T-cell activation	protein binding /// coreceptor activity /// MHC class I protein binding	integral to plasma membrane /// T-cell receptor complex	---
211496_s_at	PDC	0.245	0.154	T	electron transport /// G-protein coupled receptor protein signaling pathway /// sensory perception /// visual perception /// phototransduction	phospholipase inhibitor activity /// electron transporter activity	soluble fraction /// cytoplasm	---
205890_s_at	UBD	0.309	0.154	T	proteolysis and peptidolysis /// ubiquitin cycle /// antimicrobial humoral response (sensu Vertebrata)	---	---	---
244736_at	UBP1	-0.139	0.154	L	regulation of transcription from Pol II promoter /// negative regulation of transcription /// viral genome replication	transcription factor activity /// transcription corepressor activity /// specific transcriptional repressor activity	nucleus	---
242260_at	MATR3	0.107	0.154	L	---	RNA binding /// structural molecule activity /// zinc ion binding	nucleus /// nuclear inner membrane	---
238108_at	TNKS	-0.208	0.154	L	telomerase-dependent telomere maintenance	NAD+ ADP-ribosyltransferase activity /// protein binding /// transferase activity, transferring glycosyl groups	chromosome, telomeric region /// nucleus /// Golgi apparatus	---
218947_s_at	PAPD1	0.215	0.153	T	---	nucleic acid binding	---	---
203378_at	PCF11	-0.196	0.153	B	mRNA cleavage	pre-mRNA cleavage factor activity	nucleus /// mRNA cleavage factor complex	mRNA Processing, Transcription, Gene Expression, Cleavage and Polyadenylation
237634_at	C1QTNF3	-0.098	0.153	B	phosphate transport	---	cytoplasm	---

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230705_at	SLC2A5	-0.128	0.152	L	carbohydrate metabolism /// carbohydrate transport /// fructose transport /// glucose transport	transporter activity /// sugar porter activity /// fructose transporter activity /// glucose transporter activity	plasma membrane /// integral to membrane	---
238655_at	ACAD10	-0.116	0.152	B	electron transport /// metabolism	acyl-CoA dehydrogenase activity /// hydrolase activity	---	---
1561161_at	SCMH1	0.051	0.151	T	regulation of transcription, DNA-dependent /// development /// gene silencing /// negative regulation of transcription	transcriptional repressor activity	nucleus	---
202498_s_at	SLC2A3	-0.08	0.151	L	carbohydrate metabolism /// carbohydrate transport /// glucose transport	transporter activity /// sugar porter activity /// glucose transporter activity	membrane fraction /// integral to membrane	---
218030_at	GIT1	-0.178	0.151	L	regulation of G-protein coupled receptor protein signaling pathway /// regulation of GTPase activity	GTPase activator activity	---	---
215933_s_at	HHEX	0.274	0.15	B	regulation of transcription, DNA-dependent /// development /// antimicrobial humoral response (sensu Vertebrata)	transcription factor activity	nucleus	---
211419_s_at	CHN2	0.081	0.149	T	intracellular signaling cascade	SH3/SH2 adaptor activity /// GTPase activator activity /// GTPase activator activity /// diacylglycerol binding	---	---
1554303_at	HNMT	0.346	0.149	T	respiratory gaseous exchange	methyltransferase activity /// S-adenosylmethionine-dependent methyltransferase activity /// transferase activity /// histamine N-methyltransferase activity	---	Histidine metabolism
222666_at	CGI-90	-0.139	0.149	L	---	binding	---	---
1553544_at	GPR101	-0.043	0.149	B	G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity	integral to membrane	---
216724_at	MGC45428	-0.119	0.149	B	protein amino acid phosphorylation /// intracellular signaling cascade	protein serine/threonine kinase activity /// ATP binding /// transferase activity	---	---
1566079_at	ELOVL5	-0.022	0.149	B	---	---	integral to membrane	---
204291_at	ZNF518	-0.068	0.149	B	---	nucleic acid binding /// zinc ion binding	nucleus	---
209337_at	PSIP1	-0.072	0.148	T	regulation of transcription, DNA-dependent	DNA binding	nucleus	neuroactive ligand-receptor interaction
240542_at	MAP4	-0.179	0.148	L	negative regulation of microtubule depolymerization	structural molecule activity	microtubule associated complex	---
229707_at	ZNF606	0.273	0.147	T	transcription /// regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
212157_at	SDC2	-0.193	0.147	L	---	cytoskeletal protein binding	integral to plasma membrane /// integral to membrane	---

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205191_at	RP2	0.029	0.146	T	beta-tubulin folding /// sensory perception /// visual perception	unfolded protein binding	membrane	---
229193_at	CROP	0.227	0.146	T	apoptosis /// response to stress /// RNA splicing	---	nucleus	---
241278_at	FCRH3	0.34	0.146	B	---	receptor activity	---	---
1556783_a_at	LASS5	0.078	0.146	B	regulation of transcription, DNA-dependent /// lipid biosynthesis	transcription factor activity	nucleus /// endoplasmic reticulum /// integral to membrane	---
222957_at	NEU4	-0.25	0.145	L	carbohydrate metabolism	exo-alpha-sialidase activity /// hydrolase activity, acting on glycosyl bonds	lysosome /// inner membrane	N-Glycan degradation /// Glycosphingolipid metabolism
226999_at	RNPC3	-0.2	0.145	L	---	RNA binding	---	---
204979_s_at	SH3BGR	0.257	0.144	T	protein complex assembly	SH3/SH2 adaptor activity	---	---
230929_s_at	UBE2J2	-0.299	0.144	L	ubiquitin cycle	ubiquitin-protein ligase activity /// ligase activity	endoplasmic reticulum /// integral to membrane	Parkinson's disease
216970_at	RGS7	-0.189	0.144	L	regulation of G-protein coupled receptor protein signaling pathway /// intracellular signaling cascade /// negative regulation of signal transduction	regulator of G-protein signaling activity /// signal transducer activity	heterotrimeric G-protein complex	---
237146_at	LRP4	-0.304	0.144	L	endocytosis	receptor activity /// calcium ion binding	integral to membrane	---
216322_at	CD58	0.122	0.144	B	cell-cell adhesion /// antimicrobial humoral response (sensu Vertebrata)	protein binding	integral to plasma membrane	---
224259_at	WNT8A	-0.111	0.144	B	frizzled-2 signaling pathway /// development	signal transducer activity	extracellular region	WNT signaling pathway
211428_at	SERPINA1	0.127	0.143	T	acute-phase response	serine-type endopeptidase inhibitor activity /// serine-type endopeptidase inhibitor activity /// protein binding	extracellular region	Complement and coagulation cascades /// hemostasis
204726_at	CDH13	0.335	0.143	T	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	membrane	---
215860_at	SYT12	-0.425	0.143	L	transport	transporter activity	synaptic vesicle /// integral to membrane /// synapse	---
1569078_at	C17orf27	-0.113	0.143	B	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
220663_at	IL1RAPL1	0.24	0.142	T	signal transduction /// learning and/or memory	transmembrane receptor activity	membrane /// integral to membrane	---
243868_at	RFX3	-0.321	0.142	T	regulation of transcription, DNA-dependent /// negative regulation of transcription	RNA polymerase II transcription factor activity, enhancer binding /// transcriptional repressor activity	nucleus	---

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241027_at	OPA1	0.16	0.142	T	inner mitochondrial membrane organization and biogenesis/// mitochondrial fission/// sensory perception /// visual perception /// mitochondrial fusion /// biosynthesis /// axon transport of mitochondrion /// positive regulation of anti-apoptosis	magnesium ion binding /// motor activity /// GTPase activity /// GTPase activity /// GTP binding /// hydroxymethyl-, formyl- and related transferase activity	mitochondrial outer membrane /// mitochondrial intermembrane space /// mitochondrial crista /// dendrite	---
230075_at	RAB39B	-0.09	0.142	L	small GTPase mediated signal transduction /// protein transport	GTP binding	---	---
1555890_at	OR2A9P	0.064	0.142	B	cell surface receptor linked signal transduction/// G-protein coupled receptor protein signaling pathway/// signal transduction/// cell communication/// cellular process	signal transducer activity/// receptor activity/// G-protein coupled receptor activity/// rhodopsin-like receptor activity	---	---
1565696_at	HECTD2	0.424	0.141	T	ubiquitin cycle	ubiquitin-protein ligase activity	intracellular	---
228131_at	ERCC1	0.232	0.141	T	DNA repair /// nucleotide-excision repair /// morphogenesis	damaged DNA binding /// endonuclease activity /// endodeoxyribonuclease activity /// hydrolase activity	nucleus /// nucleus	DNA Repair, Formation of ERCC1-XPF heterodimeric complex
1552283_s_at	ZDHHC11	-0.211	0.141	L	---	metal ion binding	integral to membrane	---
234970_at	MTAC2D1	0.166	0.14	T	transport	transporter activity	nucleus /// synaptic vesicle /// membrane	---
209571_at	CIR	-0.176	0.14	L	---	transcription factor activity /// transcription corepressor activity	---	---
208198_x_at	KIR2DS1	0.386	0.139	T	immune response	transmembrane receptor activity	integral to membrane	---
235165_at	PARD6B	0.089	0.138	B	cytokinesis /// intercellular junction assembly /// cell cycle /// establishment and/or maintenance of cell polarity /// axonogenesis /// regulation of cell migration	protein binding	plasma membrane /// tight junction	Tight junction
1553468_at	HYDIN	-0.067	0.138	B	---	---	integral to membrane	---
218180_s_at	EPS8L2	-0.083	0.138	B	---	receptor activity	---	---
215915_at	GULP1	-0.046	0.138	B	apoptosis/// phagocytosis, engulfment	Signal transducer activity	---	---
1553982_a_at	RAB7B	0.225	0.137	L	small GTPase mediated signal transduction /// protein transport	GTP binding	lysosome	---
242136_x_at	MGC70870	0.302	0.137	B	L-serine biosynthesis	oxidoreductase activity /// oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	---	---

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		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
213552_at	GLCE	-0.024	0.137	B	peptidoglycan biosynthesis /// heparan sulfate proteoglycan biosynthesis /// heparin biosynthesis	isomerase activity /// racemase and epimerase activity, acting on carbohydrates and derivatives	Golgi apparatus /// integral to membrane	Chondroitin/ Heparan sulfate biosynthesis
236930_at	NUMB	0.005	0.137	B	development	---	integral to plasma membrane /// membrane	Notch signaling pathway
212943_at	KIAA0528	-0.14	0.137	B	transport	transporter activity	synaptic vesicle /// membrane	---
1564822_at	CNGA3	0.266	0.136	T	ion transport /// potassium ion transport /// signal transduction /// sensory perception /// visual perception	nucleotide binding /// receptor activity /// ion channel activity /// voltage-gated potassium channel activity /// ligand-gated ion channel activity /// 3',5'-cGMP binding	membrane fraction /// integral to plasma membrane /// membrane	---
230360_at	COLM	0.183	0.136	T	phosphate transport /// cell adhesion	structural molecule activity /// protein binding	cytoplasm	---
208234_x_at	FGFR2	0.26	0.136	T	protein amino acid phosphorylation /// protein amino acid phosphorylation /// cell growth	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// protein-tyrosine kinase activity /// receptor activity /// fibroblast growth factor receptor activity /// ATP binding /// heparin binding /// transferase activity	membrane /// integral to membrane	MAPK signaling pathway/// Regulation of actin cytoskeleton
205729_at	OSMR	-0.02	0.135	T	cell surface receptor linked signal transduction /// cell proliferation	receptor activity /// oncostatin-M receptor activity	oncostatin-M receptor complex	Cytokine-cytokine receptor interaction/// Jak-STAT signaling pathway
210998_s_at	HGF	0.288	0.135	T	proteolysis and peptidolysis /// mitosis	chymotrypsin activity /// trypsin activity /// growth factor activity	---	Cytokine-cytokine receptor interaction/// focal adhesion/// hemostasis
207210_at	GABRA3	0.495	0.135	L	ion transport /// chloride transport /// gamma-aminobutyric acid signaling pathway /// synaptic transmission	GABA-A receptor activity /// ion channel activity /// extracellular ligand-gated ion channel activity /// benzodiazepine receptor activity	integral to plasma membrane /// postsynaptic membrane	Neuroactive ligand-receptor interaction
216254_at	PARVB	-0.103	0.135	L	cell adhesion	actin binding /// protein binding	cytoskeleton	---
233343_at	DEFB127	-0.08	0.135	B	innate immune response/// defense response to bacteria	nucleic acid binding	---	---
243560_at	HSF1	0.406	0.134	T	regulation of transcription,DNA-dependent/// protein folding	transcription factor activity	nucleus	---
207400_at	NPY5R	0.466	0.133	T	signal transduction /// G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity /// receptor activity /// neuropeptide Y receptor activity	integral to plasma membrane	GPCRDB Class A Rhodopsin like /// Peptide GPCRs
236630_at	AQP2	-0.114	0.133	L	transport /// water transport /// excretion	transporter activity /// water channel activity	integral to plasma membrane	---

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217574_at	CDH8	-0.192	0.133	L	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	integral to membrane	---
1554876_a_at	S100Z	-0.07	0.133	B	---	calcium ion binding	---	---
238072_at	CLK3	0.298	0.132	T	protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	nucleus	mRNA processing
240400_at	PSCD3	0.098	0.132	L	vesicle-mediated transport	ARF guanyl-nucleotide exchange factor activity /// phosphatidylinositol binding /// inositol-1,4,5-triphosphate receptor activity	membrane fraction /// plasma membrane	---
1553409_at	ADAMTS20	-0.19	0.132	L	proteolysis and peptidolysis	metalloendopeptidase activity /// zinc ion binding /// hydrolase activity	extracellular matrix (sensu Metazoa)	---
220451_s_at	BIRC7	-0.255	0.132	L	inhibition of caspase activation /// DNA fragmentation during apoptosis /// apoptosis /// activation of JNK /// protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding /// enzyme binding	ubiquitin ligase complex /// nucleus	---
229786_at	RWDD2	0.171	0.131	T	---	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides /// acylphosphatase activity /// catalytic activity /// hydrolase activity, acting on acid anhydrides	---	---
208047_s_at	NAB1	0.088	0.131	B	regulation of transcription, DNA-dependent /// negative regulation of transcription	nucleic acid binding /// transcriptional repressor activity	nucleus	---
243649_at	FBXO7	-0.003	0.13	L	ubiquitin-dependent protein catabolism /// ubiquitin cycle	ubiquitin-protein ligase activity	ubiquitin ligase complex	---
223417_at	RAD18	-0.205	0.13	L	DNA repair /// protein ubiquitination	damaged DNA binding /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex /// nucleus	---
243108_at	RANBP9	-0.088	0.13	B	microtubule nucleation	protein binding	nucleus	---
243106_at	MICL	0.154	0.129	T	---	receptor activity /// sugar binding	---	---
1563868_a_at	C9orf79	-0.065	0.128	L	---	---	integral to membrane	---
201827_at	SMARCD2	-0.031	0.128	B	chromatin remodeling /// regulation of transcription from Pol II promoter /// chromatin modification	transcription coactivator activity	nucleoplasm	---

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1565358_at	RARA	0.343	0.127	T	transcription /// regulation of transcription, DNA-dependent /// signal transduction	transcription factor activity /// steroid hormone receptor activity /// retinoic acid receptor activity /// transcription coactivator activity	nucleus	Nuclear Receptors
238732_at	COL24A1	-0.062	0.127	L	transcription /// phosphate transport /// cell adhesion	DNA binding /// DNA-directed RNA polymerase activity /// extracellular matrix structural constituent	collagen /// cytoplasm	---
202627_s_at	SERPINE1	-0.298	0.127	L	blood coagulation	serine-type endopeptidase inhibitor activity /// plasminogen activator activity	extracellular region	complement and coagulation cascades
207313_x_at	KIR3DL2	-0.1	0.127	B	cellular defense response	receptor activity	integral to plasma membrane	---
1556306_at	MLL5	0.431	0.126	B	Regulation of transcription, DNA-dependent	DNA binding	nucleus	---
237076_at	NCSTN	0.236	0.125	T	notch receptor processing///amyloid precursor protein catabolism///positive regulation of enzyme activity	protein binding	golgi apparatus///endoplasmic reticulum///integral to membrane	notch signaling pathway////Alzheimer's disease
241216_at	KIF1B	0.147	0.125	T	embryonic development/// microtubule-based movement /// nerve-nerve synaptic transmission /// neuromuscular synaptic transmission /// anterograde axon cargo transport	microtubule motor activity /// protein binding /// ATP binding /// microtubule binding /// ATPase activity /// kinesin binding	mitochondrion /// microtubule associated complex /// cytoplasmic vesicle membrane	---
244603_at	ARHGAP4	-0.053	0.125	B	cytoskeleton organization and biogenesis /// Rho protein signal transduction	SH3/SH2 adaptor protein activity /// Rho GTPase activator activity	cytoplasm	---
243066_at	NPL	-0.135	0.124	L	lysine biosynthesis /// diaminopimelate biosynthesis	lyase activity	---	---
1553383_at	FLJ32810	0.092	0.124	L	---	GTPase activator activity	---	---
1567013_at	NFE2L2	-0.134	0.124	B	regulation of transcription, DNA-dependent /// transcription from Pol II promoter	transcription factor activity	nucleus	Wnt signaling
207968_s_at	MEF2C	0.363	0.123	T	transcription /// regulation of transcription, DNA-dependent /// transcription from RNA polymerase II promoter /// neurogenesis /// muscle development	transcription factor activity /// RNA polymerase II transcription factor activity /// transcription coactivator activity	nucleus	MAPK signaling pathway
219106_s_at	KBTBD10	0.176	0.123	T	striated muscle contraction	protein binding	cytoskeleton	---

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209097_s_at	JAG1	-0.19	0.123	L	angiogenesis /// cell fate determination /// cell communication /// Notch signaling pathway /// development /// neurogenesis /// hemopoiesis /// keratinocyte differentiation /// regulation of cell migration /// regulation of cell proliferation /// myoblast differentiation /// endothelial cell differentiation	Notch binding /// structural molecule activity /// calcium ion binding /// growth factor activity	extracellular region /// integral to plasma membrane	---
1560102_at	ARHGAP26	-0.141	0.123	L	neurogenesis /// actin cytoskeleton organization and biogenesis	Rho GTPase activator activity	---	---
216854_at	GDF11	-0.242	0.123	B	mesoderm development/// neurogenesis/// skeletal development/// growth	cytokine activity/// growth factor activity	---	---
203984_s_at	CASP9	-0.208	0.123	B	proteolysis and peptidolysis /// apoptotic program /// caspase activation via cytochrome c /// regulation of apoptosis	protein binding /// enzyme activator activity /// caspase activity	intracellular	Apoptosis///MAPK signaling pathway///Parkinson's disease
235108_at	KCNK3	-0.062	0.123	B	ion transport /// potassium ion transport /// synaptic transmission	voltage-gated ion channel activity /// potassium channel activity	integral to plasma membrane	---
232695_s_at	SEC14L2	-0.257	0.122	L	transport /// intracellular protein transport /// regulation of cholesterol biosynthesis /// positive regulation of transcription, DNA-dependent	phospholipid binding /// protein carrier activity /// vitamin E binding /// transcriptional activator activity	nucleus /// cytoplasm /// membrane	---
244402_at	SLC3A1	-0.33	0.122	L	carbohydrate metabolism /// amino acid metabolism /// transport /// basic amino acid transport /// L-cystine transport	alpha-amylase activity /// basic amino acid transporter activity /// L-cystine transporter activity	membrane fraction /// integral to plasma membrane	---
234015_at	NAALADL2	-0.221	0.122	L	proteolysis and peptidolysis	peptidase activity	---	---
200066_at	IK	-0.286	0.122	L	immune response /// cell-cell signaling	cytokine activity	extracellular space /// soluble fraction	---
233318_at	FRS2	-0.052	0.122	L	transmembrane receptor protein tyrosine phosphatase signaling pathway /// G-protein coupled receptor protein signaling pathway /// fibroblast growth factor receptor signaling pathway	receptor activity /// transmembrane receptor protein tyrosine kinase adaptor protein activity /// insulin receptor binding /// protein binding /// regulator of G-protein signaling activity /// phosphatase activator activity	integral to plasma membrane	---
209901_x_at	AIF1	0.283	0.121	T	response to stress /// inflammatory response /// cell cycle arrest /// negative regulation of cell proliferation	phosphoprotein phosphatase activity /// calcium ion binding	nucleus	---

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211489_at	ADRA1A	-0.007	0.121	B	apoptosis /// smooth muscle contraction /// signal transduction /// G-protein coupled receptor protein signaling pathway /// protein kinase cascade /// cell-cell signaling /// negative regulation of cell proliferation	rhodopsin-like receptor activity /// adrenoceptor activity /// alpha1-adrenergic receptor activity	integral to plasma membrane	Neuroactive ligand-receptor interaction
206458_s_at	WNT2B	0.299	0.12	T	protein folding /// frizzled-2 signaling pathway /// morphogenesis	signal transducer activity	extracellular space	Wnt signaling pathway/// Hedgehog signaling pathway
210422_x_at	SLC11A1	-0.282	0.12	L	transport /// iron ion transport /// response to pest, pathogen or parasite /// response to bacteria	transporter activity	membrane fraction /// integral to plasma membrane /// membrane	---
227997_at	IL17RD	-0.214	0.12	L	---	transmembrane receptor activity	membrane	---
215231_at	PRKAG2	-0.102	0.12	B	fatty acid biosynthesis /// cholesterol biosynthesis	---	---	Fatty Acid Synthesis
1552910_at	SIGLEC11	-0.099	0.12	B	cell adhesion	protein binding /// sugar binding	integral to membrane	---
222785_x_at	C11orf1	0.339	0.119	T	---	---	nucleus	---
229233_at	NRG3	-0.128	0.119	L	regulation of cell growth /// embryonic development	growth factor activity /// transmembrane receptor protein tyrosine kinase activator activity /// receptor tyrosine kinase binding	extracellular region /// integral to plasma membrane	---
1555133_at	FAM9A	-0.092	0.119	L	---	---	nucleus	---
218422_s_at	C13orf10	-0.577	0.118	T	---	nucleic acid binding	---	---
203671_at	TPMT	-0.11	0.118	L	nucleobase, nucleoside, nucleotide and nucleic acid metabolism /// metabolism	thiopurine S-methyltransferase activity /// methyltransferase activity /// transferase activity	cytoplasm	---
1559210_at	UBE2S	0.129	0.118	L	ubiquitin cycle	ubiquitin conjugating enzyme activity /// ubiquitin-protein ligase activity /// ligase activity	---	Ubiquitin mediated proteolysis
236281_x_at	HTR7	-0.116	0.118	L	G-protein signaling, coupled to cyclic nucleotide second messenger /// synaptic transmission /// circadian rhythm /// circulation	rhodopsin-like receptor activity /// melanocortin receptor activity /// serotonin receptor activity	integral to plasma membrane	Neuroactive ligand-receptor interaction
205824_at	HSPB2	0.257	0.117	T	protein folding /// response to unfolded protein	protein binding /// enzyme activator activity	cytosol	MAPK signaling pathway
203596_s_at	IFIT5	0.201	0.117	T	immune response	binding	---	---
227873_at	C5orf14	0.375	0.116	T	electron transport	electron transporter activity /// isomerase activity	---	---
208601_s_at	TUBB1	0.127	0.116	T	microtubule-based movement /// protein polymerization	GTPase activity /// structural molecule activity /// GTP binding	microtubule /// protein complex	---

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		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
220727_at	KCNK10	-0.23	0.116	L	ion transport /// potassium ion transport /// signal transduction	voltage-gated ion channel activity /// potassium channel activity	membrane fraction /// integral to plasma membrane	---
230114_at	HOXB8	-0.336	0.116	L	development/// regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
214422_at	RAD23B	0.291	0.116	L	nucleotide-excision repair /// protein modification	single-stranded DNA binding	nucleus	---
207031_at	BAPX1	0.073	0.116	B	skeletal development /// regulation of transcription, DNA-dependent /// transcription from Pol II promoter	transcription factor activity /// RNA polymerase II transcription factor activity	nucleus	---
219934_s_at	SULT1E1	0.302	0.115	T	steroid metabolism	estrone sulfotransferase activity /// steroid binding /// transferase activity	---	Androgen and estrogen metabolism /// Sulfur metabolism
206592_s_at	AP3D1	-0.218	0.115	L	eye pigment biosynthesis /// intracellular protein transport	transporter activity /// binding	Golgi apparatus	---
209320_at	ADCY3	-0.211	0.115	L	cAMP biosynthesis /// intracellular signaling cascade /// perception of smell	magnesium ion binding /// adenylate cyclase activity /// guanylate cyclase activity /// calmodulin binding /// lyase activity	integral to plasma membrane	Cholera-infection /// Purine metabolism
238566_at	ZNF334	-0.271	0.115	L	regulation of transcription, DNA-dependent	nucleic acid binding /// DNA binding /// zinc ion binding	nucleus	---
223425_at	RAVER1	-0.115	0.115	B	nuclear mRNA splicing, via spliceosome	nucleic acid binding	---	---
244068_at	STS-1	0.284	0.114	T	metabolism	catalytic activity	---	---
1558501_at	DNM3	-0.142	0.114	T	protein biosynthesis /// endocytosis	structural constituent of ribosome /// motor activity /// GTPase activity /// GTP binding /// hydrolase activity	intracellular /// ribosome	---
241644_at	LAT1-3TM	-0.317	0.114	L	transport /// amino acid transport	amino acid-polyamine transporter activity	integral to membrane	---
229370_at	INSIG1	-0.229	0.114	L	metabolism /// cell proliferation	---	---	---
204692_at	LRCH4	-0.261	0.114	L	neurogenesis	---	---	---
211619_s_at	ALPP /// ALPI	-0.176	0.114	B	metabolism /// phosphorylation	magnesium ion binding /// alkaline phosphatase activity /// hydrolase activity	integral to membrane /// membrane	gamma-Hexachlorocyclohexane degradation /// Folate biosynthesis/// glycerolipid metabolism
1557674_s_at	MGC12458	-0.099	0.114	B	---	calcium ion binding	---	---
236168_at	ACSL3	-0.169	0.113	B	lipid metabolism /// fatty acid metabolism /// metabolism	magnesium ion binding /// catalytic activity /// fatty-acyl-CoA synthase activity /// long-chain-fatty-acid-CoA ligase activity /// ligase activity	---	Fatty Acid Degradation /// Mitochondrial fatty acid betaoxidation /// Fatty acid metabolism
213207_s_at	GOSR2	0.091	0.112	T	intracellular protein transport /// ER to Golgi transport /// membrane fusion	receptor activity /// transporter activity /// v-SNARE activity	Golgi apparatus /// integral to membrane	---
244692_at	FLJ39501	-0.207	0.112	L	electron transport	monooxygenase activity	---	---
203276_at	LMNB1	-0.274	0.112	L	---	structural molecule activity	nucleus /// lamin filament	---

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1559172_at	ANK1	-0.185	0.111	B	exocytosis /// cytoskeleton organization and biogenesis /// signal transduction /// maintenance of epithelial cell polarity	structural molecule activity /// structural constituent of cytoskeleton /// protein binding /// cytoskeletal adaptor activity /// enzyme binding /// spectrin binding	cytoskeleton /// plasma membrane /// actin cytoskeleton /// basolateral plasma membrane	---
218307_at	RSAD1	0.25	0.11	T	porphyrin biosynthesis	magnesium ion binding /// catalytic activity /// coproporphyrinogen oxidase activity /// iron ion binding /// oxidoreductase activity	cytoplasm	---
219265_at	MOBKL2B	0.267	0.11	T	---	zinc ion binding /// metal ion binding	---	---
225488_at	DERL1	-0.433	0.11	B	protein transport /// viral intracellular protein transport /// ER-associated protein catabolism /// unfolded protein response /// retrograde protein transport, ER to cytosol	receptor activity /// protein binding	endoplasmic reticulum /// integral to endoplasmic reticulum membrane	---
235998_at	RHPN1	-0.16	0.109	L	signal transduction	protein binding	intracellular	---
227166_at	MGC29463	0.24	0.109	L	protein folding	heat shock protein binding /// unfolded protein binding	---	---
204456_s_at	GAS1	0.301	0.109	B	cell cycle arrest /// negative regulation of cell proliferation /// negative regulation of S phase of mitotic cell cycle	---	anchored to plasma membrane	Hedgehog signaling pathway
220378_at	TCP11	-0.029	0.108	B	development	---	---	---
44617_at	FLJ13491	0.22	0.108	B	apoptosis /// protein metabolism	oxidoreductase activity /// oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen /// oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	---	---
1554786_at	C20orf32	0.109	0.108	B	signal transduction	two-component sensor molecule activity	membrane	---
1555884_at	p44S10	-0.033	0.108	B	ATP-dependent proteolysis	binding /// ATPase activity	proteasome complex (sensu Eukaryota)	Proteasome Degradation
210750_s_at	DLGAP1	0.243	0.107	T	cell-cell signaling /// synaptic transmission	protein binding	membrane	---
230044_at	NPB	-0.417	0.107	L	neuropeptide signaling pathway	---	---	Neuroactive ligand-receptor interaction
244404_at	STXBP4	-0.232	0.107	L	---	protein binding	---	---

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1561167_at	ETV6	-0.114	0.107	B	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	Circadian Exercise
210282_at	ZNF198	-0.041	0.107	B	regulation of transcription, DNA-dependent	zinc ion binding	nucleus	---
222635_s_at	MED28	-0.107	0.106	L	regulation of transcription, DNA-dependent	actin binding	nucleus /// cytoskeleton /// membrane	---
237968_at	ARL6IP2	-0.122	0.106	B	immune response	GTPase activity /// GTP binding	---	---
1559142_at	MYST3	0.147	0.105	T	DNA packaging /// nucleosome assembly /// regulation of transcription, DNA-dependent /// protein ubiquitination	DNA binding /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex /// nucleosome /// nucleus	---
212806_at	KIAA0367	0.25	0.105	T	apoptosis	---	---	---
233053_at	PB1	0.133	0.105	T	chromatin remodeling /// regulation of transcription, DNA-dependent /// cell cycle /// mitosis	DNA binding /// chromatin binding	nuclear chromosome /// nucleus	---
222106_at	PRND	0.154	0.105	T	---	---	membrane	---
231883_at	FBXW8	-0.12	0.105	B	ubiquitin cycle /// oxygen transport	heme binding	---	---
240206_at	TARS	-0.223	0.104	B	protein biosynthesis /// threonyl-tRNA aminoacylation	threonine-tRNA ligase activity /// ATP binding /// ligase activity	soluble fraction /// cytoplasm	Glycine, serine and threonine metabolism /// Aminoacyl-tRNA biosynthesis
231693_at	FABP1	0.327	0.103	T	transport /// fatty acid metabolism /// cell-cell signaling /// organogenesis	lipid transporter activity /// lipid binding	cytoplasm	---
228168_at	ATP6G3	-0.348	0.103	L	generation of precursor metabolites and energy /// ATP synthesis coupled proton transport /// proton transport	transporter activity /// lipid binding /// hydrogen-transporting ATP synthase activity, rotational mechanism /// hydrogen-transporting ATPase activity, rotational mechanism	membrane fraction /// mitochondrion /// proton-transporting ATP synthase complex (sensu Eukaryota) /// proton-transporting two-sector ATPase complex	Oxidative phosphorylation /// Purine metabolism /// ATP synthesis
220292_at	ZNF434	0.363	0.103	L	regulation of transcription, DNA-dependent	nucleic acid binding /// DNA binding /// transcription factor activity /// zinc ion binding	nucleus	---

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234354_x_at	ERBB2	-0.161	0.102	L	electron transport /// protein amino acid phosphorylation /// transmembrane receptor protein tyrosine kinase signaling pathway /// cell proliferation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// non-membrane spanning protein tyrosine kinase activity /// receptor signaling protein tyrosine kinase activity /// receptor activity /// epidermal growth factor receptor activity /// electron transporter activity /// iron ion binding /// ATP binding /// transferase activity /// ErbB-3 class receptor binding	extracellular region /// membrane /// integral to membrane	---
229368_s_at	ZA20D2	0.32	0.101	T	---	DNA binding /// zinc ion binding	---	---
207533_at	CCL1	-0.187	0.101	B	calcium ion homeostasis /// chemotaxis /// inflammatory response /// signal transduction /// cell-cell signaling /// viral life cycle	chemokine activity	extracellular space	Cytokine-cytokine receptor interaction
228610_at	SMBP	0.32	0.101	B	transport	transporter activity	integral to membrane	---
224762_at	TDE2L	0.307	0.1	T	---	---	membrane /// integral to membrane	---
231269_at	DJ467N11.1	-0.117	0.1	B	DNA restriction	nucleotide binding /// nucleic acid binding /// ATP binding /// ATP-dependent helicase activity /// type III site-specific deoxyribonuclease activity /// nucleoside-triphosphatase activity	nucleus	---
210016_at	MYT1L	0.248	0.099	T	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
1564972_x_at	SETDB2	-0.189	0.099	L	chromatin modification	DNA binding /// methyltransferase activity /// zinc ion binding /// transferase activity /// histone-lysine N-methyltransferase activity	nucleus	---
1563899_at	KLPH	-0.067	0.099	B	carbohydrate metabolism	hydrolase activity, hydrolyzing O-glycosyl compounds	integral to membrane	---
233783_at	VPS16	-0.381	0.098	L	intracellular protein transport	---	cytoplasm /// membrane	Cell cycle

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244044_at	ENPP3	-0.141	0.098	L	phosphate metabolism /// nucleotide metabolism	nucleic acid binding /// endonuclease activity /// phosphodiesterase I activity /// nucleotide diphosphatase activity /// hydrolase activity	integral to plasma membrane	Purine metabolism /// Starch and sucrose metabolism /// Riboflavin metabolism /// Nicotinate and nicotinamide metabolism /// Pantothenate and CoA biosynthesis
210570_x_at	MAPK9	0.266	0.097	T	protein amino acid phosphorylation /// response to stress /// JNK cascade	protein serine/threonine kinase activity /// JUN kinase activity /// MAP kinase activity /// protein binding /// ATP binding /// transferase activity	---	MAPK signaling pathway/// Toll-like receptor signaling pathway/// Wnt signaling pathway/// focal adhesion
1570136_at	NOVA1	0.229	0.097	T	RNA splicing/// synaptic transmission /// synaptic transmission /// locomotory behavior /// locomotory behavior	RNA binding /// RNA binding	nucleus	---
219815_at	GAL3ST4	-0.156	0.097	L	sulfur metabolism /// cell-cell signaling /// biosynthesis /// glycoprotein metabolism /// oligosaccharide metabolism /// proteoglycan biosynthesis	galactosylceramide sulfotransferase activity /// transferase activity /// 3'-phosphoadenosine 5'-phosphosulfate binding /// proteoglycan sulfotransferase activity	membrane fraction /// Golgi apparatus /// integral to membrane	---
233459_at	POLR3E	0.308	0.097	L	Transcription	transferase activity	nucleus	Transcription
202169_at	FARSLA	-0.198	0.097	L	protein biosynthesis /// phenylalanyl-tRNA aminoacylation	phenylalanine-tRNA ligase activity /// ATP binding /// ligase activity	soluble fraction /// cytoplasm	phenylalanine,tyrosine and tryptophan biosynthesis/// aminoacyl-tRNA biosynthesis
244125_at	MGC70870	0.023	0.097	B	L-serine biosynthesis	oxidoreductase activity /// oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	---	---
235520_at	SUHW3	-0.083	0.096	T	---	nucleic acid binding /// zinc ion binding	nucleus	---
224464_at	ETNK1	-0.098	0.096	L	phosphatidylethanolamine biosynthesis	ethanolamine kinase activity /// kinase activity /// transferase activity	cytoplasm	Glycerophospholipid metabolism
1557575_at	GENX-3414	-0.12	0.096	B	carbohydrate metabolism /// muscle contraction	catalytic activity	membrane fraction /// integral to plasma membrane	Circadian Exercise
230078_at	RAPGEF6	-0.107	0.096	B	Ras protein signal transduction /// regulation of GTPase activity	guanyl-nucleotide exchange factor activity /// Ras interactor activity /// GTP-dependent protein binding	plasma membrane	---

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239465_at	UQCRC2	-0.259	0.096	B	electron transport /// oxidative phosphorylation /// proteolysis and peptidolysis /// aerobic respiration	metalloendopeptidase activity /// ubiquinol-cytochrome-c reductase activity /// oxidoreductase activity	mitochondrion /// mitochondrial electron transport chain	Oxidative phosphorylation
228366_at	PPA2	-0.119	0.095	T	metabolism	magnesium ion binding /// inorganic diphosphatase activity /// hydrolase activity	cytoplasm /// mitochondrion	Oxidative phosphorylation
1552263_at	MAPK1	-0.181	0.095	T	protein amino acid phosphorylation /// induction of apoptosis /// chemotaxis /// response to stress /// cell cycle /// signal transduction /// synaptic transmission	protein serine/threonine kinase activity /// MAP kinase activity /// MAP kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	—	MAPK signaling pathway/// regulation of actin cytoskeleton/// TGF-beta signaling pathway/// focal adhesion/// adherens junction
1552694_at	SLC2A13	-0.016	0.095	L	carbohydrate transport	transporter activity /// sugar porter activity	integral to membrane	—
211514_at	RIPK5	-0.09	0.095	B	protein amino acid phosphorylation	protein kinase activity /// protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// receptor activity /// ATP binding	—	—
202612_s_at	CRSP2	0.33	0.094	T	transcription /// regulation of transcription from RNA polymerase II promoter /// transcription initiation from RNA polymerase II promoter /// androgen receptor signaling pathway	receptor activity /// RNA polymerase II transcription mediator activity /// transcriptional activator activity /// ligand-dependent nuclear receptor transcription coactivator activity /// vitamin D receptor binding /// thyroid hormone receptor binding	mediator complex /// nucleus	—
214088_s_at	FUT3	-0.254	0.094	L	carbohydrate metabolism /// protein amino acid glycosylation	transferase activity, transferring glycosyl groups /// 3-galactosyl-N-acetylglucosaminide 4-alpha-L-fucosyltransferase activity	membrane fraction /// Golgi apparatus /// integral to membrane	Blood group glycolipid biosynthesis-lactoseries
1564190_x_at	ZNF519	-0.221	0.093	L	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	—
227485_at	DDX26B	-0.191	0.093	L	—	helicase activity	—	—
242038_at	TA-LRRP	-0.099	0.093	B	—	—	integral to membrane	—
207459_x_at	GYPB	0.17	0.092	T	—	—	plasma membrane /// integral to plasma membrane /// membrane	—
243629_x_at	MFI2	-0.204	0.092	L	iron ion transport	ferric iron binding	integral to plasma membrane	—
201798_s_at	FER1L3	0.237	0.091	T	muscle contraction /// circulation	—	nuclear membrane /// plasma membrane /// integral to membrane	—

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232352_at	ISL2	0.34	0.091	T	regulation of transcription, DNA-dependent /// development	transcription factor activity /// zinc ion binding	nucleus	---
237398_at	ARHGEF12	0.246	0.091	T	---	GTPase activator activity /// protein binding	---	---
209600_s_at	ACOX1	0.236	0.09	T	electron transport /// lipid metabolism /// fatty acid beta-oxidation /// prostaglandin metabolism	acyl-CoA dehydrogenase activity /// acyl-CoA oxidase activity /// acyl-CoA oxidase activity /// electron donor activity /// oxidoreductase activity	peroxisome /// peroxisome	Fatty acid metabolism
1552340_at	SP7	0.325	0.09	T	transcription /// regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
225039_at	RPE	0.243	0.09	B	carbohydrate metabolism	ribulose-phosphate 3-epimerase activity /// isomerase activity	---	Pentose phosphate pathway/// pentose and glucuronate interconversions/// metabolism of sugars/// carbon fixation
233470_at	PTPN5	-0.126	0.09	B	protein metabolism/// dephosphorylation/// physiological process/// protein amino acid dephosphorylation/// phosphate metabolism/// protein modification	phosphoprotein phosphatase activity/// phosphoric monoester hydrolase activity/// protein tyrosine phosphatase activity/// catalytic activity	---	MAPK signaling pathway
1556212_x_at	AIG1	0.118	0.089	T	---	---	integral to membrane	---
1552299_at	C6orf199	0.251	0.089	T	---	ATP binding /// kinase activity /// transferase activity /// nucleotide kinase activity	---	---
208828_at	POLE3	0.248	0.089	T	DNA replication	DNA binding /// epsilon DNA polymerase activity /// transferase activity	nucleus	Purine metabolism/// pyrimidine metabolism/// DNA polymerase
1558466_at	UGCGL2	-0.023	0.089	L	protein amino acid glycosylation	UDP-glucose:glycoprotein glucosyltransferase activity /// transferase activity, transferring glycosyl groups	endoplasmic reticulum	Blood group glycolipid biosynthesis-lactoseries/// fructose and mannose metabolism/// n-glycans biosynthesis/// glycosphingolipid metabolism/// ganglioside biosynthesis/// globoside metabolism/// o-glycans biosynthesis/// blood group glycolipid biosynthesis-neolactoseries/// glycosylphosphatidylinositol(gpi)-anchor biosynthesis/// glycerolipid metabolism
238819_at	ZNF347	-0.105	0.089	B	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---

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45288_at	ABHD6	-0.183	0.088	T	aromatic compound metabolism /// hydrolase activity xenobiotic metabolism /// response to toxin	---	---	---
204758_s_at	TMEM24	0.181	0.088	T	---	---	integral to membrane	---
231804_at	LGR7	-0.105	0.088	T	G-protein coupled receptor protein signaling pathway///signal transduction	rhodopsin-like receptor activity	integral to membrane	neuroactive ligand-receptor interaction
239816_at	POLD3	-0.089	0.088	L	mismatch repair	DNA binding/// transferase activity/// delta DNA polymerase activity	delta DNA polymerase complex/// nucleus	cell cycle
216318_at	MGC27165	-0.118	0.088	B	immune response	antigen binding	integral to membrane	---
221209_s_at	OTOR	0.287	0.087	T	perception of sound	---	---	---
235050_at	SLC2A12	0.255	0.087	L	carbohydrate transport	transporter activity /// sugar porter activity	integral to membrane	---
242947_at	DNAJC16	-0.216	0.087	L	electron transport /// protein folding	electron transporter activity/// heat shock protein binding	---	---
233599_at	C9orf3	-0.156	0.087	L	proteolysis and peptidolysis	aminopeptidase activity /// membrane alanyl aminopeptidase activity /// metallopeptidase activity	---	---
224326_s_at	PCGF6	-0.188	0.087	L	protein ubiquitination	DNA binding /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
1560378_at	GRIK1	0.252	0.086	T	ion transport /// potassium ion transport /// glutamate signaling pathway /// synaptic transmission /// central nervous system development	receptor activity /// transporter activity /// ion channel activity /// glutamate-gated ion channel activity /// potassium channel activity /// kainate selective glutamate receptor activity	integral to plasma membrane /// membrane	neuroactive ligand-receptor interaction
217498_at	CIP29	0.309	0.086	T	transcription /// regulation of transcription, DNA-dependent /// regulation of translation	DNA binding	nucleus	---
226619_at	SENP1	-0.345	0.086	L	proteolysis and peptidolysis /// ubiquitin cycle	endopeptidase activity /// cysteine-type peptidase activity	nucleus	---
242952_at	HDAC9	-0.094	0.086	L	regulation of cell cycle /// regulation of transcription, DNA-dependent /// inflammatory response /// chromatin modification /// histone deacetylation /// B-cell differentiation /// negative regulation of myogenesis	histone deacetylase activity /// transcription factor binding /// repressor activity /// hydrolase activity	histone deacetylase complex /// nucleus /// cytoplasm	---
233866_at	KLHL5	-0.19	0.086	L	actin cytoskeleton organization and biogenesis	actin binding /// protein binding	cytoplasm /// cytoskeleton	---

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211097_s_at	PBX2	0.153	0.086	B	regulation of transcription, DNA-dependent /// anterior compartment specification /// posterior compartment specification	transcription factor activity	nucleus	---
206734_at	JRKL	-0.172	0.085	L	central nervous system development	nucleic acid binding	nucleus	---
240841_at	INSM2	0.296	0.085	B	---	nucleic acid binding /// zinc ion binding	nucleus	---
230750_at	RAB23	0.16	0.084	L	intracellular protein transport /// small GTPase mediated signal transduction	GTP binding	---	Hedgehog signaling pathway
224334_s_at	MRPL51	-0.44	0.084	L	---	structural constituent of ribosome	mitochondrion	---
226216_at	INSR	0.341	0.083	T	carbohydrate metabolism /// generation of precursor metabolites and energy /// protein amino acid phosphorylation /// signal transduction /// transmembrane receptor protein tyrosine kinase signaling pathway /// development	receptor signaling protein tyrosine kinase activity /// receptor activity /// epidermal growth factor receptor activity /// transmembrane receptor protein tyrosine kinase signaling protein activity /// ATP binding /// transferase activity	plasma membrane /// integral to plasma membrane	Insulin receptor mediated signalling
211615_s_at	LRPPRC	-0.122	0.083	T	---	single-stranded DNA binding /// RNA binding /// binding	nucleus /// nucleus /// mitochondrion /// mitochondrion	---
1553165_at	AP1GBP1	-0.221	0.083	L	intracellular protein transport	calcium ion binding	Golgi apparatus /// AP-1 adaptor complex	---
238871_at	MLLT4	-0.214	0.083	L	cell adhesion /// signal transduction /// cell-cell signaling	motor activity /// protein binding /// protein C-terminus binding	intercellular junction /// myosin	---
215722_s_at	SNRPA1	-0.211	0.083	L	RNA splicing	RNA binding	snRNP U2	mRNA processing Reactome
206347_at	PDK3	0.172	0.083	B	glucose metabolism /// protein amino acid phosphorylation	protein kinase activity /// [pyruvate dehydrogenase (lipoamide)] kinase activity /// ATP binding	mitochondrion	Krebs-TCA Cycle
243900_at	RPL35	0.291	0.082	T	protein biosynthesis	mRNA binding /// structural constituent of ribosome	cytosolic large ribosomal subunit /// intracellular /// ribosome /// nucleolus	ribosome
211907_s_at	PARD6B	0.3	0.082	T	cytokinesis /// intercellular junction assembly /// cell cycle /// establishment and/or maintenance of cell polarity /// axonogenesis /// regulation of cell migration	protein binding	plasma membrane /// tight junction	Tight junction
1553084_at	STARD6	0.251	0.081	T	lipid transport	lipid binding	---	---

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Geneontology Pathway
215455_at	TIMELESS	-0.132	0.081	T	development/// morphogenesis of an epithelium /// transcription /// regulation of transcription, DNA-dependent /// circadian rhythm /// negative regulation of transcription	protein binding /// protein heterodimerization activity	nucleus	---
205207_at	IL6	-0.043	0.081	T	acute-phase response /// humoral immune response /// cell surface receptor linked signal transduction /// cell-cell signaling /// positive regulation of cell proliferation /// negative regulation of cell proliferation /// neuron cell differentiation /// B-cell differentiation	cytokine activity /// interleukin-6 receptor binding	extracellular space	Cytokine-cytokine receptor interaction/// Jak-STAT signaling pathway/// Toll-like receptor signaling pathway
1564911_at	MATR3	0.163	0.081	T	---	nucleotide binding /// RNA binding /// structural molecule activity /// zinc ion binding	nucleus /// nuclear inner membrane	---
203168_at	CREBL1	-0.131	0.081	L	regulation of transcription, DNA-dependent /// response to unfolded protein	DNA binding	nucleus /// endoplasmic reticulum /// integral to membrane	G1 to S cell cycle Reactome /// Smooth muscle contraction
1553924_at	LOC116123	0.171	0.08	T	electron transport	monooxygenase activity /// dimethylaniline monooxygenase (N-oxide-forming) activity	microsome	---
210399_x_at	FUT6	0.184	0.08	T	protein amino acid glycosylation /// L-fucose catabolism	transferase activity, transferring glycosyl groups /// 3-galactosyl-N-acetylglucosaminide 4-alpha-L-fucosyltransferase activity /// alpha(1,3)-fucosyltransferase activity	extracellular region /// Golgi apparatus /// membrane /// integral to membrane	Blood group glycolipid biosynthesis-lactoseries
214520_at	FOXC2	0.166	0.08	T	transcription /// regulation of transcription, DNA-dependent /// transcription from RNA polymerase II promoter /// mesoderm development	transcription factor activity	nucleus	---
204012_s_at	LCMT2	0.278	0.08	T	---	protein binding /// methyltransferase activity /// transferase activity	---	---
211114_x_at	SIP1	-0.126	0.08	L	spliceosome assembly	pre-mRNA splicing factor activity	spliceosome complex /// cytoplasm	---
232828_at	VGCNL1	0.452	0.079	T	cation transport	cation channel activity	membrane	---
242577_at	LOC285458	-0.035	0.079	T	microtubule cytoskeleton organization and biogenesis	---	microtubule	---
231572_at	LOC136242	0.355	0.079	L	proteolysis and peptidolysis	chymotrypsin activity /// trypsin activity	---	---

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238958_at	UBE2E1	-0.146	0.079	B	ubiquitin-dependent protein catabolism /// ubiquitin cycle	ubiquitin conjugating enzyme activity /// ubiquitin-protein ligase activity /// ligase activity	---	Ubiquitin mediated proteolysis
215043_s_at	SMA3 /// SMA	-0.107	0.079	B	skeletal development /// carbohydrate metabolism /// neurogenesis	hydrolase activity, hydrolyzing O-glycosyl compounds	---	---
204329_s_at	ZNF202	0.193	0.078	T	negative regulation of transcription from RNA polymerase II promoter /// transcription /// regulation of transcription, DNA-dependent /// lipid metabolism	transcription factor activity /// specific RNA polymerase II transcription factor activity /// zinc ion binding	nucleus	---
207106_s_at	LTK	-0.36	0.078	L	protein amino acid phosphorylation /// signal transduction /// transmembrane receptor protein tyrosine kinase signaling pathway	protein serine/threonine kinase activity /// transmembrane receptor protein tyrosine kinase activity /// receptor activity /// ATP binding /// transferase activity	soluble fraction /// integral to plasma membrane /// membrane	---
1554251_at	HP1-BP74	0.314	0.078	B	nucleosome assembly	DNA binding	nucleosome /// nucleus /// chromosome	---
1557820_at	AFG3L2	-0.175	0.076	T	protein catabolism/// proteolysis	ATP binding/// metal ion binding/// metalloendopeptidase activity/// nucleoside-triphosphatase activity/// nucleotide binding/// unfolded protein binding/// zinc ion binding	mitochondrion/// integral to membrane	---
219228_at	ZNF331	0.25	0.076	T	transcription /// regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
1559048_at	KIAA1447	0.193	0.076	T	---	DNA binding	---	---
229925_at	SLC6A17	-0.239	0.076	L	neurotransmitter transport	neurotransmitter:sodium symporter activity /// symporter activity	integral to plasma membrane	---
1570507_at	SFRS2IP	-0.07	0.076	L	mRNA processing /// RNA splicing	pre-mRNA splicing factor activity	DNA-directed RNA polymerase II, core complex	Apoptosis
238443_at	TFAM	0.118	0.075	T	DNA-dependent DNA replication /// transcription /// regulation of transcription, DNA-dependent /// regulation of transcription from RNA polymerase I promoter /// transcription from mitochondrial promoter	DNA binding /// transcription factor activity	nucleus /// mitochondrion	---

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222462_s_at	BACE1	0.271	0.075	T	proteolysis and peptidolysis /// membrane protein ectodomain proteolysis /// membrane protein ectodomain proteolysis /// beta-amyloid metabolism /// beta-amyloid metabolism	pepsin A activity /// peptidase activity /// beta-aspartyl-peptidase activity /// aspartic-type signal peptidase activity	endosome /// endosome /// Golgi apparatus /// Golgi apparatus /// integral to plasma membrane /// integral to membrane	Alzheimer's disease
210273_at	PCDH7	0.384	0.075	T	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	plasma membrane /// integral to plasma membrane	---
218364_at	LRRFIP2	-0.542	0.075	L	---	LRR domain binding	---	---
243166_at	SLC30A5	-0.086	0.074	T	cation transport /// zinc ion transport /// zinc ion homeostasis /// response to zinc ion /// regulation of proton transport	zinc ion transporter activity /// zinc ion binding /// cation transporter activity /// electrochemical potential-driven transporter activity /// cation diffusion facilitator activity	membrane fraction /// integral to plasma membrane /// membrane /// apical plasma membrane	---
230732_s_at	MAPK4	0.354	0.074	T	protein amino acid phosphorylation /// cell cycle	protein serine/threonine kinase activity /// MAP kinase activity /// ATP binding /// transferase activity	---	MAPK signaling pathway/// regulation of actin cytoskeleton/// TGF-beta signaling pathway/// focal adhesion/// adherens junction
217549_at	HEM1	-0.245	0.074	T	---	catalytic activity	integral to plasma membrane	regulation of actin cytoskeleton
205959_at	MMP13	-0.161	0.073	L	proteolysis and peptidolysis /// collagen catabolism	metalloendopeptidase activity /// calcium ion binding /// collagenase activity /// zinc ion binding /// hydrolase activity	extracellular matrix (sensu Metazoa) /// extracellular space	Matrix Metalloproteinases
223750_s_at	TLR10	0.249	0.072	T	inflammatory response	transmembrane receptor activity	membrane /// integral to membrane	---
208776_at	PSMD11	-0.168	0.072	T	---	binding	proteasome complex (sensu Eukaryota)	Proteasome
222716_s_at	SNX24	-0.379	0.072	L	intracellular signaling cascade /// protein transport	---	---	---
1557677_a_at	FLJ36180	0.27	0.072	L	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
242750_at	MMAA	0.212	0.071	T	---	ATP binding	mitochondrion	---
1570156_s_at	FMN1	-0.235	0.071	B	Development/// cell organization and biogenesis	actin binding	nucleus	---

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1554536_at	DPYD	0.031	0.071	B	electron transport /// 'de novo' pyrimidine base biosynthesis /// uracil catabolism /// thymidine catabolism	dihydroorotate dehydrogenase activity /// dihydroorotate oxidase activity /// electron transporter activity /// iron ion binding /// disulfide oxidoreductase activity /// oxidoreductase activity /// dihydropyrimidine dehydrogenase (NADP+) activity	cytoplasm /// mitochondrion /// membrane	Pyrimidine metabolism /// beta-Alanine metabolism /// Pantothenate and CoA biosynthesis
202516_s_at	DLG1	-0.24	0.07	L	---	guanylate kinase activity /// cytoskeletal protein binding	cytoplasm /// plasma membrane /// intercellular junction	---
215835_at	SCARB1	0.203	0.069	T	transport /// apoptosis /// cell adhesion /// cholesterol metabolism	receptor activity /// transporter activity	membrane fraction /// plasma membrane /// integral to membrane	Statin Pathway
207065_at	KGHF	0.309	0.069	T	---	structural molecule activity	intermediate filament	---
228788_at	YPEL1	-0.197	0.069	L	---	---	nucleus	---
234645_at	MAML2	-0.11	0.069	L	---	receptor activity	---	---
228157_at	ZNF207	-0.036	0.069	B	regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	nucleus	---
231509_at	C7orf16	0.295	0.068	T	protein amino acid phosphorylation /// signal transduction /// protein kinase cascade /// central nervous system development /// behavior	protein phosphatase inhibitor activity	soluble fraction	---
220281_at	SLC12A1	0.168	0.068	L	ion transport /// potassium ion transport /// sodium ion transport /// chloride transport /// amino acid transport	transporter activity /// amino acid-polyamine transporter activity /// sodium:potassium:chloride symporter activity /// symporter activity	membrane fraction /// plasma membrane /// integral to membrane	---
243158_at	NT5C2	0.19	0.068	B	---	5'-nucleotidase activity /// hydrolase activity	cytosol	---
231472_at	FBXO15	0.215	0.067	T	ubiquitin cycle	---	---	---
201148_s_at	TIMP3	0.351	0.067	B	visual perception /// induction of apoptosis by extracellular signals	metalloendopeptidase inhibitor activity	extracellular matrix (sensu Metazoa)	Matrix Metalloproteinases
240690_at	DKFZp761P0	0.303	0.066	T	protein amino acid phosphorylation	protein kinase activity /// ATP binding	---	---
222032_s_at	USP7	-0.167	0.066	L	ubiquitin-dependent protein catabolism /// ubiquitin cycle	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity /// hydrolase activity	nucleus	---
219138_at	RPL14	0.371	0.065	T	protein biosynthesis	RNA binding /// structural constituent of ribosome	ribosome /// cytosolic large ribosomal subunit (sensu Eukaryota)	Ribosome

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218202_x_at	MRPL44	0.336	0.065	T	RNA processing	double-stranded RNA binding /// structural constituent of ribosome /// endonuclease activity /// ribonuclease III activity /// hydrolase activity	mitochondrion /// ribonucleoprotein complex	---
1563465_at	PKD1L1	-0.122	0.065	B	---	---	integral to membrane	---
204339_s_at	RGS4	0.272	0.064	T	inactivation of MAPK /// signal transduction /// regulation of G-protein coupled receptor protein signaling pathway	signal transducer activity /// GTPase activator activity /// calmodulin binding	---	Calcium regulation in cardiac cells /// Smooth muscle contraction
244443_at	CHD2	-0.23	0.064	T	chromosome organization and biogenesis/// regulation of transcription from RNA polymerase II promoter	ATP binding/// ATP-dependent DNA helicase activity/// chromatin binding/// hydrolase activity	chromatin/// nucleus	---
1558522_at	MPP6	-0.058	0.064	L	protein complex assembly	protein binding	membrane	---
201675_at	AKAP1	0.206	0.063	L	---	RNA binding	mitochondrion /// integral to membrane /// outer membrane	G Protein Signaling
230838_s_at	CIAPIN1	-0.131	0.063	B	---	transferase activity, transferring one-carbon groups/// transferase activity/// methyltransferase activity/// catalytic activity	---	---
1570030_at	ZNF396	0.183	0.062	T	transcription /// negative regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding /// transcriptional repressor activity	nucleus /// cytoplasm	---
227090_at	BHC80	-0.116	0.062	L	regulation of transcription, DNA-dependent /// protein ubiquitination	DNA binding /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex /// nucleus	---
222856_at	APLN	-0.295	0.062	L	immune response /// signal transduction /// lactation	hormone activity	---	---
238821_at	CSTF2	0.278	0.062	B	mRNA polyadenylylation /// mRNA cleavage	RNA binding	nucleus	mRNA processing
224048_at	USP44	-0.297	0.061	T	ubiquitin-dependent protein catabolism /// ubiquitin cycle	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity	---	---
201292_at	TOP2A	-0.286	0.061	T	DNA topological change	DNA topoisomerase (ATP-hydrolyzing) activity /// ATP binding	nucleus	---
232875_at	KIAA1797	0.114	0.061	T	mitotic chromosome condensation	---	---	---
203486_s_at	ARMC8	-0.259	0.061	L	cell adhesion	structural molecule activity /// protein binding	cytoskeleton	---
222424_s_at	NUCKS	-0.401	0.061	L	---	---	nucleus	---
218340_s_at	FLJ10808	-0.424	0.06	T	ubiquitin cycle	catalytic activity /// ubiquitin activating enzyme activity	---	---
228526_at	NANOS1	0.311	0.06	T	regulation of translation	RNA binding /// zinc ion binding	---	---

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230686_s_at	SLC13A3	0.475	0.06	L	transport /// sodium ion transport	transporter activity /// symporter activity	membrane /// integral to membrane	—
228682_at	MASA E-1 en	-0.203	0.06	L	metabolism	catalytic activity	—	—
201578_at	PODXL	-0.232	0.06	L	—	—	integral to plasma membrane	—
214806_at	BICD1	-0.237	0.06	L	—	—	Golgi apparatus	—
203898_at	RCP9	0.197	0.06	B	acrosome reaction	calcitonin receptor activity	—	Smooth muscle contraction
201409_s_at	PPP1CB	-0.311	0.059	T	carbohydrate metabolism/// cytokinesis /// glycogen metabolism /// cell cycle	phosphoprotein phosphatase activity /// hydrolase activity /// manganese ion binding	—	Regulation of actin cytoskeleton/// focal adhesion
1552504_a_at	BRSK1	-0.196	0.059	L	protein amino acid phosphorylation	protein serine/threonine kinase activity /// ATP binding /// transferase activity	—	—
233875_at	EDIL3	-0.23	0.059	B	cell adhesion /// development	integrin binding /// calcium ion binding /// protein binding	—	—
225447_at	GPD2	-0.165	0.058	L	glucose catabolism /// glycerol-3-phosphate metabolism /// electron transport	glycerol-3-phosphate dehydrogenase activity /// calcium ion binding /// oxidoreductase activity	mitochondrion /// glycerol-3-phosphate dehydrogenase complex	Glycerolipid metabolism
226560_at	SGPP2	0.175	0.057	T	—	hydrolase activity	integral to membrane	—
1567080_s_at	CLN6	0.233	0.057	T	—	—	endoplasmic reticulum /// integral to membrane	—
219866_at	CLIC5	-0.342	0.057	L	ion transport /// chloride transport /// pregnancy	voltage-gated chloride channel activity /// chloride transporter activity	insoluble fraction /// Golgi apparatus /// actin cytoskeleton /// membrane	—
242627_at	LOC56902	-0.14	0.057	L	—	RNA binding	—	—
1552661_at	PCDHGB7	-0.073	0.057	B	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	integral to membrane	—
218832_x_at	ARRB1	0.584	0.054	L	signal transduction /// sensory perception	enzyme inhibitor activity	soluble fraction /// cytoplasm /// heterotrimeric G-protein complex /// plasma membrane	MAPK signaling pathway
244541_x_at	FOXD4L1	-0.306	0.054	L	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	—
216964_at	USP22	-0.234	0.054	B	ubiquitin-dependent protein catabolism/// ubiquitin cycle	cysteine-type endopeptidase activity/// ubiquitin thiolesterase activity	—	—
235925_at	TCF12	-0.492	0.053	T	transcription /// regulation of transcription from RNA polymerase II promoter /// immune response /// development /// muscle development	DNA binding /// RNA polymerase II transcription factor activity	nucleus	—
234438_at	KIAA1043	-0.172	0.053	T	—	binding	—	—
238793_at	TIGD7	0.137	0.052	T	—	DNA binding	chromosome, pericentric region /// nucleus	—

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		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
216283_s_at	PVR	0.188	0.052	T	---	receptor activity	extracellular space /// cytoplasm /// integral to membrane	---
212025_s_at	FLII	0.667	0.052	L	regulation of transcription, DNA-dependent /// muscle contraction /// development /// metabolism	actin binding /// lyase activity	nucleus /// cytoskeleton	---
244745_at	RERG	0.176	0.051	B	small GTPase mediated signal transduction /// negative regulation of cell proliferation /// response to hormone stimulus /// negative regulation of cell growth	GTPase activity /// GTP binding /// GDP binding /// estrogen receptor binding	nucleus /// cytosol	---
244684_at	PGGT1B	0.199	0.05	T	protein amino acid geranylgeranylation	prenyltransferase activity /// CAAX-protein geranylgeranyltransferase activity /// transferase activity	CAAX-protein geranylgeranyltransferase complex	N-Glycan biosynthesis
1552946_at	MGC17986	0.459	0.05	L	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
239058_at	FOXC2	-0.197	0.05	L	regulation of transcription, DNA-dependent /// transcription from Pol II promoter /// mesoderm development	transcription factor activity	nucleus	---
205636_at	SH3GL3	-0.208	0.05	B	central nervous system development /// signal transduction	protein binding	cytoplasm	---
208525_s_at	OR2F1 /// OR	-0.155	0.049	B	signal transduction /// G-protein coupled receptor protein signaling pathway /// perception of smell	receptor activity /// olfactory receptor activity	integral to plasma membrane /// integral to membrane	---
201499_s_at	USP7	-0.459	0.048	L	ubiquitin-dependent protein catabolism /// ubiquitin cycle	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity /// hydrolase activity	nucleus	---
204171_at	RPS6KB1	-0.092	0.048	B	protein amino acid phosphorylation /// signal transduction	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	---	TGF-Beta signaling pathway
218244_at	NOL8	-0.347	0.047	L	nuclear mRNA splicing, via spliceosome	nucleic acid binding	---	---
1559663_at	ACSL4	-0.108	0.046	T	lipid metabolism /// fatty acid metabolism /// learning and/or memory /// metabolism	magnesium ion binding /// long-chain-fatty-acid-CoA ligase activity /// ligase activity	integral to membrane	Fatty Acid Degradation /// Mitochondrial fatty acid betaoxidation /// Fatty acid metabolism
202319_at	SENP6	0.134	0.046	L	proteolysis and peptidolysis /// ubiquitin cycle	cysteine-type peptidase activity	---	---

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242652_at	EPB41L2	-0.29	0.046	L	cortical actin cytoskeleton organization and biogenesis	actin binding /// structural molecule activity /// structural constituent of cytoskeleton ///	cytoplasm /// cytoskeleton /// plasma membrane /// spectrin	---
222011_s_at	TCP1	0.215	0.045	T	protein folding /// tubulin folding	ATP binding /// unfolded protein binding /// unfolded protein binding	cytosol	---
232059_at	DSCAML1	0.233	0.045	T	cell adhesion	---	membrane	---
210868_s_at	ELOVL6	-0.187	0.045	L	---	---	integral to membrane	---
208514_at	KCNE1	0.335	0.044	T	ion transport /// potassium ion transport /// muscle contraction /// perception of sound /// regulation of heart contraction rate	delayed rectifier potassium channel activity /// potassium channel regulator activity	voltage-gated potassium channel complex /// membrane /// integral to membrane	---
205406_s_at	SPA17	0.202	0.044	T	signal transduction /// spermatogenesis /// fertilization (sensu Metazoa)	cAMP-dependent protein kinase regulator activity	membrane	---
212424_at	PDCD11	-0.294	0.044	L	regulation of transcription, DNA-dependent /// rRNA processing /// apoptosis /// positive regulation of I-kappaB kinase/NF-kappaB cascade	RNA binding /// transcription factor binding	nucleus	---
219423_x_at	TNFRSF25	0.238	0.044	L	apoptosis /// immune response /// signal transduction /// cell surface receptor linked signal transduction /// induction of apoptosis by extracellular signals /// regulation of apoptosis	receptor activity /// transmembrane receptor activity /// tumor necrosis factor receptor activity /// protein binding	cytosol /// integral to plasma membrane /// membrane	Apoptosis/// cytokine-cytokine receptor interaction
216727_at	STK38	-0.337	0.044	L	protein amino acid phosphorylation /// protein kinase cascade	magnesium ion binding /// protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	nucleus	---
222204_s_at	RRN3	-0.241	0.043	T	transcription from RNA polymerase I promoter	RNA polymerase I transcription factor activity /// translation initiation factor activity	---	---
216907_x_at	KIR3DL2	0.251	0.043	T	cellular defense response	receptor activity	integral to plasma membrane	---
233166_at	DEFB129	0.163	0.043	T	defense response to bacteria	---	---	---
238751_at	ARGBP2	-0.152	0.043	T	---	nucleic acid binding /// structural constituent of cytoskeleton /// protein binding /// cytoskeletal adaptor activity /// zinc ion binding /// structural constituent of muscle	nucleus /// nucleus /// cytoskeleton /// actin cytoskeleton /// Z disc	---

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205051_s_at	KIT	-0.482	0.043	L	protein amino acid phosphorylation /// protein amino acid dephosphorylation /// signal transduction /// transmembrane receptor protein tyrosine kinase signaling pathway	receptor signaling protein tyrosine kinase activity /// receptor activity /// vascular endothelial growth factor receptor activity /// ATP binding /// transferase activity	integral to membrane	cytokine-cytokine receptor interaction
236192_at	HOOK3	-0.291	0.043	B	Golgi organization and biogenesis/// microtubule cytoskeleton organization and biogenesis	microtubule binding	Golgi membrane/// cytoskeleton	—
1554319_at	RPS6KA5	-0.057	0.042	T	regulation of transcription, DNA-dependent /// protein amino acid phosphorylation /// proteolysis and peptidolysis /// DNA damage induced protein phosphorylation /// response to oxidative stress /// signal transduction /// epidermal growth factor receptor signaling pathway /// protein kinase cascade /// response to external stimulus /// histone phosphorylation /// response to chemical substance	catalytic activity /// protein serine/threonine kinase activity /// protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// ATP binding /// metallopeptidase activity /// zinc ion binding /// transferase activity	nucleus /// nucleus	MAPK signaling pathway
1552814_a_at	KLF14	-0.152	0.042	L	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	—
1565906_at	NADSYN1	0.256	0.041	T	nitrogen compound metabolism /// NAD biosynthesis	NAD+ synthase (glutamine-hydrolyzing) activity /// ATP binding /// hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds /// ligase activity	—	Glutamate metabolism /// Nicotinate and nicotinamide metabolism
207501_s_at	FGF12	0.359	0.04	L	—	growth factor activity	nucleus	MAPK signaling pathway
223137_at	ZDHHC4	-0.397	0.04	L	—	metal ion binding	integral to membrane	—
236024_at	GPM6A	0.216	0.039	T	—	—	integral to plasma membrane	—
1562775_at	NUDT12	0.2	0.038	T	isoprenoid biosynthesis	magnesium ion binding /// hydrolase activity	—	—
204924_at	TLR2	0.236	0.037	T	induction of apoptosis /// inflammatory response /// signal transduction	lipopolysaccharide receptor activity /// transmembrane receptor activity /// protein binding /// peptidoglycan binding /// Gram-positive bacterial binding	plasma membrane /// integral to plasma membrane /// cell surface	Toll-like receptor signaling pathway
244204_at	PRR3	0.208	0.037	T	—	nucleic acid binding	—	—
229395_at	STX4A	-0.215	0.037	L	neurotransmitter transport /// intracellular protein transport	protein transporter activity	integral to membrane	—
209394_at	ASMTL	-0.278	0.036	T	melatonin biosynthesis	acetylserotonin O-methyltransferase activity	—	—

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226573_at	DIRAS1	-0.314	0.036	T	small GTPase mediated signal transduction	GTP binding	---	---
211313_s_at	BAZ1B	0.3	0.036	T	transcription /// regulation of transcription, DNA-dependent /// protein ubiquitination	DNA binding /// transcription factor activity /// ubiquitin-protein ligase activity /// zinc ion binding /// zinc ion binding	ubiquitin ligase complex /// nucleus	---
224168_at	TXNDC2	0.382	0.036	T	thioredoxin pathway /// thioredoxin pathway /// spermatogenesis /// spermatogenesis	thioredoxin-disulfide reductase activity /// thioredoxin-disulfide reductase activity	cytoplasm /// cytoplasm	---
205503_at	PTPN14	0.303	0.036	L	protein amino acid dephosphorylation	protein tyrosine phosphatase activity /// receptor activity /// structural molecule activity /// binding /// hydrolase activity	cytoskeleton	---
225317_at	ACBD6	-0.156	0.035	T	---	acyl-CoA binding	---	---
242988_at	DCST2	0.205	0.034	T	protein targeting/// macromolecule metabolism/// intracellular transport/// protein metabolism/// cellular physiological process/// cell growth and/or maintenance/// protein transport/// intracellular protein transport	RNA binding	---	---
1555852_at	PSMB8	0.218	0.033	T	immune response/// proteolysis and peptidolysis/// ubiquitin-dependent protein catabolism	threonine endopeptidase activity	proteasome core complex	cell cycle/// DNA replication
1557597_at	CHD1L	-0.108	0.034	L	---	DNA binding /// helicase activity /// ATP binding	nucleus	---
223138_s_at	DHX36	-0.574	0.033	L	---	nucleic acid binding /// ATP binding /// ATP-dependent helicase activity	---	---
1561329_s_at	RPUSD3	0.255	0.033	B	RNA processing	RNA binding /// pseudouridine synthase activity	---	---
1553295_at	ABCA13	-0.087	0.033	B	transport/// cellular physiological process/// cell growth and/or maintenance	ATP binding/// ATPase activity	---	---
1563487_at	PDLIM5	0.213	0.032	T	heart development	actin binding /// protein kinase C binding /// protein binding /// zinc ion binding /// receptor signaling complex scaffold activity /// actinin binding	membrane fraction /// cytosol	---
230257_s_at	C1orf19	0.22	0.032	T	mRNA processing /// tRNA processing	---	nucleus	---
226678_at	UNC13D	-0.181	0.032	T	exocytosis	---	---	---

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
211471_s_at	RAB36	0.225	0.032	L	intracellular protein transport /// small GTPase mediated signal transduction	GTPase activity /// GTP binding	Golgi apparatus	---
209575_at	IL10RB	0.345	0.032	L	inflammatory response /// signal transduction /// blood coagulation	receptor activity /// hematopoietin/interferon-class (D200-domain) cytokine receptor activity /// interleukin-10 receptor activity	plasma membrane /// integral to membrane	cytokine-cytokine receptor interaction/// JAK-stat signaling pathway
230918_at	FGF7	0.187	0.032	B	regulation of cell cycle /// signal transduction /// cell-cell signaling /// cell proliferation /// positive regulation of cell proliferation /// epidermis development /// response to wounding	growth factor activity	extracellular region	MAPK signaling pathway/// Regulation of actin cytoskeleton
1554907_a_at	HYDIN	-0.196	0.032	B	---	---	integral to membrane	---
203646_at	FDX1	0.311	0.03	L	electron transport /// vitamin metabolism /// steroid metabolism	iron ion binding /// electron carrier activity	mitochondrion	---
218935_at	EHD3	0.429	0.03	L	---	nucleic acid binding /// GTPase activity /// calcium ion binding /// ATP binding /// GTP binding	nucleus	---
235879_at	MBNL1	-0.157	0.029	T	embryonic development (sensu Mammalia) /// neurogenesis /// muscle development /// embryonic limb morphogenesis /// myoblast differentiation	nucleic acid binding /// double-stranded RNA binding	nucleus /// nucleus /// cytoplasm	---
225084_at	SEC10L1	-0.289	0.028	T	post-Golgi transport /// exocytosis /// protein transport /// vesicle docking	---	cytoplasm	---
207978_s_at	NR4A3	0.161	0.028	T	transcription /// regulation of transcription, DNA-dependent	transcription factor activity /// steroid hormone receptor activity /// steroid hormone receptor activity /// thyroid hormone receptor activity /// binding	nucleus /// nucleus	Hypertrophy model
204061_at	PRKX	0.236	0.028	T	protein amino acid phosphorylation	protein serine/threonine kinase activity /// cAMP-dependent protein kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	---	MAPK signaling pathway/// Wnt signaling pathway/// Hedgehog signaling pathway/// Calcium signaling pathway
213845_at	GRIK2	-0.228	0.028	L	glutamate signaling pathway /// potassium ion transport /// synaptic transmission	kainate selective glutamate receptor activity	integral to plasma membrane	Neuroactive ligand-receptor interaction
237279_at	MARVELD2	0.309	0.028	L	---	---	integral to membrane	---

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values):	Expression change (log2 Values):		Geneontology	Geneontology	Geneontology	
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
204432_at	SOX12	-0.451	0.028	B	regulation of transcription from Pol II promoter	DNA binding /// RNA polymerase II transcription factor activity	nucleus	---
237427_at	COL9A3	-0.424	0.028	B	phosphate transport	structural molecule activity	extracellular matrix (sensu Metazoa) /// collagen type IX /// cytoplasm	---
1555421_at	AP1S3	-0.071	0.026	L	intracellular protein transport /// endocytosis	protein transporter activity	Golgi trans face /// coated pit /// AP-1 adaptor complex /// clathrin vesicle coat	---
204675_at	SRD5A1	0.314	0.025	T	cell-cell signaling /// sex determination /// sex differentiation	3-oxo-5-alpha-steroid 4-dehydrogenase activity /// electron transporter activity /// oxidoreductase activity	endoplasmic reticulum /// microsome /// integral to membrane	Bile acid biosynthesis /// Androgen and estrogen metabolism
233877_at	GOLPH4	0.197	0.024	T	---	---	Golgi lumen /// Golgi cis-face /// integral to membrane /// endocytic vesicle	---
229701_at	TTC18	-0.135	0.024	L	---	binding	---	---
1560713_a_at	KIAA1904	0.096	0.023	T	---	---	cell surface	---
215644_at	ZNF518	0.2	0.022	T	---	nucleic acid binding /// zinc ion binding	nucleus	---
239143_x_at	RNF138	-0.083	0.022	L	protein ubiquitination	nucleic acid binding /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex /// nucleus	---
207854_at	GYPE	-0.197	0.022	L	---	---	integral to plasma membrane	---
221297_at	GPRC5D	0.372	0.022	L	G-protein coupled receptor protein signaling pathway /// visual perception	sevenless binding /// metabotropic glutamate, GABA-B-like receptor activity	integral to membrane	GPCRDB Class C Metabotropic glutamate pheromone
208294_x_at	CSHL1	0.27	0.022	L	---	hormone activity /// structural constituent of chorion (sensu Insecta)	extracellular region	---
242397_at	OLR1	0.297	0.021	T	proteolysis and peptidolysis /// circulation	receptor activity /// sugar binding	membrane fraction /// integral to plasma membrane	---
209226_s_at	TNPO1	-0.706	0.021	L	protein-nucleus import, docking /// protein-nucleus import, translocation /// protein transport	binding /// nuclear localization sequence binding /// protein transporter activity	nucleus /// nuclear pore /// cytoplasm	---
1552632_a_at	KIAA1001	0.492	0.021	L	metabolism	sulfuric ester hydrolase activity /// hydrolase activity	---	---
207120_at	FLJ14011	-0.165	0.021	L	regulation of transcription, DNA-dependent	nucleic acid binding /// DNA binding /// zinc ion binding	nucleus	---
235579_at	SFRS2IP	-0.208	0.021	L	mRNA processing /// RNA splicing	pre-mRNA splicing factor activity	DNA-directed RNA polymerase II, core complex	Apoptosis.
1558779_at	H2AFY	0.16	0.021	B	nucleosome assembly /// chromosome organization and biogenesis (sensu Eukaryota)	DNA binding	nucleosome /// nucleus /// chromosome	---

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
222133_s_at	PHF20L1	-0.579	0.019	T	regulation of transcription, DNA-dependent	nucleic acid binding /// DNA binding	---	---
209385_s_at	PROSC	0.233	0.019	T	---	---	cytoplasm	---
1559452_a_at	SIAT4A	0.177	0.019	L	protein amino acid glycosylation	beta-galactoside alpha-2,3-sialyltransferase activity	Golgi apparatus /// integral to membrane	O-Glycan biosynthesis /// Keratan sulfate biosynthesis /// Globoside metabolism /// Ganglioside biosynthesis
220868_s_at	SLC7A10	-0.3	0.018	L	transport /// neutral amino acid transport	amino acid-polyamine transporter activity /// L-serine transporter activity	integral to plasma membrane	---
243445_at	BNC2	0.298	0.017	T	---	zinc ion binding /// nucleic acid binding	nucleus	---
204219_s_at	PSMC1	-0.316	0.017	L	protein catabolism	nucleotide binding /// ATP binding /// hydrolase activity /// nucleoside-triphosphatase activity	nucleus /// cytosol	Proteasome degradation
222696_at	AXIN2	0.249	0.017	L	signal transduction /// frizzled signaling pathway /// development	signal transducer activity	intracellular	Wnt signaling pathway
211208_s_at	CASK	-0.736	0.017	L	protein amino acid phosphorylation /// cell adhesion	guanylate kinase activity /// protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// protein binding /// calmodulin binding /// ATP binding /// transferase activity	plasma membrane /// actin cytoskeleton	Benzoate degradation via coa ligation/// inositol phosphate metabolism/// starch and sucrose metabolism/// nicotinate and nicotinamide metabolism
207609_s_at	CYP1A2	0.275	0.017	B	electron transport	electron transporter activity /// oxygen binding /// unspecific monooxygenase activity	endoplasmic reticulum /// microsome /// membrane	Fatty acid metabolism /// gamma-Hexachlorocyclohexane degradation /// Tryptophan metabolism
1553168_at	GRIK5	0.184	0.016	T	ion transport /// potassium ion transport /// synaptic transmission /// synaptic transmission	receptor activity /// ionotropic glutamate receptor activity /// transporter activity /// ion channel activity /// glutamate-gated ion channel activity /// potassium channel activity /// kainate selective glutamate receptor activity	membrane /// integral to membrane /// integral to membrane	neuroactive ligand-receptor interaction
216719_s_at	CYP2U1	0.207	0.016	T	electron transport	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	---	---

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		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
214498_at	ASIP	0.237	0.016	T	generation of precursor metabolites and energy /// signal transduction /// cell-cell signaling /// hormone-mediated signaling	receptor binding	extracellular space	---
202178_at	PRKCZ	-0.27	0.016	T	protein amino acid phosphorylation /// anti-apoptosis /// intracellular signaling cascade	protein serine/threonine kinase activity /// atypical protein kinase C activity /// ATP binding /// transferase activity /// diacylglycerol binding	membrane fraction /// cytoplasm /// plasma membrane	G Protein Signaling /// Wnt signaling /// Calcium regulation in cardiac cells /// Smooth muscle contraction /// Phosphatidylinositol signaling system
217210_at	DNCL1	0.244	0.016	L	microtubule-based process	microtubule motor activity	dynein complex/// microtubule	Apoptosis
208303_s_at	CRLF2	-0.235	0.016	B	---	receptor activity /// hematopoietin/interferon-class (D200-domain) cytokine receptor activity	integral to membrane	Cytokine-cytokine receptor interaction
223639_s_at	ZNRD1	-0.287	0.015	T	nucleobase, nucleoside, nucleotide and nucleic acid metabolism /// RNA elongation /// regulation of transcription, DNA-dependent	transcription factor activity	---	Purine metabolism/// Pyrimidine metabolism/// RNA polymerase
208574_at	SOX14	-0.091	0.015	L	regulation of transcription, DNA-dependent /// neurogenesis	transcription factor activity	chromatin /// nucleus	---
209992_at	PFKFB2	0.28	0.014	T	fructose 2,6-bisphosphate metabolism /// metabolism	6-phosphofructo-2-kinase activity /// fructose-2,6-bisphosphate 2-phosphatase activity /// ATP binding /// kinase activity /// transferase activity /// hydrolase activity	---	Fructose and mannose metabolism
202734_at	TRIP10	0.146	0.014	L	signal transduction /// actin cytoskeleton organization and biogenesis	protein binding	cytoplasm	---
238466_at	ZNF91	-0.125	0.014	L	regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	nucleus	---
215549_x_at	CTAGE6	-0.554	0.014	L	---	protein binding/// enzyme activator activity	---	---
206772_at	PTHR2	0.259	0.014	B	G-protein coupled receptor protein signaling pathway	G-protein coupled receptor activity /// parathyroid hormone receptor activity	integral to plasma membrane	Neuroactive ligand-receptor interaction
226787_at	ZNF18	0.166	0.013	T	regulation of transcription, DNA-dependent	nucleic acid binding /// transcription factor activity /// zinc ion binding	nucleus	---
213332_at	PAPPA2	0.289	0.013	T	regulation of cell growth /// regulation of cell growth /// proteolysis and peptidolysis /// proteolysis and peptidolysis /// cell differentiation	metallopeptidase activity /// metallopeptidase activity /// zinc ion binding /// zinc ion binding	intracellular /// intracellular /// membrane	---
240485_at	TTC8	0.136	0.013	B	visual perception	binding	---	---

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229785_at	CCM1	-0.063	0.013	B	small GTPase mediated signal transduction	small GTPase regulatory/interacting protein activity /// binding	cytoskeleton	---
212975_at	KIAA0870	-0.206	0.012	L	signal transduction	signal transducer activity	---	---
243561_at	YAF2	0.221	0.012	L	regulation of transcription, DNA-dependent /// negative regulation of transcription /// positive regulation of transcription	transcription coactivator activity /// transcription corepressor activity /// protein binding	nucleus	---
1553293_at	MRGX3	0.289	0.012	L	G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity	integral to membrane	---
204330_s_at	MRPS12	-0.213	0.012	L	protein biosynthesis	nucleic acid binding /// structural constituent of ribosome	intracellular /// mitochondrion /// mitochondrial ribosome /// small ribosomal subunit	---
221380_at	HHCM	0.358	0.011	T	cell growth and/or maintenance/// physiological process/// cellular physiological process/// cellular process	---	---	---
207486_x_at	CHN2	0.218	0.01	T	intracellular signaling cascade	SH3/SH2 adaptor activity /// GTPase activator activity /// GTPase activator activity /// diacylglycerol binding	---	---
216677_at	ZNF154	0.226	0.01	T	transcription /// regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	nucleus	---
238676_at	C21orf59	-0.212	0.01	L	metabolism	oxidoreductase activity	---	---
2079333_at	ZP2	0.467	0.01	L	fertilization (sensu Metazoa) /// binding of sperm to zona pellucida	coreceptor activity	extracellular matrix (sensu Metazoa) /// extracellular space /// integral to membrane	Ovarian Infertility Genes
238512_at	ST7L	-0.158	0.01	B	---	binding	---	---
240631_at	MASS1	0.184	0.009	T	cell communication /// neuropeptide signaling pathway /// neurogenesis /// cell-cell adhesion	receptor activity /// G-protein coupled receptor activity /// calcium ion binding	membrane /// integral to membrane	GPCRDB Other
238960_s_at	LOC113251	-0.28	0.009	L	nuclear mRNA splicing, via spliceosome	nucleic acid binding	---	---
207600_at	KCNC3	0.188	0.008	T	cation transport /// potassium ion transport	voltage-gated potassium channel activity /// protein binding	membrane fraction /// voltage-gated potassium channel complex /// membrane /// integral to membrane	---
1569508_at	PRDM5	0.2	0.008	T	transcription /// regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
1552307_a_at	C18orf17	0.221	0.008	T	---	---	---	---
207786_at	CYP2R1	-0.144	0.008	L	electron transport	monooxygenase activity	---	---
210115_at	RPL39L	-0.194	0.007	L	protein biosynthesis	structural constituent of ribosome	intracellular /// ribosome	ribosome

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1558777_at	MKL2	0.263	0.006	T	transcription /// regulation of transcription, DNA-dependent /// myogenesis /// cell differentiation /// positive regulation of myogenesis /// positive regulation of transcription from RNA polymerase II promoter	DNA binding /// transcription coactivator activity /// protein binding	nucleus	---
229526_at	AQP11	0.277	0.005	T	transport	transporter activity	membrane /// integral to membrane	---
218740_s_at	CDK5RAP3	0.439	0.005	L	regulation of cyclin dependent protein kinase activity /// brain development /// cell proliferation /// regulation of neuron differentiation	neuronal Cdc2-like kinase binding	---	---
237198_at	MGC24039	-0.168	0.005	B	---	nucleic acid binding	---	---
231561_s_at	APOC2	-0.486	0.004	L	circulation/// lipid transport/// lipid catabolism	lipid transporter activity	extracellular region	---
218619_s_at	SUV39H1	0.291	0.004	L	DNA replication and chromosome cycle /// chromatin assembly or disassembly /// chromatin modification	chromatin binding /// protein binding /// methyltransferase activity /// zinc ion binding /// S-adenosylmethionine-dependent methyltransferase activity /// transferase activity /// histone-lysine N-methyltransferase activity /// histone lysine N-methyltransferase activity (H3-K9 specific)	chromatin /// condensed nuclear chromosome /// nucleus	lysine degradation
233834_at	NCOA2	0.239	0.003	T	transcription /// regulation of transcription, DNA-dependent /// signal transduction	transcription coactivator activity /// signal transducer activity	nucleus	---
231754_at	PCDHGC4	0.122	0.003	T	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	membrane /// integral to membrane	---
202835_at	TXNL4A	-0.356	0.003	L	spliceosome assembly /// electron transport /// cell cycle /// mitosis	electron transporter activity /// pre-mRNA splicing factor activity	spliceosome complex	mRNA processing
201958_s_at	PPP1R12B	-0.3	0.003	L	regulation of muscle contraction /// signal transduction	enzyme activator activity	---	---
227689_at	ZNF227	-0.186	0.003	L	regulation of transcription, DNA-dependent	nucleic acid binding /// DNA binding /// zinc ion binding	nucleus	---
233523_at	C20orf186	0.479	0.003	L	---	lipid binding	---	---
222687_s_at	PHCA	0.188	0.002	T	protein biosynthesis /// ceramide metabolism	structural constituent of ribosome /// hydrolase activity /// hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	Golgi membrane /// intracellular /// endoplasmic reticulum membrane /// ribosome /// integral to membrane	Glycosphingolipid metabolism

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202626_s_at	LYN	-0.287	0.002	L	protein amino acid phosphorylation /// intracellular signaling cascade	receptor signaling protein tyrosine kinase activity /// ATP binding /// transferase activity	---	---
212207_at	THRAP2	-0.265	0.002	L	---	receptor activity	---	---
201571_s_at	DCTD	0.224	0.002	B	pyrimidine nucleotide metabolism /// nucleotide biosynthesis	dCMP deaminase activity /// zinc ion binding /// hydrolase activity	---	Pyrimidine metabolism /// Type II secretion system
214535_s_at	ADAMTS2	-0.141	0.001	T	collagen catabolism	collagenase activity /// procollagen N-endopeptidase activity	extracellular matrix (sensu Metazoa)	---
211519_s_at	KIF2C	-0.205	0.001	T	microtubule-based movement /// mitosis /// cell proliferation	microtubule motor activity /// ATP binding /// centromeric DNA binding	chromosome, pericentric region /// nucleus /// kinesin complex	---
218243_at	RUFY1	0.21	0	T	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
232930_at	DOCK1	-0.318	0	L	phagocytosis, engulfment /// apoptosis /// signal transduction /// integrin-mediated signaling pathway /// small GTPase mediated signal transduction	guanyl-nucleotide exchange factor activity /// GTPase activator activity /// GTP binding /// GTPase binding	cytoplasm /// cytoskeleton /// membrane	Integrin-mediated cell adhesion
213707_s_at	DLX5	0.135	0	L	skeletal development /// regulation of transcription, DNA-dependent /// development /// neurogenesis	transcription factor activity	nucleus	---
203863_at	ACTN2	-0.13	0	L	---	actin binding /// calcium ion binding /// protein binding /// structural constituent of muscle	cytoskeleton /// actin filament	Striated muscle contraction
212225_at	SUI1	-0.221	0	L	protein biosynthesis /// translational initiation /// regulation of translation /// regulation of translational initiation /// response to stress	translation initiation factor activity	cytoplasm	Translation Factors
214514_at	MCM3AP	-0.191	0	L	DNA replication /// protein-nucleus import	DNA binding	nucleus	---

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200832_s_at	SCD	-1.806	-2.304	L	fatty acid biosynthesis	stearoyl-CoA 9-desaturase activity /// iron ion binding /// oxidoreductase activity	endoplasmic reticulum /// integral to membrane	Fatty Acid Synthesis
200831_s_at	SCD	-0.583	-0.986	L	fatty acid biosynthesis	stearoyl-CoA 9-desaturase activity /// iron ion binding /// oxidoreductase activity	endoplasmic reticulum /// integral to membrane	Fatty Acid Synthesis
220551_at	SLC17A6	-1.682	-0.9	B	transport	transporter activity	integral to membrane	---
211708_s_at	SCD	-0.452	-0.845	L	fatty acid biosynthesis	stearoyl-CoA 9-desaturase activity /// iron ion binding /// oxidoreductase activity	endoplasmic reticulum /// integral to membrane	Fatty Acid Synthesis
203395_s_at	HES1	-0.328	-0.706	B	regulation of transcription, DNA-dependent /// neurogenesis	DNA binding	nucleus	Notch signaling pathway
238996_x_at	ALDOA	-0.16	-0.697	B	fructose metabolism /// glycolysis /// striated muscle contraction	fructose-bisphosphate aldolase activity /// lyase activity	---	Glycolysis and Gluconeogenesis /// Glycolysis / Gluconeogenesis /// Pentose phosphate pathway /// Inositol metabolism /// Fructose and mannose metabolism /// Carbon fixation
210143_at	ANXA10	0.165	-0.676	L	negative regulation of coagulation	calcium ion binding /// calcium-dependent phospholipid binding	---	---
208964_s_at	FADS1	-0.715	-0.645	L	fatty acid desaturation /// fatty acid desaturation /// cell-cell signaling /// phospholipid biosynthesis /// cellular response to starvation /// regulation of transcription /// regulation of cell differentiation /// icosanoid biosynthesis	oxidoreductase activity /// oxidoreductase activity /// oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	membrane fraction /// microsome /// membrane /// integral to membrane	---
224451_x_at	ARHGAP9	-0.138	-0.619	B	---	GTPase activator activity	---	---
202289_s_at	TACC2	-0.393	-0.618	T	---	---	nucleus	---
1560733_at	ALG5	-0.421	-0.597	L	protein aminoacid glycosylation	transferase activity	endoplasmic reticulum/// integral to membrane	N-Glycan biosynthesis
204647_at	HOMER3	0.006	-0.587	B	protein targeting	protein binding	---	---
221256_s_at	HDHD3	-0.403	-0.579	B	metabolism	phosphoglycolate phosphatase activity /// hydrolase activity	---	---
211534_x_at	PTPRN2	0.03	-0.575	B	protein amino acid dephosphorylation	protein tyrosine phosphatase activity /// receptor activity /// transmembrane receptor protein tyrosine phosphatase activity /// hydrolase activity	integral to plasma membrane	Phosphatidylinositol signaling system
210587_at	INHBE	-0.469	-0.575	L	---	hormone activity /// growth factor activity	extracellular region	cytokine-cytokine receptor interaction/// TGF-beta signaling pathway
205839_s_at	BZRAP1	-0.17	-0.574	B	---	benzodiazepine receptor binding	mitochondrion	---
222113_s_at	EPS15L1	-0.028	-0.573	L	endocytosis	calcium ion binding	nucleus /// coated pit	---
244128_x_at	GLIS1	-0.09	-0.567	B	negative regulation of transcription from Pol II promoter /// regulation of transcription, DNA-dependent /// positive regulation of transcription from Pol II promoter	DNA binding /// specific RNA polymerase II transcription factor activity /// zinc ion binding	nucleus	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
203889_at	SGNE1	-0.471	-0.558	L	protein folding /// transport /// intracellular protein transport /// neuropeptide signaling pathway /// peptide hormone processing /// regulation of hormone secretion	enzyme inhibitor activity /// GTP binding /// enzyme activator activity /// unfolded protein binding	secretory granule	---
202662_at	FAH	-0.158	-0.551	B	L-phenylalanine catabolism /// tyrosine catabolism /// metabolism /// aromatic amino acid family metabolism	fumarylacetoacetase activity /// hydrolase activity	---	Tyrosine metabolism /// Styrene degradation
211380_s_at	PRKG1	-0.251	-0.545	L	protein amino acid phosphorylation /// regulation of smooth muscle contraction /// signal transduction /// actin cytoskeleton organization and biogenesis	protein serine/threonine kinase activity /// cGMP-dependent protein kinase activity /// ATP binding /// cAMP-dependent protein kinase regulator activity /// transferase activity /// 3',5'-cGMP binding	cAMP-dependent protein kinase complex	Phosphatidylinositol signaling system
238306_at	CA8	-0.048	-0.542	L	one-carbon compound metabolism	carbonate dehydratase activity /// zinc ion binding	---	Nitrogen metabolism
1559351_at	SLC16A9	0.1	-0.539	L	transport	transporter activity	integral to membrane	---
214291_at	RPL17	-0.318	-0.538	L	protein biosynthesis /// positive regulation of I-kappaB kinase/NF-kappaB cascade	RNA binding /// structural constituent of ribosome /// signal transducer activity	intracellular /// large ribosomal subunit	Ribosome
209364_at	BAD	0.325	-0.533	B	induction of apoptosis /// apoptotic program	protein binding	cytoplasm /// mitochondrial outer membrane	Apoptosis /// neurodegenerative diseases /// focal adhesion /// amyotrophic lateral sclerosis
232837_at	KIF13A	-0.259	-0.533	L	microtubule-based movement /// protein transport	microtubule motor activity /// ATP binding	microtubule associated complex	---
219088_s_at	ZNF576	-0.073	-0.524	B	---	nucleic acid binding /// zinc ion binding	nucleus	---
229118_at	PRRG3	0.023	-0.522	B	---	calcium ion binding	extracellular region /// integral to membrane	---
225005_at	PHF13	0.012	-0.52	L	regulation of transcription, DNA-dependent	DNA binding	---	---
218995_s_at	EDN1	-0.139	-0.515	L	signal transduction /// cell-cell signaling /// regulation of blood pressure /// positive regulation of cell proliferation /// pathogenesis /// regulation of vasoconstriction	hormone activity	extracellular space /// soluble fraction	Neuroactive ligand-receptor interaction
223862_s_at	MGC4796	0.019	-0.507	B	protein amino acid phosphorylation	protein kinase activity /// protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	membrane	---
206681_x_at	GP2	-0.323	-0.507	B	---	---	membrane fraction /// membrane	---
210764_s_at	CYR61	-0.173	-0.505	B	regulation of cell growth /// chemotaxis /// cell adhesion /// cell proliferation /// morphogenesis	insulin-like growth factor binding /// heparin binding	extracellular region	Hypertrophy_model
244858_at	TGIF	-0.202	-0.504	B	negative regulation of transcription from Pol II promoter /// regulation of transcription, DNA-dependent /// development	transcription factor activity /// transcription corepressor activity	nucleus	TGF Beta Signaling Pathway

No.		Value): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
221418_s_at	THRAP5	-0.186	-0.5	B	regulation of transcription from Pol II promoter /// transcription from Pol II promoter /// transcription initiation from Pol II promoter /// androgen receptor signaling pathway	transcription cofactor activity /// transcription coactivator activity /// receptor activity /// RNA polymerase II transcription mediator activity /// transcriptional activator activity /// thyroid hormone receptor coactivator activity /// vitamin D receptor binding /// thyroid hormone receptor binding	mediator complex /// nucleus	---
216300_x_at	RARA	-0.207	-0.497	B	regulation of transcription, DNA-dependent /// signal transduction	transcription factor activity /// steroid hormone receptor activity /// retinoic acid receptor activity /// transcription coactivator activity	nucleus	Nuclear Receptors
203023_at	HSPC111	-0.076	-0.494	B	---	---	nucleus	---
218575_at	ANAPC1	0.047	-0.49	B	regulation of cell cycle /// cytokinesis /// ubiquitin cycle /// mitosis	---	---	ubiquitin mediated proteolysis
201582_at	SEC23B	-0.001	-0.483	L	intracellular protein transport /// ER to Golgi transport /// vesicle-mediated transport	protein binding	endoplasmic reticulum /// Golgi apparatus /// membrane /// COPII vesicle coat	---
209888_s_at	MYL1	-0.054	-0.483	L	muscle development	calcium ion binding /// structural constituent of muscle	muscle myosin /// myosin	G13 Signaling Pathway /// Striated muscle contraction
226255_at	ZBTB33	-0.978	-0.479	L	intracellular signaling cascade	nucleic acid binding /// protein binding /// zinc ion binding	nucleus	---
211719_x_at	FN1	-0.799	-0.479	T	acute-phase response /// cell adhesion /// metabolism /// response to wounding /// cell migration	extracellular matrix structural constituent /// collagen binding /// heparin binding /// oxidoreductase activity	extracellular region /// extracellular matrix (sensu Metazoa)	Inflammatory Response Pathway
201743_at	CD14	-0.302	-0.477	B	phagocytosis /// apoptosis /// inflammatory response /// cell surface receptor linked signal transduction	peptidoglycan receptor activity	plasma membrane /// extrinsic to membrane	MAPK signaling pathway/// Regulation of actin cytoskeleton/// Toll-like receptor signaling pathway
220243_at	HSPC063	0.051	-0.476	L	---	nucleic acid binding /// protein binding /// zinc ion binding	nucleus	---
202737_s_at	LSM4	0.044	-0.474	L	nuclear mRNA splicing, via spliceosome /// RNA splicing	RNA binding /// pre-mRNA splicing factor activity	snRNP U6 /// small nucleolar ribonucleoprotein complex	---
209164_s_at	CYB561	0.116	-0.473	B	electron transport	cytochrome-b5 reductase activity	integral to plasma membrane	---
224666_at	NSMCE1	-0.222	-0.472	B	intracellular signaling cascade /// protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
215124_at	ZNF560	-0.1	-0.472	L	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
209783_at	GRIA1	-0.043	-0.468	B	ion transport /// potassium ion transport /// signal transduction /// synaptic transmission	receptor activity /// alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor activity /// transporter activity /// ion channel activity /// glutamate-gated ion channel activity /// potassium channel activity /// kainate selective glutamate receptor activity	plasma membrane /// integral to membrane	neuroactive ligand-receptor interaction

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
229004_at	ADAMTS15	-0.296	-0.467	B	proteolysis and peptidolysis	metalloendopeptidase activity /// zinc ion binding /// hydrolase activity	extracellular matrix (sensu Metazoa)	---
201945_at	FURIN	-0.224	-0.466	B	proteolysis and peptidolysis /// cell-cell signaling	furin activity /// subtilase activity /// hydrolase activity	Golgi apparatus /// integral to membrane	---
229337_at	USP2	-0.284	-0.465	L	ubiquitin-dependent protein catabolism /// ubiquitin cycle	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity /// hydrolase activity	---	---
203438_at	STC2	-0.178	-0.464	L	cell surface receptor linked signal transduction /// cell-cell signaling /// response to nutrients	hormone activity	extracellular region	---
205759_s_at	SULT2B1	0.05	-0.46	B	steroid metabolism	alcohol sulfotransferase activity /// transferase activity	---	---
222828_at	IL20RA	-0.035	-0.46	B	Coagulation/// physiological process/// blood coagulation/// regulation of body fluids/// organismal physiological process/// hemostasis	Signal transducer activity/// receptor activity	---	Cytokine-cytokine receptor interaction/// JAK-STATsignaling pathway
221906_at	TXNRD3	0.102	-0.458	L	thioredoxin pathway	thioredoxin-disulfide reductase activity /// disulfide oxidoreductase activity /// oxidoreductase activity, acting on NADH or NADPH, disulfide as acceptor /// FAD binding	cytoplasm	---
220542_s_at	PLUNC	-0.044	-0.455	B	response to pathogenic bacteria /// innate immune response	lipid binding	extracellular region	---
216282_x_at	POLR2C	0.028	-0.454	B	transcription /// transcription from Pol II promoter	DNA binding /// DNA-directed RNA polymerase activity /// transferase activity /// protein dimerization activity	nucleus /// DNA-directed RNA polymerase II, core complex	pyrimidine metabolism/// purine metabolism/// RNA polymerase
207332_s_at	TFRC	-0.405	-0.454	L	proteolysis and peptidolysis /// iron ion transport /// iron ion homeostasis /// endocytosis	receptor activity /// transferrin receptor activity /// peptidase activity	extracellular region /// endosome /// integral to plasma membrane	---
202786_at	STK39	-0.717	-0.45	L	protein amino acid phosphorylation /// response to stress	receptor signaling protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	nucleus /// cytoplasm	---
205718_at	ITGB7	-0.08	-0.448	B	cell-matrix adhesion /// integrin-mediated signaling pathway /// development	receptor activity /// protein binding	integrin complex /// integral to membrane	Integrin-mediated cell adhesion
214265_at	ITGA8	-0.237	-0.447	L	cell-matrix adhesion /// integrin-mediated signaling pathway /// cell-cell adhesion	receptor activity /// protein binding	integrin complex /// integral to membrane	Integrin-mediated cell adhesion
210432_s_at	SCN3A	-0.15	-0.446	L	cation transport /// sodium ion transport	voltage-gated sodium channel activity /// cation channel activity	voltage-gated sodium channel complex /// integral to membrane	---
244145_at	FYCO1	-0.521	-0.446	T	intracellular protein transport	zinc ion binding /// protein carrier activity	membrane /// integral to membrane	---
215085_x_at	DLEC1	-0.139	-0.444	L	negative regulation of cell proliferation	---	---	---
232669_at	HIF3A	0.012	-0.443	L	regulation of transcription, DNA-dependent /// signal transduction /// rhythmic process	transcription factor activity /// signal transducer activity	nucleus	---
239190_at	VRK3	-0.262	-0.443	L	protein amino acid phosphorylation	protein serine/threonine kinase activity /// ATP binding /// transferase activity	---	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
216959_at	HOXC10	-0.206	-0.436	L	regulation of transcription, DNA-dependent /// positive regulation of cell proliferation /// morphogenesis	transcription factor activity /// RNA polymerase II transcription factor activity	nucleus	---
204718_at	EPHB6	-0.583	-0.435	T	protein amino acid phosphorylation /// transmembrane receptor protein tyrosine kinase signaling pathway	protein-tyrosine kinase activity /// receptor activity /// ephrin receptor activity /// ATP binding	membrane /// integral to membrane	---
225135_at	SIN3A	-0.129	-0.434	L	negative regulation of transcription, DNA-dependent	protein binding	nucleus	---
220851_at	RFX3	0.006	-0.433	L	regulation of transcription, DNA-dependent /// negative regulation of transcription	RNA polymerase II transcription factor activity, enhancer binding /// transcriptional repressor activity	nucleus	---
215526_at	WWOX	-0.027	-0.432	L	metabolism /// steroid metabolism	electron transporter activity /// protein binding /// oxidoreductase activity	---	---
211062_s_at	CPZ	-0.076	-0.431	B	proteolysis and peptidolysis /// development	carboxypeptidase A activity /// transmembrane receptor activity /// peptidase activity	integral to membrane	---
238416_x_at	LOC124245	-0.458	-0.431	B	---	nucleic acid binding	---	---
214070_s_at	ATP10B	-0.187	-0.431	L	calcium transport	magnesium ion binding /// phospholipid-translocating ATPase activity /// ATP binding /// hydrolase activity /// ATPase activity	integral to membrane	---
232550_at	ABHD1	-0.252	-0.427	B	Metabolism/// nucleobase, nucleoside, nucleotide and nucleic acid metabolism/// regulation of transcription, DNA-dependent/// physiological process/// regulation of physiological process	nucleic acid binding/// DNA binding	---	---
207503_at	TCP10	-0.127	-0.427	B	---	---	---	---
223481_s_at	MRPL47	-0.085	-0.425	L	protein biosynthesis	structural constituent of ribosome	mitochondrial ribosome	---
201003_x_at	Kua-UEV	0.028	-0.424	L	ubiquitin cycle	ubiquitin-like activating enzyme activity	---	---
232333_at	MAML2	-0.095	-0.422	L	---	receptor activity	---	---
220625_s_at	ELF5	-0.226	-0.421	L	regulation of transcription, DNA-dependent /// transcription from Pol II promoter /// cell proliferation	DNA binding /// transcription factor activity	nucleus	---
1554889_at	TIA1	-0.164	-0.421	L	apoptosis /// induction of apoptosis	RNA binding /// poly(A) binding	---	---
205390_s_at	ANK1	0.027	-0.42	B	exocytosis /// cytoskeleton organization and biogenesis /// signal transduction /// maintenance of epithelial cell polarity	structural molecule activity /// structural constituent of cytoskeleton /// protein binding /// cytoskeletal adaptor activity /// enzyme binding /// spectrin binding	cytoskeleton /// plasma membrane /// actin cytoskeleton /// basolateral plasma membrane	---
229422_at	NRD1	0.041	-0.42	L	proteolysis and peptidolysis /// neuromuscular junction development	hydrolase activity /// nardilysin activity	---	---
232995_at	PDGFD	-0.159	-0.42	L	---	growth factor activity	membrane	---

No.		Values):	(log2 Values):					
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
223331_s_at	DDX20	-0.481	-0.419	L	assembly of spliceosomal tri-snRNP /// mRNA processing	nucleic acid binding /// DNA binding /// ATP-dependent RNA helicase activity /// ATP binding /// ATP-dependent helicase activity /// hydrolase activity	spliceosome complex /// cytoplasm /// cytoskeleton	mRNA processing Reactome
1569061_at	IQGAP3	-0.195	-0.418	B	small GTPase mediated signal transduction	Ras GTPase activator activity /// calmodulin binding	---	Regulation of actin cytoskeleton
227131_at	MAP3K3	-0.211	-0.413	B	MAPKKK cascade /// protein amino acid phosphorylation /// positive regulation of I-kappaB kinase/NF-kappaB cascade	magnesium ion binding /// protein serine/threonine kinase activity /// MAP kinase kinase kinase activity /// signal transducer activity /// ATP binding /// transferase activity	---	MAPK Cascade
226061_s_at	NUDT3	-0.204	-0.412	L	cell-cell signaling/// diadenosine polyphosphate catabolism/// intracellular transport	diphosphoinositol-polyphosphate diphosphatase activity/// hydrolase activity/// magnesium ion binding	intracellular	---
1553118_at	CTMP	0.026	-0.412	L	---	serine esterase activity /// hydrolase activity	---	---
238737_at	FLJ32112	0.147	-0.41	B	transcription /// defense response	---	---	---
218681_s_at	SDF2L1	0.019	-0.408	B	---	hydrolase activity	membrane	---
203912_s_at	DNASE1L1	0.151	-0.407	L	DNA catabolism	DNA binding /// endonuclease activity /// deoxyribonuclease activity /// hydrolase activity	membrane	---
203423_at	RBP1	-0.44	-0.406	T	transport/// vitamin A metabolism	transporter activity /// lipid binding /// retinol binding	---	---
1555606_a_at	GDPD1	-0.235	-0.405	L	glycerol metabolism	glycerophosphodiester phosphodiesterase activity	---	---
226163_at	ZBTB9	0.074	-0.402	B	regulation of transcription, DNA-dependent	DNA binding /// protein binding /// zinc ion binding	nucleus	---
233902_at	GUCA1C	-0.173	-0.402	L	signal transduction/// visual perception	calcium ion binding/// calcium sensitive guanylate cyclase activator activity	---	---
224004_at	ZNF226	-0.126	-0.402	L	regulation of transcription, DNA-dependent	nucleic acid binding /// DNA binding /// zinc ion binding	nucleus	---
222668_at	KCTD15	-0.079	-0.4	L	potassium ion transport	voltage-gated potassium channel activity /// protein binding	voltage-gated potassium channel complex /// membrane	---
232283_at	SB145	-0.087	-0.398	L	cell wall catabolism	---	---	---
207566_at	MR1	-0.04	-0.397	B	antigen presentation	MHC class I receptor activity	MHC class I protein complex	---
210635_s_at	KLHL20	0.108	-0.396	B	cytoskeleton organization and biogenesis	actin binding /// protein binding	actin cytoskeleton	---
213219_at	ADCY2	0.026	-0.395	B	cAMP biosynthesis /// intracellular signaling cascade	magnesium ion binding /// adenylate cyclase activity /// guanylate cyclase activity /// lyase activity	integral to membrane	purine metabolism
223909_s_at	HDAC8	0.211	-0.395	B	regulation of transcription, DNA-dependent /// chromatin modification /// histone deacetylation	histone deacetylase activity /// transcription factor binding /// hydrolase activity	histone deacetylase complex /// nucleus /// cytoplasm	cell cycle
206666_at	GZMK	0.053	-0.395	L	proteolysis and peptidolysis	chymotrypsin activity /// trypsin activity /// hydrolase activity	cytoplasm	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
210565_at	GCGR	-0.084	-0.393	B	Regulation of blood pressure/// circulation/// cyclic-nucleotide-mediated signaling/// metabolism/// response to nutrients/// response to external stimulus/// intracellular signaling cascade/// physiological process/// response to abiotic stimulus/// cell surface receptor linked signal transduction/// G-protein coupled receptor protein signaling pathway/// response to stimulus/// response to chemical substance/// signal transduction/// cell communication/// regulation of physiological process/// regulation of biological process/// organismal physiological process/// response to extracellular stimulus/// cellular process	Signal transducer activity/// receptor activity/// secretin-like receptor activity/// G-protein coupled receptor activity	---	Neuroactive ligand-receptor interaction
221932_s_at	C14orf87	0.089	-0.393	B	---	---	mitochondrion	---
213722_at	SOX2	0.018	-0.393	L	establishment and/or maintenance of chromatin architecture /// regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
222856_at	APLN	-0.091	-0.39	B	immune response /// signal transduction /// lactation	hormone activity	---	Neuroactive ligand-receptor interaction
205440_s_at	NPY1R	-0.639	-0.39	B	Behavior/// cyclic-nucleotide-mediated signaling/// intracellular signaling cascade/// cell surface receptor linked signal transduction/// G-protein coupled receptor protein signaling pathway/// feeding behavior/// signal transduction/// cell communication/// cellular process	Peptide binding/// neuropeptide y receptor activity/// signal transducer activity/// binding/// neuropeptide binding/// receptor activity/// peptide receptor activity/// neuropeptide receptor activity/// G-protein coupled receptor activity/// rhodopsin-like receptor activity	---	Neuroactive ligand-receptor interaction
217967_s_at	C1orf24	0.117	-0.39	L	protein folding	heat shock protein binding /// unfolded protein binding	---	---
218847_at	IMP-2	-0.01	-0.39	L	translational attenuation /// morphogenesis	RNA binding	cytoplasm	---
216535_at	IGSF4B	0.047	-0.39	L	---	receptor activity	integral to membrane	---
210495_x_at	FN1	-0.66	-0.39	T	acute-phase response /// cell adhesion /// metabolism /// response to wounding /// cell migration	extracellular matrix structural constituent /// collagen binding /// heparin binding /// oxidoreductase activity	extracellular region /// extracellular matrix (sensu Metazoa)	ECM-receptor interaction/// focal adhesion/// regulation of actin cytoskeleton
208717_at	OXA1L	0.178	-0.388	B	electron transport /// protein complex assembly /// aerobic respiration /// protein insertion into membrane	---	mitochondrion /// mitochondrial electron transport chain /// integral to membrane /// inner membrane	protein export
1559426_at	SMURF1	-0.255	-0.388	L	ubiquitin cycle /// ectoderm development /// cell differentiation /// negative regulation of BMP signaling pathway /// protein ubiquitination during ubiquitin-dependent protein catabolism	ubiquitin-protein ligase activity /// ligase activity	intracellular	TGF-Beta signaling pathway
208473_s_at	GP2	-0.063	-0.386	B	---	---	membrane fraction /// membrane	---
204604_at	PFTK1	-0.259	-0.386	L	protein amino acid phosphorylation	protein serine/threonine kinase activity /// ATP binding /// transferase activity	nucleus /// cytoplasm	---

No.		Value): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Value): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
203678_at	KIAA1018	-0.241	-0.386	L	DNA repair	DNA binding	---	---
1570237_at	FGL1	0.15	-0.396	L	---	---	fibrinogen complex	---
235528_at	GUCA1B	-0.198	-0.384	T	cell-cell signaling/// fluid secretion/// receptor guanylyl cyclase signaling pathway/// sensory perception/// visual perception	calcium ion binding/// calcium sensitive guanylate cyclase activator activity	---	---
205752_s_at	GSTM5	-0.444	-0.383	T	metabolism	glutathione transferase activity /// glutathione transferase activity /// transferase activity	---	Glutathione metabolism
1565674_at	FCGR2A	0.007	-0.382	B	immune response	receptor activity /// receptor signaling protein activity /// IgG binding	plasma membrane /// integral to membrane	---
204191_at	IFNAR1	0.207	-0.382	L	cell surface receptor linked signal transduction /// JAK-STAT cascade /// response to virus	receptor activity /// hematopoietin/interferon-class (D200-domain) cytokine receptor activity /// interferon-alpha/beta receptor activity	integral to plasma membrane	---
226019_at	OMA1	-0.089	-0.381	L	proteolysis and peptidolysis	metalloendopeptidase activity	membrane	---
215524_x_at	A@ /// MGC40	-0.074	-0.381	L	cellular defense response	receptor activity /// MHC protein binding /// peptide antigen binding	integral to plasma membrane	---
221368_at	GPR8	0.203	-0.381	L	G-protein coupled receptor protein signaling pathway /// synaptic transmission	rhodopsin-like receptor activity /// receptor activity /// opioid receptor activity	integral to plasma membrane /// integral to membrane	Neuroactive ligand-receptor interaction
201079_at	SYNGR2	-0.062	-0.38	B	---	---	integral to plasma membrane	---
228771_at	ADRBK2	-0.02	-0.38	L	protein amino acid phosphorylation /// signal transduction	G-protein coupled receptor kinase activity /// signal transducer activity /// ATP binding /// transferase activity /// beta-adrenergic-receptor kinase activity	---	---
227538_at	CRSP7	0.122	-0.379	B	Metabolism/// nucleobase, nucleoside, nucleotide and nucleic acid metabolism/// response to external stimulus/// regulation of transcription from pol II promoter/// regulation of transcription, DNA-dependent/// physiological process/// transcription, DNA-dependent/// transcription initiation/// response to biotic stimulus/// regulation of metabolism/// defense response/// transcription from pol II promoter/// regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism/// regulation of physiological process/// regulation of biological process	Signal transducer activity/// transcription cofactor activity/// binding/// receptor activity/// transcription regulator activity/// transcription coactivator activity/// transcription factor binding/// protein binding	---	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
207462_at	GLRA2	0.06	-0.379	B	Ion transport /// chloride transport /// cell surface receptor linked signal transduction /// synaptic transmission	GABA-A receptor activity /// glycine-inhibited chloride channel activity /// ion channel activity /// extracellular ligand-gated ion channel activity /// glycine-gated chloride channel activity /// neurotransmitter receptor activity	integral to plasma membrane /// postsynaptic membrane	Neuroactive ligand-receptor interaction
207724_s_at	SPG4	-0.285	-0.379	L	---	ATP binding	nucleus	---
209092_s_at	C17orf25	-0.076	-0.378	L	---	lyase activity	---	---
202892_at	CDC23	-0.168	-0.377	B	G1 phase of mitotic cell cycle /// cytokinesis /// ubiquitin cycle /// cell cycle /// mitosis /// mitotic metaphase plate congression /// regulation of mitotic metaphase/anaphase transition	ubiquitin-protein ligase activity /// ubiquitin-protein ligase binding	anaphase-promoting complex	ubiquitin mediated proteolysis
204693_at	ICAM2	0.028	-0.377	L	cell-cell adhesion	integrin binding /// protein binding	integral to plasma membrane	---
219910_at	HYPE	0.112	-0.377	L	regulation of cell cycle	protein binding	---	---
219837_s_at	CYTL1	-0.001	-0.376	B	signal transduction	receptor binding	extracellular space /// soluble fraction	---
1566973_at	MGAT3	0.067	-0.375	L	N-linked glycosylation	beta-1,4-mannosylglycoprotein 4-beta-N-acetylglucosaminyltransferase activity /// transferase activity, transferring glycosyl groups	Golgi apparatus /// integral to membrane	N-Glycan biosynthesis
215545_at	ERCC3	-0.046	-0.374	L	DNA topological change /// transcription-coupled nucleotide-excision repair /// regulation of transcription, DNA-dependent /// transcription from Pol II promoter /// induction of apoptosis /// perception of sound	damaged DNA binding /// ATP-dependent DNA helicase activity /// helicase activity /// protein binding /// ATP binding /// hydrolase activity /// 3'-5' DNA helicase activity	nucleus /// transcription factor TFIIH complex	RNA transcription reactome
1565579_at	TATDN2	-0.01	-0.373	B	---	nuclease activity /// hydrolase activity	---	---
1564403_at	TOPORS	-0.147	-0.372	L	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
234640_s_at	OR9V1	-0.128	-0.372	L	G-protein coupled receptor protein signaling pathway /// perception of smell	olfactory receptor activity	integral to membrane	GPCRDB Class A Rhodopsin-like
242937_at	FOXI2	-0.301	-0.371	L	regulation of transcription, DNA-dependent /// regulation of transcription from Pol II promoter	transcription factor activity /// RNA polymerase II transcription factor activity	nucleus	---
227223_at	RNPC2	-0.86	-0.371	T	nuclear mRNA splicing, via spliceosome /// transcription /// regulation of transcription, DNA-dependent /// mRNA processing	nucleotide binding /// RNA binding	nucleus /// nucleoplasm	mRNA processing
205057_s_at	IDUA	0.049	-0.37	B	carbohydrate metabolism /// disaccharide metabolism /// glycosaminoglycan metabolism	L-iduronidase activity	lysosome	Glycosaminoglycan degradation
207246_at	ZFY	-0.218	-0.37	L	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding /// transcription regulator activity /// metal ion binding	nucleus	---

No.		Values):	(log2 Values):					
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
228145_s_at	ZNF398	0.025	-0.37	L	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding /// transcriptional activator activity	nucleus	---
224069_x_at	P2RX2	-0.027	-0.369	B	ion transport	receptor activity /// ion channel activity /// ATP binding /// ligand-gated ion channel activity	membrane /// integral to membrane	Neuroactive ligand-receptor interaction
1555777_at	POSTN	0.164	-0.369	L	skeletal development /// cell adhesion	protein binding /// heparin binding	extracellular matrix (sensu Metazoa)	---
209267_s_at	SLC39A8	-0.277	-0.369	T	transport /// metal ion transport	metal ion transporter activity	membrane /// integral to membrane	---
222102_at	GSTA3	-0.149	-0.368	B	response to stress /// metabolism	glutathione transferase activity /// transferase activity	---	Glutathione metabolism
215135_at	DNPEP	-0.27	-0.368	L	proteolysis and peptidolysis /// peptide metabolism	aminopeptidase I activity /// metallopeptidase activity /// hydrolase activity	vacuole	---
1564621_a_at	MGC40042	0.054	-0.366	L	---	binding	---	---
224054_at	ARMCX3	0.038	-0.366	L	---	binding	---	---
1555252_a_at	TRPM3	0.02	-0.365	L	cation transport	receptor activity /// cation channel activity /// calcium channel activity	membrane /// integral to membrane	---
214609_at	PHOX2A	-0.064	-0.364	B	regulation of transcription, DNA-dependent /// transcription from Pol II promoter /// neurotransmitter metabolism	transcription factor activity	nucleus	---
223438_s_at	PPARA	-0.017	-0.363	L	generation of precursor metabolites and energy /// transcription /// regulation of transcription, DNA-dependent /// transcription from Pol II promoter /// lipid metabolism /// fatty acid metabolism	transcription factor activity /// steroid hormone receptor activity /// ligand-dependent nuclear receptor activity	nucleus	Nuclear Receptors
40837_at	TLE2	-0.056	-0.362	B	regulation of transcription, DNA-dependent /// signal transduction /// frizzled signaling pathway /// organogenesis	---	nucleus	---
240188_at	TGFBR3	-0.026	-0.362	L	signal transduction /// transforming growth factor beta receptor signaling pathway /// development	receptor activity /// glycosaminoglycan binding	integral to membrane	TGF-Beta Signaling Pathway
239616_at	DKFZP566E14	-0.127	-0.361	L	nucleotide metabolism	3'-5' exonuclease activity /// hydrolase activity /// manganese ion binding	nucleus /// mitochondrion	---
204472_at	GEM	-0.091	-0.361	L	immune response /// cell surface receptor linked signal transduction /// small GTPase mediated signal transduction	calmodulin binding /// GTP binding	membrane	---
226562_at	FLJ35867	-0.292	-0.361	T	regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	nucleus	---
231274_s_at	SLC25A37	0.132	-0.36	L	transport	binding	mitochondrial inner membrane /// membrane /// integral to membrane	---
239931_at	MYC	0.078	-0.36	L	regulation of transcription from Pol II promoter /// iron ion homeostasis /// cell cycle arrest /// cell proliferation	transcription factor activity /// protein binding	nucleus	TGF-beta signaling pathway/// JAK stat signaling pathway/// Wnt signaling pathway/// MAPK signaling pathway

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
211438_at	TRHR	0.007	-0.359	L	G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity /// thyrotropin-releasing hormone receptor activity	integral to plasma membrane	Neuroactive ligand-receptor interaction
244126_at	PEX11G	0.026	-0.358	B	peroxisome division	---	peroxisomal membrane	---
207605_x_at	ZNF117	0.407	-0.357	L	regulation of transcription, DNA-dependent	nucleic acid binding /// transcription factor activity /// zinc ion binding	nucleus	---
201516_at	SRM	-0.761	-0.357	T	spermidine biosynthesis	spermidine synthase activity /// S-adenosylmethionine-dependent methyltransferase activity /// transferase activity	---	Arginine and proline metabolism/// urea cycle and metabolism of amino groups/// beta-Alanine metabolism
203792_x_at	PCGF2	-0.001	-0.356	B	regulation of transcription, DNA-dependent /// protein ubiquitination	transcription factor activity /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex /// nucleus	---
221528_s_at	ELMO2	0.097	-0.356	L	phagocytosis /// apoptosis	---	cytoskeleton /// membrane	---
225353_s_at	C1QG	-0.155	-0.355	B	phosphate transport /// immune response /// complement activation, classical pathway	---	extracellular region /// cytoplasm	complement and coagulation cascades
207746_at	POLQ	-0.066	-0.355	L	DNA replication /// DNA repair	DNA binding /// damaged DNA binding /// DNA-directed DNA polymerase activity /// ATP binding /// ATP-dependent helicase activity /// transferase activity	nucleoplasm	Purine metabolism /// Pyrimidine metabolism /// DNA polymerase
241827_at	ZNF615	-0.106	-0.354	L	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
235312_s_at	NRAP	0.099	-0.354	L	---	actin binding /// zinc ion binding	---	---
201869_s_at	TBL1X	-0.065	-0.352	B	regulation of transcription, DNA-dependent /// ubiquitin cycle /// signal transduction /// visual perception /// perception of sound	---	nucleus	Wnt signaling
225442_at	DDR2	-0.039	-0.352	L	protein amino acid phosphorylation /// cell adhesion /// signal transduction /// transmembrane receptor protein tyrosine kinase signaling pathway	transmembrane receptor protein tyrosine kinase activity /// receptor activity /// ATP binding /// transferase activity	integral to plasma membrane	---
210765_at	CSE1L	-0.348	-0.351	L	protein-nucleus import, docking /// apoptosis /// cell proliferation /// protein transport	binding /// importin-alpha export receptor activity /// protein transporter activity	nucleus /// nuclear pore /// cytoplasm	---
229901_at	ZNF488	-0.195	-0.35	L	---	nucleic acid binding /// zinc ion binding	nucleus	---
209151_x_at	TCF3	0.082	-0.349	B	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
209167_at	GPM6B	-0.379	-0.348	L	neurogenesis	---	integral to membrane	---
224822_at	DLC1	-0.039	-0.347	L	cytoskeleton organization and biogenesis /// regulation of cell adhesion /// negative regulation of cell growth	Rho GTPase activator activity /// protein binding	extracellular region /// cytoplasm	---
222173_s_at	TBC1D2	-0.157	-0.346	B	---	GTPase activator activity	---	---
208157_at	SIM2	0.263	-0.346	L	regulation of transcription, DNA-dependent /// signal transduction /// development /// neurogenesis	transcription factor activity /// signal transducer activity	nucleus	---
225436_at	LOC58489	-0.256	-0.346	L	---	catalytic activity	---	---
221908_at	FLJ14627	-0.082	-0.344	L	electron transport	electron transporter activity	---	---
203702_s_at	TTLL4	0.047	-0.344	L	protein modification	tubulin-tyrosine ligase activity /// ligase activity	---	---
233306_at	C1orf1	-0.255	-0.344	L	---	---	---	Circadian Exercise
				B		---	nucleus	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
227449_at	EPHA4	-0.264	-0.343	L	protein amino acid phosphorylation /// signal transduction /// transmembrane receptor protein tyrosine kinase signaling pathway	receptor activity /// ephrin receptor activity /// ATP binding /// transferase activity	integral to plasma membrane	---
201838_s_at	TAF6l(gamm	-0.035	-0.342	L	regulation of transcription, DNA-dependent	---	nucleus	---
202476_s_at	TUBGCP2	0.09	-0.341	B	microtubule cytoskeleton organization and biogenesis	---	spindle pole /// microtubule organizing center	---
218347_at	RSAFD1	-0.141	-0.341	B	electron transport	electron transporter activity /// iron ion binding /// FMN binding /// oxidoreductase activity	outer membrane (sensu Gram-negative Bacteria)	---
207979_s_at	CD8B1	-0.51	-0.341	T	immune response /// transmembrane receptor protein tyrosine kinase signaling pathway /// T-cell activation	protein binding /// coreceptor activity /// MHC class I protein binding	plasma membrane /// integral to plasma membrane /// T-cell receptor complex	---
202875_s_at	PBX2	0.068	-0.34	B	regulation of transcription, DNA-dependent /// anterior compartment specification /// posterior compartment specification	transcription factor activity	nucleus	---
203101_s_at	MGAT2	-0.093	-0.339	B	N-linked glycosylation /// oligosaccharide biosynthesis	alpha-1,6-mannosylglycoprotein 2-beta-N-acetylglucosaminyltransferase activity /// transferase activity, transferring glycosyl groups	membrane fraction /// Golgi stack /// integral to membrane	N-Glycan biosynthesis
231766_s_at	COL12A1	-0.446	-0.339	T	skeletal development /// phosphate transport /// cell adhesion /// collagen fibril organization	structural molecule activity /// protein binding /// extracellular matrix structural constituent conferring tensile strength	extracellular matrix (sensu Metazoa) /// collagen type XII /// collagen type XII /// cytoplasm	---
217198_x_at	IGH@ /// IGHG	-0.467	-0.339	T	immune response /// immune response	sugar porter activity /// UDP-N-acetylgalactosamine transporter activity	membrane fraction /// integral to membrane	---
209713_s_at	SLC35D1	-0.13	-0.338	L	transport /// UDP-N-acetylgalactosamine transport /// chondroitin sulfate biosynthesis	guanyl-nucleotide exchange factor activity /// binding	endoplasmic reticulum /// integral to endoplasmic reticulum membrane	---
237443_at	ARFGEF2	-0.216	-0.338	L	exocytosis	ATP binding /// protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// transferase activity	---	---
229212_at	CSNK2A1	-0.13	-0.337	L	protein amino acid phosphorylation			Adherens junction /// tight junction /// Wnt signaling pathway
213928_s_at	HRB	-0.469	-0.335	T	mRNA-nucleus export /// transport /// regulation of GTPase activity	DNA binding /// RNA binding	nucleus /// nuclear pore	---
218282_at	C20orf31	-0.517	-0.335	T	carbohydrate metabolism /// N-linked glycosylation	mannosyl-oligosaccharide 1,2-alpha-mannosidase activity /// calcium ion binding /// hydrolase activity, acting on glycosyl bonds	membrane	---

No.		Values):	(log2 Values):					
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
209325_s_at	RGS16	0.014	-0.333	B	signal transduction /// visual perception /// regulation of G-protein coupled receptor protein signaling pathway	signal transducer activity /// GTPase activator activity /// calmodulin binding	---	Calcium regulation in cardiac cells /// Smooth muscle contraction
44783_s_at	HEY1	-0.559	-0.333	L	regulation of transcription, DNA-dependent /// neurogenesis	DNA binding /// transcription factor activity	nucleus	---
241009_at	FOXN4	-0.269	-0.33	B	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
232405_at	SEC24D	-0.076	-0.33	L	intracellular protein transport /// ER to Golgi transport	protein binding	endoplasmic reticulum /// Golgi apparatus /// COPII vesicle coat	---
202495_at	TBCC	-0.102	-0.33	L	protein folding /// post-chaperonin tubulin folding pathway /// beta-tubulin folding	unfolded protein binding /// chaperone binding	cytoskeleton /// microtubule /// membrane	---
234479_at	PCDHB18	0.248	-0.33	L	homophilic cell adhesion	calcium ion binding	membrane	---
202493_x_at	CSH1	0.178	-0.33	L	---	hormone activity	extracellular region	Neuroactive ligand-receptor interaction/// cytokine-cytokine receptor interaction
219726_at	NLGN3	-0.079	-0.329	B	cell adhesion	catalytic activity /// protein binding	integral to membrane	---
1553096_s_at	BCL2L11	0.192	-0.329	L	apoptosis /// induction of apoptosis /// positive regulation of apoptosis	---	membrane fraction /// membrane	Apoptosis
234978_at	SLC36A4	0.259	-0.328	L	transport /// amino acid transport	amino acid-polyamine transporter activity	integral to membrane	---
228516_at	CDAN1	-0.081	-0.328	L	---	---	---	cell cycle
239341_at	VDP	-0.066	-0.327	B	Secretory pathway/// transport/// intracellular transport/// physiological process/// vesicle docking during exocytosis/// exocytosis/// vesicle docking/// cellular physiological process/// cell growth and/or maintenance/// vesicle-mediated transport/// protein transport/// intracellular protein transport/// cellular process	Protein transporter activity	---	---
201213_at	PPP1R7	-0.03	-0.327	B	---	protein phosphatase type 1 regulator activity /// enzyme regulator activity	nucleus /// cytoplasm	---
1553541_at	LMX1A	-0.325	-0.327	L	regulation of transcription, DNA-dependent /// development	transcription factor activity /// zinc ion binding	nucleus	---
1554787_at	C9orf96	-0.103	-0.327	L	protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding	---	---
1567304_at	CDC14A	-0.153	-0.327	L	cytokinesis /// protein amino acid dephosphorylation /// cell cycle	protein tyrosine phosphatase activity /// protein tyrosine/serine/threonine phosphatase activity /// hydrolase activity	nucleus	cell cycle
205218_at	POLR3F	0.104	-0.325	B	transcription	DNA binding /// DNA-directed RNA polymerase activity /// transferase activity	nucleus /// DNA-directed RNA polymerase III complex	pyrimidine metabolism/// purine metabolism/// RNA polymerase

No.		Value(s): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Value(s): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
206580_x_at	HIST1H4I	-0.636	-0.324	T	DNA metabolism /// chromosome organization and biogenesis (sensu eukarya) /// nucleobase, nucleoside, nucleotide and nucleic acid metabolism /// nuclear organization and biogenesis /// cell growth and/or maintenance /// cell organization and biogenesis	nucleic acid binding /// DNA binding	---	---
209874_s_at	NOL5A	-0.035	-0.323	B	rRNA processing	RNA binding	nucleolus	---
205770_at	GSR	0.348	-0.323	B	electron transport /// glutathione metabolism /// response to pest, pathogen or parasite	glutathione-disulfide reductase activity /// disulfide oxidoreductase activity /// FAD binding	mitochondrion	glutamate metabolism /// glutathione metabolism
208823_x_at	HIST1H2BK	-0.365	-0.323	T	chromosome organization and biogenesis (sensu Eukaryota) /// nucleosome assembly	DNA binding	chromosome /// nucleosome /// nucleus	---
1561434_at	SGNE1	-0.289	-0.323	T	protein folding /// transport /// intracellular protein transport /// neuropeptide signaling pathway /// peptide hormone processing /// regulation of hormone secretion	enzyme inhibitor activity /// GTP binding /// enzyme activator activity /// unfolded protein binding	secretory granule	---
221792_at	RAB6B	-0.076	-0.32	L	intracellular protein transport /// retrograde transport, Golgi to ER /// small GTPase mediated signal transduction	GTPase activity /// GTP binding	Golgi apparatus	---
214287_s_at	CDC2L5	0.244	-0.32	L	development /// positive regulation of cell proliferation /// protein amino acid phosphorylation /// regulation of mitosis	ATP binding /// nucleotide binding /// protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// transferase activity	---	Benzoate degradation via CoA ligation /// inositol phosphate metabolism /// nicotinate and nicotinamide metabolism /// phosphatidylinositol signaling system
206169_at	UNC5C	-0.154	-0.319	L	apoptosis /// signal transduction /// development /// axon guidance /// brain development	receptor activity /// netrin receptor activity /// protein binding	integral to membrane	---
209504_s_at	PLEKHB1	-0.575	-0.319	T	signal transduction /// phototransduction	signal transducer activity	membrane fraction /// integral to membrane	---
205406_s_at	SPA17	0.023	-0.318	L	signal transduction /// spermatogenesis /// fertilization (sensu Metazoa)	cAMP-dependent protein kinase regulator activity	plasma membrane /// membrane	---
1553526_at	NALP8	0.074	-0.318	L	---	ATP binding	---	---
208971_at	UROD	-0.48	-0.318	T	heme biosynthesis	uroporphyrinogen decarboxylase activity /// lyase activity	---	Heme Biosynthesis /// Porphyrin and chlorophyll metabolism
236200_at	FAF1	-0.535	-0.317	L	apoptosis	---	nucleus	---
207122_x_at	SULT1A2	-0.476	-0.317	T	catecholamine metabolism /// lipid metabolism /// steroid metabolism /// amine biosynthesis	aryl sulfotransferase activity /// transferase activity	---	Sulfur metabolism
217748_at	COPG	-0.328	-0.316	T	retrograde transport, Golgi to ER /// intra-Golgi transport /// protein transport	binding	Golgi apparatus /// membrane /// COPI vesicle coat	---
217372_at	IL15	0.04	-0.315	L	cell-cell signaling /// immune response /// positive regulation of cell proliferation	signal transducer activity	golgi apparatus /// endosome /// extracellular space /// integral to plasmamembrane	Cytokine-cytokine receptor interaction /// Jak-STAT signaling pathway
213081_at	ZNF297	-0.261	-0.314	B	regulation of transcription, DNA-dependent	DNA binding /// protein binding /// zinc ion binding	nucleus	---

No.		Values):	(log2 Values):					
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
222781_s_at	C9orf40	-0.231	-0.314	L	---	actin binding	---	---
208242_at	RAX	-0.137	-0.312	B	regulation of transcription, DNA-dependent /// development /// visual perception	transcription factor activity /// RNA polymerase II transcription factor activity	nucleus	---
1552598_at	KCNG4	-0.108	-0.311	L	cation transport /// potassium ion transport	voltage-gated potassium channel activity /// protein binding	voltage-gated potassium channel complex /// integral to membrane	---
204408_at	APEX2	0.166	-0.311	L	DNA repair	endonuclease activity /// zinc ion binding	---	---
219878_s_at	KLF13	-0.706	-0.311	T	transcription /// regulation of transcription, DNA-dependent /// transcription from RNA polymerase II promoter	DNA binding /// RNA polymerase II transcription factor activity /// zinc ion binding	nucleus	---
213713_s_at	LOC89944	0.137	-0.31	L	carbohydrate metabolism	beta-galactosidase activity	beta-galactosidase complex	---
206558_at	SIM2	-0.061	-0.31	L	regulation of transcription, DNA-dependent /// signal transduction /// development /// neurogenesis	transcription factor activity /// signal transducer activity	nucleus	---
236951_at	NSFL1C	-0.11	-0.309	L	---	lipid binding	nucleus /// Golgi apparatus	---
211222_s_at	HAP1	0.167	-0.308	B	synaptic transmission /// development	---	actin cytoskeleton	Huntington's disease
217319_x_at	CYP4A11	0.27	-0.308	L	electron transport /// fatty acid metabolism	fatty acid (omega-1)-hydroxylase activity /// alkane 1-monooxygenase activity	endoplasmic reticulum /// microsome /// membrane	Fatty acid metabolism
227294_at	LOC115509	-0.017	-0.306	B	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
202870_s_at	CDC20	-0.622	-0.306	T	regulation of cell cycle /// cytokinesis /// ubiquitin-dependent protein catabolism /// ubiquitin cycle /// mitosis	---	spindle	Cell cycle/// ubiquitin mediated proteolysis/// cell cycle checkpoints
217149_x_at	TNK1	0.01	-0.305	B	Macromolecule metabolism/// metabolism///phosphorus metabolism/// physiological process/// protein amino acid phosphorylation/// phosphate metabolism/// phosphorylation/// protein metabolism/// protein modification	Kinase activity/// signal transducer activity/// purine nucleotide binding/// binding/// nucleotide binding/// receptor activity/// adenyl nucleotide binding/// transferase activity/// protein kinase activity/// catalytic activity/// phosphotransferase activity, alcohol group as acceptor/// protein-tyrosine kinase activity/// ATP binding/// transferase activity, transferring phosphorus-containing groups	---	---
234682_at	BTBD9	0.22	-0.305	L	cell adhesion	protein binding	---	---
206480_at	LTC4S	-0.407	-0.304	B	leukotriene biosynthesis	glutathione transferase activity /// leukotriene-C4 synthase activity /// enzyme activator activity /// lyase activity	membrane fraction /// microsome /// integral to membrane	prostaglandin and leukotriene metabolism
224152_s_at	PB1	0.014	-0.304	B	chromatin remodeling /// regulation of transcription, DNA-dependent /// mitosis	DNA binding /// chromatin binding	nuclear chromosome	---
240359_at	C20orf71	0.154	-0.304	B	---	lipid binding	---	---
214192_at	NUP88	0.297	-0.304	L	protein transport	transporter activity	nucleus /// nuclear pore	---

No.		Value(s): 1x LCPUFA (1.1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (1.3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
203515_s_at	PMVK	-0.292	-0.304	T	lipid metabolism /// protein amino acid phosphorylation /// cholesterol biosynthesis	phosphomevalonate kinase activity /// transferase activity	cytoplasm /// peroxisome	Biosynthesis of steroids
211474_s_at	SERPINB6	-0.041	-0.303	B	---	serine-type endopeptidase inhibitor activity /// protein binding	cytosol	---
1554801_at	MGC27121	0.007	-0.303	L	---	---	integral to membrane	---
223749_at	C1QTNF2	-0.249	-0.303	T	phosphate transport	---	cytoplasm	---
211151_x_at	GH1	-0.103	-0.302	B	signal transduction	hormone activity	extracellular region	neuroactive ligand-receptor interaction /// cytokine-cytokine receptor interaction
215584_at	HECW1	-0.168	-0.302	L	ubiquitin cycle	ubiquitin-protein ligase activity	intracellular	---
237845_at	KIF27	-0.119	-0.302	L	microtubule-based movement	ATP binding /// microtubule motor activity	microtubule associated complex	---
224077_at	WHSC1L1	-0.176	-0.301	B	regulation of transcription, DNA-dependent /// cell growth /// protein ubiquitination /// cell differentiation	DNA binding /// ubiquitin-protein ligase activity /// protein binding /// zinc ion binding	ubiquitin ligase complex /// nucleus	---
237762_at	RHAG	-0.379	-0.301	L	protein complex assembly /// circulation /// ammonium transport	ammonium transporter activity /// ankyrin binding	integral to plasma membrane /// membrane	---
1562074_a_at	UNC13C	-0.105	-0.301	L	exocytosis /// intracellular signaling cascade	diacylglycerol binding	synaptosome	---
212912_at	RPS6KA2	0.152	-0.301	L	protein amino acid phosphorylation /// protein kinase cascade	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	nucleus	Ribosomal Proteins
219647_at	POPDC2	-0.146	-0.301	L	---	---	integral to membrane	Electron Transport Chain
232392_at	SFRS3	-0.146	-0.301	L	nuclear mRNA splicing, via spliceosome	nucleic acid binding /// RNA binding	nucleus	---
242872_at	CIT	-0.364	-0.3	T	protein amino acid phosphorylation /// intracellular signaling cascade	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// small GTPase regulator activity /// ATP binding /// transferase activity /// diacylglycerol binding	intracellular	G13 Signaling Pathway
219741_at	C220rf18	-0.545	-0.3	T	---	---	nucleus	---
1567319_at	LOC57802	0.196	-0.299	B	Transport /// physiological process /// cellular physiological process /// cell growth and/or maintenance /// cellular process	Purine nucleotide binding /// ATPase activity /// primary active transporter activity /// hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides /// nucleotide binding /// adenyl nucleotide binding /// hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances /// P-P-bond-hydrolysis-driven transporter activity /// ATPase activity, coupled to transmembrane movement of substances /// catalytic activity /// hydrolase activity /// ATP binding /// carrier activity /// ATPase activity, coupled /// transporter activity /// hydrolase activity, acting on acid anhydrides	---	---

No.		Values):	(log2 Values):					
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
207029_at	KITLG	-0.366	-0.299	T	cell adhesion /// signal transduction /// cell proliferation /// hemopoiesis	stem cell factor receptor binding /// stem cell factor receptor binding /// protein binding /// growth factor activity	plasma membrane /// membrane /// integral to membrane	Cytokine-cytokine receptor interaction
203690_at	TUBGCP3	0.173	-0.298	B	microtubule nucleation	structural constituent of cytoskeleton /// gamma-tubulin binding	centriole /// polar microtubule	---
234635_at	KRTAP4-10	0.104	-0.298	L	---	---	keratin filament	---
1559228_at	CLU	-0.201	-0.297	L	lipid metabolism/// apoptosis/// cell death/// immune response/// fertilization (sensu Metazoa)	---	extracellular space	---
205840_x_at	GH1	0.07	-0.297	L	signal transduction	hormone activity	extracellular region	Neuroactive ligand-receptor interaction/// cytokine-cytokine receptor interaction
235367_at	MYPN	-0.055	-0.297	L	---	kinase activity	---	---
235768_at	SH3RF2	0.122	-0.296	L	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
203754_s_at	BRF1	-0.22	-0.295	B	transcription /// transcription initiation /// regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	transcription factor TFIIIB complex /// nucleus	Transcription, RNA Polymerase III
218104_at	TEX10	-0.046	-0.295	L	transport	carrier activity	extracellular space	---
203058_s_at	PAPSS2	0.049	-0.295	L	sulfate assimilation /// skeletal development /// nucleobase, nucleoside, nucleotide and nucleic acid metabolism	adenylyl-sulfate kinase activity /// sulfate adenylyltransferase (ATP) activity /// ATP binding /// nucleotidyltransferase activity	intracellular	selenoamino acid metabolism/// purine metabolism/// sulfur metabolism
221075_s_at	NCR2	0.137	-0.295	L	cellular defense response /// signal transduction	transmembrane receptor activity	integral to plasma membrane	---
210075_at	3B413	-0.31	-0.295	T	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex /// integral to membrane	---
230760_at	ZFY	-0.228	-0.294	L	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding /// transcription regulator activity /// metal ion binding	nucleus	---
225078_at	EMP2	0.025	-0.293	B	development /// cell death /// cell proliferation	---	integral to membrane	---
230603_at	COL27A1	0.043	-0.293	L	phosphate transport /// cell adhesion	extracellular matrix structural constituent /// protein binding	collagen /// cytoplasm	---
1555082_a_at	NEK11	-0.086	-0.292	B	protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding	---	---
230839_at	HRMT1L4	-0.183	-0.292	B	---	S-adenosylmethionine-dependent methyltransferase activity /// transferase activity	---	selenoamino acid metabolism/// tryptophan metabolism/// histidine metabolism/// ubiquinone biosynthesis/// nitrobenzene degradation/// aminophosphonate metabolism/// androgen and estrogen metabolism/// tyrosine metabolism
240666_at	FOXP1	0.243	-0.292	L	regulation of transcription, DNA-dependent	nucleic acid binding /// transcription factor activity /// zinc ion binding	nucleus	---
240777_at	SYNE2	-0.183	-0.292	T	---	actin binding /// structural molecule activity	cytoskeleton /// integral to membrane	---
210032_s_at	SPAG6	-0.04	-0.291	B	spermatid cell development	binding	axoneme /// flagellum	---
1555236_a_at	PGC	-0.008	-0.291	B	proteolysis and peptidolysis /// digestion	pepsin A activity /// hydrolase activity	extracellular space	---
215796_at	TRA@	0.009	-0.291	L	cellular defense response	receptor activity /// MHC protein binding /// peptide antigen binding	integral to plasma membrane	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
229707_at	ZNF606	0.234	-0.29	L	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
228233_at	FREM1	-0.282	-0.29	L	cell communication /// homophilic cell adhesion	calcium ion binding /// sugar binding	membrane /// integral to membrane	---
222065_s_at	FLII	-0.047	-0.289	B	regulation of transcription, DNA-dependent /// muscle contraction /// development /// metabolism	actin binding /// lyase activity	nucleus /// cytoskeleton	---
210832_x_at	PTGER3	0.136	-0.289	L	transcription, DNA-dependent /// G-protein coupled receptor protein signaling pathway /// cell death	rhodopsin-like receptor activity /// receptor activity /// ligand-dependent nuclear receptor activity /// prostaglandin E receptor activity /// thromboxane receptor activity	nuclear membrane /// integral to plasma membrane /// integral to membrane	Neuroactive ligand-receptor interaction
230949_at	SLC23A3	-0.043	-0.288	L	transport	transporter activity	membrane	---
210329_s_at	SGCD	-0.347	-0.288	T	cytoskeleton organization and biogenesis /// muscle development	---	cytoskeleton /// plasma membrane /// sarcoglycan complex /// sarcoglycan complex /// integral to membrane	---
226082_s_at	SFRS15	-0.332	-0.288	T	---	RNA binding	nucleus	---
204096_s_at	ELL	-0.205	-0.287	B	regulation of transcription, DNA-dependent /// RNA elongation from Pol II promoter	positive transcription elongation factor activity	nucleus	Transcription, Gene Expression, Elongating transcript encounters
204263_s_at	CPT2	0.027	-0.286	B	fatty acid metabolism /// fatty acid beta-oxidation /// transport	carnitine O-palmitoyltransferase activity /// acyltransferase activity /// transferase activity	mitochondrion /// mitochondrial inner membrane	Fatty Acid Degradation /// Mitochondrial fatty acid betaoxidation /// Fatty acid metabolism
1564414_a_at	PNLDC1	-0.059	-0.286	L	negative regulation of transcription	transcriptional repressor activity	nucleus	---
214754_at	MGC22014	-0.184	-0.285	L	regulation of transcription, DNA-dependent	transcription factor activity /// iron ion binding	---	---
204267_x_at	PKMYT1	0.258	-0.285	L	regulation of cyclin dependent protein kinase activity /// protein amino acid phosphorylation /// cell cycle /// regulation of mitosis	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	membrane fraction /// endoplasmic reticulum /// Golgi apparatus /// membrane	cell cycle
208579_x_at	H2BFS	-0.369	-0.285	T	nucleosome assembly /// chromosome organization and biogenesis (sensu Eukaryota)	DNA binding	nucleosome /// nucleus /// chromosome	---
220127_s_at	FBXL12	-0.481	-0.285	T	ubiquitin cycle	---	---	---
218780_at	HOOK2	-0.241	-0.284	B	microtubule cytoskeleton organization and biogenesis	microtubule binding	cytoplasm /// cytoskeleton	---
207693_at	CACNB4	0.267	-0.284	L	ion transport /// calcium ion transport	voltage-gated calcium channel activity	membrane fraction /// voltage-gated calcium channel complex	---
233194_at	STARD13	-0.015	-0.284	L	---	GTPase activator activity	---	---
220807_at	HBQ1	0.016	-0.283	B	transport /// oxygen transport	oxygen transporter activity /// oxygen binding /// heme binding	hemoglobin complex	---
237624_at	COL4A2	-0.179	-0.283	B	phosphate transport /// extracellular matrix organization and biogenesis	extracellular matrix structural constituent	collagen /// collagen type IV /// cytoplasm	ECM-receptor interaction
238036_at	SHE	-0.134	-0.283	L	intracellular signaling cascade	---	---	---
208606_s_at	WNT4	-0.308	-0.283	T	frizzled-2 signaling pathway /// cell-cell signaling /// development	signal transducer activity /// extracellular matrix structural constituent	extracellular region	Wnt signaling
236783_at	KCNIP4	-0.045	-0.282	L	---	ion channel activity /// calcium ion binding	---	---
203489_at	SIVA	-0.555	-0.282	T	apoptosis /// defense response /// induction of apoptosis by extracellular signals	receptor signaling protein activity /// CD27 receptor binding /// CD70 receptor binding	cytoplasm /// integral to plasma membrane	---

No.		Values):	(log2 Values):					
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
220944_at	PGLYRP4	-0.084	-0.281	L	peptidoglycan catabolism /// detection of bacteria /// innate immune response /// defense response to Gram-positive bacteria	protein binding /// N-acetylmuramoyl-L-alanine amidase activity /// peptidoglycan receptor activity	intracellular /// membrane	---
212910_at	THAP11	-0.466	-0.281	T	---	DNA binding	nucleus	---
203407_at	PPL	-0.097	-0.281	T	---	structural constituent of cytoskeleton	cytoskeleton	---
235946_at	RIBC1	-0.224	-0.281	T	---	---	flagellum	---
217551_at	OR7E18P	-0.054	-0.28	L	G-protein coupled receptor protein signaling pathway /// perception of smell	receptor activity /// olfactory receptor activity	integral to membrane	GPCRDB Other
205379_at	CBR3	-0.105	-0.279	B	metabolism	carbonyl reductase (NADPH) activity /// oxidoreductase activity	cytosol	Prostaglandin and leukotriene metabolism
206019_at	RBM19	0.036	-0.279	B	nuclear mRNA splicing, via spliceosome	nucleic acid binding /// RNA binding	---	---
221817_at	DOLPP1	-0.055	-0.279	B	N-linked glycosylation	hydrolase activity /// dolichyldiphosphatase activity	endoplasmic reticulum /// integral to endoplasmic reticulum membrane	---
1554318_at	FKBP6	0.001	-0.279	L	protein folding	peptidyl-prolyl cis-trans isomerase activity /// binding /// FK506 binding /// isomerase activity	---	---
204412_s_at	NEFH	-0.09	-0.279	T	nucleosome assembly /// neurogenesis	DNA binding /// structural molecule activity	nucleosome /// nucleus /// chromosome /// neurofilament /// axon	Amyotrophic lateral sclerosis
218183_at	C16orf5	-0.436	-0.279	T	---	---	nucleus /// integral to membrane	---
215260_s_at	TCF3	-0.355	-0.278	B	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
240323_at	FXYD6	0.287	-0.278	L	ion transport	ion channel activity	extracellular space/// integral to membrane	---
218788_s_at	SMYD3	0.047	-0.278	L	chromatin modification	methyltransferase activity /// transferase activity /// histone-lysine N-methyltransferase activity	nucleus	---
232072_at	ASAHL	-0.356	-0.278	T	---	hydrolase activity	---	---
221285_at	ST8SIA2	0.063	-0.277	L	carbohydrate metabolism /// protein amino acid glycosylation /// N-glycan processing /// neurogenesis /// oligosaccharide biosynthesis	sialyltransferase activity	Golgi apparatus /// integral to membrane	Ganglioside biosynthesis/// globoside metabolism/// blood group glycolipid biosynthesis-neolactoseries
202535_at	FADD	-0.243	-0.277	T	cell surface receptor linked signal transduction /// induction of apoptosis via death domain receptors /// antimicrobial humoral response (sensu Vertebrata) /// regulation of apoptosis /// positive regulation of I-kappaB kinase/NF-kappaB cascade	signal transducer activity /// death receptor binding /// protein binding	cytoplasm	apoptosis/// Toll-like receptor signaling pathway
218848_at	WDR58	-0.409	-0.277	T	---	kinase activity	---	---
217515_s_at	CACNA1S	-0.16	-0.276	B	cation transport /// calcium ion transport /// muscle contraction	voltage-gated calcium channel activity /// cation channel activity /// calcium ion binding /// dihydropyridine-sensitive calcium channel activity	membrane fraction /// voltage-gated calcium channel complex /// integral to membrane	MAPK signaling pathway
226375_at	LMTK2	-0.443	-0.276	B	autophosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// protein phosphatase inhibitor activity /// protein binding /// ATP binding	integral to membrane	---
1564307_a_at	FLJ25179	-0.232	-0.276	B	---	endopeptidase inhibitor activity	---	---
220320_at	DOK3	-0.018	-0.276	B	---	insulin receptor binding	---	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
203872_at	ACTA1	-0.46	-0.276	T	muscle development	motor activity /// structural constituent of cytoskeleton /// protein binding	actin filament	Smooth muscle contraction /// Striated muscle contraction
216210_x_at	HRIHFB2122	-0.283	-0.276	T	actin modification /// barbed-end actin filament capping	actin binding /// GTP-Rho binding /// myosin II binding	nucleus /// actin cytoskeleton	---
227650_at	HSPA14	0.022	-0.275	L	protein folding /// response to unfolded protein	ATP binding	---	---
214440_at	NAT1	-0.185	-0.274	L	metabolism	arylamine N-acetyltransferase activity /// acetyltransferase activity /// transferase activity	---	---
241079_at	PUM1	-0.092	-0.274	L	regulation of translation /// mRNA metabolism	RNA binding /// binding	---	---
213974_at	ADAMTSL3	-0.427	-0.274	L	development	peptidase activity /// metallopeptidase activity	---	---
203460_s_at	PSEN1	-0.109	-0.274	T	membrane protein ectodomain proteolysis /// anti-apoptosis /// chromosome organization and biogenesis (sensu Eukaryota) /// chromosome segregation /// Notch receptor processing /// intracellular signaling cascade /// protein processing /// amyloid precursor protein catabolism /// positive regulation of enzyme activity	protein binding	kinetochore /// membrane fraction /// integral to nuclear inner membrane /// mitochondrion /// endoplasmic reticulum /// Golgi apparatus /// integral to plasma membrane /// membrane /// integral to membrane	Alzheimer's disease/// Wnt signaling pathway/// Notch signaling pathway
1554932_at	ZSWIM2	-0.044	-0.273	L	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
204123_at	LIG3	-0.193	-0.273	T	cytokinesis /// DNA replication /// DNA repair /// cell cycle /// meiotic recombination /// spermatogenesis	DNA binding /// DNA ligase (ATP) activity /// ATP binding /// ligase activity	nucleus	DNA Repair
223035_s_at	FARSLB	-0.083	-0.272	B	protein biosynthesis /// phenylalanyl-tRNA aminoacylation	phenylalanine-tRNA ligase activity /// ATP binding /// ligase activity	soluble fraction /// cytoplasm	phenylalanine, tyrosine and tryptophan biosynthesis/// aminoacyl-tRNA biosynthesis
211545_at	GHRHR	-0.061	-0.272	B	skeletal development /// G-protein coupled receptor protein signaling pathway /// adenylate cyclase activation	receptor activity /// G-protein coupled receptor activity /// growth hormone-releasing hormone receptor activity	plasma membrane /// integral to membrane	Neuroactive ligand-receptor interaction
201580_s_at	DJ971N18.2	-0.116	-0.272	L	electron transport	electron transporter activity	integral to membrane	---
235086_at	THBS1	0.01	-0.272	L	cell motility /// cell adhesion /// development /// neurogenesis /// blood coagulation	endopeptidase inhibitor activity /// signal transducer activity /// structural molecule activity /// calcium ion binding /// protein binding /// heparin binding	extracellular region	TGF Beta signaling pathway /// Inflammatory response pathway
226136_at	HRB2	0.028	-0.272	L	---	nucleic acid binding	nucleus	---
223531_x_at	GPR89	-0.009	-0.272	L	positive regulation of I-kappaB kinase/NF-kappaB cascade	receptor activity	---	---
212116_at	RFP	-0.371	-0.272	T	transcription /// regulation of transcription, DNA-dependent /// spermatogenesis /// cell proliferation /// protein ubiquitination	DNA binding /// transmembrane receptor protein tyrosine kinase activity /// ubiquitin-protein ligase activity /// zinc ion binding /// metal ion binding	ubiquitin ligase complex /// membrane fraction /// nucleus /// integral to plasma membrane	---
208293_x_at	CSHL1	-0.222	-0.271	B	---	hormone activity /// structural constituent of chorion (sensu Insecta)	extracellular region	---
210407_at	PPM1A	-0.214	-0.271	L	protein amino acid dephosphorylation /// positive regulation of I-kappaB kinase/NF-kappaB cascade	magnesium ion binding /// signal transducer activity /// protein phosphatase type 2C activity /// hydrolase activity /// manganese ion binding	protein serine/threonine phosphatase complex	MAPK signaling pathway

No.		Values):	(log2 Values):					
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
1557411_s_at	LOC203427	-0.037	-0.27	L	protein biosynthesis /// transport	nucleic acid binding /// structural constituent of ribosome /// transporter activity /// binding	mitochondrial inner membrane /// ribosome /// integral to membrane	---
224347_x_at	UBE2J2	-0.126	-0.27	T	ubiquitin cycle	ubiquitin conjugating enzyme activity /// ubiquitin-protein ligase activity /// ligase activity	endoplasmic reticulum /// integral to membrane	Ubiquitin mediated proteolysis
1569243_at	PLEKHE1	-0.179	-0.269	B	---	catalytic activity	---	---
220788_s_at	RNF31	-0.125	-0.269	B	---	---	---	JAK-STAT signaling pathway
207990_x_at	ACRV1	0.196	-0.269	L	development	---	---	---
240598_s_at	EXOSC2	-0.248	-0.269	T	rRNA processing	7sRNA binding/// 3'-5'-exoribonuclease activity/// hydrolase activity	cytoplasm/// nucleus	---
210843_s_at	MFAP3L	0.016	-0.268	B	---	---	integral to membrane	---
204644_at	COVA1	-0.219	-0.268	L	nuclear mRNA splicing, via spliceosome /// regulation of cell growth /// electron transport /// ultradian rhythm	nucleic acid binding /// protein disulfide oxidoreductase activity /// oxidoreductase activity	cytosol /// external side of plasma membrane /// membrane	---
216426_at	TCEB1	0.099	-0.267	B	Metabolism/// nucleobase, nucleoside, nucleotide and nucleic acid metabolism/// regulation of transcription from pol II promoter/// regulation of transcription/// regulation of transcription, DNA-dependent/// physiological process/// transcription, DNA-dependent/// transcription/// regulation of metabolism/// transcription from pol II promoter/// regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism/// regulation of physiological process/// regulation of biological process	Protein binding/// transcription regulator activity	---	Ubiquitin mediated proteolysis
223709_s_at	WNT10A	0.004	-0.267	B	frizzled-2 signaling pathway /// development	signal transducer activity	extracellular region	Wnt signaling
200646_s_at	NUCB1	-0.331	-0.267	T	---	DNA binding /// calcium ion binding	extracellular space /// Golgi apparatus	---
201168_x_at	ARHGDIA	0.083	-0.266	B	negative regulation of cell adhesion /// Rho protein signal transduction	Rho GDP-dissociation inhibitor activity /// GTPase activator activity /// protein binding	cytoplasm	---
227385_at	LOC403313	-0.234	-0.266	L	---	hydrolase activity	integral to membrane	---
211616_s_at	HTR2A	-0.178	-0.266	T	signal transduction /// serotonin receptor signaling pathway /// synaptic transmission	rhodopsin-like receptor activity /// receptor activity /// serotonin receptor activity	integral to plasma membrane	Neuroactive ligand-receptor interaction/// calcium signaling pathway
203032_s_at	FH	-0.073	-0.265	B	tricarboxylic acid cycle /// fumarate metabolism /// negative regulation of cell cycle	fumarate hydratase activity /// lyase activity	mitochondrion /// tricarboxylic acid cycle enzyme complex	Krebs-TCA Cycle /// Citrate cycle (TCA cycle) /// Reductive carboxylate cycle (CO2 fixation)
209907_s_at	ITSN2	0.302	-0.265	B	endocytosis	SH3/SH2 adaptor protein activity /// calcium ion binding	---	---
213124_at	ZNF473	0.232	-0.265	L	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
214442_s_at	PIAS2	-0.162	-0.265	L	regulation of transcription, DNA-dependent /// ubiquitin cycle /// development	DNA binding /// zinc ion binding	nucleus	JAK-Stat signaling pathway
231218_at	CASP8	0.118	-0.265	L	proteolysis and peptidolysis /// apoptotic program /// regulation of apoptosis /// positive regulation of I-kappaB kinase/NF-kappaB cascade	signal transducer activity /// protein binding /// cysteine-type peptidase activity /// hydrolase activity /// caspase activity	mitochondrion /// cytoskeleton	Apoptosis/// Huntington's disease/// toll-like receptor signaling pathway/// MAPK signaling pathway/// dentatorubropallidoluysian atrophy (drpla)

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
1554942_a_at	KLHL14	0.083	-0.264	B	---	protein binding	---	---
231382_at	FGF18	0.321	-0.264	L	signal transduction /// cell-cell signaling /// positive regulation of cell proliferation /// morphogenesis	growth factor activity	extracellular space	MAPK signaling pathway
232252_at	LOC92235	-0.211	-0.264	L	protein amino acid dephosphorylation	protein tyrosine/serine/threonine phosphatase activity	---	---
205486_at	TESK2	-0.434	-0.264	T	protein amino acid phosphorylation /// apoptosis /// intracellular signaling cascade /// spermatogenesis /// actin cytoskeleton organization and biogenesis /// focal adhesion formation	magnesium ion binding /// protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity /// manganese ion binding	nucleus	Benzoate degradation via CoA ligation/// Inositol phosphate metabolism/// Nicotinate and nicotinamide metabolism/// Phosphatidylinositol signaling system
215938_s_at	PLA2G6	-0.124	-0.262	B	phospholipid metabolism /// lipid catabolism	phospholipase A2 activity /// hydrolase activity	cytoplasm /// membrane	phospholipid degradation/// prostaglandin and leukotriene metabolism/// MAPK signaling pathway/// glycerolipid metabolism
229216_s_at	CSNK2A1	-0.132	-0.262	L	---	---	---	Wnt signaling pathway/// tight junction/// adherens junction
209650_s_at	TBC1D22A	0.124	-0.261	B	---	GTPase activator activity	---	---
1554193_s_at	MANEA	-0.158	-0.261	L	carbohydrate metabolism	glycoprotein endo-alpha-1,2-mannosidase activity /// hydrolase activity, acting on glycosyl bonds	---	---
203158_s_at	GLS	-0.087	-0.261	L	glutamine catabolism	glutaminase activity /// hydrolase activity	mitochondrion	Glutamate metabolism /// D-Glutamine and D-glutamate metabolism /// Nitrogen metabolism
1570351_at	ADAMTS6	-0.054	-0.261	L	proteolysis and peptidolysis	metalloendopeptidase activity /// peptidase activity /// zinc ion binding /// hydrolase activity	extracellular matrix (sensu Metazoa)	---
1569401_at	CLEC12A	-0.184	-0.261	L	---	receptor activity /// sugar binding	---	---
200060_s_at	RNPS1	-0.478	-0.261	L	nuclear mRNA splicing, via spliceosome /// transcription /// RNA splicing	nucleic acid binding /// RNA binding	nucleus	mRNA processing Reactome
229008_at	KIAA2002	-0.158	-0.26	L	protein amino acid phosphorylation	protein kinase activity /// ATP binding	---	---
223474_at	C14orf4	-0.576	-0.26	T	---	---	nucleus	---
226364_at	HIP1	-0.023	-0.259	B	---	actin binding /// structural constituent of cytoskeleton /// phospholipid binding	membrane fraction /// cytoplasm /// cytoskeleton	Huntington's disease
221575_at	SCLY	-0.238	-0.259	L	amino acid metabolism /// metabolism	transaminase activity /// selenocysteine lyase activity /// transferase activity /// lyase activity	cytosol	Selenoamino acid metabolism
235305_s_at	FLJ10948	0.065	-0.259	L	metabolism	catalytic activity	---	---
207768_at	EGR4	-0.289	-0.259	L	regulation of transcription, DNA-dependent /// positive regulation of cell proliferation	transcription factor activity /// zinc ion binding	nucleus	---
205765_at	CYP3A5	0.019	-0.258	T	electron transport /// xenobiotic metabolism /// transport /// steroid metabolism	monooxygenase activity /// oxygen binding /// unspecific monooxygenase activity	membrane fraction /// endoplasmic reticulum /// microsome /// membrane	Irinotecan pathway /// Fatty acid metabolism /// gamma-Hexachlorocyclohexane degradation /// Tryptophan metabolism
222484_s_at	CXCL14	0.07	-0.256	L	chemotaxis /// inflammatory response /// signal transduction /// cell-cell signaling	chemokine activity	extracellular region	cytokine-cytokine receptor interaction

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
227811_at	FGD3	-0.291	-0.256	T	cytoskeleton organization and biogenesis /// regulation of cell shape /// actin cytoskeleton organization and biogenesis /// regulation of Cdc42 GTPase activity /// filopodium formation	guanyl-nucleotide exchange factor activity /// protein binding /// zinc ion binding /// small GTPase binding	ruffle /// Golgi apparatus /// cytoskeleton /// lamellipodium	Regulation of actin cytoskeleton
241493_at	MYO1E	0.046	-0.255	B	actin filament-based movement	microfilament motor activity /// actin binding /// calmodulin binding /// ATP binding /// ATPase activity, coupled	myosin	---
210310_s_at	FGF5	0.111	-0.254	B	regulation of cell cycle /// cell-cell signaling /// neurogenesis /// cell proliferation /// fibroblast growth factor receptor signaling pathway	growth factor activity	extracellular space	MAPK signaling pathway
204810_s_at	CKM	0.124	-0.254	B	---	creatine kinase activity	cytoplasm	Urea cycle and metabolism of amino groups /// Arginine and proline metabolism
235129_at	PPP1R1A	0.008	-0.254	L	glycogen metabolism /// signal transduction	type 1 serine/threonine specific protein phosphatase inhibitor activity	---	---
219622_at	RAB20	-0.103	-0.254	L	small GTPase mediated signal transduction /// protein transport	GTP binding	---	---
230093_at	TSGA2	-0.318	-0.254	L	meiosis	---	---	---
201106_at	GPX4	-0.525	-0.254	T	phospholipid metabolism /// response to oxidative stress /// development	glutathione peroxidase activity /// electron transporter activity /// oxidoreductase activity /// phospholipid-hydroperoxide glutathione peroxidase activity	mitochondrion	Glutathione metabolism
222633_at	TBL1XR1	-0.688	-0.254	T	transcription /// regulation of transcription, DNA-dependent /// ubiquitin cycle	---	nucleus	Wnt signaling pathway
222778_s_at	WHSC1	0.028	-0.254	T	regulation of transcription, DNA-dependent /// morphogenesis /// protein ubiquitination	DNA binding /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex /// nucleus	---
224332_s_at	MRPL43	-0.289	-0.254	T	---	structural constituent of ribosome	mitochondrion /// ribonucleoprotein complex	---
227543_at	HTATIP	-0.312	-0.252	T	androgen receptor signaling pathway/// chromatin assembly or disassembly/// chromatin modification/// double-strand break repair/// histone acetylation/// positive regulation of transcription, DNA-dependent/// regulation of cell growth/// transcription from RNA polymerase II promoter	acyltransferase activity/// androgen receptor binding/// chromatin binding/// histone acetyltransferase activity/// metal ion binding/// protein binding/// transcription coactivator activity/// transferase activity/// zinc ion binding	TIP60 histone acetyltransferase complex/// chromatin/// nucleus	---
209946_at	VEGFC	0.032	-0.252	T	regulation of cell cycle /// angiogenesis /// substrate-bound cell migration /// signal transduction /// lymph gland development /// cell proliferation /// positive regulation of cell proliferation /// cell differentiation	growth factor activity	membrane	Cytokine-cytokine receptor interaction/// focal adhesion/// hemostasis
214958_s_at	EVER1	-0.518	-0.252	T	---	---	integral to membrane	---
208553_at	HIST1H1E	-0.249	-0.251	B	nucleosome assembly /// chromosome organization and biogenesis (sensu Eukaryota)	DNA binding	nucleosome /// nucleus /// chromosome	---
235476_at	TRIM59	0.08	-0.251	L	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
217332_at	CTAGE5	0.048	-0.251	L	RNA processing	RNA binding/// protein binding/// enzyme activator activity/// 3'-5'-exoribonuclease activity	---	---
205136_s_at	NUFIP1	-0.179	-0.251	L	RNA processing	RNA binding /// protein binding /// zinc ion binding	nucleus	---
1568596_a_at	TROAP	-0.118	-0.25	B	cell adhesion	protein binding	cytoplasm	---
238508_at	DRF1	0.113	-0.25	B	---	nucleic acid binding /// zinc ion binding /// kinase activity	---	---
205374_at	SLN	0.132	-0.25	L	transport	enzyme regulator activity	smooth endoplasmic reticulum /// integral to membrane /// sarcoplasmic reticulum	---
204735_at	PDE4A	-0.265	-0.25	L	signal transduction /// cyclic nucleotide metabolism	3',5'-cyclic-nucleotide phosphodiesterase activity /// cAMP-specific phosphodiesterase activity /// hydrolase activity	membrane fraction /// soluble fraction /// insoluble fraction	Purine metabolism
201314_at	STK25	-0.462	-0.25	T	protein amino acid phosphorylation /// response to oxidative stress /// signal transduction	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	---	---
228168_at	ATP5G3	-0.079	-0.249	B	generation of precursor metabolites and energy /// ATP synthesis coupled proton transport /// proton transport	transporter activity /// lipid binding /// hydrogen-transporting ATP synthase activity, rotational mechanism /// hydrogen-transporting ATPase activity, rotational mechanism	membrane fraction /// mitochondrion /// proton-transporting ATP synthase complex (sensu Eukaryota) /// proton-transporting two-sector ATPase complex	oxidative phosphorylation/// ATP synthesis
228650_at	POLR2D	0.127	-0.248	B	Metabolism/// nucleobase, nucleoside, nucleotide and nucleic acid metabolism/// physiological process/// transcription, DNA-dependent/// transcription/// transcription from pol II promoter	Obsolete molecular function/// transferase activity/// DNA-directed RNA polymerase activity/// DNA-directed RNA polymerase I activity/// catalytic activity/// DNA-directed RNA polymerase III activity/// DNA-directed RNA polymerase II activity/// nucleotidyltransferase activity/// transferase activity, transferring phosphorus-containing groups	---	Pyrimidine metabolism/// Purine metabolism/// RNA polymerase
205439_at	GSTT2	0.127	-0.248	L	---	glutathione transferase activity /// transferase activity	---	Glutathione metabolism
219529_at	CLIC3	-0.503	-0.248	T	ion transport /// chloride transport /// signal transduction	voltage-gated chloride channel activity	membrane fraction /// nucleus /// membrane	---
202495_at	TBCC	0.243	-0.247	B	protein folding /// post-chaperonin tubulin folding pathway /// beta-tubulin folding	unfolded protein binding /// chaperone binding	cytoskeleton /// microtubule /// membrane	---
1558369_at	MPHOSPH9	0.237	-0.247	L	regulation of cell cycle /// M phase of mitotic cell cycle	---	Golgi apparatus /// membrane	---
214433_s_at	SELENBP1	-0.585	-0.247	T	---	selenium binding /// selenium binding	---	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.60% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
214159_at	PLCE1	-0.148	-0.246	B	activation of MAPK /// regulation of cell growth /// lipid metabolism /// phospholipid metabolism /// diacylglycerol biosynthesis /// regulation of smooth muscle contraction /// cytoskeleton organization and biogenesis /// epidermal growth factor receptor signaling pathway /// positive regulation of cytosolic calcium ion concentration /// protein kinase C activation /// small GTPase mediated signal transduction /// Ras protein signal transduction /// heart development /// regulation of G-protein coupled receptor protein signaling pathway /// cell proliferation /// calcium-mediated signaling /// regulation of protein kinase activity /// regulation of Ras protein signal transduction /// inositol phosphate-mediated signaling	1phosphoinositide phospholipase C activity /// receptor signaling protein activity /// guanyl-nucleotide exchange factor activity /// calcium ion binding /// Ras interactor activity /// enzyme binding	membrane fraction /// cytosol /// plasma membrane	Wnt signaling
226808_at	KIAA0543	0.222	-0.246	L	regulation of transcription, DNA-dependent /// cell adhesion	nucleic acid binding /// protein dimerization activity	intracellular	---
225868_s_at	BIRC4	0.02	-0.246	L	apoptosis /// anti-apoptosis /// protein ubiquitination	ubiquitin-protein ligase activity /// cysteine protease inhibitor activity /// zinc ion binding /// caspase inhibitor activity	ubiquitin ligase complex /// cytosol	Apoptosis
201521_s_at	NCBP2	-0.005	-0.245	B	mRNA processing /// mRNA-nucleus export /// snRNA-nucleus export /// transport	RNA cap binding /// nucleic acid binding	nucleus	mRNA processing
207385_at	TFDP3	-0.063	-0.245	B	regulation of cell cycle /// transcription /// regulation of transcription, DNA-dependent	transcription factor activity	nucleus /// transcription factor complex	cell cycle
225382_at	ZNF275	-0.086	-0.245	L	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
205515_at	PRSS12	0.312	-0.245	L	proteolysis and peptidolysis	chymotrypsin activity /// trypsin activity /// protein-lysine 6-oxidase activity /// scavenger receptor activity /// copper ion binding /// hydrolase activity	membrane	---
210988_s_at	PRUNE	0.242	-0.244	L	---	pyrophosphatase activity	cytoplasm	---
229316_at	NGC2749	-0.331	-0.244	T	two-component signal transduction system (phosphorelay)	two-component sensor molecule activity	---	---
239273_s_at	MMP28	-0.338	-0.244	T	proteolysis and peptidolysis /// proteolysis and peptidolysis	metalloendopeptidase activity /// metalloendopeptidase activity /// zinc ion binding	extracellular matrix (sensu Metazoa) /// extracellular matrix (sensu Metazoa)	Matrix Metalloproteinases
213071_at	DPT	0.009	-0.243	L	cell adhesion	protein binding	extracellular matrix (sensu Metazoa)	---
214175_x_at	PDLIM4	-0.012	-0.242	B	---	protein binding /// zinc ion binding	---	---
204349_at	CRSP9	-0.141	-0.242	L	regulation of transcription from Pol II promoter /// transcription initiation from Pol II promoter /// positive regulation of transcription	transcription coactivator activity /// receptor activity	nucleus	---
219938_at	RARRES1	-0.065	-0.242	L	negative regulation of cell proliferation	---	integral to membrane	---
206156_at	GJB5	-0.223	-0.242	T	epidermis development /// cell communication	connexon channel activity	connexon complex /// integral to membrane	Calcium regulation in cardiac cells
240336_at	HBM	-0.083	-0.241	B	transport /// oxygen transport	oxygen transporter activity /// oxygen binding	hemoglobin complex	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
239098_at	KCNRG	-0.107	-0.241	L	potassium ion transport	ion channel activity /// voltage-gated potassium channel activity /// protein binding	voltage-gated potassium channel complex /// membrane	---
214870_x_at	DC339047 /// L	-0.097	-0.241	L	neuropeptide signaling pathway	---	integral to membrane	---
1556029_at	PHACTR3	-0.209	-0.241	T	---	actin binding /// protein phosphatase inhibitor activity	nucleus	---
204931_at	TCF21	-0.155	-0.24	B	regulation of transcription, DNA-dependent /// mesoderm development	DNA binding /// RNA polymerase II transcription factor activity	nucleus	---
1556689_a_at	WNT4	-0.194	-0.24	L	frizzled-2 signaling pathway /// cell-cell signaling /// development	signal transducer activity /// extracellular matrix structural constituent	extracellular region	Wnt signaling pathway
213323_s_at	RoXaN	0.06	-0.24	L	---	nucleic acid binding /// zinc ion binding	nucleus	---
222944_s_at	FLJ21687	0.005	-0.24	L	---	protein binding	---	---
219693_at	AGPAT4	-0.125	-0.24	T	metabolism /// phospholipid biosynthesis	1-acylglycerol-3-phosphate O-acyltransferase activity /// acyltransferase activity /// transferase activity	integral to membrane	Glycerolipid metabolism/// Glycerophospholipid metabolism
227953_at	CKLFSF6	-0.143	-0.239	L	chemotaxis	cytokine activity	integral to membrane	---
232117_at	ZNF471	-0.247	-0.239	T	transcription /// regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
238544_at	IGF1R	-0.014	-0.239	T	regulation of cell cycle /// protein amino acid phosphorylation /// anti-apoptosis /// signal transduction /// positive regulation of cell proliferation /// insulin receptor signaling pathway	receptor activity /// epidermal growth factor receptor activity /// insulin-like growth factor receptor activity /// protein binding /// ATP binding /// transferase activity	membrane /// integral to membrane	Adherens junction/// focal adhesion
243238_at	PYGB	0.146	-0.238	L	carbohydrate metabolism /// glycogen catabolism	phosphorylase activity /// transferase activity, transferring glycosyl groups	---	Glycogen Metabolism /// Starch and sucrose metabolism
205930_at	GTF2E1	-0.555	-0.238	L	regulation of transcription, DNA-dependent /// transcription initiation from Pol II promoter	general RNA polymerase II transcription factor activity	nucleus /// transcription factor TFIIE complex	basal transcription factors
205689_at	PCNXL2	0.049	-0.238	L	---	---	integral to membrane	---
227769_at	GPR27	-0.532	-0.238	L	signal transduction /// G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity	integral to membrane	GPCRDB Class A Rhodopsin-like
226882_x_at	WDR4	0.081	-0.238	L	tRNA processing	---	---	---
222998_at	MAF1	-0.456	-0.238	T	transcription /// regulation of transcription, DNA-dependent	---	nucleus	---
217840_at	DDX41	-0.184	-0.238	T	RNA processing /// apoptosis /// development	RNA binding /// ATP binding /// ATP-dependent helicase activity /// hydrolase activity	nucleus	---
225860_at	LOC400843	0.048	-0.237	B	macromolecule metabolism/// physiological process/// proteolysis and peptidolysis	peptidase activity/// enzyme regulator activity/// metal ion binding/// metalloendopeptidase activity/// catalytic activity/// hydrolase activity/// transition metal ion binding/// zinc ion binding	---	---
244484_at	C20orf161	-0.345	-0.237	L	intracellular signaling cascade /// protein transport	binding	---	---
220468_at	FLJ22595	-0.211	-0.237	L	small GTPase mediated signal transduction	GTP binding	---	---
203151_at	MAP1A	0.236	-0.237	L	---	structural molecule activity	microtubule associated complex	---
218168_s_at	CABC1	-0.377	-0.237	T	protein folding	unfolded protein binding	mitochondrion	---
1563091_at	HDHD1A	-0.11	-0.236	B	metabolism	catalytic activity	---	---
229661_at	SALL4	0.017	-0.236	B	regulation of transcription, DNA-dependent	nucleic acid binding /// DNA binding /// zinc ion binding	nucleus	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
208539_x_at	SPRR2A	0.052	-0.236	B	keratinocyte differentiation	structural molecule activity /// binding	cornified envelope /// cytoplasm	---
223753_s_at	CFC1	-0.312	-0.236	B	determination of left/right symmetry	---	---	---
204420_at	FOSL1	0.046	-0.236	L	regulation of transcription from Pol II promoter /// chemotaxis /// cellular defense response /// positive regulation of cell proliferation /// response to virus	transcription factor activity	nucleus	Wnt signaling pathway
240224_at	PRDM10	0.16	-0.236	L	regulation of transcription, DNA-dependent /// transport	nucleic acid binding /// DNA binding /// transporter activity /// zinc ion binding /// lipid binding	nucleus	---
203188_at	B3GNT6	-0.216	-0.236	T	poly-N-acetyllactosamine biosynthesis	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase activity /// transferase activity, transferring glycosyl groups	Golgi apparatus /// integral to membrane /// integral to Golgi membrane	Blood group glycolipid biosynthesis-neolactoseries/// Keratan sulfate biosynthesis
201391_at	TRAP1	-0.359	-0.236	T	protein folding	receptor activity /// tumor necrosis factor receptor binding /// ATP binding /// unfolded protein binding	mitochondrion	---
201804_x_at	CKAP1	-0.309	-0.236	T	protein folding	unfolded protein binding	microtubule cytoskeleton	---
1555044_a_at	KBTBD5	0.257	-0.235	L	---	protein binding	---	---
210046_s_at	IDH2	-0.495	-0.235	T	carbohydrate metabolism /// glyoxylate cycle /// tricarboxylic acid cycle /// metabolism /// metabolism	isocitrate dehydrogenase (NADP+) activity /// isocitrate dehydrogenase (NADP+) activity /// oxidoreductase activity	mitochondrion /// mitochondrion	Citrate cycle/// Glutathione metabolism/// Reductive carboxylate cycle (CO2 fixation)
233324_at	TRERF1	-0.206	-0.235	T	regulation of transcription, DNA-dependent /// steroid biosynthesis /// cholesterol catabolism /// development /// homeostasis /// positive regulation of transcription, DNA-dependent /// regulation of hormone biosynthesis	DNA binding /// transcription factor activity /// transcription factor binding /// zinc ion binding /// DNA bending activity /// RNA polymerase II transcription mediator activity /// ligand-dependent nuclear receptor transcription coactivator activity	nucleus /// nucleus	---
1568598_at	KAZALD1	-0.004	-0.235	T	regulation of cell growth	insulin-like growth factor binding/// peptidase activity	extracellular region	---
234902_s_at	FLJ20557	0.066	-0.234	B	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
211153_s_at	TNFSF11	-0.009	-0.234	L	immune response /// cell differentiation /// osteoclast differentiation	receptor activity /// tumor necrosis factor receptor binding	extracellular region /// integral to plasma membrane	cytokine-cytokine receptor interaction
203235_at	THOP1	-0.355	-0.234	T	proteolysis and peptidolysis	metalloendopeptidase activity /// metalloendopeptidase activity /// zinc ion binding	---	---
215918_s_at	SPTBN1	0.27	-0.233	L	---	actin binding /// structural constituent of cytoskeleton /// calmodulin binding	cytoskeleton /// spectrin /// membrane	---
227492_at	OCLN	0.14	-0.233	L	protein complex assembly	structural molecule activity	plasma membrane/// integral to membrane/// tight junction	tight junction
230481_at	ACY3	-0.258	-0.233	T	metabolism	hydrolase activity, acting on ester bonds /// aspartoacylase activity	---	---
1559739_at	CHPT1	-0.135	-0.233	T	regulation of cell growth /// CDP-choline pathway /// platelet activating factor biosynthesis	diacylglycerol cholinephosphotransferase activity /// transferase activity /// diacylglycerol binding	microsome /// membrane /// integral to membrane	Glycerophospholipid metabolism/// Aminophosphonate metabolism
1554577-a_at	PSMD10	0.111	-0.232	B	---	---	cytosol /// proteasome regulatory particle (sensu Eukaryota)	Proteasome Degradation
217521_at	HAL	0.019	-0.232	L	histidine catabolism /// biosynthesis	histidine ammonia-lyase activity /// ammonia ligase activity /// lyase activity	cytosol	Histidine metabolism /// Nitrogen metabolism

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
216250_s_at	LPXN	0.205	-0.232	L	protein complex assembly /// cell adhesion /// signal transduction	zinc ion binding	cytoplasm	---
205034_at	CCNE2	-0.229	-0.232	L	regulation of cell cycle /// cell cycle checkpoint /// regulation of cyclin dependent protein kinase activity /// cytokinesis	---	nucleus	cell cycle
230393_at	CUL5	-0.11	-0.232	T	G1/S transition of mitotic cell cycle /// ubiquitin cycle /// cell cycle arrest /// cell proliferation /// negative regulation of cell proliferation /// induction of apoptosis by intracellular signals	receptor activity /// calcium channel activity /// protein binding	---	---
1554663_a_at	NUMA1	-0.083	-0.232	T	mitotic anaphase /// nuclear organization and biogenesis	structural molecule activity	nucleus /// spindle microtubule	---
207951_at	CSN2	0.157	-0.23	L	transport /// calcium ion transport	enzyme inhibitor activity /// transporter activity /// calcium ion binding	extracellular region	---
210580_x_at	SULT1A3	-0.417	-0.23	T	catecholamine metabolism /// lipid metabolism /// synaptic transmission /// steroid metabolism	aryl sulfotransferase activity /// transferase activity	cytoplasm	Sulfur metabolism
228308_at	FKBP11	-0.052	-0.229	B	protein folding	peptidyl-prolyl cis-trans isomerase activity /// isomerase activity	---	---
204159_at	CDKN2C	-0.073	-0.229	B	cell cycle /// cell cycle arrest /// negative regulation of cell proliferation	cyclin-dependent protein kinase inhibitor activity	nucleus /// cytoplasm	cell cycle
1552897_a_at	KCNG3	-0.142	-0.229	L	cation transport /// potassium ion transport	voltage-gated potassium channel activity /// protein binding	endoplasmic reticulum /// plasma membrane /// voltage-gated potassium channel complex /// integral to membrane	---
1557126_a_at	PLD1	0.163	-0.229	L	phospholipid metabolism /// chemotaxis /// Ras protein signal transduction /// metabolism /// lipid catabolism	phospholipase D activity /// hydrolase activity	endoplasmic reticulum /// Golgi apparatus /// membrane	phospholipid degradation/// glycerolipid metabolism
229991_s_at	SYTL4	-0.351	-0.228	L	transport /// intracellular protein transport /// exocytosis	transporter activity /// phospholipid binding /// zinc ion binding /// Rab interactor activity /// neurexin binding	synaptic vesicle /// membrane /// extrinsic to plasma membrane	---
1566165_at	KIAA2024	-0.109	-0.228	L	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
201415_at	GSS	-0.368	-0.228	T	amino acid metabolism /// glutathione biosynthesis /// response to oxidative stress /// neurogenesis	glutathione synthase activity /// ATP binding /// ligase activity	---	Glutamate metabolism /// Glutathione metabolism
1552412_a_at	DEFB106A	-0.152	-0.228	T	defense response to bacteria	---	extracellular region	---
220158_at	LGALS14	-0.051	-0.227	L	---	sugar binding	---	---
233123_at	SLC40A1	-0.227	-0.227	T	transport /// iron ion transport /// iron ion homeostasis /// morphogenesis	iron ion transporter activity	cytoplasm /// integral to plasma membrane	---
222963_s_at	IL1RAPL1	0.043	-0.227	T	signal transduction /// learning and/or memory	transmembrane receptor activity	membrane /// integral to membrane	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
210511_s_at	INHBA	-0.524	-0.226	L	skeletal development /// ovarian follicle development /// induction of apoptosis /// defense response /// cell cycle arrest /// cell surface receptor linked signal transduction /// cell-cell signaling /// neurogenesis /// mesoderm development /// response to external stimulus /// cell differentiation /// erythrocyte differentiation /// growth /// negative regulation of phosphorylation /// hemoglobin biosynthesis /// negative regulation of interferon-gamma biosynthesis /// negative regulation of B-cell differentiation /// negative regulation of macrophage differentiation /// negative regulation of cell cycle /// positive regulation of follicle-stimulating hormone secretion /// negative regulation of follicle-stimulating hormone secretion	cytokine activity /// transforming growth factor beta receptor binding /// hormone activity /// protein binding /// growth factor activity /// activin inhibitor activity	extracellular region	TGF-Beta signaling pathway/// cytokine-cytokine receptor interaction
221330_at	CHRM2	0.078	-0.226	L	G-protein signaling, coupled to cAMP nucleotide second messenger /// muscarinic acetylcholine receptor, adenylate cyclase inhibiting pathway /// muscarinic acetylcholine receptor, phospholipase C activating pathway /// synaptic transmission /// neurogenesis /// regulation of heart contraction rate	rhodopsin-like receptor activity /// muscarinic acetylcholine receptor activity	integral to plasma membrane	Neuroactive ligand-receptor interaction
230622_at	MLLT4	-0.372	-0.226	T	cell adhesion /// cell adhesion /// signal transduction /// signal transduction /// cell-cell signaling	motor activity /// protein binding /// protein C-terminus binding	intercellular junction /// myosin	Adherens junction/// tight junction
214649_s_at	MTMR2	-0.135	-0.225	B	protein amino acid dephosphorylation /// phospholipid dephosphorylation	inositol or phosphatidylinositol phosphatase activity /// protein tyrosine phosphatase activity /// protein binding /// protein tyrosine/serine/threonine phosphatase activity /// hydrolase activity	nucleus /// cytoplasm	Riboflavin metabolism/// thiamine metabolism/// vitamin B6 metabolism/// aminosugars metabolism/// fructose and mannose metabolism/// nicotinate and nicotinamide metabolism
221241_s_at	BCL2L14	-0.263	-0.225	L	regulation of apoptosis	---	---	---
241293_x_at	SPTLC2	-0.487	-0.225	T	biosynthesis	serine C-palmitoyltransferase activity /// acyltransferase activity /// transferase activity, transferring nitrogenous groups	endoplasmic reticulum /// integral to membrane	Glycosphingolipid metabolism
227809_at	ZC3HDC6	-0.185	-0.225	T	---	nucleic acid binding	---	---
201321_s_at	SMARCC2	0.285	-0.224	L	chromatin assembly or disassembly /// regulation of transcription, DNA-dependent /// chromatin modification	chromatin binding	chromatin /// nucleus	---
241403_at	CLK4	-0.161	-0.224	L	protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	nucleus	mRNA processing
1558120_at	DDX3X	-0.142	-0.224	L	---	DNA binding /// RNA binding /// ATP-dependent RNA helicase activity /// ATP binding	nucleus /// cytoplasm	---
204283_at	FARS2	0.415	-0.224	L	protein biosynthesis /// phenylalanyl-tRNA aminoacylation /// tRNA processing	tRNA binding /// phenylalanine-tRNA ligase activity /// ATP binding	soluble fraction /// mitochondrion	phenylalanine, tyrosine and tryptophan biosynthesis/// aminoacyl-tRNA biosynthesis

No.		Value(s): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Value(s): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
234202_at	NTN4	-0.238	-0.224	L	---	structural molecule activity	extracellular matrix (sensu Metazoa)	---
230306_at	MGC10485	-0.367	-0.224	T	intracellular protein transport /// retrograde transport, endosome to Golgi	protein binding /// protein transporter activity	cytosol	---
201607_at	PWP1	-0.069	-0.224	T	transcription	---	nucleus	---
240014_at	LOC51619	-0.163	-0.223	B	ubiquitin cycle	ubiquitin conjugating enzyme activity /// ligase activity	---	---
206691_s_at	PDIP	0.023	-0.223	B	electron transport /// protein folding /// protein-ER retention	protein disulfide isomerase activity /// electron transporter activity /// isomerase activity	endoplasmic reticulum	G13 Signaling Pathway
238646_at	CLTC	-0.177	-0.223	L	intracellular protein transport	structural molecule activity /// binding	coated pit /// clathrin vesicle coat	Huntington's disease
207621_s_at	PEMT	-0.295	-0.223	T	lipid metabolism /// phospholipid metabolism /// phosphatidylcholine biosynthesis /// cell proliferation /// phospholipid biosynthesis	phosphatidylethanolamine N-methyltransferase activity /// N-methyltransferase activity	mitochondrion /// endoplasmic reticulum /// integral to membrane	Acetylcholine Synthesis /// Glycine, serine and threonine metabolism /// Glycerophospholipid metabolism
207632_at	MUSK	-0.174	-0.223	T	protein amino acid phosphorylation /// transmembrane receptor protein tyrosine kinase signaling pathway /// development /// muscle development	transmembrane receptor protein tyrosine kinase activity /// transmembrane receptor activity /// ATP binding /// transferase activity	integral to plasma membrane /// membrane	---
228234_at	TICAM2	0.077	-0.222	L	intracellular protein transport /// inflammatory response /// positive regulation of I-kappaB kinase/NF-kappaB cascade	signal transducer activity /// transmembrane receptor activity /// protein carrier activity	membrane	---
244823_at	NEK6	-0.145	-0.222	T	protein amino acid phosphorylation /// positive regulation of I-kappaB kinase/NF-kappaB cascade	magnesium ion binding /// protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// signal transducer activity /// ATP binding /// transferase activity	nucleus	Proteasome Degradation
205437_at	ZNF211	0.029	-0.221	L	regulation of transcription, DNA-dependent	nucleic acid binding /// transcription factor activity /// zinc ion binding	nucleus	---
205509_at	CPB1	0.258	-0.22	L	proteolysis and peptidolysis	carboxypeptidase B activity /// carboxypeptidase A activity /// metallopeptidase activity /// hydrolase activity /// carboxypeptidase B activity	---	---
226465_s_at	SON	-0.704	-0.22	T	anti-apoptosis	nucleic acid binding /// DNA binding /// double-stranded RNA binding	intracellular /// nucleus	---
1554686_a_at	RHOBTB2	0.109	-0.219	L	small GTPase mediated signal transduction	protein binding /// GTP binding	---	---
241145_at	PDE1C	0.069	-0.219	L	signal transduction	3',5'-cyclic-nucleotide phosphodiesterase activity /// calmodulin-dependent cyclic-nucleotide phosphodiesterase activity /// calmodulin binding /// hydrolase activity	---	Purine metabolism
202743_at	PIK3R3	-0.112	-0.219	L	intracellular signaling cascade /// insulin receptor signaling pathway	phosphatidylinositol 3-kinase activity	phosphoinositide 3-kinase complex	phosphatidylinositol signaling system /// apoptosis
220698_at	CARD14	-0.159	-0.219	T	regulation of apoptosis /// activation of NF-kappaB-inducing kinase	protein binding /// protein binding	intracellular /// plasma membrane	---
211459_at	MAP3K2	-0.188	-0.218	B	protein amino acid phosphorylation /// activation of JNK	magnesium ion binding /// protein serine/threonine kinase activity /// ATP binding /// transferase activity	---	MAPK Cascade
235639_at	CDH19	0.145	-0.218	L	homophilic cell adhesion	calcium ion binding /// protein binding	integral to membrane	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
237183_at	GALNT5	-0.159	-0.218	L	---	polypeptide N-acetylgalactosaminyltransferase activity /// sugar binding /// transferase activity, transferring glycosyl groups /// manganese ion binding	Golgi apparatus /// integral to membrane	---
223112_s_at	NDUFB10	-0.469	-0.218	T	---	NADH dehydrogenase activity /// NADH dehydrogenase (ubiquinone) activity /// oxidoreductase activity	membrane fraction /// mitochondrion	Electron Transport Chain
236648_at	GMPS	0.036	-0.217	B	purine nucleotide biosynthesis /// GMP biosynthesis /// glutamine metabolism /// biosynthesis /// purine base biosynthesis	GMP synthase activity /// GMP synthase (glutamine-hydrolyzing) activity /// anthranilate synthase activity /// ATP binding /// ligase activity	---	Purine metabolism /// Glutamate metabolism
217614_at	POLR2E	0.097	-0.217	L	transcription /// transcription from Pol II promoter	DNA binding /// DNA-directed RNA polymerase activity /// protein binding /// transferase activity	nucleus /// DNA-directed RNA polymerase II, core complex	Purine metabolism /// Pyrimidine metabolism /// RNA polymerase
1555299_s_at	ERVWE1	0.095	-0.217	L	DNA transposition	structural molecule activity	integral to membrane /// viral capsid /// viral envelope	---
204941_s_at	ALDH3B2	0.074	-0.216	B	alcohol metabolism /// lipid metabolism /// metabolism	aldehyde dehydrogenase [NAD(P)+] activity /// oxidoreductase activity	---	Glycolysis / Gluconeogenesis /// Histidine metabolism /// Tyrosine metabolism /// Phenylalanine metabolism
1570433_at	TMPRSS2	-0.117	-0.216	B	proteolysis and peptidolysis	chymotrypsin activity /// trypsin activity /// scavenger receptor activity /// hydrolase activity	integral to plasma membrane	---
221501_x_at	LOC339047	0.04	-0.216	L	neuropeptide signaling pathway	---	integral to membrane	---
240515_at	CBARA1	0.009	-0.216	L	defense response	calcium ion binding	intracellular	---
1566948_at	FLJ37266	-0.074	-0.216	L	---	nucleic acid binding /// pancreatic ribonuclease activity	---	---
232187_at	PALMD	-0.181	-0.216	T	regulation of cell shape	---	membrane	---
232912_at	ITR	-0.164	-0.215	L	---	receptor activity	---	---
206876_at	SIM1	-0.216	-0.213	B	regulation of transcription, DNA-dependent /// signal transduction /// development /// neurogenesis	transcription factor activity /// signal transducer activity	nucleus	---
235688_s_at	TRAF4	-0.321	-0.213	L	apoptosis /// development /// protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex /// nucleus	---
206131_at	CLPS	0.022	-0.212	B	digestion /// lipid catabolism	enzyme activator activity	extracellular region /// soluble fraction	---
243660_at	CHD9	-0.097	-0.212	L	---	DNA binding /// helicase activity /// ATP binding	nucleus /// integral to membrane	---
228012_at	MATR3	-0.154	-0.212	L	---	RNA binding /// structural molecule activity /// zinc ion binding	nucleus /// nuclear inner membrane	---
217162_at	TSPY1	-0.119	-0.212	T	gonadal mesoderm development/// nucleosome assembly /// spermatogenesis /// sex differentiation /// cell proliferation /// cell differentiation	---	nucleus	---
1561853_a_at	IL23R	-0.025	-0.211	L	---	receptor activity	---	cytokine-cytokine receptor interaction/// Jak-Stat signaling pathway
1555469_a_at	CLASP2	-0.271	-0.211	L	---	binding	---	---
241743_at	NKTR	-0.025	-0.211	T	protein folding	cyclosporin A binding/// isomerase activity/// peptidyl-prolyl cis-trans isomerase activity	plasma membrane	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
233171_at	GRIN3A	-0.484	-0.211	T	protein biosynthesis /// ion transport /// synaptic transmission	magnesium ion binding /// DNA binding /// receptor activity /// ionotropic glutamate receptor activity /// transporter activity /// ion channel activity /// glutamate-gated ion channe activ ty	membrane /// integral to membrane	---
205665_at	TSPAN9	-0.351	-0.211	T	---	---	membrane fraction /// integral to plasma membrane	Ribosomal Proteins
206326_at	GRP	-0.213	-0.21	B	signal transduction /// neuropeptide signaling pathway	growth factor activity	soluble fraction	Neuroactive ligand-receptor interaction
234942_s_at	DNTTIP1	-0.458	-0.21	T	---	---	nucleus	---
37631_at	SIPA1L3	-0.056	-0.209	B	---	GTPase activator activity /// protein binding	---	---
222612_at	PSPC1	0.005	-0.209	L	nuclear mRNA splicing, via spliceosome	nucleic acid binding	---	---
225309_at	PHF5A	0.074	-0.208	B	nuclear mRNA splicing, via spliceosome /// positive regulation of transcription, DNA-dependent	transcription factor activity /// pre-mRNA splicing factor activity	spliceosome complex /// snRNP U2	mRNA processing
1555673_at	KRTAP2-4	-0.211	-0.208	L	---	---	keratin filament	---
237439_at	USP43	-0.313	-0.208	T	ubiquitin-dependent protein catabolism /// ubiquitin cycle	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity	---	---
233748_x_at	PRKAG2	0.234	-0.207	B	fatty acid biosynthesis /// cholesterol biosynthesis	---	---	Fatty Acid Synthesis
208429_x_at	HNF4A	0.08	-0.207	B	transcription /// regulation of transcription, DNA-dependent /// regulation of transcription from Pol II promoter /// lipid metabolism /// blood coagulation	transcription factor activity /// RNA polymerase II transcription factor activity /// steroid hormone receptor activity /// ligand-dependent nuclear receptor activity /// steroid binding	nucleus	Nuclear Receptors
236067_at	MBNL2	-0.265	-0.207	L	---	nucleic acid binding	---	---
230140_at	PTPN9	0.074	-0.207	T	transport/// protein amino acid dephosphorylation	non-membrane spanning protein tyrosine phosphatase activity /// transporter activity /// hydrolase activity	intracellular	---
218503_at	KIAA1797	-0.297	-0.207	T	mitotic chromosome condensation	---	---	---
218773_s_at	MSRB2	-0.39	-0.207	T	protein repair	protein-methionine-R-oxide reductase activity /// transcription factor activity /// zinc ion binding /// oxidoreductase activity	mitochondrion	---
1553258_at	FLJ30679	0.004	-0.206	B	proteolysis and peptidolysis	trypsin activity	---	---
201249_at	SLC2A1	0.043	-0.206	B	carbohydrate transport /// glucose transport	transporter activity /// sugar porter activity /// glucose transporter activity	membrane fraction /// integral to membrane	Metabolism of sugars
1560253_at	LHX9	0.144	-0.206	L	regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	nucleus	---
1559054_a_at	PPP1R7	-0.231	-0.206	L	---	protein phosphatase type 1 regulator activity /// enzyme regulator activity	nucleus /// cytoplasm	---
1556618_at	ELK4	-0.156	-0.206	T	regulation of transcription, DNA dependent/// transcription from RNA polymerase II promoter	protein binding/// transcription cofactor activity	nucleus	MAPK signaling pathway
218014_at	PCNT1	-0.385	-0.206	T	---	porin activity	integral to membrane /// outer membrane	---

No.		Value(s): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
223596_at	SLC12A6	0.219	-0.205	B	Chloride transport/// regulation of blood pressure/// circulation/// cell proliferation/// regulation of cell cycle/// metal ion transport/// regulation of cellular process/// transport/// carboxylic acid transport/// monovalent inorganic cation transport/// physiological process/// amino acid transport/// amine/polyamine transport/// homeostasis/// ion homeostasis/// cellular physiological process/// cation transport/// inorganic anion transport/// cell growth and/or maintenance/// ion transport/// organic acid transport/// anion transport/// cell homeostasis/// cell ion homeostasis/// cell cycle/// potassium ion transport/// regulation of physiological process/// regulation of biological process/// regulation of cell volume/// organismal physiological process/// sodium ion	Porter activity/// symporter activity/// amine/polyamine transporter activity/// organic acid transporter activity/// polyamine transporter activity/// amino acid transporter activity/// electrochemical potential-driven transporter activity/// carboxylic acid transporter activity/// cation:chloride symporter activity/// anion:cation symporter activity/// carrier activity/// potassium:chloride symporter activity/// transporter activity	---	---
1552334_at	HRIHFB2122	-0.147	-0.205	L	regulation of transcription, DNA-dependent actin modification	transcription factor activity GTP-Rho binding/// actin binding/// myosin II binding	nucleus actin cytoskeleton/// nucleus	---
210536_s_at	SPAM1	-0.053	-0.205	T	carbohydrate metabolism /// carbohydrate metabolism /// cell adhesion /// binding of sperm to zona pellucida /// fusion of sperm to egg plasma membrane	hyaluronoglucosaminidase activity /// protein binding /// hydrolase activity, acting on glycosyl bonds	plasma membrane	---
235727_at	BTBD5	-0.561	-0.205	T	---	protein binding	---	---
239441_at	LOC284323	-0.278	-0.204	L	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
209591_s_at	BMP7	0.162	-0.204	L	skeletal development /// growth	cytokine activity /// growth factor activity	---	cytokine-cytokine receptor interaction
206277_at	P2RY2	0.254	-0.204	L	cell ion homeostasis /// G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	rhodopsin-like receptor activity /// receptor activity /// purinergic nucleotide receptor activity, G-protein coupled	integral to plasma membrane	Neuroactive ligand-receptor interaction
230153_at	NEK9	-0.338	-0.203	L	cell cycle/// cell division/// protein amino acid phosphorylation	ATP binding/// magnesium ion binding/// transferase activity/// protein serine/threonine kinase activity	---	---
206600_s_at	SLC16A5	-0.035	-0.203	T	transport /// organic anion transport /// monocarboxylic acid transport	transporter activity /// symporter activity /// monocarboxylate porter activity	membrane fraction /// integral to plasma membrane	---
241506_at	LPHN3	-0.089	-0.202	B	neuropeptide signaling pathway	G-protein coupled receptor activity /// sugar binding /// latrotoxin receptor activity	integral to membrane	GPCRDB Class B Secretin-like
1553243_at	ITIH5	-0.313	-0.202	T	hyaluronan metabolism	serine-type endopeptidase inhibitor activity	---	---
1561181_at	ARID5B	-0.168	-0.202	T	transcription /// regulation of transcription, DNA-dependent	DNA binding	nucleus	---
230583_s_at	ZNF75	0.032	-0.202	T	transcription /// regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
207865_s_at	BMP8B	-0.014	-0.202	T	skeletal development /// cell differentiation	cytokine activity /// growth factor activity	extracellular region	TGF-beta signaling pathway /// Hedgehog signaling pathway

No.			(log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
213539_at	CD3D		0.052	-0.201	B	protein complex assembly /// cell surface receptor linked signal transduction /// T-cell activation /// positive thymic T-cell selection	transmembrane receptor activity /// protein binding /// protein heterodimerization activity	cytoplasm /// integral to membrane /// T-cell receptor complex	---
219998_at	ZNF589		0.231	-0.201	B	regulation of transcription, DNA-dependent	nucleic acid binding /// DNA binding /// zinc ion binding	nucleus	---
239057_at	LMOD2		0.066	-0.201	B	---	tropomyosin binding	cytoskeleton	---
209590_at	BMP7		-0.274	-0.201	L	skeletal development /// growth	cytokine activity /// growth factor activity	---	---
225261_x_at	TH1L		-0.312	-0.201	T	transcription /// regulation of transcription, DNA-dependent /// negative regulation of transcription	---	nucleus	Transcription, Gene Expression, Formation of NELF
38703_at	DNPEP		-0.277	-0.201	T	proteolysis and peptidolysis /// peptide metabolism	aminopeptidase I activity /// metallopeptidase activity	vacuole	---
206733_at	TULP2		0.099	-0.2	B	visual perception	---	---	---
242561_at	IPO9		-0.018	-0.2	B	protein-nucleus import, docking /// protein transport	binding /// protein transporter activity	nucleus /// nuclear pore /// cytoplasm	---
209203_s_at	ARL4A		-0.201	-0.2	L	small GTPase mediated signal transduction	GTPase activity /// GTP binding	nucleus	---
204879_at	T1A-2		0.102	-0.2	L	---	---	integral to plasma membrane /// integral to membrane	---
1555653_at	HNRPA3		0.26	-0.2	L	---	RNA binding	ribonucleoprotein complex /// nucleus	mRNA processing
217747_s_at	RPS9		-0.365	-0.2	T	protein biosynthesis	RNA binding /// structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukaryota)	Ribosomal Proteins
213192_at	THAP3		-0.259	-0.2	T	---	nucleic acid binding /// DNA binding	---	---
215346_at	CD40		-0.804	-0.199	B	protein complex assembly /// apoptosis /// inflammatory response /// immune response /// signal transduction /// development /// antimicrobial humoral response (sensu Vertebrata) /// platelet activation /// B-cell proliferation /// positive regulation of I-kappaB kinase/NF-kappaB cascade	transmembrane receptor activity	integral to plasma membrane /// membrane	Cytokine-cytokine receptor interaction
213516_at	AKAP13		-0.072	-0.199	B	intracellular signaling cascade	cAMP-dependent protein kinase activity /// signal transducer activity /// receptor activity /// Rho guanyl-nucleotide exchange factor activity /// kinase activity	membrane fraction	---
202846_s_at	PIGC		-0.362	-0.199	L	GPI anchor biosynthesis	transferase activity, transferring glycosyl groups /// phosphatidylinositol N-acetylglucosaminyltransferase activity	endoplasmic reticulum membrane /// integral to membrane	glycosylphosphatidylinositol(gpi)-anchor biosynthesis
239358_at	FDFT1		0.248	-0.199	L	steroid biosynthesis /// cholesterol biosynthesis /// isoprenoid biosynthesis	magnesium ion binding /// farnesyl-diphosphate farnesyltransferase activity /// oxidoreductase activity /// transferase activity	endoplasmic reticulum /// integral to membrane	Cholesterol biosynthesis /// Biosynthesis of steroids /// Terpenoid biosynthesis
209724_s_at	ZFP161		-0.234	-0.199	L	negative regulation of transcription from Pol II promoter /// regulation of transcription, DNA-dependent	DNA binding /// protein binding /// zinc ion binding	nucleus	---
217242_at	ZNF154		-0.123	-0.199	L	regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	nucleus	---
222300_at	CAPZA1		-0.284	-0.199	L	protein complex assembly /// cell motility /// actin cytoskeleton organization and	actin binding	F-actin capping protein complex	---

No.		Value): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
218496_at	RNASEH1	0.006	-0.198	B	RNA catabolism	magnesium ion binding /// RNA binding /// endonuclease activity /// ribonuclease H activity /// ribonuclease activity /// hydrolase activity	---	---
204595_s_at	STC1	0.018	-0.198	B	calcium ion homeostasis /// cell surface receptor linked signal transduction /// cell-cell signaling /// response to nutrients	hormone activity	extracellular region	---
231394_at	PCDHB3	0.302	-0.198	L	cell adhesion /// homophilic cell adhesion /// synaptic transmission /// synaptogenesis /// calcium-dependent cell cell adhesion	calcium ion binding /// protein binding	integral to plasma membrane	---
233429_at	FLJ23577	0.149	-0.198	L	---	protein dimerization activity	---	---
210037_s_at	NOS2A	-0.263	-0.198	T	electron transport /// superoxide metabolism /// nitric oxide biosynthesis /// inflammatory response /// defense response to bacteria /// positive regulation of cytotoxic T-cell differentiation	nitric-oxide synthase activity /// electron transporter activity /// calcium ion binding /// calmodulin binding /// FMN binding /// oxidoreductase activity /// heme binding	cytosol	Arginine and proline metabolism
206118_at	STAT4	0.331	-0.197	L	regulation of transcription from Pol II promoter /// intracellular signaling cascade /// JAK-STAT cascade	transcription factor activity /// signal transducer activity /// calcium ion binding	nucleus	JAK-Stat signaling pathway
238773_at	FLJ33979	0.035	-0.197	L	---	---	---	---
221708_s_at	SMAP-1	-0.312	-0.197	T	---	methyltransferase activity	---	---
50965_at	RAB26	0.069	-0.195	B	small GTPase mediated signal transduction	GTP binding	---	---
218129_s_at	NFYB	-0.463	-0.196	T	transcription /// regulation of transcription, DNA-dependent	transcription factor activity	nucleus /// CCAAT-binding factor complex	---
209434_s_at	PPAT	0.12	-0.195	B	purine nucleotide biosynthesis /// glutamine metabolism /// metabolism /// purine base biosynthesis /// nucleoside metabolism	magnesium ion binding /// amidophosphoribosyltransferase activity /// transferase activity, transferring glycosyl groups	---	Purine metabolism /// Glutamate metabolism
201571_s_at	DCTD	0.348	-0.195	L	pyrimidine nucleotide metabolism /// nucleotide biosynthesis	dCMP deaminase activity /// zinc ion binding /// hydrolase activity	---	Pyrimidine metabolism /// Type II secretion system
210536_s_at	SPAM1	-0.114	-0.195	L	carbohydrate metabolism /// cell adhesion /// binding of sperm to zona pellucida /// fusion of sperm to egg plasma membrane	hyaluronoglucosaminidase activity /// protein binding /// hydrolase activity, acting on glycosyl bonds	plasma membrane	---
242157_at	CHD9	0.094	-0.195	L	---	DNA binding /// helicase activity /// ATP binding	nucleus /// integral to membrane	---
222889_at	DCLRE1B	0.035	-0.195	L	---	hydrolase activity	---	---
1552502_s_at	RHBDL2	-0.366	-0.195	L	---	serine-type endopeptidase activity /// peptidase activity	integral to membrane	---
203536_s_at	WDR39	-0.393	-0.195	T	regulation of transcription from RNA polymerase II promoter /// positive regulation of cell proliferation	---	nucleus	---
226871_s_at	APG4D	-0.406	-0.195	T	proteolysis and peptidolysis /// autophagic vacuole formation /// protein-membrane targeting /// protein-vacuolar targeting /// autophagy /// protein transport	cysteine-type endopeptidase activity /// protein binding /// microtubule binding	cytosol /// microtubule associated complex	---
221016_s_at	TCF7L1	0.187	-0.194	L	establishment and/or maintenance of chromatin architecture /// regulation of transcription, DNA-dependent /// regulation of Wnt receptor signaling	transcription factor activity	nucleus	Wnt signaling pathway

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
231684_at	ANGPTL3	0.136	-0.194	T	triacylglycerol metabolism /// cell-matrix adhesion /// integrin-mediated signaling pathway /// lipid catabolism /// positive regulation of cell migration /// positive regulation of angiogenesis /// positive regulation of lipid metabolism	enzyme inhibitor activity /// integrin binding	extracellular region	---
213742_at	SFRS11	-0.914	-0.194	T	nuclear mRNA splicing, via spliceosome /// RNA splicing	nucleotide binding /// RNA binding	nucleus	mRNA Processing, Transcription, Gene Expression
209680_s_at	KIFC1	-0.485	-0.194	T	mitotic sister chromatid segregation /// microtubule-based movement	microtubule motor activity /// ATP binding	microtubule associated complex	---
1560225_at	CNR1	-0.091	-0.193	B	Behavior/// cyclic-nucleotide-mediated signaling/// intracellular signaling cascade/// cell surface receptor linked signal transduction/// G-protein coupled receptor protein signaling pathway/// signal transduction/// cell communicatin	Cannabinoid receptor activity/// signal transducer activity/// receptor activity/// G-protein coupled receptor activity/// rhodopsin-like receptor activity	---	Neuroactive ligand-receptor interaction
1565306_a_at	SLC8A1	0.195	-0.192	L	transport /// sodium ion transport /// calcium ion transport /// muscle contraction /// cell communication	calcium:sodium antiporter activity /// calmodulin binding /// sodium ion transporter activity /// calcium ion transporter activity /// antiporter activity	integral to plasma membrane /// membrane	Calcium regulation in cardiac cells /// Smooth muscle contraction
218707_at	ZNF444	-0.482	-0.192	T	transcription /// regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	nucleus	---
216699_s_at	KLK1	-0.254	-0.192	T	proteolysis and peptidolysis	chymotrypsin activity /// tissue kallikrein activity /// trypsin activity /// peptidase activity	---	---
224695_at	C2orf29	-0.339	-0.192	T	cell proliferation	---	---	---
206203_at	RCVI	0.224	-0.191	L	signal transduction /// visual perception	calcium ion binding /// calcium sensitive guanylate cyclase activator activity	---	---
213966_at	HMG20B	-0.223	-0.191	T	transcription /// regulation of transcription, DNA-dependent /// regulation of transcription, DNA-dependent /// cell cycle /// chromatin modification	DNA binding /// transcription factor activity	chromatin /// nucleus	---
202600_s_at	NRIP1	-1.055	-0.191	T	transcription /// regulation of transcription, DNA-dependent	transcription coactivator activity	nucleus	Ovarian Infertility Genes
206237_s_at	NRG1	0.081	-0.191	T	neurogenesis /// embryonic development /// cell differentiation	receptor binding /// growth factor activity /// growth factor activity /// transmembrane receptor protein tyrosine kinase activator activity /// receptor tyrosine kinase binding	extracellular region /// membrane /// integral to membrane	---
202750_s_at	TFIP11	-0.37	-0.191	T	ossification /// cell differentiation /// extracellular matrix organization and biogenesis /// secretory pathway	nucleic acid binding /// protein binding	intracellular /// nucleus	---
231668_x_at	IGHG4	-0.244	-0.191	T	immune response	antigen binding	membrane fraction	---
241473_at	SULF1	-0.15	-0.191	T	apoptosis /// metabolism /// heparan sulfate proteoglycan metabolism	arylsulfatase activity /// hydrolase activity	extracellular space /// endoplasmic reticulum /// Golgi apparatus /// cell surface	---
1555437_at	KIAA1970	-0.086	-0.19	B	protein biosynthesis /// glutamyl-tRNA aminoacylation	glutamate-tRNA ligase activity /// ATP binding /// ligase activity	cytoplasm /// aminoacyl-tRNA synthetase multienzyme complex	---
221940_at	RPUSD2	0.042	-0.19	B	RNA processing	RNA binding /// pseudouridylate synthase activity /// pseudouridine synthase activity	---	---
1552649_a_at	RFFL	0.059	-0.19	B	protein ubiquitination	DNA binding /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
				L	development	DNA binding /// zinc ion binding	nucleus	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
1565080_at	SRC	0.188	-0.19	L	protein amino acid phosphorylation /// signal complex formation /// protein kinase cascade	protein-tyrosine kinase activity /// SH3/SH2 adaptor protein activity /// protein binding /// ATP binding /// transferase activity	---	Integrin-mediated cell adhesion
244870_at	TES	0.14	-0.19	L	---	zinc ion binding	---	---
221601_s_at	TOSO	-0.231	-0.189	B	anti-apoptosis /// cellular defense response	---	---	---
1555626_a_at	SLAMF1	-0.161	-0.189	L	positive regulation of cell proliferation /// antimicrobial humoral response (sensu Vertebrata) /// lymphocyte activation	antigen binding /// transmembrane receptor activity	cell surface /// integral to membrane	---
223109_at	TRUB2	-0.21	-0.188	B	RNA processing /// telomerase-dependent telomere maintenance	RNA binding /// pseudouridylate synthase activity	chromosome, telomeric region	---
236345_at	TBXAS1	-0.288	-0.188	L	prostaglandin biosynthesis /// electron transport /// blood coagulation	monooxygenase activity /// thromboxane-A synthase activity /// isomerase activity	integral to membrane	Eicosanoid synthesis /// Prostaglandin synthesis regulation /// Prostaglandin and leukotriene metabolism
1555993_at	CACNA1D	0.051	-0.188	T	cation transport /// calcium ion transport	calcium ion binding /// dihydropyridine-sensitive calcium channel activity	voltage-gated calcium channel complex /// membrane /// integral to membrane	Calcium regulation in cardiac cells
209782_s_at	DBP	-0.373	-0.188	T	transcription /// regulation of transcription from RNA polymerase II promoter /// rhythmic process	DNA binding /// RNA polymerase II transcription factor activity	nucleus	---
210632_s_at	SGCA	-0.164	-0.188	T	muscle development/// muscle contraction	calcium ion binding /// protein binding	cytoskeleton /// dystrophin-associated glycoprotein complex /// sarcoglycan complex /// integral to membrane	---
238458_at	EFHA2	-0.036	-0.188	T	---	calcium ion binding	---	---
208339_at	XKRY /// XKRY2	-0.076	-0.187	B	fertilization (sensu Metazoa)	---	integral to membrane	---
207407_x_at	CYP4A11	0.29	-0.187	L	electron transport /// fatty acid metabolism	fatty acid (omega-1)-hydroxylase activity /// alkane 1-monooxygenase activity	endoplasmic reticulum /// microsome /// membrane	Fatty acid metabolism
204004_at	PAWR	-0.294	-0.187	L	negative regulation of transcription from Pol II promoter /// apoptosis /// negative regulation of cell proliferation	transcription corepressor activity	nucleus /// cytoplasm	---
202541_at	SCYE1	-0.342	-0.187	L	protein biosynthesis /// tRNA aminoacylation for protein translation /// chemotaxis /// inflammatory response /// signal transduction /// cell-cell signaling	tRNA binding /// cytokine activity	extracellular space	---
216256_at	GRM8	-0.175	-0.187	T	signal transduction /// G-protein coupled receptor protein signaling pathway /// negative regulation of adenylate cyclase activity /// synaptic transmission /// visual perception /// perception of smell	receptor activity /// metabotropic glutamate, GABA-B-like receptor activity /// metabotropic glutamate, GABA-B-like receptor activity	integral to plasma membrane /// membrane	neuroactive ligand-receptor interaction
205013_s_at	ADORA2A	-0.384	-0.187	T	cAMP biosynthesis/// neurotransmitter transport/// phagocytosis /// apoptosis /// inflammatory response /// cellular defense response /// signal transduction /// G-protein coupled receptor protein signaling pathway /// G-protein signaling, coupled to cAMP nucleotide second messenger /// adenylate cyclase activation /// cell-cell signaling /// central nervous system development /// blood coagulation /// sensory perception /// circulation	rhodopsin-like receptor activity /// A2A adenosine receptor activity, G-protein coupled /// A3 adenosine receptor activity, G-protein coupled /// receptor activity /// gastric inhibitory peptide receptor activity	membrane fraction /// plasma membrane /// integral to plasma membrane /// integral to membrane	Neuroactive ligand-receptor interaction/// calcium signaling pathway

No.		Values):	(log2 Values):					
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
213980_s_at	CTBP1	-0.546	-0.197	T	protein amino acid phosphorylation /// L-serine biosynthesis /// negative regulation of cell proliferation /// viral genome replication	protein C-terminus binding /// oxidoreductase activity /// oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	nucleus /// Golgi apparatus	Notch signaling pathway /// Wnt signaling pathway
229321_s_at	BID	0.029	-0.186	L	induction of apoptosis via death domain receptors /// apoptotic mitochondrial changes /// positive regulation of apoptosis	death receptor binding	membrane fraction /// cytoplasm /// Apoptosis mitochondrion /// cytosol	---
214783_s_at	ANXA11	-0.392	-0.186	T	immune response	calcium ion binding /// protein binding /// calcium-dependent phospholipid binding	nuclear membrane /// nucleoplasm /// cytoplasm	---
218216_x_at	ARL6IP4	-0.267	-0.186	T	RNA splicing	---	nucleus /// nucleus	---
1561236_at	UXS1	-0.084	-0.185	L	nucleotide-sugar metabolism	catalytic activity	---	---
207317_s_at	CASQ2	0.19	-0.185	L	striated muscle contraction /// heart development /// muscle development	calcium ion binding	smooth endoplasmic reticulum	Calcium regulation in cardiac cells
239794_at	IARS	0.258	-0.185	L	protein biosynthesis /// isoleucyl-tRNA aminoacylation	isoleucine-tRNA ligase activity /// ATP binding /// ligase activity	soluble fraction /// cytoplasm	Valine, leucine and isoleucine biosynthesis /// Aminoacyl-tRNA biosynthesis
226495_at	KIAA1271	-0.192	-0.185	T	positive regulation of I-kappa B kinase/NF-kappa B cascade	signal transducer activity	---	---
224601_at	SIAT7B	0.097	-0.185	T	protein amino acid glycosylation	sialyltransferase activity	Golgi apparatus /// membrane /// integral to membrane	Blood group glycolipid biosynthesis-neolactoseries /// Ganglioside biosynthesis /// Globoside metabolism
209983_x_at	CD59	0.241	-0.184	L	immune response /// cell surface receptor linked signal transduction /// blood coagulation	---	membrane fraction /// plasma membrane	complement and coagulation cascades
223919_at	PS3AIP1	0.068	-0.184	L	apoptosis	---	mitochondrion	---
210058_at	MAPK13	-0.032	-0.184	L	regulation of translation /// protein amino acid phosphorylation /// response to stress /// cell cycle /// protein kinase cascade	protein serine/threonine kinase activity /// MAP kinase activity /// protein-tyrosine kinase activity /// ATP binding /// MP kinase activity /// transferase activity	---	MAPK signaling pathway /// toll-like receptor signaling pathway /// Parkinson's disease
208544_at	ADRA2B	-0.244	-0.184	T	signal transduction /// G-protein coupled receptor protein signaling pathway /// cell-cell signaling	rhodopsin-like receptor activity /// receptor activity /// adrenoceptor activity /// alpha2-adrenergic receptor activity	plasma membrane /// integral to plasma membrane	neuroactive ligand-receptor interaction
232012_at	CAPN1	-0.052	-0.184	T	proteolysis and peptidolysis /// positive regulation of cell proliferation	calpain activity /// calcium ion binding	intracellular	Integrin-mediated cell adhesion
205434_s_at	AAK1	-0.544	-0.184	T	protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	---	---
1556346_at	COTL1	-0.071	-0.184	T	---	actin binding /// actin binding /// enzyme binding	intracellular /// cytoskeleton	---
223412_at	KBTBD7	-0.23	-0.184	T	---	protein binding	---	---
203686_at	MPG	-0.376	-0.183	T	base-excision repair /// DNA dealkylation	damaged DNA binding /// alkylbase DNA N-glycosylase activity /// hydrolase activity	nucleoplasm	DNA Repair
213152_s_at	SRP46	-0.13	-0.182	B	nuclear mRNA splicing, via spliceosome	nucleic acid binding	---	---
210797_s_at	OASL	0.077	-0.182	B	protein modification /// immune response	DNA binding /// double-stranded RNA binding /// ATP binding /// transferase activity /// thyroid hormone receptor binding	nucleolus /// cytoplasm	Porphyrin and chlorophyll metabolism /// Ubiquinone biosynthesis
209828_s_at	IL16	0.087	-0.182	L	chemotaxis /// immune response	cytokine activity /// protein binding	extracellular space	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
212703_at	TLN2	-0.157	-0.182	T	cell adhesion	actin binding /// structural molecule activity /// protein binding	actin cytoskeleton /// synapse	focal adhesion
45653_at	KCTD13	0.155	-0.181	L	potassium ion transport	voltage-gated potassium channel activity /// protein binding	nucleus /// voltage-gated potassium channel complex /// membrane	---
224137_at	CACNG7	-0.233	-0.181	T	ion transport /// calcium ion transport	voltage-gated calcium channel activity	voltage-gated calcium channel complex /// membrane /// integral to membrane	---
1555500_s_at	SLC2A4RG	0.18	-0.181	T	transcription /// regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	nucleus	---
1562282_at	ZNF568	-0.031	-0.181	T	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
1562442_a_at	SSBP1	-0.194	-0.181	T	DNA replication	single-stranded DNA binding	mitochondrion	---
225552_x_at	AKIP	-0.474	-0.181	T	negative regulation of mitosis	protein binding	nucleus	---
206121_at	AMPD1	0.526	-0.18	L	nucleotide metabolism /// purine ribonucleoside monophosphate biosynthesis	AMP deaminase activity /// hydrolase activity	---	Purine metabolism
243498_at	GABPA	-0.083	-0.18	L	regulation of transcription, DNA-dependent /// transcription from Pol II promoter	transcription factor activity /// RNA polymerase II transcription factor activity /// transcription coactivator activity /// protein binding	nucleus	Smooth muscle contraction
213681_at	CYHR1	-0.35	-0.18	T	---	zinc ion binding	---	---
1563856_at	INSAF	-0.073	-0.179	B	regulation of transcription, DNA-dependent	transcriptional activator activity	insulin control element activator complex	---
214358_at	ACACA	-0.347	-0.179	L	fatty acid biosynthesis /// metabolism	acetyl-CoA carboxylase activity /// biotin carboxylase activity /// ATP binding /// biotin binding /// ligase activity	biotin carboxylase complex	Fatty acid biosynthesis (path 1) /// Tetracycline biosynthesis /// Pyruvate metabolism /// Propanoate metabolism
235249_at	RDH13	-0.345	-0.179	L	metabolism	oxidoreductase activity	---	---
226534_at	KITLG	-0.074	-0.179	L	cell adhesion /// signal transduction /// cell proliferation /// organogenesis	stem cell factor receptor binding /// protein binding /// growth factor activity	membrane /// integral to membrane	cytokine-cytokine receptor interaction
205600_x_at	HOXB5	0.105	-0.179	L	regulation of transcription, DNA-dependent /// morphogenesis	transcription factor activity	nucleus	---
221113_s_at	WNT16	0.066	-0.179	L	frizzled-2 signaling pathway /// cell-cell signaling /// development	signal transducer activity /// extracellular matrix structural constituent	extracellular region	Wnt signaling pathway
207364_at	CXorf2	0.177	-0.179	L	---	---	integral to membrane	---
209740_s_at	PNPLA4	-0.041	-0.179	L	---	catalytic activity /// nutrient reservoir activity	---	---
207561_s_at	ACCN3	-0.128	-0.179	T	ion transport /// sodium ion transport /// signal transduction /// sensory perception	ion channel activity /// amiloride-sensitive sodium channel activity	plasma membrane /// integral to plasma membrane /// membrane /// integral to membrane	---
1554921_a_at	SCEL	-0.014	-0.178	B	epidermis development	zinc ion binding	cytoplasm	---
1560020_at	DNAJC13	-0.292	-0.178	L	protein folding	heat shock protein binding /// unfolded protein binding	---	---
241753_at	DISC1	0.056	-0.178	L	DNA methylation	DNA binding /// N-methyltransferase activity	---	---
40524_at	PTPN21	-0.062	-0.178	T	protein amino acid dephosphorylation	protein tyrosine phosphatase activity /// structural molecule activity /// binding /// hydrolase activity	cytoskeleton	---
227483_s_at	KRTAP5-11	-0.276	-0.178	T	---	---	keratin filament	---
1570357_at	STX8	0.012	-0.177	L	transport	---	endoplasmic reticulum /// integral to plasma membrane	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
242320_at	FOXO3A	0.082	-0.177	L	regulation of transcription, DNA-dependent /// transcription from Pol II promoter /// apoptosis /// induction of apoptosis	transcription factor activity	nucleus /// cytoplasm	---
1565082_x_at	SRC	0.185	-0.177	L	protein amino acid phosphorylation /// signal complex formation /// protein kinase cascade	protein-tyrosine kinase activity /// SH3/SH2 adaptor protein activity /// protein binding /// ATP binding /// transferase activity	---	Integrin-mediated cell adhesion
231621_at	MPZL1	-0.016	-0.177	T	transmembrane receptor protein tyrosine kinase signaling pathway /// cell-cell signaling	structural molecule activity /// protein binding	integral to plasma membrane /// membrane	---
225006_x_at	TH1L	-0.32	-0.177	T	transcription /// regulation of transcription, DNA-dependent /// negative regulation of transcription	---	nucleus	Transcription, Gene Expression, Formation of NELF
207106_s_at	LTK	-0.283	-0.177	T	protein amino acid phosphorylation /// protein amino acid phosphorylation /// signal transduction /// transmembrane receptor protein tyrosine kinase signaling pathway	protein serine/threonine kinase activity /// transmembrane receptor protein tyrosine kinase activity /// transmembrane receptor protein tyrosine kinase activity /// receptor activity /// ATP binding /// transferase activity	soluble fraction /// plasma membrane /// integral to plasma membrane /// membrane	---
203736_s_at	PPFIBP1	-0.034	-0.177	T	cell adhesion	protein binding	plasma membrane	---
221614_s_at	RPH3AL	-0.262	-0.176	B	intracellular protein transport /// exocytosis	protein binding /// cytoskeletal protein binding /// zinc ion binding /// Rab interactor activity	cytoplasm	---
203198_at	CDK9	0.361	-0.175	B	regulation of cell cycle /// transcription initiation from Pol II promoter /// RNA elongation from Pol II promoter /// protein amino acid phosphorylation /// cell proliferation	cyclin-dependent protein kinase activity /// protein binding /// ATP binding /// transferase activity	nucleus /// transcription elongation factor complex	Sphingoglycolipid metabolism/// inositol phosphate metabolism/// starch and sucrose metabolism/// porphyrin and chlorophyll metabolism/// benzoate degradation via CoA ligation/// nicotinate and nicotinamide metabolism
1553685_s_at	SP1	0.169	-0.175	L	regulation of transcription, DNA-dependent	DNA binding /// RNA polymerase II transcription factor activity /// zinc ion binding /// transcriptional activator activity	nucleus	TGF-Beta signaling pathway
229529_at	TCF21	0.137	-0.175	L	regulation of transcription, DNA-dependent /// mesoderm development	DNA binding /// RNA polymerase II transcription factor activity	nucleus	---
243165_at	BTF3	0.146	-0.175	L	regulation of transcription, DNA-dependent /// transcription from Pol II promoter	RNA polymerase II transcription factor activity	nucleus	---
223382_s_at	ZNRF1	-0.385	-0.175	T	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---

No.		Values):	(log2 Values):					
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
1556341_s_at	MAPK12	-0.024	-0.174	B	Cell proliferation/// macromolecule metabolism/// regulation of cell cycle/// negative regulation of cell cycle/// metabolism/// mapkkk cascade/// DNA damage induced protein phosphorylation/// phosphorus metabolism/// intracellular signaling cascade/// physiological process/// protein kinase cascade/// protein amino acid phosphorylation/// muscle development/// response to DNA damage stimulus/// phosphate metabolism/// cell cycle arrest/// phosphorylation/// protein metabolism/// cellular physiological process/// cell growth and/or maintenance/// organogenesis/// morphogenesis/// response to stimulus/// protein modification/// myoblast differentiation/// response to stress/// signal transduction/// cell communication/// development/// cell cycle/// cellular process/// response to endogenous stimulus/// cell differentiation	Kinase activity/// signal transducer activity/// purine nucleotide binding/// MAP kinase activity/// camp-dependent protein kinase activity/// binding/// nucleotide binding/// adenyl nucleotide binding/// transferase activity/// magnesium ion binding/// metal ion binding/// ion binding/// sap kinase activity/// protein kinase activity/// protein kinase ck2 activity/// catalytic activity/// phosphotransferase activity/// alcohol group as acceptor/// ATP binding/// protein serine/threonine kinase activity/// transferase activity, transferring phosphorus-containing groups	---	Parkinson's disease/// focal adhesion/// MAPK signaling pathway/// sphingoglycolipid metabolism/// inositol phosphate metabolism/// starch and sucrose metabolism/// cadherin-mediated cell adhesion/// integrin-mediated cell adhesion/// porphyrin and chlorophyll metabolism/// Toll-like receptor signaling pathway/// benzoate degradation via CoA ligation/// nicotinate and nicotinamide metabolism
210047_at	SLC11A2	-0.249	-0.174	L	transport /// iron ion transport	transporter activity /// iron ion transporter activity	integral to plasma membrane	---
215337_at	THRAP4	-0.034	-0.174	T	transcription /// regulation of transcription, DNA-dependent /// transcription initiation from RNA polymerase II promoter /// androgen receptor signaling pathway	transcription cofactor activity /// receptor activity /// ATP binding /// RNA polymerase II transcription mediator activity /// transcriptional activator activity /// ligand-dependent nuclear receptor transcription coactivator activity /// vitamin D receptor binding /// thyroid hormone receptor binding	mediator complex /// nucleus	---
203798_s_at	VSNL1	-0.218	-0.174	T	---	calcium ion binding	---	---
242046_at	ACMSD	0.082	-0.173	L	metabolism /// quinolinate metabolism	aminocarboxymuconate-semialdehyde decarboxylase activity /// lyase activity	cytosol	Tryptophan metabolism
220559_at	EN1	0.029	-0.173	L	skeletal development /// regulation of transcription, DNA-dependent /// morphogenesis	transcription factor activity	nucleus	---
242657_at	IGFBP4	-0.047	-0.173	T	skeletal development /// regulation of cell growth /// DNA metabolism /// signal transduction /// cell proliferation	insulin-like growth factor binding	extracellular region	Smooth muscle contraction
1552804_a_at	TIRAP	-0.417	-0.173	T	inflammatory response	transmembrane receptor activity	membrane	Toll-like receptor signaling pathway
219244_s_at	MRPL46	-0.377	-0.173	T	---	structural constituent of ribosome	mitochondrion /// ribonucleoprotein complex	---
202049_s_at	ZNF262	-0.432	-0.172	L	development	DNA binding /// zinc ion binding	nucleus	---
244602_at	KIAA1340	0.193	-0.172	T	---	protein binding	---	---
225298_at	MR-1	-0.306	-0.172	T	---	hydrolase activity	---	---
224900_at	ANKFY1	-0.176	-0.171	B	endocytosis	protein binding /// zinc ion binding	endosome membrane /// membrane	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
218807_at	VAV3	-0.002	-0.171	B	intracellular signaling cascade /// small GTPase mediated signal transduction	SH3/SH2 adaptor protein activity /// guanyl-nucleotide exchange factor activity /// GTPase activator activity /// diacylglycerol binding	---	Integrin-mediated cell adhesion
1552314_a_at	EYA3	-0.221	-0.171	L	regulation of transcription, DNA-dependent /// development /// visual perception /// metabolism /// morphogenesis	magnesium ion binding /// catalytic activity /// phosphoprotein phosphatase activity /// protein tyrosine phosphatase activity /// hydrolase activity	nucleus	---
219548_at	ZNF16	0.22	-0.171	L	---	nucleic acid binding /// zinc ion binding	nucleus	---
208714_at	NDUFV1	-0.449	-0.171	T	electron transport /// mitochondrial electron transport, NADH to ubiquinone	NADH dehydrogenase activity /// iron ion binding /// NADH dehydrogenase (ubiquinone) activity /// FMN binding /// NAD binding	membrane fraction /// mitochondrion /// mitochondrial inner membrane	Electron Transport Chain /// Oxidative phosphorylation
234746_at	IL1RAPL1	-0.285	-0.171	T	signal transduction /// learning and/or memory	transmembrane receptor activity	membrane /// integral to membrane	---
217465_at	NCKAP1	0.046	-0.171	T	central nervous system development/// apoptosis	---	integral to membrane	regulation of actin cytoskeleton
209464_at	AURKB	-0.31	-0.171	T	protein amino acid phosphorylation /// cell cycle	protein serine/threonine kinase activity /// ATP binding /// transferase activity	---	Phosphatidylinositol signaling system
243658_at	FDFT1	0.02	-0.17	B	steroid biosynthesis /// cholesterol biosynthesis /// isoprenoid biosynthesis /// biosynthesis	magnesium ion binding /// farnesyl-diphosphate farnesyltransferase activity /// oxidoreductase activity /// transferase activity	endoplasmic reticulum /// integral to membrane	Cholesterol Biosynthesis /// Biosynthesis of steroids /// Terpenoid biosynthesis
238546_at	SLC8A1	-0.006	-0.17	L	transport /// sodium ion transport /// calcium ion transport /// muscle contraction /// cell communication	calcium:sodium antiporter activity /// calmodulin binding /// sodium ion transporter activity /// calcium ion transporter activity /// antiporter activity	integral to plasma membrane /// membrane	Calcium regulation in cardiac cells /// Smooth muscle contraction
209369_at	ANXA3	0.106	-0.17	L	---	calcium ion binding /// calcium-dependent phospholipid binding /// diphosphoinositol-polyphosphate diphosphatase activity /// phospholipase A2 inhibitor activity	cytoplasm	Prostaglandin synthesis regulation
244872_at	RBBP4	-0.304	-0.17	T	DNA replication /// DNA repair /// transcription /// regulation of transcription, DNA-dependent /// cell cycle /// negative regulation of cell proliferation	---	nucleus	---
223790_at	KATNAL1	-0.141	-0.169	B	---	nucleotide binding /// ATP binding /// nucleoside-triphosphatase activity	---	---
1552715_a_at	LGR7	0.023	-0.169	T	signal transduction /// G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity /// receptor activity	membrane /// integral to membrane	neuroactive ligand-receptor interaction
1561767_at	NTNG1	0.039	-0.169	T	neurogenesis /// axonogenesis /// cell differentiation	structural molecule activity /// protein binding	extracellular matrix (sensu Metazoa) /// membrane /// anchored to plasma membrane	---
241857_at	RAET1E	-0.302	-0.169	T	antigen presentation	MHC class I receptor activity/// protein binding	integral to membrane/// plasma membrane/// MHC class I protein complex	---
212168_at	RBM12	-0.449	-0.169	T	---	nucleotide binding /// nucleic acid binding /// RNA binding	nucleus	---

No.		Values): 1x LCPUFA (1.1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (1.3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
223898_s_at	LARS	-0.366	-0.168	L	protein biosynthesis /// RNA aminoacylation for protein translation	tRNA ligase activity /// leucine-tRNA ligase activity /// ATP binding ///	cytoplasm	aminoacyl-tma biosynthesis/// valine, leucine and isoleucine biosynthesis
238220_at	UTX	-0.032	-0.168	L	---	binding	nucleus	---
202942_at	ETFB	-0.544	-0.168	T	electron transport /// transport	electron carrier activity	mitochondrial matrix	---
227538_at	CRSP7	-0.455	-0.168	T	transcription /// regulation of transcription from RNA polymerase II promoter /// transcription initiation from RNA polymerase II promoter /// defense response	transcription coactivator activity /// receptor activity	nucleus	---
240282_at	WDR1	-0.151	-0.168	T	perception of sound	actin binding /// protein binding	cytoskeleton	Hypertrophy model
1552494_at	TBN	-0.04	-0.167	B	---	---	nucleus	---
243322_at	DPYSL3	0.173	-0.167	L	nucleobase, nucleoside, nucleotide and nucleic acid metabolism /// signal transduction /// neurogenesis	dihydropyrimidinase activity /// hydrolase activity	---	---
222317_at	PDE3B	0.127	-0.167	L	signal transduction	3',5'-cyclic-nucleotide phosphodiesterase activity /// cGMP-inhibited cyclic-nucleotide phosphodiesterase activity /// hydrolase activity	membrane	Purine metabolism
238289_at	LASS5	-0.221	-0.167	L	regulation of transcription, DNA-dependent /// lipid biosynthesis	transcription factor activity	nucleus /// endoplasmic reticulum /// integral to membrane	---
211668_s_at	PLAU	0.271	-0.167	L	proteolysis and peptidolysis /// chemotaxis /// signal transduction /// blood coagulation /// negative regulation of blood coagulation	chymotrypsin activity /// trypsin activity /// plasminogen activator activity /// kinase activity /// hydrolase activity	extracellular space	complement and coagulation cascades
212666_at	SMURF1	0.351	-0.167	L	ubiquitin cycle /// ectoderm development /// cell differentiation /// negative regulation of BMP signaling pathway /// protein ubiquitination during ubiquitin-dependent protein catabolism	ubiquitin-protein ligase activity /// ligase activity	intracellular	TGF-Beta signaling pathway
222246_at	TMSB10	-0.01	-0.167	L	cytoskeleton organization and biogenesis	actin binding	cytoskeleton /// cytoplasm	---
225389_at	BTBD6	-0.28	-0.167	L	---	receptor activity /// protein binding	---	---
1553131_a_at	GATA4	-0.166	-0.167	T	transcription /// transcription /// regulation of transcription, DNA-dependent /// transcription from RNA polymerase II promoter /// heart development /// positive regulation of transcription, DNA-dependent /// positive regulation of transcription	DNA binding /// transcription factor activity /// transcription factor activity /// RNA polymerase II transcription factor activity /// protein binding /// zinc ion binding /// transcriptional activator activity	nucleus /// nucleus	---
216566_at	IGLC2	0.024	-0.167	T	immune response	antigen binding	---	---
1552716_at	FLJ23577	0.049	-0.166	B	---	protein dimerization activity	---	---
1557362_at	PHIP	0.392	-0.166	L	insulin receptor signaling pathway	insulin receptor binding /// protein binding	---	---
205106_at	MTCP1	0.111	-0.166	L	regulation of cell cycle /// cell proliferation	---	mitochondrion	---
234574_at	MYO1F	-0.256	-0.166	L	---	microfilament motor activity /// motor activity /// actin binding /// calmodulin binding /// ATP binding	myosin /// unconventional myosin	---
213570_at	EIF4E2	0.158	-0.166	L	translational initiation /// regulation of translation	RNA cap binding /// translation initiation factor activity	cytoplasm	---
230701_x_at	KIF9	-0.126	-0.165	L	microtubule-based movement	microtubule motor activity /// ATP binding	microtubule associated complex	---
228186_s_at	THSD2	0.002	-0.165	T	electron transport	electron transporter activity /// iron ion binding	---	---

No.		Values): 1x LCPUFA (L-1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
229919_at	PCNXL2	-0.037	-0.165	T	---	---	integral to membrane	---
223693_s_at	FLJ10324	-0.169	-0.164	B	signal transduction	motor activity /// protein binding	myosin	---
1554384_at	PADI2	0.122	-0.164	B	protein modification	protein-arginine deiminase activity /// calcium ion binding /// hydrolase activity	---	---
40284_at	FOXA2	-0.369	-0.164	L	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
232188_at	AKAP13	0.008	-0.164	T	intracellular signaling cascade	cAMP-dependent protein kinase activity /// signal transducer activity /// receptor activity /// Rho guanyl-nucleotide exchange factor activity /// kinase activity	membrane fraction	---
208528_x_at	SSX5	0.049	-0.164	T	transcription /// regulation of transcription, DNA-dependent	nucleic acid binding	intracellular	---
1570078_a_at	DOCK5	-0.185	-0.163	B	---	guanyl-nucleotide exchange factor activity /// GTP binding /// GTPase binding	---	---
226518_at	KCTD10	-0.245	-0.163	T	potassium ion transport	ion channel activity /// voltage-gated potassium channel activity /// protein complex /// membrane binding	voltage-gated potassium channel complex /// membrane	---
202846_s_at	PIGC	-0.259	-0.163	T	GPI anchor biosynthesis	transferase activity, transferring glycosyl groups /// phosphatidylinositol N-acetylglucosaminyltransferase activity	endoplasmic reticulum membrane /// integral to membrane	Glycosylphosphatidylinositol(GPI)-anchor biosynthesis
204647_at	HOMER3	-0.347	-0.163	T	protein targeting /// metabotropic glutamate receptor signaling pathway	protein binding	---	---
1553891_at	ZNF393	-0.334	-0.163	T	---	nucleic acid binding /// zinc ion binding	nucleus	---
241819_at	TNFSF8	0.173	-0.162	L	induction of apoptosis /// immune response /// signal transduction /// cell-cell signaling /// cell proliferation	tumor necrosis factor receptor	integral to plasma membrane	cytokine-cytokine receptor interaction
1560148_at	FLJ39207	0.073	-0.162	L	glycolysis	phosphoglycerate kinase activity	---	---
205567_s_at	PHF20	-0.41	-0.152	T	transcription /// regulation of transcription, DNA-dependent	nucleic acid binding /// DNA binding /// zinc ion binding	nucleus	---
1554047_at	TXNDC9	-0.017	-0.161	L	electron transport	electron transporter activity	---	---
206868_s_at	HOXC6	-0.097	-0.161	L	regulation of transcription, DNA-dependent /// regulation of transcription from Pol II promoter /// development	transcription factor activity /// transcription corepressor activity	nucleus	---
244070_at	SYNE1	0.075	-0.161	L	nuclear organization and biogenesis /// Golgi organization and biogenesis /// muscle cell differentiation	actin binding /// structural molecule activity /// tamin binding	nuclear membrane /// Golgi apparatus /// cytoskeleton /// integral to membrane /// postsynaptic membrane	---
230736_at	SVIL	-0.31	-0.161	L	myogenesis	actin filament binding	actin cytoskeleton /// nucleus /// cytoplasm /// plasma membrane /// costamere	---
1558822_at	ARID1B	-0.131	-0.161	T	chromatin-mediated maintenance of transcription /// chromatin-mediated maintenance of transcription	DNA binding /// transcription coactivator activity /// transcription coactivator activity /// protein binding	intracellular /// SWI/SNF complex /// SWI/SNF complex	---
244661_at	SOAT1	-0.125	-0.16	B	circulation /// cholesterol metabolism	sterol O-acyltransferase activity /// acyltransferase activity /// transferase activity	endoplasmic reticulum /// integral to membrane	bile acid biosynthesis
225076_s_at	KIAA1404	0.103	-0.16	B	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
225418_at	PVRL2	0.08	-0.16	B	---	coreceptor activity	plasma membrane /// integral to membrane	Adherens junction

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
232276_s_at	DEPDC1	0.206	-0.16	L	intracellular signaling cascade	GTPase activator activity	---	---
202526_at	SMAD4	-0.104	-0.16	L	regulation of transcription, DNA-dependent /// SMAD protein heteromerization	transcription factor activity /// transcription cofactor activity	nucleus /// cytoplasm	Cell cycle /// TGF-Beta signaling pathway/// Wnt signaling pathway
217040_x_at	SOX15	-0.265	-0.16	T	establishment and/or maintenance of chromatin architecture /// regulation of transcription from RNA polymerase II promoter /// male gonad development	transcription factor activity /// RNA polymerase II transcription factor activity	chromatin /// nucleus	---
205846_at	PTPRB	0.231	-0.159	B	protein amino acid dephosphorylation /// phosphate metabolism	transmembrane receptor protein tyrosine phosphatase activity /// hydrolase activity	membrane fraction /// integral to plasma membrane	Adherens junction/// cadherin-mediated cell adhesion/// phosphatidylinositol signaling system
237234_at	PSCD2	-0.431	-0.159	T	endocytosis /// actin cytoskeleton organization and biogenesis	ARF guanyl-nucleotide exchange factor activity	membrane fraction /// plasma membrane	---
220265_at	GPR107	-0.156	-0.159	T	---	receptor activity	integral to membrane	---
1552852_a_at	ZSCAN4	0.057	-0.158	L	regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	nucleus	---
237513_at	TRY1	0.117	-0.158	L	proteolysis and peptidolysis	chymotrypsin activity /// trypsin activity /// peptidase activity	---	---
1552737_s_at	WWP2	0.017	-0.158	L	ubiquitin cycle /// viral entry into host cell	ubiquitin-protein ligase activity /// protein binding /// ligase activity	ubiquitin ligase complex /// intracellular	ubiquitin mediated proteolysis/// dentatorubropallidoluysian atrophy (drpla)
1569700_s_at	AK7	0.193	-0.158	L	---	adenylate kinase activity /// ATP binding /// kinase activity /// transferase activity	---	---
232508_at	RAI17	-0.192	-0.158	T	transcription /// regulation of transcription, DNA-dependent	zinc ion binding	nucleus	---
206361_at	GPR44	-0.439	-0.158	T	immune response /// signal transduction /// G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity /// receptor activity /// N-formyl peptide receptor activity	plasma membrane /// integral to plasma membrane	GPCRDB Class A Rhodopsin-like
205343_at	SULT1C1	0.126	-0.157	B	amine metabolism	sulfotransferase activity /// transferase activity	cytoplasm	cysteine metabolism
209295_at	TNFRSF10B	0.036	-0.157	L	electron transport /// induction of apoptosis /// caspase activation /// signal transduction /// activation of NF-kappaB-inducing kinase /// induction of apoptosis via death domain receptors /// regulation of apoptosis /// positive regulation of I-kappaB kinase/NF-kappaB cascade	receptor activity /// electron transporter activity /// iron ion binding /// protein binding /// caspase activator activity /// TRAIL binding	integral to membrane	Apoptosis/// cytokine-cytokine receptor interaction
240224_at	PRDM10	0.149	-0.157	T	transcription /// regulation of transcription, DNA-dependent /// transport	nucleic acid binding /// DNA binding /// transporter activity /// zinc ion binding /// lipid binding	nucleus	---
225245_x_at	H2AFJ	-0.433	-0.157	T	nucleosome assembly /// chromosome organization and biogenesis (sensu Eukaryota)	DNA binding	nucleosome /// nucleus	---
208879_x_at	C20orf14	0.077	-0.156	B	spliceosome assembly	binding /// pre-mRNA splicing factor activity	spliceosome complex	mRNA processing
1561146_at	VPS35	-0.184	-0.156	L	protein transport /// retrograde transport, endosome to Golgi	protein binding	cytosol	---
223369_at	AD-003	-0.358	-0.156	T	---	S-adenosylmethionine-dependent methyltransferase activity /// transferase activity	---	---
209974_s_at	BUB3	0.256	-0.155	B	mitosis /// mitotic spindle checkpoint /// cell proliferation	---	kinetochore /// nucleus	cell cycle

No.		Values:	(log2 Values):					
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
228343_at	POU2F2	0.024	-0.155	B	regulation of transcription, DNA-dependent /// transcription from Pol II promoter /// humoral immune response	DNA binding /// transcription factor activity	nucleus	---
210324_at	C8G	-0.227	-0.155	B	transport /// complement activation, alternative pathway /// complement activation, classical pathway /// cytolysis	transporter activity /// binding /// retinol binding	membrane attack complex	complement and coagulation cascades
210864_x_at	HFE	0.136	-0.155	B	protein complex assembly /// transport /// iron ion transport /// iron ion homeostasis /// receptor-mediated endocytosis /// antigen presentation /// antigen presentation, endogenous antigen /// antigen processing, endogenous antigen via MHC class I	MHC class I receptor activity	cytoplasm /// integral to plasma membrane /// MHC class I protein complex	---
218594_at	FLJ10359	0.113	-0.165	B	---	binding	---	---
220158_at	LGALS14	0.16	-0.155	B	---	sugar binding	---	---
226864_at	PKIA	-0.012	-0.155	L	negative regulation of protein kinase activity	cAMP-dependent protein kinase inhibitor activity	---	Calcium regulation in cardiac cells /// Smooth muscle contraction
201705_at	PSMD7	-0.22	-0.155	L	---	---	proteasome regulatory particle (sensu Eukaryota)	Proteasome
217663_at	CLOCK	-0.261	-0.155	T	transcription /// regulation of transcription from RNA polymerase II promoter /// signal transduction /// circadian rhythm /// response to photoperiod	transcription factor activity /// signal transducer activity	nucleus	Circadian Exercise
208205_at	PCDHA9	0.017	-0.155	T	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	membrane /// integral to membrane	---
204169_at	IMPDH1	-0.265	-0.154	B	purine nucleotide biosynthesis /// GMP biosynthesis /// GTP biosynthesis /// visual perception	catalytic activity /// IMP dehydrogenase activity /// oxidoreductase activity	---	Nucleotide Metabolism /// Purine metabolism
244362_at	YES1	0.073	-0.154	T	protein amino acid phosphorylation /// intracellular signaling cascade	protein-tyrosine kinase activity /// ATP binding /// transferase activity	---	Adherens junction /// tight junction
224972_at	C20orf52	-0.433	-0.154	T	---	---	integral to membrane	---
1563036_at	GPR111	-0.224	-0.153	T	signal transduction /// neuropeptide signaling pathway	receptor activity /// G-protein coupled receptor activity	membrane /// integral to membrane	---
215987_at	RAPGEF2	-0.211	-0.153	T	MAPKKK cascade /// small GTPase mediated signal transduction /// cAMP-mediated signaling	signal transducer activity /// calcium ion binding /// protein binding /// Rap guanyl-nucleotide exchange factor activity /// diacylglycerol binding /// Rap GTPase activator activity	integral to plasma membrane /// integral to membrane	---
208275_x_at	UTF1	0.099	-0.152	B	regulation of transcription from Pol II promoter	RNA polymerase II transcription factor activity /// transcription coactivator activity	---	---
220310_at	TUBAL3	-0.172	-0.152	L	microtubule-based movement /// microtubule polymerization	GTPase activity /// structural molecule activity /// GTP binding	tubulin	---
236609_at	PMS1	-0.159	-0.152	T	mismatch repair /// regulation of transcription, DNA-dependent /// cell cycle /// negative regulation of cell cycle	DNA binding /// ATP binding	nucleus /// nucleus /// inner membrane	---
222535_s_at	DATF1	-0.255	-0.152	T	transcription /// regulation of transcription, DNA-dependent /// apoptosis	DNA binding	nucleus	---
243303_at	KIAA1340	-0.164	-0.152	T	---	protein binding	---	---
222067_x_at	HIST1H2BD	0.195	-0.151	B	nucleosome assembly /// chromosome organization and biogenesis (sensu Eukaryota)	DNA binding	nucleosome /// nucleus /// chromosome	---
226799_at	FGD6	-0.123	-0.151	L	---	zinc ion binding	---	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
208020_s_at	CACNA1C	-0.314	-0.151	T	ion transport /// cation transport /// calcium ion transport /// regulation of heart contraction rate	ion channel activity /// voltage-gated calcium channel activity /// voltage-gated calcium channel activity /// calcium ion binding	voltage-gated calcium channel complex /// voltage-gated calcium channel complex /// membrane /// integral to membrane	Calcium regulation in cardiac cells
237751_x_at	RARS	-0.172	-0.151	T	protein biosynthesis /// arginyl-tRNA aminoacylation	arginine-tRNA ligase activity /// ATP binding /// ligase activity	soluble fraction /// cytoplasm	Arginine and proline metabolism /// Aminoacyl-tRNA biosynthesis
212167_s_at	SMARCB1	-0.378	-0.151	T	chromatin remodeling /// transcription /// regulation of transcription from RNA polymerase II promoter /// cell cycle /// DNA integration /// negative regulation of cell cycle	---	nuclear chromosome /// nucleoplasm	---
244382_at	TBC1D10	-0.242	-0.151	T	---	PDZ domain binding	microvillus	---
231523_at	FGF14	0.02	-0.15	B	signal transduction /// cell-cell signaling /// neurogenesis	growth factor activity	extracellular space	MAPK signaling pathway
204129_at	BCL9	0.045	-0.15	L	Wnt receptor signaling pathway	---	nucleus	---
1558636_s_at	ADAMTS5	-0.157	-0.15	L	proteolysis and peptidolysis	metalloendopeptidase activity /// integrin binding /// zinc ion binding /// hydrolase activity	extracellular matrix (sensu Metazoa)	---
1552922_at	RIMS1	-0.076	-0.15	T	neurotransmitter transport /// protein complex assembly/// intracellular protein transport /// membrane fusion /// sensory perception /// visual perception /// synaptic vesicle exocytosis /// calcium ion-dependent exocytosis /// secretion	small GTPase regulator activity /// protein binding /// zinc ion binding /// Rab GTPase binding	presynaptic membrane	---
212346_s_at	MXD4	-0.353	-0.15	T	negative regulation of transcription from RNA polymerase II promoter /// transcription /// regulation of transcription, DNA-dependent /// negative regulation of cell proliferation	DNA binding /// transcription corepressor activity /// protein binding	nucleus	---
232457_at	KIAA1102	-0.259	-0.15	T	smooth muscle contraction	actin binding /// zinc ion binding	---	---
1552797_s_at	PROM2	0.02	-0.149	L	---	---	integral to membrane	---
234276_at	USP6NL	0.353	-0.149	L	---	GTPase activator activity	---	---
224301_x_at	H2AFJ	-0.388	-0.149	T	nucleosome assembly /// chromosome organization and biogenesis (sensu Eukaryota)	DNA binding	nucleosome /// nucleus	---
204333_s_at	AGA	-0.15	-0.148	L	protein deglycosylation	N4-(beta-N-acetylglucosaminyl)-L-asparaginase activity /// hydrolase activity	lysosome	N-Glycan degradation
205208_at	ALDH1L1	-0.517	-0.148	T	protein biosynthesis /// one-carbon compound metabolism /// biosynthesis /// 10-formyltetrahydrofolate catabolism	electron transporter activity /// methyltransferase activity /// formyltetrahydrofolate dehydrogenase activity /// oxidoreductase activity /// hydroxymethyl-, formyl- and related transferase activity /// cofactor binding	cytoplasm	One carbon pool by folate
244333_at	KIAA1727	0.128	-0.148	T	cell organization and biogenesis	actin binding	---	---
227473_at	CTTN	-0.101	-0.148	T	---	protein binding	ruffle /// soluble fraction /// cytoskeleton /// cell cortex /// lamellipodium	Tight junction
203044_at	CHSY1	-0.397	-0.148	T	---	transferase activity /// glucuronosyl-N-acetylgalactosaminyl-proteoglycan 4-beta-N-acetylgalactosaminyltransferase activity /// N-acetylgalactosaminyl-proteoglycan 3-beta-glucuronosyltransferase activity	Golgi apparatus /// integral to membrane	---

No.		Values):	(log2 Values):					
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
243437_at	GCC1	0.174	-0.148	T	---	---	Golgi apparatus	---
1560038_at	COCH	0.021	-0.147	B	perception of sound	---	---	---
204306_s_at	CD151	-0.399	-0.147	T	cell adhesion /// visual perception /// perception of sound	protein binding	membrane fraction /// plasma membrane /// integral to plasma membrane /// integral to membrane	---
226305_at	LYNX1	-0.148	-0.147	T	pathogenesis	---	membrane	---
208917_x_at	FLJ13052	0.161	-0.146	B	metabolism /// phosphorylation /// ATP metabolism	NAD+ kinase activity /// transferase activity	cytosol	nicotinate and nicotinamide metabolism
211533_at	PDGFRA	0.04	-0.146	L	protein amino acid phosphorylation /// cell surface receptor linked signal transduction /// transmembrane receptor protein tyrosine kinase signaling pathway /// cell proliferation	receptor activity /// platelet-derived growth factor alpha-receptor activity /// vascular endothelial growth factor receptor activity /// ATP binding /// transferase activity	integral to plasma membrane	MAPK signaling pathway/// cytokine-cytokine receptor interaction
231508_s_at	DNAJA2	-0.29	-0.146	L	regulation of cell cycle /// G1 phase of mitotic cell cycle /// protein folding /// positive regulation of cell proliferation	heat shock protein binding /// unfolded protein binding	membrane	---
220030_at	STYK1	-0.078	-0.146	T	protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	integral to membrane	---
237380_at	FBXO46	0.153	-0.146	T	ubiquitin cycle	---	---	---
202870_s_at	CDC20	-0.259	-0.145	B	regulation of cell cycle /// cytokinesis /// ubiquitin-dependent protein catabolism /// ubiquitin cycle /// mitosis	---	spindle	cell cycle
241909_at	TNKS2	-0.008	-0.145	T	protein amino acid ADP-ribosylation /// telomerase-dependent telomere maintenance	NAD+ ADP-ribosyltransferase activity /// transferase activity, transferring glycosyl groups	chromosome, telomeric region /// nucleus /// Golgi apparatus	---
219372_at	CDV1	-0.002	-0.144	B	spermatogenesis	---	---	---
242986_at	NAV1	0.042	-0.144	B	DNA methylation	nucleotide binding /// DNA binding /// ATP binding /// nucleoside-triphosphatase activity	---	---
1570342_at	NKTR	-0.18	-0.144	T	protein folding	peptidyl-prolyl cis-trans isomerase activity /// cyclosporin A binding /// isomerase activity	plasma membrane	---
201995_at	EXT1	-0.369	-0.144	T	skeletal development /// glycosaminoglycan biosynthesis /// cell cycle /// signal transduction /// negative regulation of cell cycle	transferase activity, transferring glycosyl groups /// N-acetylglucosaminyl-proteoglycan 4-beta-glucuronosyltransferase activity	endoplasmic reticulum membrane /// Golgi apparatus /// membrane /// integral to membrane	Chondroitin / Heparan sulfate biosynthesis
224726_at	MIB1	-0.671	-0.144	T	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
206411_s_at	ABL2	0.36	-0.143	L	protein amino acid phosphorylation /// intracellular signaling cascade	protein-tyrosine kinase activity /// ATP binding /// transferase activity	cytoplasm	---
211276_at	TCEAL2	0.044	-0.143	T	---	translation elongation factor activity	---	---
222414_at	MLL3	0.076	-0.142	B	regulation of transcription, DNA-dependent /// ATP synthesis coupled proton transport /// protein ubiquitination /// chromatin modification	DNA binding /// ubiquitin-protein ligase activity /// ATP binding /// methyltransferase activity /// zinc ion binding /// transferase activity /// histone-lysine N-methyltransferase activity /// metal ion binding /// hydrogen-transporting ATP synthase activity, rotational mechanism /// hydrogen-transporting ATPase activity, rotational mechanism	ubiquitin ligase complex /// nucleus /// proton-transporting two-sector ATPase complex	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
206140_at	LHX2	0.284	-0.142	L	regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	nucleus	---
206022_at	NDP	-0.115	-0.142	T	vacuole organization and biogenesis /// signal transduction /// cell-cell signaling /// neurogenesis /// sensory perception /// visual perception /// perception of sound /// cell proliferation	growth factor activity	extracellular space	---
233318_at	FRS2	-0.148	-0.142	T	G-protein coupled receptor protein signaling pathway/// fibroblast growth factor receptor signaling pathway/// transmembrane receptor protein tyrosine phosphatase signaling pathway/// signal transduction	insulin receptor binding/// phosphatase activator activity/// protein binding/// receptor activity/// regulator of G-protein signaling activity/// transmembrane receptor protein tyrosine kinase adaptor protein activity	integral to plasma membrane/// membrane fraction	---
219951_s_at	C20orf12	0.157	-0.141	B	G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity	integral to membrane	---
1556699_at	RBPMS	0.21	-0.141	L	RNA processing	RNA binding	---	---
211212_s_at	ORC5L	0.054	-0.14	B	DNA replication /// DNA replication initiation	nucleotide binding /// DNA replication origin binding /// ATP binding	nucleus /// nuclear origin of replication recognition complex	Cell cycle /// DNA replication /// G1 to S cell cycle
233395_at	RGS3	-0.33	-0.14	L	inactivation of MAPK /// signal transduction /// regulation of G-protein coupled receptor protein signaling pathway	signal transducer activity /// GTPase activator activity /// protein binding	cytosol	Calcium regulation in cardiac cells /// Smooth muscle contraction
1558720_at	KNS2	0.097	-0.14	L	---	protein binding/// microtubule motor activity	kinesin complex/// microtubule	---
211759_x_at	CKAP1	-0.247	-0.14	T	protein folding	unfolded protein binding	microtubule cytoskeleton	---
240269_at	MGC16169	-0.175	-0.14	T	protein amino acid phosphorylation	protein kinase activity /// protein serine/threonine kinase activity /// ATP binding	---	---
224065_at	HIPK2	0.021	-0.14	T	regulation of cell cycle /// transcription /// regulation of transcription, DNA-dependent /// protein amino acid phosphorylation /// apoptosis /// induction of apoptosis by intracellular signals /// virus-host interaction /// positive regulation of transforming growth factor beta receptor signaling pathway /// positive regulation of JNK cascade	transcription corepressor activity /// protein serine/threonine kinase activity /// protein binding /// ATP binding /// transferase activity /// virion binding	nucleus /// cytoplasm /// nuclear body	Benzoate degradation via CoA ligation/// Inositol phosphate metabolism/// Nicotinate and nicotinamide metabolism/// Phosphatidylinositol signaling system
219597_at	TTC12	-0.361	-0.14	T	---	binding	---	---
240168_at	XPO7	-0.316	-0.139	T	protein transport/// protein-nucleus export	nuclear export signal receptor activity/// protein transporter activity/// binding	cytoplasm/// nuclear pore/// nucleus	---
202115_s_at	DKFZP564C18	-0.287	-0.139	T	---	---	nucleus	---
204210_s_at	PCYT1A	-0.078	-0.139	T	phospholipid biosynthesis /// biosynthesis	choline-phosphate cytidylyltransferase activity /// transferase activity /// nucleotidyltransferase activity	soluble fraction /// membrane	Acetylcholine Synthesis /// Aminophosphonate metabolism /// Glycerophospholipid metabolism
226506_at	FLJ13710	-0.177	-0.139	T	---	metalloendopeptidase activity /// peptidase activity	extracellular matrix	---
238323_at	TEAD2	0.309	-0.138	L	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
233502_at	CNTN3	0.194	-0.138	L	cell adhesion	protein binding	membrane	---
1553146_at	FLJ32859	0.095	-0.138	L	---	kinase activity	---	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
237722_at	FLI1	-0.131	-0.137	L	regulation of transcription, DNA-dependent /// hemostasis /// organogenesis	transcription factor activity	nucleus	---
241732_at	CDKAL1	-0.156	-0.137	L	---	catalytic activity /// iron ion binding	---	---
1562759_at	MYOM1	-0.192	-0.137	T	muscle development/// striated muscle contraction	structural constituent of muscle	myofibril/// striated muscle thick filament	---
240735_at	CDC42BPA	-0.137	-0.137	T	protein amino acid phosphorylation /// protein amino acid phosphorylation /// intracellular signaling cascade	protein serine/threonine kinase activity /// protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// small GTPase regulator activity /// ATP binding	membrane	---
201700_at	CCND3	-0.368	-0.137	T	regulation of cell cycle /// cytokinesis	---	nucleus	Cell cycle/// Wnt signaling pathway/// Jak-STAT signaling pathway/// focal adhesion
201388_at	PSMD3	-0.356	-0.137	T	---	binding	proteasome complex (sensu Eukaryota) /// cytosol	Proteasome Degradation
228800_x_at	AKIP	-0.218	-0.137	T	negative regulation of mitosis	protein binding	nucleus	---
205386_s_at	MDM2	-0.167	-0.136	B	regulation of cell cycle /// negative regulation of transcription from Pol II promoter /// protein complex assembly /// negative regulation of cell proliferation /// protein ubiquitination /// regulation of protein catabolism	ubiquitin-protein ligase activity /// protein binding /// zinc ion binding /// ligase activity /// negative regulator of basal transcription activity	ubiquitin ligase complex /// nucleus /// nucleoplasm /// nucleolus	tryptophan metabolism/// cell cycle
207246_at	ZFY	0.05	-0.135	B	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding /// transcription regulator activity /// metal ion binding	nucleus	---
214466_at	GJA5	0.122	-0.135	L	transport /// muscle contraction /// intercellular junction assembly /// cell communication	connexon channel activity	connexon complex /// integral to membrane	Calcium regulation in cardiac cells
228343_at	POU2F2	-0.232	-0.135	L	regulation of transcription, DNA-dependent /// transcription from Pol II promoter /// humoral immune response	DNA binding /// transcription factor activity	nucleus	---
217691_x_at	SLC16A3	-0.225	-0.135	T	transport /// organic anion transport /// monocarboxylic acid transport	transporter activity /// symporter activity /// monocarboxylate porter activity	membrane fraction /// integral to plasma membrane	---
234173_s_at	NXF2	-0.116	-0.134	B	mRNA processing /// mRNA-nucleus export /// protein-nucleus import /// transport /// development /// RNA transport	RNA binding /// protein binding /// protein transporter activity	nucleus /// cytoplasm /// nuclear RNA export factor complex	---
229790_at	TERF2	0.108	-0.134	B	telomerase-dependent telomere maintenance /// cell cycle /// regulation of transcription	telomeric DNA binding	chromosome, telomeric region /// nucleus	---
212728_at	DLG3	0.145	-0.134	L	negative regulation of cell proliferation	guanylate kinase activity /// protein binding	---	---
1552532_a_at	ATP6V1C2	-0.19	-0.134	T	ATP synthesis coupled proton transport	ATP binding /// hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	proton-transporting two-sector ATPase complex	Oxidative phosphorylation /// ATP synthesis /// Photosynthesis /// Flagellar assembly /// Type III secretion system
222621_at	DNAJC1	-0.557	-0.134	T	protein folding /// regulation of transcription /// negative regulation of proteolysis and peptidolysis /// regulation of protein secretion	ATPase stimulator activity /// DNA binding /// Hsp70/Hsc70 protein regulator activity /// heat shock protein binding /// ribosome binding /// unfolded protein binding	nucleus /// endoplasmic reticulum lumen /// microsome /// integral to membrane	---
217095_x_at	NCR1	0.217	-0.134	T	cellular defense response /// signal transduction /// natural killer cell activation	receptor activity /// receptor signaling protein activity	integral to plasma membrane	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): -3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
220901_at	GPR157	-0.284	-0.134	T	G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity /// receptor activity /// G-protein coupled receptor activity	membrane /// integral to membrane	---
1553286_at	ZNF555	-0.282	-0.133	T	regulation of transcription, DNA-dependent	nucleic acid binding /// DNA binding /// zinc ion binding	nucleus	---
232409_x_at	FBXL16	0.017	-0.133	T	ubiquitin cycle	---	---	---
1561094_a_at	LOC387601	-0.015	-0.132	L	transport	transporter activity	integral to membrane	---
204886_at	PLK4	0.065	-0.132	L	regulation of cell cycle /// protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	---	---
213892_s_at	APRT	-0.335	-0.132	T	purine ribonucleoside salvage /// adenine salvage /// nucleoside metabolism	adenine phosphoribosyltransferase activity /// transferase activity, transferring glycosyl groups	---	Purine metabolism
200688_at	SF3B3	-0.33	-0.132	T	nuclear mRNA splicing, via spliceosome /// protein complex assembly /// RNA splicing	nucleic acid binding /// RNA splicing factor activity, transesterification mechanism	spliceosome complex /// small nuclear ribonucleoprotein complex	mRNA Processing, Gene Expression
220317_at	LRAT	-0.024	-0.132	T	sensory perception /// visual perception	acyltransferase activity /// transferase activity /// phosphatidylcholine-retinol O-acyltransferase activity	endoplasmic reticulum /// integral to membrane	---
225806_at	JUB	0.131	-0.131	B	---	zinc ion binding	---	---
208569_at	HIST1H2AB	-0.307	-0.131	T	nucleosome assembly /// chromosome organization and biogenesis (sensu Eukaryota)	DNA binding	nucleosome /// nucleus /// chromosome	---
212307_s_at	OGT	0.237	-0.13	B	O-linked glycosylation /// signal transduction /// response to nutrients	binding /// protein binding /// acetylglucosaminyltransferase activity /// transferase activity, transferring glycosyl groups	nucleus /// cytosol	blood group glycolipid biosynthesis lactoseries/// fructose and mannose metabolism/// n-glycans biosynthesis/// glycosphingolipid metabolism/// globoside metabolism/// glycosylphosphatidylinositol/// glycolipid biosynthesis-neolactoseries/// o-glycans biosynthesis/// glycerolipid metabolism
241938_at	QKI	-0.469	-0.13	L	---	nucleic acid binding /// RNA binding	---	---
1564339_a_at	CHRM3	0.195	-0.13	L	protein modification /// signal transduction /// G-protein coupled receptor protein signaling pathway /// synaptic transmission /// neurogenesis /// cell proliferation	rhodopsin-like receptor activity /// phosphoinositide phospholipase C activity /// receptor activity /// muscarinic acetylcholine receptor activity	integral to plasma membrane	neuroactive ligand-receptor interaction
74694_s_at	RABEP2	-0.43	-0.13	T	protein transport/// endocytosis	GTPase activator activity /// growth factor activity	---	---
221934_s_at	DALRD3	-0.236	-0.13	T	protein biosynthesis /// arginyl-tRNA aminoacylation	arginine-tRNA ligase activity /// ATP binding /// ligase activity	---	---
243090_at	KIAA0427	-0.17	-0.13	T	---	RNA binding	---	---
1559780_at	DDAH1	0.131	-0.129	B	arginine catabolism /// nitric oxide mediated signal transduction	dimethylargininase activity /// hydrolase activity	---	---
227752_at	SPTLC2L	0.427	-0.129	L	biosynthesis	transferase activity, transferring nitrogenous groups	---	---
227467_at	RDH10	0.334	-0.129	T	metabolism	oxidoreductase activity	---	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
1552582_at	ABCC13	0.288	-0.128	L	transport	ATP binding /// ATPase activity, coupled to transmembrane movement of substances	nucleus /// integral to membrane	---
219336_s_at	ASCC1	-0.243	-0.128	L	regulation of transcription, DNA-dependent /// regulation of transcription	nucleic acid binding	cytoplasm	---
221657_s_at	ASB6	-0.192	-0.127	B	intracellular signaling cascade	---	---	---
205092_x_at	ZBTB1	-0.062	-0.127	L	regulation of transcription, DNA-dependent	DNA binding /// protein binding /// zinc ion binding	nucleus	---
1562462_at	DNAH10	0.003	-0.127	T	microtubule-based movement	microtubule motor activity /// ATP binding /// ATPase activity	flagellum /// dynein complex	---
1554970_at	PDILT	-0.144	-0.126	B	electron transport	electron transporter activity /// isomerase activity	---	---
1557829_at	SLC8A1	0.14	-0.126	L	transport /// sodium ion transport /// calcium ion transport /// muscle contraction /// cell communication	calcium:sodium antiporter activity /// calmodulin binding /// sodium ion transporter activity /// calcium ion transporter activity /// antiporter activity	integral to plasma membrane /// membrane	Calcium regulation in cardiac cells /// Smooth muscle contraction
1558532_at	TPM1	0.203	-0.126	L	regulation of muscle contraction /// muscle development /// regulation of heart contraction rate	actin binding /// structural constituent of cytoskeleton /// structural constituent of muscle	cytoskeleton /// muscle thin filament tropomyosin	Striated muscle contraction
219710_at	KIAA1985	0.281	-0.126	L	---	binding	---	Neuroactive ligand-receptor interaction
243447_at	RYR2	-0.138	-0.126	T	cation transport /// calcium ion transport /// calcium ion homeostasis /// muscle contraction /// signal transduction /// regulation of heart contraction rate	receptor activity /// ryanodine-sensitive calcium-release channel activity /// calcium ion binding /// calmodulin binding /// calcium-release channel activity	plasma membrane /// integral to plasma membrane	Calcium regulation in cardiac cells /// Smooth muscle contraction
207235_s_at	GRM5	0.051	-0.126	T	signal transduction /// G-protein coupled receptor protein signaling pathway /// metabotropic glutamate receptor, phospholipase C activating pathway /// synaptic transmission	receptor activity /// metabotropic glutamate, GABA-B-like receptor activity	integral to plasma membrane /// membrane	Neuroactive ligand-receptor interaction/// calcium signaling pathway
213521_at	PTPN18	0.028	-0.126	T	protein amino acid dephosphorylation /// protein amino acid dephosphorylation	protein tyrosine phosphatase activity /// non-membrane spanning protein tyrosine phosphatase activity /// hydrolase activity	---	---
233424_at	NRXN1	-0.408	-0.126	T	cell adhesion /// axon guidance	receptor activity /// structural molecule activity /// protein binding /// protein binding	integral to plasma membrane /// integral to membrane	---
231716_at	MNAB	-0.504	-0.126	T	protein ubiquitination	nucleic acid binding /// DNA binding /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex /// membrane fraction /// cell surface	---
201558_at	RAE1	-0.208	-0.126	T	mRNA-nucleus export	RNA binding	nucleus /// nuclear outer membrane /// nuclear pore /// cytoplasm /// cytoskeleton	---
202922_at	GCLC	-0.525	-0.125	L	cysteine metabolism /// glutamate metabolism /// glutathione biosynthesis /// circulation	nucleic acid binding /// glutamate-cysteine ligase activity /// ligase activity	---	Glutamate metabolism /// Glutathione metabolism
240045_at	PRDM16	0.13	-0.125	L	regulation of transcription, DNA-dependent	DNA binding /// transcription factor activity /// zinc ion binding	nucleus	---
224652_at	C10orf9	-0.178	-0.125	T	regulation of cell cycle /// cytokinesis	---	---	---
237569_at	PB1	0.136	-0.124	B	chromatin remodeling /// regulation of transcription, DNA-dependent /// mitosis	DNA binding /// chromatin binding	nuclear chromosome	---

No.		Values):	(log2 Values):					
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
229724_at	GABRB3	-0.185	-0.124	L	ion transport /// signal transduction /// synaptic transmission	GABA-A receptor activity /// ion channel activity /// extracellular ligand-gated ion channel activity /// neurotransmitter receptor activity	integral to plasma membrane /// postsynaptic membrane	Neuroactive ligand-receptor interaction
239935_at	MAMDC1	0.062	-0.124	L	---	---	membrane /// integral to membrane	---
1555246_a_at	SCN1A	0.116	-0.124	T	cation transport /// sodium ion transport	voltage-gated sodium channel activity /// cation channel activity	voltage-gated sodium channel complex /// membrane /// integral to membrane	---
208638_at	TXNDC7	0.155	-0.123	B	electron transport /// protein folding	protein disulfide isomerase activity /// electron transporter activity /// isomerase activity	endoplasmic reticulum	---
218739_at	ABHD5	-0.189	-0.123	L	proteolysis and peptidolysis /// aromatic compound metabolism	aminopeptidase activity /// peptidase activity	---	---
1561136_at	GYPE	0.037	-0.123	L	---	---	integral to plasma membrane	---
233039_at	SPRED1	-0.091	-0.123	T	development /// inactivation of MAPK /// regulation of signal transduction	stem cell factor receptor binding /// protein binding	membrane	Jak-STAT signaling pathway
221317_x_at	PCDHB6	-0.1	-0.122	B	cell adhesion /// homophilic cell adhesion /// synaptic transmission /// synaptogenesis /// calcium-dependent cell cell adhesion	calcium ion binding /// protein binding	integral to plasma membrane	---
1553704_x_at	FLJ90396	0.156	-0.122	B	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
223426_s_at	EPB41L4B	-0.328	-0.122	T	---	structural molecule activity /// structural constituent of cytoskeleton /// binding /// cytoskeletal protein binding	cytoplasm /// cytoskeleton /// cytoskeleton /// membrane	---
1560228_at	SNAI3	-0.142	-0.121	L	---	nucleic acid binding /// zinc ion binding	nucleus	---
1556067_a_at	JMJD3	0.26	-0.121	L	---	binding	---	---
220955_x_at	RAB23	0.067	-0.121	T	small GTPase mediated signal transduction /// protein transport	GTP binding	---	Hedgehog signaling pathway
204085_s_at	CLN5	-0.231	-0.121	T	---	---	lysosome /// integral to membrane	---
210693_at	SPPL2B	0.172	-0.12	B	proteolysis and peptidolysis	peptidase activity /// D-alanyl-D-alanine endopeptidase activity	integral to membrane	---
1554393_a_at	ODC-p	0.161	-0.12	L	polyamine biosynthesis /// spermatogenesis	ornithine decarboxylase activity /// lyase activity	---	---
228358_at	SOX12	-0.123	-0.12	L	regulation of transcription from Pol II promoter	DNA binding /// RNA polymerase II transcription factor activity	nucleus	---
202515_at	DLG1	-0.644	-0.12	L	---	guanylate kinase activity /// cytoskeletal protein binding	cytoplasm /// plasma membrane /// intercellular junction	---
204058_at	ME1	-0.221	-0.12	T	carbohydrate metabolism /// tricarboxylic acid cycle /// malate metabolism	malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity /// electron transporter activity /// oxidoreductase activity	cytosol	Pyruvate metabolism /// Carbon fixation
213426_s_at	CAV2	-0.136	-0.12	T	---	---	integral to membrane /// caveolar membrane	Integrin-mediated cell adhesion
241970_at	PVRL3	-0.126	-0.12	T	---	receptor activity	---	Adherens junction
207709_at	PRKAA2	-0.146	-0.119	L	protein amino acid phosphorylation /// fatty acid biosynthesis /// cholesterol biosynthesis /// signal transduction	protein serine/threonine kinase activity /// ATP binding /// transferase activity	---	Fatty Acid Synthesis
201651_s_at	PACSIN2	-0.228	-0.119	T	intracellular protein transport /// endocytosis /// actin cytoskeleton organization and biogenesis	transporter activity	cytoplasm	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
1558487_a_at	TMED4	-0.143	-0.119	T	positive regulation of signal transduction/// regulation of i-kappab kinase/nf-kappab cascade/// intracellular transport/// protein kinase cascade/// cellular physiological process/// cell growth and/or maintenance/// protein transport	signal transducer activity/// binding/// protein transporter activity/// protein binding	---	---
207544_s_at	ADH6	-0.217	-0.119	T	ethanol oxidation	alcohol dehydrogenase activity /// alcohol dehydrogenase activity /// electron transporter activity /// zinc ion binding /// oxidoreductase activity	---	Glycolysis / Gluconeogenesis /// Fatty acid metabolism /// Bile acid biosynthesis /// Tyrosine metabolism /// Glycerolipid metabolism
212767_at	GTP	-0.156	-0.118	B	---	GTP binding	---	---
220624_s_at	ELF5	0.408	-0.118	L	regulation of transcription, DNA-dependent /// transcription from Pol II promoter /// cell proliferation	DNA binding /// transcription factor activity	nucleus	---
244333_at	KIAA1727	-0.263	-0.118	L	cell organization and biogenesis	actin binding	---	---
235345_at	RUFY2	-0.215	-0.118	L	---	zinc ion binding	---	---
239725_at	PGAP1	-0.195	-0.118	T	---	hydrolase activity	---	---
1553340_s_at	IAC1L2 /// AMA	-0.136	-0.118	T	---	---	membrane	---
206720_at	MGAT5	0.032	-0.118	T	N-linked glycosylation	transferase activity, transferring glycosyl groups /// alpha-1,6-mannosyl-glycoprotein 6-beta-N-acetylglucosaminyltransferase activity	Golgi membrane /// integral to membrane	N-Glycan biosynthesis
1557744_at	TRPC4AP	0.248	-0.117	L	protein complex assembly /// intracellular protein transport /// peptide transport /// antigen processing, endogenous antigen via MHC class I /// cytosol to ER transport /// antigen presentation, endogenous peptide antigen	ATP binding /// peptide transporter activity /// peptide antigen-transporting ATPase activity /// MHC class I protein binding /// phosphate binding /// peptide antigen binding /// protein homodimerization activity /// TAP1 binding /// TAP2 binding /// tapasin binding /// protein heterodimerization activity	endoplasmic reticulum lumen /// cytosol	---
1569481_s_at	SNX22	0.202	-0.117	L	intracellular signaling cascade /// protein transport	---	---	---
210229_s_at	CSF2	0.428	-0.117	L	cellular defense response /// cell surface receptor linked signal transduction /// development	cytokine activity /// granulocyte macrophage colony-stimulating factor receptor binding	extracellular space	cytokine-cytokine receptor interaction
221703_at	BRIP1	-0.154	-0.116	L	nucleobase, nucleoside, nucleotide and nucleic acid metabolism /// nucleotide-excision repair	DNA binding /// ATP-dependent DNA helicase activity /// ATP binding /// hydrolase activity /// hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	nucleus	---
243876_at	FOXP1	-0.007	-0.116	L	regulation of transcription, DNA-dependent	nucleic acid binding /// transcription factor activity /// zinc ion binding	nucleus	---
210690_at	KLRC4	-0.029	-0.115	T	cellular defense response /// signal transduction /// antimicrobial humoral response (sensu Vertebrata)	receptor activity /// receptor activity /// protein binding /// sugar binding	integral to plasma membrane /// integral to membrane	---
1557837_a_at	ELMOD2	-0.068	-0.115	T	apoptosis/// phagocytosis	---	cytoskeleton	---
233973_at	YZL1 /// LYZL	0.251	-0.114	L	cell wall catabolism	lysozyme activity	extracellular region	---
1556449_at	TTC15	0.041	-0.114	T	---	binding	---	---
217526_at	NFATC2IP	-0.179	-0.114	T	protein modification	---	---	---

No.		Value): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
1558163_at	PEX13	-0.002	-0.113	L	protein transport /// peroxisome matrix protein import, docking	---	membrane fraction /// peroxisome /// integral to peroxisomal membrane	---
244215_at	BTD	0.087	-0.113	T	biotin metabolism /// nitrogen compound metabolism /// central nervous system development /// epidermis development	biotin carboxylase activity /// hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds /// biotinidase activity	---	Biotin metabolism
208909_at	UQCRFS1	-0.379	-0.112	T	electron transport /// transport	ubiquinol-cytochrome-c reductase activity /// oxidoreductase activity	mitochondrion /// ubiquinol-cytochrome-c reductase complex (sensu Eukaryota) /// integral to membrane /// inner membrane	Oxidative phosphorylation
224694_at	SNX12	-0.16	-0.112	T	intracellular signaling cascade /// protein transport	---	---	---
226774_at	KIAA1838	0.107	-0.111	B	carbohydrate metabolism	---	---	---
214791_at	LOC93349	0.33	-0.111	L	---	DNA binding	nucleus	---
223767_at	GPR84	0.138	-0.111	L	G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity /// receptor activity /// G-protein coupled receptor activity, unknown ligand	integral to membrane	GPCRDB Other
223640_at	HCST	-0.414	-0.111	T	---	---	integral to membrane	---
225307_at	ZNF511	-0.355	-0.111	T	---	nucleic acid binding /// zinc ion binding	nucleus	---
220119_at	EPB41L4A	0.099	-0.111	T	---	structural molecule activity /// binding /// cytoskeletal protein binding	cytoplasm /// cytoskeleton /// membrane	---
202817_s_at	SS18	0.375	-0.11	B	---	---	nucleus	---
229822_at	PARVG	0.125	-0.11	B	cell-matrix adhesion	actin binding /// protein binding	cytoskeleton	Focal adhesion
220658_s_at	ARNTL2	0.163	-0.11	B	regulation of transcription, DNA-dependent /// signal transduction /// entrainment of circadian clock	transcription factor activity /// signal transducer activity	nucleus	circadian rhythm
201714_at	TUBG1	-0.356	-0.11	T	meiotic spindle organization and biogenesis /// microtubule-based movement /// microtubule nucleation /// mitotic spindle organization and biogenesis /// protein polymerization	GTPase activity /// structural constituent of cytoskeleton /// protein binding /// GTP binding	condensed nuclear chromosome /// gamma-tubulin complex /// centrosome /// spindle pole body /// polar microtubule /// microtubule	---
244376_at	KFZP586A052	0.097	-0.11	T	---	S-adenosylmethionine-dependent methyltransferase activity	---	---
227535_at	C15orf24	0.108	-0.11	T	---	purine nucleotide binding	cytoplasm	---
203387_s_at	TBC1D4	0.201	-0.109	B	---	GTPase activator activity	---	---
200596_s_at	EIF3S10	-0.541	-0.109	L	protein biosynthesis /// regulation of translational initiation	translation initiation factor activity	eukaryotic translation initiation factor 3 complex	Translation Factors
222250_s_at	DKFZP434B16	0.329	-0.109	L	---	binding	---	---
1565777_at	ABCA1	-0.208	-0.109	T	lipid metabolism /// transport /// transport /// sterol metabolism /// cholesterol metabolism	nucleotide binding /// ATP binding /// ATP binding /// ATP binding /// anion transporter activity /// sterol transporter activity /// ATPase activity	membrane fraction /// integral to plasma membrane	Statin Pathway
203793_x_at	PCGF2	0.164	-0.109	T	transcription /// regulation of transcription, DNA-dependent /// protein ubiquitination	transcription factor activity /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex /// nucleus	---
219837_s_at	CYTL1	0.25	-0.108	L	signal transduction	receptor binding	extracellular space /// soluble fraction	---
220468_at	FLJ22595	0.042	-0.108	T	small GTPase mediated signal transduction	GTP binding	---	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
214322_at	CAMK2G	0.174	-0.107	B	protein amino acid phosphorylation /// signal transduction /// insulin secretion	protein serine/threonine kinase activity /// calcium- and calmodulin-dependent protein kinase activity /// protein-tyrosine kinase activity /// calcium-dependent protein serine/threonine phosphatase activity /// calmodulin binding /// ATP binding /// kinase activity /// transferase activity	---	Wnt signaling
220463_at	TRPM3	0.115	-0.107	T	calcium transport /// calcium ion transport	receptor activity /// calcium channel activity	membrane /// integral to membrane	---
225109_at	FLJ10826	-0.285	-0.106	L	protein metabolism	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	---	---
1569205_at	PRCP	0.199	-0.106	L	proteolysis and peptidolysis	serine-type Pro-X carboxypeptidase activity	lysosome	hemostasis
234719_at	LAMA3	0.084	-0.106	L	epidermis development /// regulation of cell adhesion /// regulation of cell migration	structural molecule activity /// receptor binding	basement membrane	ECM-receptor interaction
233492_s_at	R2A4 /// OR2A	0.507	-0.106	L	G-protein coupled receptor protein signaling pathway /// perception of smell	olfactory receptor activity /// receptor activity	integral to membrane	---
1555423_at	SSH2	-0.067	-0.106	T	protein amino acid dephosphorylation	protein tyrosine/serine/threonine phosphatase activity	---	Regulation of actin cytoskeleton
208336_s_at	GPSN2	-0.509	-0.106	T	---	---	integral to membrane	---
237128_at	FLJ20184	0.19	-0.105	B	---	GTPase activator activity	---	---
203648_at	TATDN2	0.272	-0.105	L	---	nuclease activity /// hydrolase activity	---	---
226212_s_at	INSR	0.166	-0.105	T	carbohydrate metabolism /// generation of precursor metabolites and energy /// protein amino acid phosphorylation /// signal transduction /// transmembrane receptor protein tyrosine kinase signaling pathway /// development	receptor signaling protein tyrosine kinase activity /// receptor activity /// epidermal growth factor receptor activity /// transmembrane receptor protein tyrosine kinase signaling protein activity /// ATP binding /// transferase activity	plasma membrane /// integral to plasma membrane	Insulin receptor mediated signalling
222051_s_at	E2F5	0.15	-0.105	T	regulation of cell cycle /// transcription /// regulation of transcription, DNA-dependent	transcription factor activity /// protein binding	nucleus /// transcription factor complex	Cell cycle /// TGF-beta signaling pathway
232636_at	SLITRK4	0.047	-0.105	T	---	---	integral to membrane	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
213719_s_at	SMARCA4	-0.137	-0.104	B	Metabolism/// nucleobase, nucleoside, nucleotide and nucleic acid metabolism/// regulation of transcription from pol II promoter/// regulation of transcription/// regulation of transcription, DNA-dependent/// physiological process/// transcription, DNA-dependent/// regulation of metabolism/// transcription from pol II promoter/// regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism/// regulation of physiological process/// regulation of biological process	Purine nucleotide binding/// transcription factor activity/// ATPase activity/// transcription cofactor activity/// ATP-dependent helicase activity/// hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides/// nucleotide binding///adenyl nucleotide binding/// nucleic acid binding/// DNA binding/// transcription regulator activity/// transcription coactivator activity/// catalytic activity/// hydrolase activity/// ATP binding/// transcription factor binding/// ATPase activity, coupled/// hydrolase activity, acting on acid anhydrides/// protein binding///	---	---
244585_at	KIAA0590	0.196	-0.104	B	---	binding	---	---
214022_s_at	IFITM1	0.362	-0.104	L	regulation of cell cycle /// immune response /// cell surface receptor linked signal transduction /// negative regulation of cell proliferation /// response to biotic stimulus	receptor signaling protein activity	plasma membrane /// integral to membrane	---
209635_at	AP1S1	-0.245	-0.104	T	intracellular protein transport /// receptor mediated endocytosis	protein binding /// protein transporter activity	Golgi trans face /// coated pit /// AP-1 adaptor complex /// AP-1 adaptor complex	---
232643_at	POLR2F	0.146	-0.104	T	transcription, DNA-dependent /// regulation of transcription	DNA binding /// DNA-directed RNA polymerase activity /// transferase activity	nucleus /// RNA polymerase complex	RNA transcription Reactome /// Purine metabolism /// Pyrimidine metabolism /// RNA polymerase
231042_s_at	CAMK2D	-0.114	-0.104	T	regulation of cell growth /// protein amino acid phosphorylation /// protein amino acid phosphorylation	protein serine/threonine kinase activity /// calcium- and calmodulin-dependent protein kinase activity /// calmodulin binding /// ATP binding /// ATP binding /// kinase activity /// transferase activity	---	Calcium regulation in cardiac cells /// Smooth muscle contraction
204129_at	BCL9	0.164	-0.103	B	Wnt receptor signaling pathway	---	nucleus	---
216295_s_at	CLTA	-0.354	-0.103	T	intracellular protein transport	calcium ion binding	coated pit /// clathrin vesicle coat	---
226570_at	ATP1B3	-0.356	-0.103	T	transport /// potassium ion transport /// sodium ion transport	sodium:potassium-exchanging ATPase activity	sodium:potassium-exchanging ATPase complex /// membrane /// integral to membrane	Calcium regulation in cardiac cells
207214_at	SPINK4	0.259	-0.102	L	---	serine-type endopeptidase inhibitor activity	---	---
241350_at	FBXL22	0.054	-0.101	B	ubiquitin cycle	---	---	---
212320_at	TUBB	0.512	-0.101	L	microtubule-based movement /// natural killer cell mediated cytotoxicity /// microtubule polymerization	GTPase activity /// structural molecule activity /// GTP binding /// MHC class I protein binding /// unfolded protein binding	cytoplasm /// tubulin	---
1553978_at	MEF2B	-0.269	-0.101	T	transcription /// regulation of transcription, DNA-dependent /// transcription from RNA polymerase II promoter /// muscle development	transcription factor activity /// transcription coactivator activity	nucleus	---
223784_at	TMEM27	0.105	-0.101	T	---	---	integral to membrane	---
232503_at	STATIP1	0.142	-0.101	T	---	---	cytoskeleton	---

No.		Values): 1x LCPUFA (1.1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (1.3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
203358_s_at	EZH2	0.015	-0.1	B	establishment and/or maintenance of chromatin architecture /// regulation of transcription, DNA-dependent	DNA binding	nucleus	---
1562462_at	DNAH10	0.209	-0.1	L	microtubule-based movement	microtubule motor activity	flagellum /// dynein complex	---
222414_at	MLL3	-0.333	-0.1	T	transcription /// regulation of transcription, DNA-dependent /// ATP synthesis coupled proton transport /// protein ubiquitination /// chromatin modification	DNA binding /// ubiquitin-protein ligase activity /// ATP binding /// methyltransferase activity /// zinc ion binding /// transferase activity /// histone-lysine N-methyltransferase activity /// metal ion binding /// hydrogen-transporting ATP synthase activity, rotational mechanism /// hydrogen-transporting ATP activity, rotational mechanism	ubiquitin ligase complex /// nucleus --- /// proton-transporting two-sector ATPase complex	
214177_s_at	PBXIP1	-0.29	-0.1	T	negative regulation of transcription /// cell differentiation	transcription corepressor activity	nucleus /// cytosol	---
213055_at	CD47	-0.222	-0.1	T	cell-matrix adhesion /// integrin-mediated signaling pathway	protein binding	plasma membrane /// integral to plasma membrane	ECM-receptor interaction
240462_at	CLYBL	0.014	-0.1	T	---	citrate (pro-3S)-lyase activity /// lyase activity	citrate lyase complex	---
1553348_a_at	NFX1	0.185	-0.099	L	negative regulation of transcription from Pol II promoter /// regulation of transcription, DNA-dependent /// transcription from Pol II promoter /// mRNA processing /// mRNA-nucleus export /// transport /// inflammatory response /// protein ubiquitination	transcription factor activity /// ubiquitin-protein ligase activity /// zinc ion binding /// ligase activity	ubiquitin ligase complex /// nucleus	Tryptophan metabolism
230075_at	RAB39B	-0.107	-0.099	T	small GTPase mediated signal transduction /// protein transport	GTP binding	---	---
231067_s_at	AKAP12	-0.135	-0.099	T	signal transduction /// protein targeting /// G-protein coupled receptor protein signaling pathway	protein binding /// protein kinase A binding	cytoplasm	G Protein Signaling
202599_s_at	NRIP1	-0.811	-0.099	T	transcription /// regulation of transcription, DNA-dependent	transcription coactivator activity	nucleus	Ovarian Infertility Genes
228056_s_at	NAPSB	-0.241	-0.099	T	proteolysis and peptidolysis	peptidase activity /// peptidase activity	membrane	---
241805_at	GABRG1	0.101	-0.098	L	chloride transport /// gamma-aminobutyric acid signaling pathway	GABA-A receptor activity /// extracellular ligand-gated ion channel activity /// ion channel activity /// neurotransmitter receptor activity	integral to membrane /// postsynaptic membrane	Neuroactive ligand-receptor interaction
201372_s_at	CUL3	-0.182	-0.098	L	G1/S transition of mitotic cell cycle /// ubiquitin cycle /// cell cycle /// cell cycle arrest /// positive regulation of cell proliferation /// induction of apoptosis by intracellular signals	---	nucleus	Ubiquitin mediated proteolysis
1553130_at	FLJ39075	-0.215	-0.097	B	---	---	---	---
1554443_s_at	VMD2	0.172	-0.097	B	ion transport /// visual perception	ion channel activity	membrane fraction /// integral to membrane /// basolateral plasma membrane	---
1564945_at	TBX20	0.076	-0.097	T	transcription /// regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
204468_s_at	TIE1	0.446	-0.096	B	protein amino acid phosphorylation /// signal transduction /// mesoderm development	transmembrane receptor protein tyrosine kinase activity /// receptor activity /// ATP binding /// transferase activity	integral to plasma membrane	integrin-mediated cell adhesion

No.		Values):	(log2 Values):					
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
201660_at	ACSL3	-0.727	-0.096	L	lipid metabolism /// fatty acid metabolism /// metabolism	magnesium ion binding /// catalytic activity /// fatty-acyl-CoA synthase activity /// long-chain-fatty-acid-CoA ligase activity /// ligase activity	---	Fatty Acid Degradation /// Mitochondrial fatty acid betaoxidation /// Fatty acid metabolism
1555306_a_at	ECE2	0.183	-0.095	L	proteolysis and peptidolysis /// cell-cell signaling /// brain development /// heart development /// regulation of G-protein coupled receptor protein signaling pathway /// embryonic development /// cardioblast differentiation /// peptide hormone processing /// vasoconstriction	neprilysin activity /// zinc ion binding /// S-adenosylmethionine-dependent methyltransferase activity /// endothelin-converting enzyme activity /// endothelin-converting enzyme 1 activity /// transferase activity /// hydrolase activity	membrane /// integral to membrane /// cytoplasmic vesicle membrane	---
225984_at	PRKAA1	-0.163	-0.095	T	activation of MAPK /// response to hypoxia /// protein amino acid phosphorylation /// protein amino acid phosphorylation /// fatty acid biosynthesis /// cholesterol biosynthesis /// signal transduction /// negative regulation of protein biosynthesis /// positive regulation of cholesterol biosynthesis /// positive regulation of gluconeogenesis /// positive regulation of anti-apoptosis /// negative regulation of glucosylceramide biosynthesis /// positive regulation of fatty acid oxidation /// positive regulation of glucose import	protein serine/threonine kinase activity /// cAMP-dependent protein kinase activity /// ATP binding /// transferase activity /// eukaryotic elongation factor-2 kinase activator activity	intracellular	Benzoate degradation via CoA ligation/// Inositol phosphate metabolism/// Nicotinate and nicotinamide metabolism/// Phosphatidylinositol signaling system
235136_at	ORMDL3	-0.261	-0.095	T	---	---	integral to membrane	---
238825_at	ACRC	-0.22	-0.095	T	---	---	nucleus	---
206885_x_at	GH1	0.4	-0.094	L	signal transduction	hormone activity	extracellular region	Neuroactive ligand-receptor interaction/// cytokine-cytokine receptor interaction
243482_at	EPS15L1	0.055	-0.094	L	endocytosis	calcium ion binding	nucleus /// coated pit	---
205892_s_at	FABP1	-0.638	-0.093	L	fatty acid metabolism /// transport /// cell-cell signaling /// organogenesis	lipid transporter activity /// lipid binding	cytoplasm	---
204131_s_at	FOXO3A	-0.276	-0.093	T	transcription /// regulation of transcription, DNA-dependent /// transcription from RNA polymerase II promoter /// apoptosis /// induction of apoptosis	transcription factor activity	nucleus /// cytoplasm	---
218019_s_at	PDXK	-0.249	-0.093	T	---	ATP binding /// pyridoxal kinase activity /// transferase activity	---	Vitamin B6 metabolism
201315_x_at	IFITM2	0.157	-0.092	B	immune response /// response to biotic stimulus	---	integral to membrane	---
211816_x_at	FCAR	0.246	-0.092	L	immune response	receptor activity /// receptor signaling protein activity /// IgA binding	integral to plasma membrane	---
237762_at	RHAG	0.043	-0.092	T	transport /// circulation /// ammonium transport/// protein complex assembly	ammonium transporter activity /// ankyrin binding	plasma membrane /// integral to plasma membrane /// membrane	---
221940_at	RPUSD2	-0.297	-0.092	T	RNA processing	RNA binding /// pseudouridylate synthase activity /// pseudouridine synthase activity	---	---
201308_s_at	38606	0.067	-0.092	T	cytokinesis /// cell cycle	GTP binding	---	---
216185_at	FUT9	-0.05	-0.091	B	carbohydrate metabolism /// protein amino acid glycosylation /// L-fucose catabolism	transferase activity, transferring glycosyl groups /// alpha(1,3)-fucosyltransferase activity	Golgi apparatus /// integral to membrane	Blood group glycolipid biosynthesis-neolactoseries/// globoside metabolism

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
231750_at	PCDHB4	0.392	-0.091	L	cell adhesion /// homophilic cell adhesion /// synaptic transmission /// synaptogenesis /// calcium-dependent cell cell adhesion	calcium ion binding /// protein binding	integral to plasma membrane	---
215984_s_at	ARFRP1	-0.365	-0.091	T	intracellular protein transport /// signal transduction /// small GTPase mediated signal transduction	GTPase activity /// GTP binding	membrane fraction /// Golgi apparatus	---
215730_at	VGLL1	-0.133	-0.091	T	regulation of transcription, DNA-dependent	transcription coactivator activity /// transcription regulator activity	nucleus	---
242302_at	APRIN	-0.057	-0.091	T	regulation of transcription, DNA-dependent /// mitotic chromosome condensation /// cell proliferation /// negative regulation of cell proliferation	DNA binding /// binding /// ATP binding	nucleus	---
203318_s_at	ZNF148	-0.671	-0.09	L	negative regulation of transcription from Pol II promoter /// regulation of transcription, DNA-dependent /// cellular defense response	nucleic acid binding /// DNA binding /// specific RNA polymerase II transcription factor activity /// zinc ion binding /// transcriptional activator activity	nucleus /// DNA-directed RNA polymerase II, core complex	---
201960_s_at	MYCBP2	-1.054	-0.09	L	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
214071_at	GNAL	0.186	-0.09	L	signal transduction /// G-protein coupled receptor protein signaling pathway	GTPase activity /// signal transducer activity /// GTP binding	---	G Protein Signaling
201709_s_at	NIPSNAP1	-0.154	-0.09	T	---	---	mitochondrion	---
1569312_at	ZNF146	-0.213	-0.089	B	regulation of transcription, DNA-dependent	DNA binding /// heparin binding /// zinc ion binding	nucleus	---
211151_x_at	GH1	0.201	-0.089	L	signal transduction	hormone activity	extracellular region	---
231329_at	ITPR1	-0.162	-0.089	T	cation transport /// calcium ion transport /// signal transduction	inositol 1,4,5-triphosphate-sensitive calcium-release channel activity /// calcium channel activity /// inositol-1,4,5-triphosphate receptor activity /// calcium ion transporter activity	endoplasmic reticulum membrane /// integral to plasma membrane /// membrane	G Protein Signaling /// Calcium regulation in cardiac cells /// Smooth muscle contraction
219826_at	ZNF419	0.156	-0.088	B	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
219610_at	RGNEF	0.314	-0.088	L	intracellular signaling cascade	---	---	---
211794_at	FYB	-0.401	-0.088	L	protein amino acid phosphorylation /// NLS-bearing substrate-nucleus import /// immune response /// signal transduction /// protein kinase cascade	receptor binding /// protein binding	nucleus /// actin cytoskeleton	---
201689_s_at	TPD52	0.123	-0.087	B	morphogenesis	---	---	---
235982_at	FCRH1	0.263	-0.087	B	---	receptor activity	---	---
216683_at	TBCA	-0.211	-0.087	L	protein folding /// chaperonin-mediated tubulin folding /// post-chaperonin tubulin folding pathway /// beta-tubulin folding	unfolded protein binding /// chaperone binding	cytoskeleton	---
1555255_a_at	KIAA0377	0.223	-0.087	L	---	acid phosphatase activity	---	---
221042_s_at	CLMN	-0.053	-0.087	T	---	actin binding	integral to membrane	---
210056_at	RND1	-0.148	-0.087	T	actin filament organization /// negative regulation of cell adhesion /// small GTPase mediated signal transduction /// neuronal remodeling	GTPase activity /// GTP binding	cytoskeleton /// adherens junction	---
214113_s_at	RBM8A	0.149	-0.086	B	nuclear mRNA splicing, via spliceosome /// mRNA-nucleus export /// transport	mRNA binding	nucleus /// cytoplasm	mRNA Processing, Gene Expression
229726_at	GRAP	-0.153	-0.086	T	intracellular signaling cascade /// Ras protein signal transduction /// cell-cell signaling	SH3/SH2 adaptor activity	cytoplasm	---

No.		Values):	(log2 Values):					
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
1569856_at	TPP2	0.102	-0.085	B	proteolysis and peptidolysis	aminopeptidase activity /// subtilase activity /// tripeptidyl-peptidase II activity /// D-alanyl-D-alanine endopeptidase activity /// hydrolase activity	cytoplasm	---
241763_s_at	FBXO32	0.305	-0.085	L	ubiquitin cycle	---	---	---
1554183_s_at	TRIM50C	-0.294	-0.085	L	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
231264_at	COL9A2	0.141	-0.085	T	phosphate transport/// skeletal development	structural molecule activity	collagen type IX /// cytoplasm/// extracellular matrix (sensu Metazoa)	---
214454_at	ADAMTS2	0.111	-0.085	T	collagen catabolism	collagenase activity /// procollagen N-endopeptidase activity	extracellular matrix (sensu Metazoa)	---
203643_at	ERF	-0.225	-0.085	T	regulation of cell cycle /// transcription /// regulation of transcription from RNA polymerase II promoter /// cell proliferation	transcription factor activity /// ligand-regulated transcription factor activity /// transcription corepressor activity	nucleus	---
207224_s_at	SIGLEC7	0.071	-0.085	T	cell adhesion	receptor activity /// protein binding /// sugar binding	integral to plasma membrane	---
230895_at	HAPLN1	0.039	-0.084	T	cell adhesion	hyaluronic acid binding	extracellular matrix (sensu Metazoa)	---
210826_x_at	RAD17	0.218	-0.083	B	DNA replication checkpoint /// DNA damage checkpoint /// DNA replication /// DNA repair /// cell cycle /// mitotic checkpoint	nucleotide binding /// DNA binding /// ATP binding /// nucleoside-triphosphatase activity	nucleus /// DNA replication factor C complex /// mitochondrion	---
243333_at	LONP	-0.029	-0.083	T	ATP-dependent proteolysis	nucleotide binding /// ATP-dependent peptidase activity /// serine-type endopeptidase activity /// ATP binding /// nucleoside-triphosphatase activity	---	---
233789_at	EPHA6	0.073	-0.082	B	protein amino acid phosphorylation	protein-tyrosine kinase activity /// ATP binding	---	---
216188_at	MYCNOS	0.317	-0.082	L	development	---	---	---
1553319_at	OXGR1	0.269	-0.082	L	G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity /// purinergic nucleotide receptor activity, G-protein coupled	integral to membrane	---
48825_at	ING4	-0.206	-0.081	T	protein amino acid acetylation /// apoptosis /// cell cycle /// cell cycle arrest /// negative regulation of cell proliferation /// negative regulation of cell cycle /// negative regulation of transcription, DNA-dependent /// negative regulation of growth	DNA binding /// protein binding	nucleus	---
207753_at	ZNF304	-0.053	-0.08	L	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
225626_at	PAG	-0.649	-0.08	T	intracellular signaling cascade /// antimicrobial humoral response (sensu Vertebrata) /// negative regulation of T-cell activation	transmembrane receptor protein tyrosine kinase adaptor protein activity /// SH3/SH2 adaptor activity /// protein binding /// SH2 domain binding	integral to plasma membrane /// lipid raft /// lipid raft	---
231326_s_at	FAM11A	0.089	-0.08	T	---	---	integral to membrane	---
224407_s_at	MST4	0.159	-0.079	L	protein amino acid phosphorylation	protein kinase activity /// protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	---	---
1555430_at	C9orf97	-0.288	-0.079	L	---	phosphoprotein phosphatase activity /// hydrolase activity	---	Striated muscle contraction

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
224825_at	DNTTIP1	-0.202	-0.079	T	---	---	nucleus	---
238464_at	ANKRD36	0.108	-0.079	T	---	catalytic activity	---	---
214219_x_at	MAP4K1	0.129	-0.078	B	protein amino acid phosphorylation /// response to stress /// protein kinase cascade /// activation of JNK /// regulation of hemocyte differentiation	protein serine/threonine kinase activity /// small GTPase regulatoryinteracting protein activity /// ATP binding /// transferase activity	---	MAPK signaling pathway
204388_s_at	MAOA	0.084	-0.078	B	electron transport /// catecholamine metabolism /// behavior /// neurotransmitter catabolism	amine oxidase activity /// oxidoreductase activity	mitochondrion /// integral to membrane	tryptophan metabolism/// histidine metabolism/// phenylalanine metabolism/// arginine and proline metabolism/// glycine, serine and threonine metabolism/// tyrosine metabolism
222457_s_at	EPLIN	-0.361	-0.077	L	---	zinc ion binding	actin cytoskeleton	---
213540_at	HSD17B8	-0.364	-0.077	T	estrogen biosynthesis /// metabolism	alcohol dehydrogenase activity /// estradiol 17-beta-dehydrogenase activity /// oxidoreductase activity	---	Androgen and estrogen metabolism
240503_at	R3HDM	0.191	-0.077	T	---	nucleic acid binding ///	---	---
214338_at	DNAJB12	-0.196	-0.076	B	protein folding	endopeptidase inhibitor activity heat shock protein binding /// unfolded protein binding	integral to membrane	---
235727_at	BTBD5	-0.255	-0.076	B	---	protein binding	---	---
233896_s_at	PAPLN	-0.42	-0.076	B	---	metalloendopeptidase activity /// serine-type endopeptidase inhibitor activity /// peptidase activity	extracellular matrix	---
239210_at	PBX1	-0.17	-0.076	L	regulation of transcription, DNA-dependent /// transcription from Pol II promoter /// C21-steroid hormone biosynthesis /// sex differentiation /// embryonic development /// hindbrain development /// regulation of transcriptional preinitiation complex formation	transcription factor activity /// protein binding	nucleus	---
202417_at	KEAP1	-0.309	-0.075	T	transcription /// regulation of transcription, DNA-dependent	protein binding	---	---
228310_at	ENAH	0.235	-0.074	L	development /// neurogenesis	---	---	---
236562_at	MLL5	0.073	-0.074	T	regulation of transcription, DNA-dependent	DNA binding	nucleus	---
216980_s_at	SPN	-0.185	-0.074	T	chemotaxis /// cellular defense response /// negative regulation of cell adhesion /// establishment and/or maintenance of cell polarity /// signal transduction	transmembrane receptor activity ///	integral to plasma membrane	---
233537_at	KRTAP3-1	0.133	-0.073	B	---	structural molecule activity	keratin filament	---
210704_at	FEZ2	-0.216	-0.073	L	signal transduction /// neurogenesis /// axon guidance /// hemopoiesis	---	---	---
218984_at	LRRC5	-0.612	-0.073	L	---	---	integral to membrane	---
208632_at	RNF10	-0.24	-0.072	B	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
1556055_at	ATP11A	-0.214	-0.072	L	cation transport /// metabolism	magnesium ion binding /// catalytic activity /// phospholipid-translocating ATPase activity /// ATP binding /// ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism /// hydrolase activity /// ATPase activity	membrane /// integral to membrane	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
230878_s_at	COG1	-0.322	-0.072	T	intra-Golgi transport /// Golgi organization and biogenesis /// protein transport	protein transporter activity	membrane /// Golgi transport complex	---
237819_at	CREB3L2	0.175	-0.072	T	regulation of transcription, DNA-dependent	DNA binding	nucleus	---
1553217_s_at	ZNF41	-0.335	-0.072	T	transcription /// regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	nucleus	---
1557857_a_at	ABHD4	-0.123	-0.072	T	proteolysis and peptidolysis /// aromatic compound metabolism	aminopeptidase activity /// hydrolase activity	---	---
209053_s_at	WHSC1	0.091	-0.071	B	regulation of transcription, DNA-dependent /// morphogenesis /// protein ubiquitination	DNA binding /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
214498_at	ASIP	0.175	-0.071	L	generation of precursor metabolites and energy /// signal transduction /// cell-cell signaling /// hormone-mediated signaling	receptor binding	extracellular space	---
224047_at	RNF12	-0.144	-0.071	L	negative regulation of transcription/// protein ubiquitination/// regulation of transcription, DNA-dependent	metal ion binding/// transcription corepressor activity/// PubMed ubiquitin-protein ligase activity/// zinc ion binding	transcriptional repressor complex/// ubiquitin ligase complex	---
239526_x_at	PTPN1	-0.243	-0.07	L	protein amino acid dephosphorylation /// signal transduction	protein tyrosine phosphatase activity /// hydrolase activity	soluble fraction /// cytoplasm	---
211824_x_at	NALP1	0.393	-0.07	L	induction of apoptosis /// caspase activation /// defense response to pathogen /// regulation of apoptosis	ATP binding /// caspase activator activity /// enzyme binding	intracellular	---
241831_at	ZNF614	0.175	-0.07	T	regulation of transcription, DNA-dependent	nucleic acid binding /// DNA binding /// zinc ion binding	intracellular /// nucleus	---
202948_at	IL1R1	0.105	-0.069	B	inflammatory response /// cell surface receptor linked signal transduction	transmembrane receptor activity /// interleukin-1, Type I, activating receptor activity	integral to plasma membrane	cytokine-cytokine receptor interaction/// apoptosis/// MAPK signaling pathway
208345_s_at	POU3F1	-0.473	-0.069	L	regulation of transcription, DNA-dependent /// nerve ensheathment	transcription factor activity	nucleus	---
235539_at	NUMA1	0.447	-0.069	L	mitotic anaphase /// nuclear organization and biogenesis	structural molecule activity	nucleus /// spindle microtubule	---
226798_at	BCL2L13	-0.258	-0.069	L	induction of apoptosis /// caspase activation /// regulation of apoptosis	caspase activator activity	integral to membrane/// mitochondrion	---
241909_at	TNKS2	-0.138	-0.069	L	telomerase-dependent telomere maintenance	NAD+ ADP-ribosyltransferase activity /// transferase activity, transferring glycosyl groups	chromosome, telomeric region /// nucleus /// Golgi apparatus	---
231558_at	INSM1	-0.187	-0.069	T	regulation of transcription, DNA-dependent	zinc ion binding/// DNA binding	nucleus	---
204458_at	LYPLA3	-0.375	-0.068	T	lipid metabolism /// fatty acid catabolism	phosphatidylcholine-sterol O-acyltransferase activity /// lysophospholipase activity /// phospholipid binding /// acyltransferase activity /// transferase activity /// hydrolase activity	lysosome	Glycerophospholipid metabolism
1555367_at	ZNF479	0.079	-0.067	B	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
223148_at	PIGS	-0.173	-0.067	L	---	---	endoplasmic reticulum /// integral to membrane	glycosylphosphatidylinositol(gpi)-anchor biosynthesis
204918_s_at	MLLT3	-0.23	-0.067	T	transcription /// regulation of transcription, DNA-dependent	---	nucleus	---

No.		Values):	(log2 Values):					
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
209881_s_at	LAT	-0.472	-0.067	T	immune response /// integrin-mediated signaling pathway /// intracellular signaling cascade /// Ras protein signal transduction /// calcium-mediated signaling /// regulation of T-cell activation	SH3/SH2 adaptor activity /// protein binding /// protein binding	immunological synapse /// membrane /// integral to membrane /// lipid raft	---
230072_at	CCND1	-0.265	-0.067	T	G1/S transition of mitotic cell cycle /// regulation of cell cycle	---	nucleus	cell cycle/// focal adhesion/// Jak-STAT signaling pathway/// Wnt signaling pathway
1555347_at	KIAA0251	-0.231	-0.066	B	amino acid metabolism	lyase activity /// carboxy-lyase activity	---	---
233921_s_at	MAD1L1	0.281	-0.066	L	---	---	---	Cell cycle
202667_s_at	SLC39A7	-0.306	-0.066	T	transport /// metal ion transport	metal ion transporter activity	membrane fraction /// membrane /// integral to membrane	---
237269_at	EVI1	-0.247	-0.065	L	development	DNA binding /// zinc ion binding	nucleus	MAPK signaling pathway
202837_at	FLN29	-0.334	-0.065	L	---	DNA binding /// zinc ion binding	nucleus	---
202470_s_at	CPSF6	0.262	-0.065	L	nuclear mRNA splicing, via spliceosome	nucleic acid binding /// RNA binding	nucleus	---
216881_x_at	PRB4	0.104	-0.064	B	G-protein coupled receptor protein signaling pathway /// visual perception	rhodopsin-like receptor activity	extracellular region /// extracellular space /// integral to membrane	---
236274_at	EIF3S9	-0.337	-0.064	L	protein biosynthesis /// translational initiation	RNA binding /// translation initiation factor activity	eukaryotic translation initiation factor 3 complex	Translation Factors
226439_s_at	NBEA	0.22	-0.063	L	post-Golgi transport	protein kinase A binding	Golgi trans face /// cytosol /// plasma membrane /// endomembrane system /// postsynaptic membrane	---
201827_at	SMARCD2	-0.343	-0.063	T	chromatin remodeling /// transcription /// regulation of transcription from RNA polymerase II promoter	transcription coactivator activity	nucleoplasm	---
223755_at	KIRREL2	0.153	-0.063	T	cell adhesion	---	integral to membrane	---
222138_s_at	WDR13	-0.405	-0.063	T	---	---	nucleus	---
210022_at	PCGF1	0.163	-0.061	L	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
219525_at	FLJ10847	0.246	-0.061	T	multidrug transport	drug transporter activity /// antiporter activity	membrane	---
208046_at	HIST1H4I	-0.293	-0.061	T	DNA metabolism/// chromosome organization and biogenesis (sensu eukarya)/// nucleobase, nucleoside, nucleotide and nucleic acid metabolism/// nuclear organization and biogenesis/// cell growth and/or maintenance/// cell organization and biogenesis	nucleic acid binding/// DNA binding	---	---
204504_s_at	HIRIP3	-0.254	-0.061	T	chromatin assembly or disassembly	---	nucleus	---
202666_s_at	ACTL6A	0.139	-0.06	B	regulation of cell growth /// chromatin remodeling /// regulation of transcription, DNA-dependent /// signal transduction /// response to pest, pathogen or parasite /// chromatin modification	chromatin binding /// motor activity /// structural constituent of cytoskeleton	nucleus /// actin filament /// TIP60 histone acetyltransferase complex	---
216217_at	PLCL2	0.177	-0.06	T	lipid metabolism /// intracellular signaling cascade	phosphoinositide phospholipase C activity /// calcium ion binding	---	---
225982_at	UBTF	-0.226	-0.06	T	transcription /// regulation of transcription, DNA-dependent /// regulation of transcription from RNA polymerase I promoter	DNA binding /// RNA polymerase I transcription factor activity	nucleus /// nucleolus	Transcription

No.			log2 Values):					
		Values): 1x LCPUFA (L1, 0.33% DNA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
216317_x_at	RHCE	0.193	-0.059	T	transport	transporter activity	integral to plasma membrane /// membrane /// integral to membrane	---
233315_at	CTBP2	-0.353	-0.059	T	L-serine biosynthesis /// negative regulation of cell proliferation /// viral genome replication	oxidoreductase activity /// oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	nucleus	Wnt signaling pathway/// Notch signaling pathway
241287_x_at	POLN	-0.177	-0.058	L	DNA replication	DNA binding /// DNA-directed DNA polymerase activity /// transferase activity	---	---
1555317_at	POLK	0.065	-0.058	L	mutagenesis /// DNA repair	DNA binding	---	DNA polymerase
205914_s_at	GRIN1	0.194	-0.058	T	cation transport /// cation transport /// potassium ion transport /// calcium ion homeostasis /// calcium ion homeostasis /// glutamate signaling pathway /// synaptic transmission /// synaptic transmission /// learning and/or memory /// learning and/or memory /// response to ethanol /// regulation of synaptic plasticity	magnesium ion binding /// motor activity /// receptor activity /// N-methyl-D-aspartate selective glutamate receptor activity /// N-methyl-D-aspartate selective glutamate receptor activity /// ion channel activity /// glutamate-gated ion channel activity /// glutamate-gated ion channel activity /// potassium channel activity /// glycine binding /// glutamate binding /// glycine-gated ion channel activity /// glycine-gated ion channel activity	membrane /// integral to membrane /// integral to membrane /// N-methyl-D-aspartate selective glutamate receptor complex /// N-methyl-D-aspartate selective glutamate receptor complex /// dendrite /// dendrite /// growth cone	Neuroactive ligand-receptor interaction/// calcium signaling pathway
220325_at	TAF7L	0.139	-0.058	T	regulation of transcription	transcription factor activity	nucleus	Basal transcription factors
222916_s_at	HDLBP	0.145	-0.057	L	lipid transport /// cholesterol metabolism	nucleic acid binding /// RNA binding /// lipid transporter activity /// lipid binding	nucleus /// plasma membrane	---
1560915_at	DPY19L1	0.015	-0.057	T	response to external stimulus/// Immune response/// defense response	signal transducer activity/// receptor binding/// chemokine receptor binding/// G-protein-coupled receptor binding/// cytokine activity	---	---
219396_s_at	NEIL1	0.241	-0.056	B	carbohydrate metabolism /// DNA repair	DNA binding /// DNA-(apurinic or apyrimidinic site) lyase activity /// endonuclease activity /// hydrolase activity, acting on glycosyl bonds /// lyase activity	nucleus	---
1552555_at	FLJ90661	0.091	-0.056	B	proteolysis and peptidolysis	chymotrypsin activity /// trypsin activity	---	---
204712_at	WIF1	-0.262	-0.056	L	signal transduction /// cell-cell signaling /// development /// Wnt receptor signaling pathway	protein-tyrosine kinase activity	---	Wnt signaling pathway
211574_s_at	MCP	0.187	-0.055	B	complement activation, classical pathway	receptor activity	integral to plasma membrane	complement and coagulation cascades
209318_x_at	PLAGL1	0.125	-0.055	B	regulation of transcription, DNA-dependent /// induction of apoptosis /// cell cycle arrest	nucleic acid binding /// DNA binding /// zinc ion binding	nucleus	---
210297_s_at	MSMB	-0.07	-0.055	L	---	---	extracellular space /// nucleus	---
243062_at	MOBKL2C	0.318	-0.055	L	---	kinase activity	---	---
214525_x_at	MLH3	0.275	-0.055	L	mismatch repair /// meiotic recombination	satellite DNA binding /// protein binding /// ATP binding	nucleus	---
235802_at	TP53INP1	0.28	-0.055	T	apoptosis	---	nucleus	---

No.		Values):	(log2 Values):					
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
236750_at	NRXN3	-0.126	-0.055	T	cell adhesion /// axon guidance	receptor activity /// structural molecule activity /// protein binding	integral to plasma membrane /// integral to membrane	---
223659_at	MSP	0.328	-0.054	L	proteolysis and peptidolysis	chymotrypsin activity /// trypsin activity /// scavenger receptor activity /// peptidase activity	integral to membrane	---
243666_at	BRUNOL4	0.088	-0.054	T	germ cell development /// embryonic development /// RNA interference	nucleotide binding /// translation repressor activity, nucleic acid binding /// nucleic acid binding /// BRE binding	nucleus /// ribonucleoprotein complex	mRNA processing
227581_at	KFZP434B033	-0.16	-0.054	T	---	---	integral to membrane	---
206790_s_at	NDUFB1	-0.265	-0.053	T	---	NADH dehydrogenase activity /// NADH dehydrogenase (ubiquinone) activity /// oxidoreductase activity	mitochondrion	Electron Transport Chain
202399_s_at	AP3S2	0.387	-0.051	B	transport /// intracellular protein transport	---	Golgi apparatus /// clathrin vesicle coat	---
205501_at	PDE10A	-0.155	-0.051	T	signal transduction	3'-5'-cyclic-nucleotide phosphodiesterase activity/// hydrolase activity/// nucleotide binding	---	purine metabolism
1556095_at	UNC13C	0.075	-0.051	T	exocytosis /// intracellular signaling cascade	diacylglycerol binding	synaptosome	---
218356_at	FTSJ2	-0.195	-0.051	T	rRNA processing	methyltransferase activity /// transferase activity	nucleus	Androgen and estrogen metabolism/// aminophosphonate metabolism/// histidine metabolism/// nitrobenzene degradation/// selenoamino acid metabolism/// Tryptophan metabolism/// tyrosine metabolism
208368_s_at	BRCA2	-0.207	-0.051	T	regulation of cell cycle /// double-strand break repair via homologous recombination /// DNA repair /// establishment and/or maintenance of chromatin architecture /// chromatin remodeling /// regulation of S phase of mitotic cell cycle /// mitotic checkpoint /// regulation of transcription	nucleic acid binding /// single-stranded DNA binding /// protein binding	extracellular space /// nucleus /// secretory granule	DNA Repair
227263_at	PDLIM2	-0.192	-0.051	T	---	protein binding/// zinc ion binding	cell surface/// cytoskeleton/// nucleus	---
232105_at	LEMD1	0.217	-0.051	T	---	---	nuclear membrane	---
242659_at	ELF4	-0.279	-0.05	L	regulation of transcription, DNA-dependent /// transcription from Pol II promoter	transcription factor activity /// transcription coactivator activity	nucleus	---
1553284_s_at	LMLN	-0.131	-0.05	T	proteolysis and peptidolysis /// cell adhesion	metalloendopeptidase activity /// hydrolase activity	membrane	---
220031_at	ZA20D1	0.166	-0.05	T	ubiquitin cycle	DNA binding /// cysteine-type peptidase activity /// zinc ion binding	nucleus	---
209369_at	ANXA3	0.33	-0.049	B	---	calcium ion binding /// calcium-dependent phospholipid binding /// diphosphoinositol-polyphosphate diphosphatase activity /// phospholipase A2 inhibitor activity	cytoplasm	Prostaglandin synthesis regulation
218725_at	SLC25A22	-0.374	-0.049	T	transport /// L-glutamate transport	L-glutamate transporter activity /// carrier activity /// binding /// symporter activity	mitochondrion /// mitochondrial inner membrane /// integral to membrane	---

No.		Values):	(log2 Values):					
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
223284_at	KLP1	-0.151	-0.049	T	transcription initiation	N-acetyltransferase activity /// transcriptional activator activity	nucleus	---
208283_at	GAGE1	0.279	-0.049	T	cellular defense response	---	---	---
206494_s_at	ITGA2B	0.093	-0.049	T	cell-matrix adhesion /// integrin-mediated signaling pathway	receptor activity /// protein binding	integrin complex	Integrin-mediated cell adhesion
1565358_at	RARA	0.439	-0.048	L	regulation of transcription, DNA-dependent /// signal transduction	transcription factor activity /// steroid hormone receptor activity /// retinoic acid receptor activity /// transcription coactivator activity	nucleus	Nuclear Receptors
241794_at	ACTR6	-0.295	-0.048	L	---	structural constituent of cytoskeleton	actin cytoskeleton	---
226731_at	PELO	-0.229	-0.048	T	protein biosynthesis	---	nucleus	---
231868_at	KIAA1443	0.199	-0.047	T	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
235175_at	GBP4	0.149	-0.047	T	immune response	GTP binding/// GTPase activity	---	---
233983_at	TGM6	0.21	-0.047	T	peptide cross-linking	protein-glutamine gamma-glutamyltransferase activity /// calcium ion binding /// acyltransferase activity /// transferase activity	---	---
217004_s_at	MCF2	-0.349	-0.046	B	intracellular signaling cascade	guanyl-nucleotide exchange factor activity	membrane fraction /// cytosol /// cytoskeleton	---
217951_s_at	PHF3	-0.348	-0.046	L	transcription /// regulation of transcription, DNA-dependent /// development	DNA binding	---	---
215647_at	C13orf10	0.133	-0.045	B	---	nucleic acid binding	---	---
203229_s_at	CLK2	0.459	-0.045	L	protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	nucleus	mRNA processing
211025_x_at	COX5B	-0.247	-0.045	T	electron transport /// respiratory gaseous exchange	cytochrome-c oxidase activity /// oxidoreductase activity	mitochondrial membrane /// inner membrane	Oxidative phosphorylation
226947_at	C6orf216	-0.201	-0.045	T	carbohydrate metabolism	hydrolase activity, hydrolyzing O-glycosyl compounds	---	---
203831_at	KIAA1002	-0.232	-0.045	T	---	nucleic acid binding	nucleus	---
1570121_at	ZNF365	0.242	-0.044	L	---	nucleic acid binding /// zinc ion binding	nucleus	---
1552481_s_at	MAN1A2	0.216	-0.044	T	carbohydrate metabolism /// N-glycan processing	mannosyl-oligosaccharide 1,2-alpha-mannosidase activity /// calcium ion binding /// hydrolase activity, acting on glycosyl bonds	membrane fraction /// Golgi apparatus /// membrane /// integral to membrane	High-mannose type N-glycan biosynthesis/// N-Glycan biosynthesis
223353_at	HCCA2	-0.278	-0.044	T	---	---	nucleus	---
213622_at	COL9A2	0.378	-0.043	B	skeletal development /// phosphate transport	structural molecule activity	extracellular matrix (sensu Metazoa) /// collagen type IX /// cytoplasm	---
229653_at	FLJ10979	-0.142	-0.043	B	response to external stimulus/// physiological process/// response to biotic stimulus/// defense response	---	---	---
218358_at	MGC11256	-0.211	-0.043	T	---	calcium ion binding	---	---
214096_s_at	SHMT2	0.181	-0.042	B	glycine metabolism /// L-serine metabolism /// one-carbon compound metabolism	glycine hydroxymethyltransferase activity /// transferase activity	mitochondrion	Glycine, serine and threonine metabolism /// Lysine degradation /// Cyanoamino acid metabolism /// One carbon pool by folate /// Methane metabolism
213019_at	RANBP6	-0.275	-0.042	T	protein transport	binding	nucleus	---

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
1560265_at	GRIK2	0.191	-0.042	T	ion transport /// potassium ion transport /// glutamate signaling pathway /// synaptic transmission /// synaptic transmission	receptor activity /// ionotropic glutamate receptor activity /// transporter activity /// ion channel activity /// glutamate-gated ion channel activity /// potassium channel activity /// kainate selective glutamate receptor activity	integral to plasma membrane /// membrane /// integral to membrane	neuroactive ligand-receptor interaction
203707_at	ZNF263	-0.428	-0.041	L	regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	nucleus	---
213994_s_at	SPON1	-0.298	-0.041	L	cell adhesion /// development	protein binding	extracellular matrix (sensu Metazoa)	---
1558896_at	STXBP5L	0.257	-0.041	T	vesicle-mediated transport	---	integral to membrane	---
1560526_at	PR47	0.18	-0.041	T	negative regulation of cell adhesion /// platelet activation /// negative regulation of blood coagulation	transmembrane receptor activity /// collagen binding	integral to membrane	---
218795_at	ACP6	-0.236	-0.041	T	---	acid phosphatase activity	---	---
209238_at	STX3A	0.236	-0.04	L	neurotransmitter transport /// intracellular protein transport	protein transporter activity	integral to membrane	---
217339_x_at	CTAG1B	-0.335	-0.04	L	---	---	integral to membrane	---
206247_at	MICB	0.522	-0.04	T	response to stress /// cellular defense response /// cell recognition /// antigen presentation	protein binding /// MHC class I receptor activity	MHC class I protein complex	---
229663_at	LONP	-0.334	-0.039	L	ATP-dependent proteolysis	nucleotide binding /// ATP-dependent peptidase activity /// serine-type endopeptidase activity /// ATP binding /// nucleoside-triphosphatase activity	---	---
240122_at	DIRAS2	0.105	-0.039	T	small GTPase mediated signal transduction	GTP binding	---	---
229529_at	TCF21	0.14	-0.039	T	transcription /// regulation of transcription, DNA-dependent /// mesoderm development	DNA binding /// RNA polymerase II transcription factor activity	nucleus	---
215565_at	DTNB	0.194	-0.039	T	---	calcium ion binding /// protein binding /// zinc ion binding	cytoskeleton	---
231917_at	GFM2	0.437	-0.038	B	protein biosynthesis /// translational elongation	translation elongation factor activity /// GTP binding	mitochondrion	---
233308_at	COPB	0.19	-0.038	T	retrograde transport, Golgi to ER /// protein targeting/// intra-Golgi transport /// protein transport	protein binding	Golgi membrane /// Golgi stack /// Golgi vesicle /// cytosol /// membrane /// COPI vesicle coat	---
222620_s_at	DNAJC1	-0.558	-0.038	T	protein folding /// regulation of transcription /// negative regulation of proteolysis and peptidolysis /// regulation of protein secretion	ATPase stimulator activity /// DNA binding /// Hsp70/Hsc70 protein regulator activity /// heat shock protein binding /// ribosome binding /// unfolded protein binding	nucleus /// endoplasmic reticulum lumen /// microsome /// integral to membrane	---
210310_s_at	FGF5	0.232	-0.036	L	regulation of cell cycle /// cell-cell signaling /// neurogenesis /// cell proliferation /// fibroblast growth factor receptor signaling pathway	growth factor activity	extracellular space	MAPK signaling pathway
230472_at	IRX1	-0.215	-0.035	B	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
204738_s_at	CCM1	-0.346	-0.035	L	small GTPase mediated signal transduction	small GTPase regulatory/interacting protein activity /// binding	cytoskeleton	---

No.		Values):	(log2 Values):					
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
1555323_at	ABCB9	0.122	-0.035	T	transport /// transport /// oligopeptide transport /// spermatogenesis	nucleotide binding /// ATP binding /// ATP binding /// oligopeptide transporter activity /// ATPase activity /// ATPase activity, coupled to transmembrane movement of substances	lysosome /// integral to membrane /// integral to membrane /// ATP-binding cassette (ABC) transporter complex	---
203618_at	FAIM2	-0.191	-0.035	T	apoptosis /// anti-apoptosis	---	integral to membrane	---
222109_at	GNL3L	-0.174	-0.035	T	---	GTP binding	---	---
224576_at	KIAA1181	-0.326	-0.034	B	transport	---	endoplasmic reticulum /// Golgi apparatus /// integral to membrane	---
228269_x_at	CSEN	0.235	-0.034	T	transcription /// regulation of transcription from RNA polymerase II promoter /// signal transduction	DNA binding /// transcription corepressor activity /// calcium ion binding /// calcium ion binding	nucleus	---
214940_s_at	C17orf31	0.177	-0.033	B	telomerase-dependent telomere maintenance	DNA binding	chromosome, telomeric region /// nucleus	---
240461_at	BICD1	-0.175	-0.033	B	---	---	Golgi apparatus	---
244511_at	PDE4DIP	-0.117	-0.033	T	protein biosynthesis /// cytoskeleton organization and biogenesis /// actin cytoskeleton organization and biogenesis	structural constituent of ribosome /// actin binding	intracellular /// ribosome /// actin cytoskeleton	---
213131_at	OLFM1	0.383	-0.032	L	development /// neurogenesis	latrotoxin receptor activity	endoplasmic reticulum /// membrane	---
235192_at	TP53RK	-0.173	-0.032	L	protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein binding /// ATP binding /// transferase activity	nucleus	---
217511_at	KAZALD1	-0.169	-0.031	B	regulation of cell growth	insulin-like growth factor binding /// peptidase activity	extracellular region	---
240450_at	PAPPA	0.365	-0.031	L	proteolysis and peptidolysis /// pregnancy /// cell differentiation	metallopeptidase activity /// zinc ion binding /// hydrolase activity	extracellular space /// membrane	---
224601_at	SIAT7B	0.339	-0.031	L	protein amino acid glycosylation	sialyltransferase activity	Golgi apparatus /// integral to membrane	ganglioside biosynthesis/// globoside metabolism/// blood group glycolipid biosynthesis-neolactoseries
1552548_at	BSND	0.181	-0.031	T	---	---	integral to membrane	---
219749_at	SH2D4A	-0.404	-0.03	L	intracellular signaling cascade	---	---	---
225393_at	P66beta	0.348	-0.03	L	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
223591_at	RNF135	0.237	-0.029	B	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
228137_s_at	PPP2R2C	-0.316	-0.029	L	signal transduction	hydrolase activity/// phosphoprotein phosphatase activity/// protein phosphatase type 2A regulator activity	protein phosphatase type 2A complex	Wnt signaling pathway/// tight junction
1553059_at	PGLYRP3	0.284	-0.029	L	peptidoglycan catabolism /// detection of bacteria /// innate immune response /// defense response to Gram-positive bacteria	N-acetylmuramoyl-L-alanine amidase activity /// peptidoglycan receptor activity	intracellular /// membrane	---
208661_s_at	TTC3	-0.669	-0.029	L	protein ubiquitination	ubiquitin-protein ligase activity /// binding /// zinc ion binding	ubiquitin ligase complex	---
222359_x_at	FVT1	0.134	-0.029	T	metabolism	oxidoreductase activity /// 3-dehydrosphinganine reductase activity	extracellular space /// endoplasmic reticulum /// integral to membrane	---
227079_at	DHX8	0.137	-0.028	B	nuclear mRNA splicing, via spliceosome /// RNA splicing	RNA binding /// ATP-dependent RNA helicase activity /// ATP binding /// pre-mRNA splicing factor activity	spliceosome complex	mRNA processing

No.		Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
214613_at	GPR3	0.085	-0.027	T	signal transduction /// G-protein coupled receptor protein signaling pathway /// G-protein signaling, adenylate cyclase activating pathway	rhodopsin-like receptor activity /// receptor activity /// G-protein coupled receptor activity, unknown ligand	integral to plasma membrane	GPCRDB Class A Rhodopsin-like
228545_at	ZNF148	-0.584	-0.027	T	negative regulation of transcription from RNA polymerase II promoter /// transcription /// regulation of transcription, DNA-dependent /// regulation of transcription, DNA-dependent /// cellular defense response	nucleic acid binding /// DNA binding /// specific RNA polymerase II transcription factor activity /// zinc ion binding /// transcriptional activator activity	nucleus /// nucleus /// DNA-directed RNA polymerase II, core complex	---
227907_at	TP53BP1	0.223	-0.027	T	transcription /// positive regulation of transcription, DNA-dependent	protein binding /// transcriptional activator activity	nucleoplasm /// cytoplasm	DNA Repair
214917_at	PRKAA1	0.122	-0.026	B	activation of MAPK /// response to hypoxia /// protein amino acid phosphorylation /// fatty acid biosynthesis /// cholesterol biosynthesis /// negative regulation of protein biosynthesis /// positive regulation of cholesterol biosynthesis /// positive regulation of gluconeogenesis /// positive regulation of anti-apoptosis /// negative regulation of glucosylceramide biosynthesis /// positive regulation of fatty acid oxidation /// positive regulation of glucose import	protein serine/threonine kinase activity /// cAMP-dependent protein kinase activity /// ATP binding /// transferase activity /// eukaryotic elongation factor-2 kinase activator activity	intracellular	Fatty Acid Synthesis
205825_at	PCSK1	0.11	-0.026	T	proteolysis and peptidolysis /// cell-cell signaling /// metabolism	proprotein convertase 1 activity /// subtilase activity /// peptidase activity	---	---
226991_at	NFATC2	0.314	-0.025	L	regulation of transcription, DNA-dependent	transcription factor activity	nucleus /// cytoplasm	Wnt signaling pathway/// MAPK signaling pathway
1566201_at	PPP3CA	0.23	-0.025	T	protein amino acid dephosphorylation	protein serine/threonine phosphatase activity /// calcium ion binding /// calmodulin binding /// hydrolase activity	calcineurin complex	G Protein Signaling
235983_at	ALS2CR3	0.407	-0.024	L	neurotransmitter transport	receptor binding /// intracellular transporter activity	cytoplasm /// plasma membrane	---
1553736_at	MGC23401	-0.235	-0.024	L	mRNA processing	binding	intracellular	---
1552970_s_at	ZNF258	0.085	-0.024	T	development	DNA binding /// zinc ion binding	nucleus	---
235312_s_at	NRAP	0.16	-0.023	T	ion transport	actin binding /// zinc ion binding	cytoskeleton	---
226718_at	AMIGO	0.158	-0.023	T	---	---	integral to membrane	---
201991_s_at	KIF5B	-0.755	-0.023	T	microtubule-based movement	microtubule motor activity /// ATP binding	kinesin complex	---
1559259_at	AKAP8	-0.159	-0.022	B	transport /// mitosis /// signal transduction	DNA binding /// sugar porter activity /// zinc ion binding /// protein kinase A binding	nucleus /// membrane	G Protein Signaling
229103_at	WNT3	0.172	-0.022	T	frizzled-2 signaling pathway /// cell-cell signaling /// morphogenesis	signal transducer activity /// extracellular matrix structural constituent	extracellular matrix (sensu Metazoa)	Wnt signaling pathway/// Hedgehog signaling pathway
207174_at	GPC5	0.159	-0.022	T	---	---	extracellular matrix (sensu Metazoa) /// integral to plasma membrane /// membrane	---
203189_s_at	NDUFS8	-0.216	-0.02	T	electron transport /// mitochondrial electron transport, NADH to ubiquinone	NADH dehydrogenase activity /// iron ion binding /// NADH dehydrogenase (ubiquinone) activity /// electron carrier activity	membrane fraction /// mitochondrion	Oxidative phosphorylation
239114_at	DELGEF	0.159	-0.02	T	signal transduction	Ran guanyl-nucleotide exchange factor activity /// protein binding	nucleus /// cytoplasm	---

No.		Value(s):	(log2 Values):					
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
233242_at	SCAND2	-0.404	-0.02	T	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
239190_at	VRK3	0.133	-0.02	T	protein amino acid phosphorylation	protein serine/threonine kinase activity /// ATP binding /// transferase activity	---	---
227880_s_at	FAM11A	-0.166	-0.02	T	---	---	integral to membrane	---
226086_at	MITF	-0.227	-0.019	B	regulation of transcription, DNA-dependent /// development /// perception of sound /// melanocyte differentiation	DNA binding /// transcriptional activator activity	nucleus	---
204385_at	KYNU	-0.367	-0.019	L	tryptophan catabolism /// NAD biosynthesis	peptidase activity /// pyridoxal phosphate binding /// kynureninase activity	cytoplasm	Tryptophan metabolism
224441_s_at	USP45	0.161	-0.019	L	electron transport /// ubiquitin-dependent protein catabolism /// ubiquitin cycle /// transport	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity /// electron transporter activity /// iron ion binding	---	---
223678_s_at	TPA1 /// SFTP	-0.232	-0.018	L	phosphate transport /// respiratory gaseous exchange /// regulation of liquid surface tension	lipid transporter activity /// sugar binding	extracellular space /// cytoplasm	---
229250_at	TPCN2	-0.463	-0.018	L	cation transport	cation channel activity	membrane	---
224537_at	PCDHGC5	0.089	-0.018	T	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	membrane /// integral to membrane	---
1554262_s_at	KBTBD9	0.21	-0.018	T	---	protein binding	nucleus	---
224126_at	DKFZP566M111	-0.138	-0.016	T	sodium ion transport	bile acid:sodium symporter activity	membrane	---
1561146_at	VPS35	0.154	-0.016	T	protein transport /// retrograde transport, endosome to Golgi	protein binding	cytosol	---
243372_at	HSPD1	0.13	-0.016	T	protein folding /// protein folding /// response to unfolded protein /// response to unfolded protein /// mitochondrial matrix protein import	ATP binding /// ATP binding /// unfolded protein binding	mitochondrial matrix	Prion disease
217094_s_at	ITCH	-0.397	-0.015	L	ubiquitin cycle /// viral entry into host cell	ubiquitin-protein ligase activity /// protein binding /// ligase activity	nucleus	ubiquitin mediated proteolysis /// dentatorubropallidoluysian atrophy (drpla)
238190_at	TUFM	-0.271	-0.015	T	protein biosynthesis /// translational elongation	translation elongation factor activity /// GTP binding	mitochondrion	---
228607_at	OAS2	0.207	-0.014	B	nucleobase, nucleoside, nucleotide and nucleic acid metabolism /// immune response	RNA binding /// ATP binding /// transferase activity /// nucleotidyltransferase activity	microsome /// membrane	Ubiquinone biosynthesis /// Porphyrin and chlorophyll metabolism
241590_at	RNF130	-0.224	-0.014	B	proteolysis and peptidolysis /// apoptosis /// protein ubiquitination	ubiquitin-protein ligase activity /// peptidase activity /// zinc ion binding	ubiquitin ligase complex /// integral to membrane	---
204243_at	RLF	-0.324	-0.014	L	---	nucleic acid binding /// zinc ion binding	nucleus	---
238073_at	ELAVL4	-0.227	-0.014	L	nuclear mRNA splicing, via spliceosome /// mRNA processing	RNA binding /// mRNA 3'-UTR binding	---	---
210357_s_at	SMOX	0.134	-0.013	B	electron transport	oxidoreductase activity	---	---
211103_at	MYO7A	-0.393	-0.013	L	visual perception /// perception of sound /// actin filament-based movement	microfilament motor activity /// actin binding /// calmodulin binding /// ATP binding /// ATPase activity, coupled	cytoskeleton /// myosin	---
240052_at	ITPR1	0.222	-0.013	T	cation transport /// calcium ion transport /// signal transduction	inositol 1,4,5-triphosphate-sensitive calcium-release channel activity /// calcium channel activity /// inositol-1,4,5-triphosphate receptor activity /// calcium ion transporter activity	endoplasmic reticulum membrane /// integral to plasma membrane /// membrane	Phosphatidylinositol signaling system /// calcium signaling pathway /// hemostasis

No.		Values: 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	(log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
1554921_a_at	SCEL	0.181	-0.013	T	epidermis development	zinc ion binding	cytoplasm	---
219033_at	PARP8	0.268	-0.013	T	protein amino acid ADP-ribosylation	NAD+-ADP-ribosyltransferase activity	nucleus	---
204509_at	CA12	-0.191	-0.012	L	one-carbon compound metabolism	carbonate dehydratase activity /// zinc ion binding /// lyase activity	integral to membrane	Nitrogen metabolism
206469_x_at	AKR7A3	0.573	-0.012	L	aldehyde metabolism	aldo-keto reductase activity /// electron transporter activity	cytosol	---
220558_x_at	PHEMX	-0.283	-0.012	L	cell-cell signaling	---	integral to membrane	---
207014_at	GABRA2	0.131	-0.012	T	ion transport /// regulation of neurotransmitter levels /// chloride transport /// gamma-aminobutyric acid signaling pathway	GABA-A receptor activity /// ion channel activity /// extracellular ligand-gated ion channel activity /// benzodiazepine receptor activity	integral to plasma membrane /// postsynaptic membrane	neuroactive ligand-receptor interaction
203978_at	NUBP1	0.11	-0.012	T	sequin ring assembly	nucleotide binding /// ATP binding	---	---
237706_at	STXBP4	0.187	-0.011	B	---	protein binding	---	---
218783_at	DKFZP434B16	-0.232	-0.011	B	---	binding	---	---
1564064_a_at	ATP11B	-0.457	-0.011	L	cation transport /// metabolism	magnesium ion binding /// phospholipid-translocating ATPase activity /// binding /// ATP binding /// ion transporter activity /// ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism /// hydrolase activity /// ATPase activity	nuclear inner membrane /// membrane /// integral to membrane	---
237199_at	TAF5L	-0.327	-0.011	L	regulation of transcription, DNA-dependent /// transcription from Pol II promoter	transcription factor activity	nucleus	basal transcription factors
1567287_at	OR5K1	0.167	-0.011	L	G-protein coupled receptor protein signaling pathway /// perception of smell /// sensory perception /// signal transduction	olfactory receptor activity	integral to membrane	---
214655_at	GPR6	0.141	-0.011	T	signal transduction /// G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity /// receptor activity /// G-protein coupled receptor activity, unknown ligand	integral to plasma membrane	GPCRDB Class A Rhodopsin-like
240384_at	WWP2	0.226	-0.01	B	Viral infectious cycle /// initiation of viral infection /// macromolecule metabolism /// metabolism /// viral entry /// physiological process /// viral life cycle /// protein metabolism /// protein modification /// ubiquitin cycle	Protein binding /// ligase activity /// ubiquitin-protein ligase activity /// catalytic activity /// ligase activity /// forming carbon-nitrogen bonds	---	Ubiquitin mediated proteolysis /// Dentatorubropallidoluysian (DRPLA)
201373_at	PLEC1	-0.377	-0.01	B	cytoskeletal anchoring	actin binding /// structural constituent of cytoskeleton /// structural constituent of muscle	cytoskeleton /// intermediate filament /// plasma membrane	---
243403_x_at	CPM	0.229	-0.01	L	proteolysis and peptidolysis /// aromatic compound metabolism /// morphogenesis	carboxypeptidase A activity /// ferric iron binding /// metallopeptidase activity /// hydrolase activity	plasma membrane	---
220086_at	ZNFN1A5	0.288	-0.01	L	---	nucleic acid binding /// zinc ion binding	nucleus	---
1555545_at	KLK2	0.225	-0.01	T	proteolysis and peptidolysis	chymotrypsin activity /// tissue kallikrein activity /// trypsin activity /// peptidase activity	---	---
216440_at	RAB6IP2	0.168	-0.009	L	protein transport	---	---	---
220051_at	PRSS21	0.231	-0.009	T	proteolysis and peptidolysis	chymotrypsin activity /// trypsin activity	membrane fraction /// cytoplasm /// plasma membrane	---

No.		Values):	log2 Values):	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)					
219145_at	LPHN1	-0.297	-0.007	T	signal transduction /// neuropeptide signaling pathway	receptor activity /// G-protein coupled receptor activity /// sugar binding /// latrotoxin receptor activity	membrane /// integral to membrane	GPCRDB Class B Secretin-like
1553465_a_at	FLJ31547	0.275	-0.007	T	---	catalytic activity /// serine esterase activity /// hydrolase activity	---	---
222855_s_at	TRPV2	0.3	-0.006	B	calcium transport /// sensory perception	receptor activity /// cation channel activity /// ion transporter activity	integral to plasma membrane	---
244300_at	LPHN3	0.229	-0.005	L	neuropeptide signaling pathway	G-protein coupled receptor activity /// sugar binding /// latrotoxin receptor activity	integral to membrane	GPCRDB Class B Secretin-like /// GPCRDB Other
233839_at	FLJ23588	0.141	-0.005	L	muscle development	motor activity /// calcium ion binding	myosin	---
234732_s_at	FLJ23588	0.165	-0.005	L	muscle development	motor activity /// calcium ion binding	myosin	---
224162_s_at	FBXO31	0.183	-0.005	L	ubiquitin cycle	---	---	---
210259_s_at	DLX4	0.16	-0.005	T	regulation of transcription, DNA-dependent /// regulation of transcription, DNA-dependent /// development	transcription factor activity /// transcription factor activity /// nucleic acid binding /// zinc ion binding	nucleus /// nucleus	---
228974_at	MGC18625	0.088	-0.005	T	regulation of transcription, DNA-dependent	transcription factor activity /// nucleic acid binding /// zinc ion binding	nucleus	---
216252_x_at	FAS	0.138	-0.005	T	protein complex assembly /// apoptosis /// anti-apoptosis /// induction of apoptosis /// immune response /// signal transduction /// regulation of apoptosis	transmembrane receptor activity /// protein binding	soluble fraction /// cytosol /// membrane /// integral to membrane	apoptosis/// cytokine-cytokine receptor interaction/// MAPK signaling pathway
209299_at	EVI5	0.234	-0.005	T	cell proliferation/// development	protein binding	---	---
1564990_at	KRTAP7-1	0.227	-0.005	T	---	---	intermediate filament	---
217518_at	FER1L3	-0.211	-0.004	T	muscle contraction /// circulation	---	nuclear membrane /// plasma membrane /// integral to membrane	---
1556903_at	LRP8	0.164	-0.004	T	proteolysis and peptidolysis /// lipid metabolism /// lipid metabolism /// endocytosis /// signal transduction /// signal transduction /// cytokine and chemokine mediated signaling pathway	receptor activity /// transmembrane receptor activity /// transmembrane receptor activity /// calcium ion binding /// lipoprotein binding /// apolipoprotein E receptor activity /// apolipoprotein E receptor activity /// apolipoprotein E receptor activity	plasma membrane /// plasma membrane /// membrane /// integral to membrane	---
202084_s_at	SEC14L1	0.129	-0.003	T	transport	transporter activity /// binding	intracellular /// Golgi apparatus /// membrane	---
217321_x_at	ATXN3	0.178	-0.003	T	nucleotide-excision repair /// transcription /// regulation of transcription, DNA-dependent /// synaptic transmission /// neurogenesis	---	nucleoplasm /// cytoplasm	---
206070_s_at	EPHA3	-0.142	-0.003	T	protein amino acid phosphorylation /// signal transduction /// transmembrane receptor protein tyrosine kinase signaling pathway	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// receptor activity /// ephrin receptor activity /// ATP binding /// transferase activity	integral to plasma membrane /// membrane	---
226953_at	IGSF4B	-0.093	-0.002	B	---	receptor activity	integral to membrane	---
200606_at	DSP	-0.448	-0.002	L	epidermis development	structural constituent of cytoskeleton	cytoskeleton /// intermediate filament /// cell-cell adherens junction	---
210605_s_at	MFGE8	-0.221	-0.002	L	cell adhesion /// fertilization (sensu Metazoa)	protein binding	lipid particle	---

No.		Values):	(log2 Values):					
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
235610_at	LOC91801	-0.157	-0.001	L	nuclear mRNA splicing, via spliceosome	nucleic acid binding	---	---
237232_at	UBE2H	-0.347	-0.001	T	ubiquitin cycle	ubiquitin conjugating enzyme activity /// ubiquitin-protein ligase activity /// ligase activity	---	Ubiquitin mediated proteolysis

Table 6. Genes without known function upregulated by 3x LCPUFA (L3, 1.00% DHA-0.67% ARA) supplementation in Brain (B), Liver (L) and Thymus (T).

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values):	Expression change (log2 Values):		Geneontology	Geneontology	Geneontology	
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
1570255_s_at	D20B /// LOC4	-0.028	1.012	T				
1552719_at	H63	0.038	0.715	B				
221925_s_at	J22490/// CSP	0.196	0.63	L				
233399_x_at	---	0.171	0.624	B				
224105_x_at	---	0.054	0.605	B				
1560276_at	LOC283403	0.043	0.596	B				
234788_x_at	FLJ13611	0.277	0.595	B				
241867_at	PARP6	-0.115	0.582	B				
212179_at	C6orf111	0.121	0.58	B				
242273_at	---	0.003	0.566	B				
216051_x_at	---	-0.014	0.562	B				
1553844_a_at	C10orf67	0.049	0.559	B				
214768_x_at	---	-0.056	0.556	B				
215604_x_at	---	-0.015	0.551	B				
242391_at	---	-0.044	0.539	B				
224143_at	TTTY8	-0.052	0.535	B				
239199_at	---	0.046	0.532	B				
211997_x_at	H3F3B	-0.37	0.531	L				
244310_at	---	0.086	0.527	B				
243285_at	LOC283335	-0.016	0.525	L				
231538_at	C11orf1	0.081	0.518	B				
216372_at	---	0.046	0.507	L				
235767_x_at	PHAX	0.047	0.504	B				
234652_at	---	-0.053	0.498	B				
235425_at	SGOL2	-0.07	0.492	B				
216943_at	---	-0.213	0.489	L				
240142_at	ASAM	-0.018	0.485	L				
234594_at	C14orf85	0.193	0.477	B				
234711_s_at	BCORL1	0.346	0.472	L				
228319_at	NSE1	-0.238	0.463	L				
1559952_x_at	// LOC440078 /	0.02	0.461	B				
224348_s_at	---	-0.165	0.456	L				
1567663_at	---	-0.194	0.453	L				
1556952_at	---	0.054	0.45	B				
200906_s_at	KIAA0992	0.12	0.449	B				
215120_s_at	SAMD4	-0.032	0.442	L				
1556414_at	C21orf71	-0.099	0.434	B				
234263_at	---	0.022	0.43	B				
232420_x_at	LOC286260	0.017	0.428	B				
231037_at	---	0.002	0.422	B				
244189_at	KIAA1648	-0.103	0.42	B				
238327_at	LOC440836	0.038	0.42	L				
241036_at	HPS3	0.209	0.418	L				
1562605_at	LOC349408	0.049	0.415	B				
234940_s_at	VEPH1	-0.029	0.414	B				
243891_at	LOC196463	-0.126	0.408	L				
239409_at	---	0.05	0.407	B				
244651_at	---	-0.188	0.4	B				
239980_at	HSPC117	-0.344	0.397	B				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (1.1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (1.3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
234517_at	---	-0.118	0.395	B				
235779_at	LOC284408	0.04	0.395	L				
241268_x_at	---	0.109	0.394	B				
240974_at	LOC153959	0.063	0.391	L				
1566779_at	---	-0.032	0.388	L				
1561205_at	---	-0.008	0.384	B				
1563484_at	---	0.104	0.382	B				
224036_s_at	C7orf2	0.085	0.382	B				
1554923_at	SAMD6	0.223	0.381	L				
1562520_at	---	-0.017	0.378	B				
244449_at	C21orf84	0.117	0.378	B				
206005_s_at	C6orf84	-0.233	0.376	B				
1560001_at	---	0.125	0.375	B				
1560560_at	KIAA0376	-0.098	0.371	B				
240796_at	IQCG	-0.034	0.37	L				
221185_s_at	FLJ12649	0.298	0.37	T				
219626_at	MGC14141	-0.12	0.369	B				
225568_at	C20orf42	-0.273	0.369	L				
229545_at	LOC96610	0.165	0.368	L				
226802_s_at	SHANK3	-0.071	0.367	L				
227923_at	---	0.392	0.367	L				
241617_x_at	---	-0.349	0.366	L				
244216_at	FLJ25222	0.151	0.365	T				
233929_x_at	KIAA0649	0.193	0.363	L				
1559026_at	Cer162	-0.178	0.358	B				
239413_at	FAD104	0.055	0.358	B				
242029_at	---	0.122	0.358	B				
239705_at	FLJ22594	-0.135	0.357	B				
1566885_at	DKFZP434H133	0.125	0.355	B				
204494_s_at	FLJ13315	0.028	0.355	B				
220718_at	---	0.074	0.354	B				
234546_at	LOC474170	0.002	0.354	B				
233519_at	H3F3A	0.025	0.353	B				
208755_x_at	---	-0.171	0.353	L				
1564691_at	FLJ11292	0.038	0.352	B				
217335_at	MGC10955	-0.061	0.352	B				
224133_at	CSPP	-0.024	0.352	B				
227105_at	FLJ40244	0.179	0.35	T				
233462_at	VKORC1L1	-0.124	0.349	L				
1553679_s_at	---	0.088	0.347	B				
234010_at	---	-0.076	0.347	L				
229793_at	---	0.168	0.346	B				
1561776_at	---	0.075	0.344	B				
220149_at	FLJ22671	-0.065	0.343	B				
1562914_a_at	FLJ25328	-0.107	0.342	B				
1563332_at	---	0.015	0.341	L				
239463_at	---	-0.171	0.341	L				
237961_at	---	0.157	0.338	B				
227933_at	LRRN6A	-0.111	0.334	L				
237872_at	---	0.045	0.329	B				
215304_at	---	0.019	0.328	L				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
233105_at	---	-0.095	0.327	B				
239577_at	---	0.16	0.327	B				
240624_x_at	---	-0.086	0.326	L				
228666_at	MGC61550	0.053	0.325	B				
239601_at	C18orf10	-0.071	0.324	L				
239386_at	---	-0.056	0.321	L				
210920_x_at	---	0.123	0.32	B				
238508_at	---	0.038	0.318	L				
241636_x_at	---	-0.174	0.315	L				
216369_at	---	-0.048	0.313	B				
243636_s_at	KFZp434D02	-0.16	0.311	B				
1562983_at	---	-0.005	0.31	B				
216263_s_at	C14orf120	-0.022	0.309	L				
217619_x_at	---	-0.04	0.306	B				
1559792_at	---	0.045	0.305	B				
1560928_at	LOC151657	0.26	0.305	B				
239487_at	FLJ30665	-0.273	0.304	B				
217378_x_at	LOC391427	0.373	0.304	L				
235994_s_at	PLAC2	-0.003	0.304	L				
237165_at	---	-0.043	0.304	L				
231612_at	NYD-SP26	0.441	0.304	T				
234201_x_at	LOC221814	-0.094	0.303	L				
1552599_at	PXT1	-0.098	0.302	B				
203941_at	FLJ10871	0.124	0.302	B				
212785_s_at	HDCMA18P	-0.108	0.302	B				
1557812_a_at	---	-0.085	0.301	B				
1558858_at	---	0.154	0.299	B				
1566959_at	GAB2	0.024	0.299	B				
216524_x_at	---	-0.041	0.299	B				
234056_at	---	0.01	0.298	B				
213512_x_at	BC8902 /// AG	0.297	0.297	T				
212840_at	KIAA0794	0.375	0.296	B				
228314_at	---	-0.068	0.295	B				
224565_at	TncRNA	-0.215	0.295	L				
1558919_a_at	---	0.172	0.294	L				
1560707_at	LOC283856	-0.007	0.293	B				
232924_at	LRRC17	0.132	0.293	B				
220352_x_at	MGC4278	0.195	0.292	B				
235023_at	VPS13C	-0.097	0.292	B				
226590_at	LOC286334	0.002	0.292	L				
238591_at	MGC4368	-0.053	0.292	L				
239022_at	---	-0.097	0.29	B				
237104_at	---	0.088	0.289	L				
237085_x_at	---	-0.107	0.287	B				
216861_at	FLJ14031	-0.176	0.285	B				
240093_x_at	FLJ20366	-0.015	0.285	B				
244232_at	---	0.052	0.285	L				
234942_at	---	-0.27	0.284	L				
239162_at	---	0.192	0.284	L				
244558_at	---	-0.031	0.283	B				
240919_at	---	-0.188	0.282	L				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
1554714_at	LOC253981	0.044	0.281	B				
238170_at	Cep63	-0.201	0.281	L				
234872_at	---	0.009	0.28	B				
242016_at	LOC284409	0.49	0.279	B				
229690_at	FLJ32356	-0.061	0.279	L				
227226_at	C6orf117	0.446	0.279	T				
1552933_at	MGC26989	-0.004	0.277	B				
219385_at	SLAMF8	-0.057	0.277	B				
240438_at	---	0.193	0.276	B				
223795_at	OCSP	-0.15	0.275	L				
1568846_at	---	-0.053	0.274	B				
231811_at	/// MGC52000 ///	0.137	0.274	B				
239402_at	---	-0.17	0.274	B				
215572_at	---	0.025	0.274	L				
231143_at	C20orf173	0.283	0.274	L				
226221_at	KIAA1432	0.104	0.273	B				
244180_at	---	-0.284	0.273	L				
222129_at	C2orf17	-0.258	0.273	T				
1553641_a_at	TSGA13	0.387	0.272	T				
1564253_at	LOC285766	0.063	0.27	B				
228872_at	PRO2964	0.101	0.27	B				
224261_at	---	-0.101	0.27	B				
235569_at	WBSCR24	-0.098	0.27	L				
238180_at	MUC11	-0.157	0.269	L				
1555392_at	---	-0.155	0.267	L				
229568_at	LOC440449	0.15	0.267	T				
229046_at	LOC389831	-0.179	0.266	B				
225714_s_at	GLCCI1	-0.04	0.265	B				
1558158_at	---	0.221	0.264	B				
1569810_at	---	0.008	0.264	B				
237303_at	---	0.084	0.264	L				
239076_at	---	-0.318	0.264	L				
231831_at	LOC90639	-0.101	0.263	L				
212478_at	FLJ13910	-0.066	0.262	L				
228887_x_at	LOC388554	0.164	0.262	L				
233298_at	FLJ20449	-0.132	0.262	L				
1561707_at	---	-0.119	0.261	B				
1563106_at	---	-0.051	0.261	B				
233286_at	---	-0.251	0.261	B				
204514_at	DPH2L2	0.02	0.26	B				
227672_at	LOC286073	-0.092	0.26	L				
1566038_at	DGCR7	0.038	0.259	L				
216612_x_at	---	-0.097	0.259	L				
1555798_at	KF2p761D191	0.032	0.258	B				
230158_at	FLJ32949	0.011	0.258	B				
242383_at	---	-0.309	0.258	L				
241724_x_at	---	-0.018	0.256	B				
207756_at	---	-0.405	0.256	L				
217536_x_at	---	0.006	0.255	B				
229835_s_at	C20orf45	0.012	0.255	L				
233508_at	---	0.074	0.254	B				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
230347_at	C7orf19	-0.194	0.254	L				
1557896_at	---	-0.009	0.252	B				
240912_x_at	FLJ33768	-0.226	0.252	B				
221068_at	ANKRD25	-0.29	0.252	L				
239295_at	SRrp35	-0.27	0.252	L				
242357_x_at	---	0.035	0.252	L				
236800_at	C10orf49	0.214	0.251	L				
233984_at	KIAA0831	0.483	0.25	T				
235347_at	---	0.02	0.248	B				
235186_at	LOC388690	-0.291	0.248	L				
239063_at	---	0.029	0.248	L				
241783_at	---	-0.104	0.248	L				
242021_at	---	-0.099	0.248	L				
1557398_at	DKFZP564C15	-0.093	0.247	B				
214858_at	---	-0.198	0.247	B				
234043_at	FLJ20071	0.083	0.247	B				
1556938_a_at	---	0.29	0.247	T				
1561998_at	---	-0.13	0.246	L				
228539_at	---	-0.033	0.246	L				
1557169_x_at	HCG11	0.015	0.244	T				
1557519_at	---	0.057	0.243	B				
239413_at	---	-0.064	0.243	L				
243186_at	ALS2CR13	-0.137	0.242	L				
243369_at	---	0.096	0.242	L				
240916_x_at	KIAA1126	-0.06	0.241	L				
242866_x_at	---	-0.179	0.241	L				
216063_at	HBBP1	0.261	0.24	B				
1554957_at	---	0.517	0.24	T				
239095_at	---	-0.305	0.239	L				
212791_at	FLJ38984	0.142	0.239	T				
1552309_a_at	NEXN	-0.043	0.238	B				
1564674_a_at	FLJ37927	-0.18	0.238	B				
208144_s_at	---	-0.104	0.238	B				
238577_at	---	-0.075	0.238	B				
1561976_at	DKFZp434E1411	-0.006	0.238	L				
206707_x_at	C6orf32	0.185	0.238	T				
228382_at	LOC90268	0.27	0.238	T				
1561096_at	LOC285419	0.081	0.237	B				
234656_x_at	---	0.068	0.237	B				
239972_at	---	-0.082	0.237	L				
226654_at	LOC202347	-0.068	0.236	L				
237184_at	ATXN2	-0.363	0.236	L				
225688_s_at	PHLDB2	0.214	0.235	B				
227105_at	FLJ22490	-0.057	0.235	B				
1552782_at	MGC34032	0.071	0.233	B				
1557710_at	---	-0.215	0.233	L				
235911_at	LOC440995	-0.06	0.233	L				
216731_s_at	---	0.035	0.232	L				
229507_at	LOC389119	-0.089	0.232	L				
214202_at	---	-0.015	0.231	B				
231346_s_at	---	-0.128	0.23	L				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Geneontology Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Geneontology Pathway
235513_at	---	-0.041	0.23	L				
204251_s_at	Cer164	-0.056	0.229	L				
234478_at	---	-0.114	0.229	L				
238213_at	---	-0.057	0.229	L				
244307_s_at	---	-0.178	0.229	L				
224115_at	---	0.06	0.228	B				
236112_at	LOC285548	-0.068	0.228	B				
239710_at	---	0.105	0.228	B				
225380_at	LOC91461	-0.278	0.228	L				
230207_s_at	---	-0.096	0.227	B				
229531_at	LOC286437	-0.021	0.227	L				
1564656_at	---	0.044	0.226	L				
1556281_at	---	-0.094	0.225	B				
241633_x_at	---	-0.23	0.225	L				
1558670_at	PLEKHM2	0.04	0.223	L				
1556253_s_at	---	0.133	0.223	T				
230840_at	LOC388588	-0.07	0.222	B				
233922_at	---	-0.208	0.222	L				
1562275_at	---	0.329	0.222	T				
1553909_a_at	C9orf71	0.221	0.22	B				
223825_at	KIAA1432	0.061	0.22	B				
239399_at	---	-0.152	0.22	B				
220329_s_at	C6orf93	-0.002	0.22	L				
228576_s_at	---	-0.241	0.219	L				
233960_s_at	LOC440555	-0.21	0.219	L				
232750_at	---	0.094	0.218	B				
231140_at	C14orf8	-0.029	0.217	B				
236353_at	---	-0.064	0.217	B				
234414_at	DKFZp434I111	-0.246	0.217	L				
244091_at	---	-0.169	0.217	L				
1568838_at	---	0.092	0.217	T				
237124_at	C14orf168	0.193	0.216	B				
1565518_at	KIAA1671	-0.086	0.216	L				
241165_at	---	0.018	0.216	L				
1559932_at	---	0.011	0.215	B				
1563528_at	LOC91149	-0.176	0.215	B				
225100_at	FBXO45	0.189	0.215	B				
238874_at	FLJ43663	0.192	0.215	T				
236580_at	---	0.496	0.214	T				
1569495_at	FLJ30655	-0.094	0.212	B				
230930_at	LOC338620	0.023	0.212	B				
202852_s_at	FLJ11506	-0.06	0.212	L				
242016_at	LOC284409	0.431	0.212	L				
229908_at	FLJ10300	0.277	0.212	T				
1562661_at	---	0.137	0.211	B				
244572_at	---	-0.166	0.211	B				
229865_at	FNDC3B	-0.025	0.21	B				
240346_at	---	0.089	0.21	B				
239810_at	KIAA1036	-0.182	0.21	L				
1565614_at	---	-0.018	0.209	B				
1569182_at	---	0.353	0.209	T				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Geneontology Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
243723_at	---	-0.031	0.208	B				
216562_at	SRMP1	0.304	0.208	L				
227816_at	---	-0.132	0.208	L				
230770_at	LOC442506	-0.061	0.208	L				
233947_x_at	---	0.053	0.207	L				
242040_at	---	0.298	0.207	L				
1560503_a_at	---	0.596	0.207	T				
215200_x_at	---	-0.046	0.206	B				
217490_at	---	0.157	0.206	B				
222339_x_at	---	-0.365	0.206	L				
242002_at	TCBA1	0.023	0.206	L				
244396_at	---	0.233	0.205	B				
233235_x_at	---	-0.171	0.205	L				
238501_at	---	-0.014	0.204	B				
235659_at	---	-0.173	0.203	L				
243620_at	---	-0.157	0.202	B				
206179_s_at	TPPP	-0.094	0.201	L				
238328_at	M-RIP	-0.107	0.201	L				
218562_s_at	FLJ10747	-0.441	0.2	L				
236351_at	LOC389023	0.15	0.2	T				
1561708_at	C5orf150	0.142	0.199	B				
239414_at	---	-0.069	0.199	B				
239435_x_at	APXL2	-0.094	0.199	L				
228221_at	MGC45474	-0.111	0.198	B				
1562788_at	LOC254099	-0.2	0.197	B				
1567374_at	---	0.063	0.197	L				
222669_s_at	SBDS	-0.205	0.197	L				
241012_at	---	-0.171	0.197	L				
1555221_at	---	0.021	0.196	B				
239418_x_at	---	-0.023	0.196	B				
1556763_at	---	0.123	0.196	L				
229804_at	DGCR5	-0.195	0.196	L				
236668_at	---	0.25	0.196	T				
244061_at	ARHGAP15	-0.725	0.196	T				
229090_at	LOC220930	-0.072	0.195	B				
203143_s_at	KIAA0040	-0.214	0.195	L				
1555148_a_at	LOC130951	-0.005	0.194	B				
230778_at	---	-0.1	0.194	B				
232578_at	---	-0.089	0.194	B				
228106_at	FLJ20280	0.137	0.193	T				
229926_x_at	ANKRD19	0.046	0.192	B				
227606_s_at	AMSH-LP	0.273	0.192	T				
1563569_at	---	0.073	0.191	B				
231608_at	---	-0.065	0.191	L				
238451_at	---	-0.032	0.19	B				
230213_at	MGC2803	-0.486	0.19	L				
238038_at	---	-0.257	0.19	L				
241039_at	---	0.073	0.187	L				
1562516_at	FLJ10300	0.225	0.187	T				
1555237_at	---	-0.022	0.186	L				
231651_at	---	-0.259	0.186	L				

Affymetrix Probe ID No.	Gene Symbol:	Expression change (log2 Values):	Expression change (log2 Values):	Geneontology		Geneontology		Geneontology	
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
228702_at	FLJ43663	0.445	0.186	T				
234830_at	FRG2	0.031	0.185	B				
237315_at	---	-0.131	0.185	B				
242012_at	FLJ31132	-0.113	0.185	L				
210837_at	CNOT4	-0.024	0.184	L				
207855_s_at	MGLC	0.074	0.182	L				
1561528_at	---	-0.01	0.181	B				
220724_at	FLJ21511	-0.132	0.18	B				
216948_at	---	-0.134	0.18	L				
230383_x_at	---	-0.044	0.18	L				
1566763_at	---	-0.051	0.179	B				
226362_at	---	-0.112	0.179	L				
228884_at	LOC440010	-0.133	0.179	L				
223914_at	FLJ38717	-0.099	0.179	L				
1563064_at	---	0.083	0.179	T				
217571_at	---	-0.027	0.178	B				
234377_at	---	-0.087	0.178	B				
241437_s_at	FLJ33915	0.039	0.178	B				
232116_at	TFCP2L4	0.464	0.178	T				
242698_at	AKAP14	0.328	0.178	T				
1559787_at	---	-0.282	0.177	B				
213882_at	BBP	-0.069	0.177	B				
216447_at	---	-0.217	0.176	L				
1559491_at	CENTG2	-0.158	0.175	B				
1559147_at	---	-0.019	0.175	B				
1559624_at	---	0.084	0.174	B				
1554813_at	---	-0.124	0.174	L				
205519_at	FLJ12973	-0.179	0.174	L				
237298_at	FLJ26850	-0.07	0.174	L				
222606_at	FLJ10036	-0.114	0.173	B				
241465_at	C17orf39	0.09	0.173	T				
1569868_s_at	EME2	0.092	0.172	L				
220221_at	VPS13D	-0.179	0.172	L				
230639_at	---	-0.273	0.172	L				
219251_s_at	FLJ10300	-0.235	0.171	L				
214801_at	LOC163590	-0.012	0.171	T				
234289_x_at	---	0.149	0.17	B				
1570191_at	---	0.373	0.17	T				
215838_at	LILRB7	0.372	0.169	T				
1562934_at	---	-0.14	0.169	B				
1566168_at	---	0.077	0.168	B				
232836_at	C20orf61	0.304	0.168	T				
1569739_at	LOC221946	-0.241	0.167	B				
232736_s_at	YP211 /// DKFZ	0.09	0.167	L				
239181_at	---	0.085	0.167	L				
1566981_at	C14orf32	-0.294	0.166	B				
235362_at	---	-0.088	0.166	B				
215356_at	FLJ13072	-0.187	0.165	L				
242670_at	LGI4	-0.135	0.166	L				
229795_at	---	-0.009	0.164	B				
234223_at	---	-0.143	0.164	L				

Affymatrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
244803_at	YAP	-0.114	0.164	L				
1552326_a_at	CCDC11	0.299	0.164	T				
1559972_at	---	0.158	0.164	T				
237519_at	LOC283922	-0.04	0.164	T				
226720_at	KIAA1935	-0.204	0.163	L				
237381_at	---	0.188	0.163	T				
1570578_at	---	-0.004	0.162	B				
234767_at	MLSTD2	0.225	0.162	B				
243861_at	---	-0.048	0.161	B				
209183_s_at	C10orf10	-0.158	0.161	L				
235263_at	ZKFZP434A013	-0.05	0.161	L				
202268_s_at	PFAAP5	0.04	0.16	B				
242721_at	---	-0.083	0.159	L				
1562841_at	LOC339665	0.406	0.159	T				
242660_at	---	0.272	0.159	T				
1565819_at	---	-0.006	0.158	B				
1568616_a_at	LOC399884	-0.272	0.158	L				
1562222_at	---	0.204	0.158	T				
1561677_at	---	-0.054	0.157	B				
1563092_at	---	-0.092	0.157	B				
219756_s_at	POF1B	-0.153	-0.157	L				
1564813_at	---	0.068	0.156	B				
1553197_at	FLJ35775	-0.035	0.156	T				
1560938_s_at	---	0.307	0.156	T				
1555243_x_at	LOC401466	-0.092	0.155	B				
220913_at	---	-0.209	0.155	L				
1563040_s_at	---	0.013	0.154	L				
232630_at	MMRP19	-0.073	0.154	L				
AFFX-LysX-5_at	---	-0.03	0.154	L				
237740_at	---	0.446	0.154	T				
241469_at	FLJ35760	0.081	0.154	T				
213466_at	SCSTDC1	0.316	0.153	B				
239845_at	---	-0.104	0.153	L				
242782_x_at	MGC99813	-0.296	0.153	L				
238777_x_at	---	0.303	0.153	T				
1558668_s_at	NYD-SP20	-0.049	0.152	B				
225579_at	C2orf22	-0.006	0.152	B				
243962_at	---	-0.127	0.152	B				
204976_s_at	AMMECR1	-0.236	0.152	L				
244426_at	---	0.254	0.152	T				
229716_at	---	-0.16	0.151	L				
243927_x_at	DKFZP434I116	-0.032	0.151	T				
221153_s_at	---	-0.021	0.15	B				
236521_at	---	-0.076	0.15	L				
217629_at	---	0.052	0.148	B				
204373_s_at	CAP350	-0.471	0.148	L				
235874_at	---	-0.211	0.148	L				
242848_x_at	CC2D1B	-0.12	0.147	L				
1554983_at	C21orf117	-0.356	0.146	B				
1558724_at	---	0.203	0.146	B				
238431_at	---	-0.191	0.146	B				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values):	Expression change (log2 Values):		Geneontology	Geneontology	Geneontology	
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
242593_at	—	-0.206	0.146	L				
49111_at	—	-0.199	0.146	L				
232794_at	LOC153682	0.241	0.146	T				
1567027_at	SH3GLP2	0.297	0.145	L				
217443_at	—	-0.108	0.145	L				
236852_at	FBXO43	-0.195	0.145	L				
1558234_at	FLJ36644	0.068	0.145	T				
1560030_at	LOC283692	0.229	0.145	T				
238282_at	—	0.23	0.145	T				
1560779_a_at	LOC126167	-0.012	0.144	B				
229023_at	MGC5391	0.299	0.144	T				
240978_at	—	-0.222	0.143	L				
243760_at	LOC387904	-0.125	0.143	L				
1570451_at	CROC4	0.387	0.143	T				
1553226_at	FLJ31461	-0.055	0.142	B				
223327_x_at	FLJ22795	-0.33	0.141	L				
238202_at	—	-0.104	0.141	L				
1560747_at	ATXN7L1	0.268	0.141	T				
232933_at	KIAA1656	-0.157	0.14	B				
1570023_at	LOC163556	0.286	0.14	T				
1556220_at	—	0.093	0.139	B				
243689_s_at	MGC72104	0.092	0.139	B				
237996_at	—	0.261	0.138	L				
226057_at	CDGAP	-0.116	0.137	B				
233904_at	—	0.068	0.137	L				
227431_at	RSBN1L	0.222	0.137	T				
1562167_a_at	DEFB122	0.184	0.136	T				
242162_at	FLJ25955	0.268	0.136	T				
228247_at	MGC72104	0.336	0.135	T				
225172_at	CRAMP1L	-0.136	0.134	B				
239635_at	MGC15912	-0.153	0.134	B				
240380_at	—	0.337	0.134	L				
229308_at	—	0.048	0.134	T				
233306_at	C1orf1	0.244	0.134	T				
1553861_at	MGC40368	0.238	0.133	B				
1566462_at	—	0.252	0.133	T				
240047_at	FAM13A1	-0.017	0.132	B				
222295_x_at	FLJ39639	-0.292	0.132	L				
243902_at	—	-0.159	0.132	L				
1558028_x_at	HCG11	-0.033	0.132	T				
243873_at	—	0.261	0.132	T				
216655_s_at	—	-0.332	0.131	L				
237562_at	—	0.106	0.131	L				
227598_at	C7orf29	-0.254	0.13	L				
222309_at	C6orf62	0.094	0.129	B				
1563484_at	—	-0.211	0.129	L				
239762_at	LOC286437	-0.197	0.129	L				
216665_s_at	TTTY2	0.32	0.129	T				
238657_at	UBXD3	0.272	0.129	T				
1562988_at	—	-0.01	0.128	B				
1560819_a_at	LOC387895	-0.014	0.127	B				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
1570931_at	---	0.188	0.127	B				
242534_at	EVI5L	-0.048	0.127	L				
1561857_at	---	-0.132	0.126	B				
1565976_at	---	0.12	0.126	B				
237754_at	---	-0.272	0.125	B				
1568870_at	---	0.328	0.125	T				
239935_at	C6orf154	0.287	0.125	T				
1562067_at	---	-0.082	0.124	B				
1561439_at	---	-0.039	0.124	L				
232096_x_at	---	-0.152	0.124	L				
231337_at	---	0.373	0.124	T				
213316_at	KIAA1462	-0.291	0.123	L				
238366_at	---	-0.2	0.123	L				
238704_at	---	-0.176	0.123	L				
1558226_a_at	---	0.117	0.122	B				
220940_at	KIAA1641	0.251	0.122	B				
239128_at	---	-0.249	0.122	B				
220529_at	FLJ11710	-0.195	0.122	L				
222322_at	---	-0.206	0.12	B				
215993_at	OD72	-0.124	0.12	L				
233777_at	---	-0.113	0.12	L				
1553462_at	---	-0.103	0.119	L				
217836_s_at	YY1AP1	-0.245	0.119	L				
220366_at	ELSPBP1	-0.128	0.118	L				
235386_at	LOC285535	-0.382	0.118	L				
242237_at	---	0.24	0.117	T				
218187_s_at	FLJ20989	-0.001	0.116	B				
243480_at	C11orf23	-0.132	0.116	L				
1562507_at	---	0.294	0.116	T				
243336_at	---	0.214	0.116	T				
234523_at	MGC21644	0.181	0.115	B				
235828_at	---	-0.029	0.114	L				
239117_at	KIAA0465	-0.212	0.114	L				
232997_at	---	-0.052	0.113	B				
1562688_at	---	0.197	0.112	T				
239979_at	EPSTI1	0.149	0.112	T				
1557338_x_at	---	0.033	0.111	B				
231691_at	CPLP	0.553	0.111	L				
1564014_at	---	0.231	0.111	T				
232049_at	---	-0.067	0.11	B				
217928_s_at	C11orf23	-0.139	0.11	L				
243397_at	FREM3	0.308	0.11	T				
209907_s_at	KIAA0992	-0.371	0.109	B				
243422_at	---	-0.166	0.109	L				
1556722_a_at	FLJ33706	0.275	0.109	T				
1556923_s_at	MAK10	0.283	0.109	T				
1557233_at	LOC285441	-0.156	0.108	B				
219037_at	CGI-115	-0.116	0.108	B				
218789_s_at	FLJ20010	0.341	0.108	L				
234522_at	---	0.214	0.108	T				
239997_at	---	0.174	0.107	B				

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		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
222244_s_at	FLJ20618	-0.507	0.107	L				
1557832_at	---	0.041	0.107	T				
1561106_at	---	0.122	0.107	T				
234139_s_at	---	0.215	0.107	T				
204335_at	FLJ10374	-0.221	0.105	L				
243383_at	---	0.507	0.105	L				
1563568_at	---	0.147	0.105	T				
220007_at	FLJ13984	-0.295	0.104	L				
220912_at	FLJ11827	-0.263	0.104	L				
239130_at	---	-0.058	0.104	L				
1562046_at	---	0.207	0.103	T				
232824_at	---	-0.064	0.102	B				
241484_x_at	---	0.019	0.102	B				
225555_x_at	---	-0.584	0.102	L				
227814_at	WDR53	-0.312	0.102	L				
231081_at	FLJ40298	0.247	0.102	L				
1555894_s_at	LOC92154	0.344	0.102	T				
1570014_at	FLJ46082	0.033	0.101	B				
1553211_at	FLJ38335	0.239	0.101	L				
233542_at	---	-0.092	0.1	B				
1561112_at	---	-0.037	0.099	L				
1562772_a_at	DAND5	-0.208	0.099	L				
1570208_at	LOC284260	0.222	0.099	T				
234485_at	LOC340947	0.389	0.098	L				
216857_at	---	0.103	0.097	B				
208869_s_at	GABARAPL1	-0.329	0.097	L				
233658_at	---	-0.444	0.097	L				
224089_at	PRO3077	0.359	0.097	T				
243405_at	---	0.471	0.097	T				
238028_at	LOC389389	-0.275	0.096	L				
225809_at	KFZP564O082	0.209	0.096	T				
229976_at	C9orf18	0.312	0.096	T				
237911_at	---	0.153	0.096	T				
222936_s_at	C1orf121	-0.148	0.095	L				
225749_at	LOC283951	-0.239	0.094	B				
241085_at	---	0.156	0.094	B				
240120_at	---	-0.174	0.093	B				
234144_at	HHIP	0.165	0.093	T				
242283_at	MGC27277	0.26	0.092	T				
237267_at	---	-0.252	0.091	L				
241807_x_at	---	-0.336	0.091	L				
218361_at	GOLPH3L	0.145	0.091	T				
1558963_at	LOC196337	-0.094	0.09	L				
234947_s_at	C10orf84	0.03	0.09	L				
230654_at	---	0.257	0.09	T				
236607_at	LOC151194	-0.097	0.089	L				
236378_at	CIB4	0.397	0.089	T				
224036_s_at	C7orf2	-0.137	0.088	L				
221687_s_at	C9orf28	-0.089	0.087	L				
239088_at	---	-0.127	0.087	L				
1570177_at	---	0.152	0.086	L				

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		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
237835_at	---	-0.175	0.086	L				
1555043_at	LHFPL5	0.313	0.086	T				
1561644_x_at	H63	0.045	0.085	T				
233579_at	---	0.071	0.085	T				
225586_at	C9orf112	0.299	0.084	L				
238106_at	---	0.417	0.084	T				
240453_at	C20orf26	0.402	0.084	T				
244797_at	---	0.284	0.084	T				
1556617_a_at	---	0.232	0.083	B				
238713_at	---	-0.059	0.083	B				
230986_at	---	-0.23	0.083	L				
221714_s_at	LOC94431	0.24	0.082	L				
1557046_x_at	---	-0.061	0.08	B				
243490_at	---	-0.124	0.079	L				
212465_at	C14orf154	-0.372	0.078	L				
225380_at	LOC91461	-0.047	0.078	T				
1555634_a_at	LIR9	-0.149	0.077	L				
240813_at	---	-0.275	0.077	L				
1558496_at	---	0.234	0.077	T				
222933_at	FLJ13941	0.31	0.077	T				
1553775_at	FLJ31715	0.18	0.076	T				
1556039_s_at	---	0.19	0.076	T				
241000_at	FLJ37794	0.195	0.076	T				
1556981_at	9KF2p762C241	-0.139	0.075	B				
1552974_at	---	-0.17	0.075	L				
1557588_at	---	-0.131	0.075	L				
212394_at	KIAA0990	0.355	0.075	L				
215163_at	---	-0.163	0.075	L				
220824_at	FLJ40083	-0.252	0.075	L				
229205_at	---	0.224	0.075	T				
213280_at	GARNL4	0.245	0.074	T				
237689_at	---	0.262	0.074	T				
1557140_at	---	0.204	0.073	L				
240619_at	---	0.064	0.072	L				
1556766_at	LOC157697	0.203	0.072	T				
235373_at	---	-0.116	0.071	B				
227739_at	LOC389822	-0.316	0.07	L				
1552319_at	FLJ39743	0.25	0.07	T				
237357_at	---	-0.123	0.07	T				
229608_at	LOC284465	0.198	0.069	T				
1562294_x_at	ANKRD30B	-0.359	0.068	B				
1562790_at	---	0.211	0.067	T				
235550_at	FLJ21159	0.221	0.067	T				
242107_x_at	---	-0.03	0.067	T				
1556392_a_at	---	-0.116	0.066	B				
238063_at	FLJ32028	0.018	0.066	L				
243972_at	MGC23908	0.252	0.066	T				
232945_at	FLJ32312	-0.164	0.065	L				
1557222_at	---	0.174	0.065	T				
233103_at	---	-0.41	0.064	L				
1557055_s_at	LOC284591	0.33	0.064	T				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values):	Expression change (log2 Values):		Geneontology	Geneontology	Geneontology	
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Biological Function	Molecular Function	Cellular Component	Pathway
1566807_a_at	—	0.248	0.063	T				
239828_at	FLJ25791	0.341	0.062	T				
241002_at	—	-0.097	0.061	T				
217663_at	—	-0.179	0.06	L				
244658_at	—	-0.154	0.06	L				
1569023_a_at	—	0.27	0.06	T				
1560911_at	—	-0.271	0.059	B				
243791_at	—	-0.115	0.057	B				
220575_at	FLJ11800	0.253	0.057	L				
234949_at	MGC72104	-0.318	0.057	L				
241856_at	—	0.227	0.057	T				
229438_at	FAM20C	-0.209	0.056	L				
236624_at	LOC284591	-0.143	0.056	L				
243892_at	—	-0.127	0.055	T				
237753_at	—	-0.264	0.054	L				
230525_at	LOC388206	0.252	0.054	T				
242588_at	—	0.128	0.054	T				
226740_x_at	0030 /// MGC8	-0.243	0.053	B				
227007_at	LOC255104	-0.144	0.053	B				
218908_at	ASPSCR1	-0.283	0.053	T				
1554340_a_at	LOC374946	0.192	0.051	L				
234571_at	LOC127406	-0.144	0.051	L				
237408_at	RP42	0.185	0.051	T				
239588_s_at	—	0.256	0.051	T				
217122_s_at	SLC35E2	0.11	0.049	L				
229073_at	LOC145786	-0.293	0.048	L				
230108_at	LOC282965	-0.271	0.048	L				
1553519_at	C21orf94	-0.172	0.048	T				
235474_at	—	-0.203	0.047	B				
215585_at	KIAA0174	-0.141	0.047	L				
1562953_s_at	FBI4	0.207	0.047	T				
224604_at	LOC401152	0.207	0.047	T				
224475_at	—	-0.323	0.046	B				
1567997_x_at	—	-0.615	0.046	L				
219699_at	LGI2	-0.404	0.045	L				
1564070_s_at	—	0.161	0.045	T				
1569034_a_at	LOC440864	0.195	0.044	T				
1561604_at	—	-0.26	0.043	B				
1554963_at	—	-0.058	0.043	L				
244178_at	COMMD7	0.32	0.043	L				
239782_at	—	-0.295	0.041	L				
1566340_at	RNU6C	0.185	0.041	T				
238468_at	—	-0.092	0.04	L				
1561090_at	LOC400654	0.299	0.04	T				
230312_at	—	0.198	0.04	T				
1560964_at	—	0.2	0.038	L				
1569537_at	—	0.239	0.038	L				
221182_at	FLJ23550	-0.357	0.037	L				
243549_at	—	-0.079	0.037	L				
1561185_at	CLONE795723	0.207	0.037	T				
1561593_at	—	0.103	0.036	T				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
241194_at	---	-0.107	0.036	T				
236899_at	---	-0.183	0.035	T				
241769_at	---	-0.326	0.035	T				
1560690_at	---	-0.265	0.033	L				
234031_at	LOC400942	-0.168	0.033	T				
238725_at	KIBRA	0.357	0.033	T				
223578_x_at	PRO1073	-0.361	0.03	L				
234018_s_at	C20orf50	0.228	0.03	L				
1565696_at	---	-0.148	0.03	T				
236503_at	---	-0.101	0.029	B				
1569831_at	---	-0.128	0.029	L				
229979_at	LOC253970	0.139	0.028	T				
230523_at	---	0.172	0.028	T				
218775_s_at	BOMB	-0.174	0.027	L				
218614_at	FLJ10552	-0.323	0.026	L				
222284_at	---	-0.33	0.026	L				
1566257_at	LOC144874	0.161	0.026	T				
1557609_s_at	TBC1D12	0.257	0.025	L				
1563121_at	---	0.221	0.025	T				
238684_at	---	-0.129	0.025	T				
214570_x_at	DKFZP434P211	-0.327	0.024	B				
212323_s_at	VPS13D	-0.351	0.024	L				
244301_at	LOC143941	-0.198	0.023	B				
232738_at	KIAA1680	0.182	0.023	T				
243551_at	---	0.22	0.023	T				
242446_at	C6orf163	-0.131	0.022	L				
1556676_a_at	---	0.294	0.021	L				
231584_s_at	BCAS4	-0.171	0.021	L				
1570040_at	---	0.215	0.021	T				
243810_at	LOC138255	0.284	0.021	T				
234525_at	KFZP761C171	-0.171	0.019	L				
234258_at	---	-0.218	0.018	L				
239292_at	---	0.183	0.018	T				
227917_at	---	-0.112	0.017	B				
219585_at	MGC1203	-0.244	0.017	L				
238637_at	---	0.13	0.017	L				
1558425_x_at	LOC349114	0.3	0.017	T				
220609_at	LOC441118	0.206	0.017	T				
1563743_at	FLJ35487	0.327	0.015	T				
225996_at	---	-0.175	0.015	T				
1562430_at	WDR17	-0.121	0.014	B				
1560184_at	MGC35118	0.207	0.014	L				
230446_at	---	0.223	0.014	T				
1566631_at	---	0.285	0.013	L				
1568813_at	---	0.199	0.013	L				
226776_at	glyt2	0.184	0.013	T				
213153_at	KIAA1076	-0.212	0.012	T				
1561202_at	---	0.416	0.011	T				
1561599_at	---	0.141	0.01	L				
242990_at	PPFIA1	-0.174	0.008	L				
230647_at	FLJ22353	0.205	0.008	T				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values):	Expression change (log2 Values):	Organ	Geneontology		Geneontology		Pathway
		1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	3x LCPUFA (L3, 1.00% DHA-0.67% ARA)		Biological Function	Molecular Function	Cellular Component		
233076_at	C10orf39	0.157	0.008	T					
238910_at	---	0.25	0.008	T					
1564446_at	LOC284930	-0.244	0.007	L					
230950_at	---	0.204	0.007	T					
1570633_at	---	-0.068	0.006	B					
1570008_at	LOC253724	-0.229	0.006	L					
238301_at	---	-0.269	0.006	L					
233438_at	C6orf162	0.11	0.006	T					
1558512_at	---	-0.094	0.005	B					
1557336_at	---	0.153	0.005	T					
1559002_at	LOC340544	0.329	0.005	T					
231670_at	---	0.22	0.005	T					
1568593_a_at	LOC152195	0.332	0.004	B					
1561489_at	---	-0.053	0.004	T					
1557850_at	LOC285954	0.289	0.003	L					
1552928_s_at	TAB3	-0.206	0.003	T					
212319_at	RUTBC1	-0.155	0.003	T					
240834_at	LOC90268	0.111	0.003	T					
215837_x_at	PRO1621	0.393	0.002	T					
233637_at	WDR42A	0.37	0.002	T					
231345_s_at	FLJ13639	-0.216	0.001	L					
237395_at	---	-0.23	0.001	L					
1562740_at	LOC285224	0.234	0.001	T					
1554547_at	FAM13C1	-0.171	0	T					
240513_at	GA17	-0.159	0	T					

Table 7. Genes without known function downregulated by 3x LCPUFA (L3, 1.00% DHA-0.67% ARA) supplementation in Brain (B), Liver (L) and Thymus (T).

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
227687_at	FLJ32915	-0.236	-0.654	L				
237847_at	---	-0.228	-0.641	B				
233739_at	---	-0.164	-0.593	L				
223018_at	NOB1P	0.019	-0.583	B				
1569721_at	---	-0.173	-0.552	L				
213429_at	---	-0.241	-0.546	L				
1557676_at	---	-0.153	-0.541	L				
230208_at	---	-0.166	-0.538	L				
1557680_at	C14orf174	-0.47	-0.535	L				
232943_at	---	-0.354	-0.528	L				
241399_at	FAM19A2	-0.449	-0.527	B				
222349_x_at	RNF126P1	-0.097	-0.516	B				
239641_at	LOC387821	-0.166	-0.504	L				
229428_at	LOC255326	-0.482	-0.503	L				
1569685_at	LOC400575	0.112	-0.494	L				
229023_at	MGC5391	-0.171	-0.493	B				
234006_s_at	RP4-622L5	-0.066	-0.490	B				
1558809_s_at	LOC284408	-0.518	-0.484	L				
236716_at	---	-0.268	-0.483	L				
1553641_a_at	TSGA13	0.017	-0.482	B				
216157_at	---	0.171	-0.478	B				
223987_at	CHRDL2	-0.188	-0.478	B				
219705_at	FLJ21924	-0.279	-0.478	L				
216567_at	---	-0.202	-0.476	B				
240529_at	FLJ31153	-0.199	-0.470	L				
226686_at	LOC493855	0.115	-0.469	L				
236180_at	---	-0.134	-0.468	L				
203829_at	ELP4	-0.083	-0.463	B				
218826_at	SLC35F2	-0.237	-0.461	L				
220941_s_at	C21orf91	-0.105	-0.459	L				
238349_at	FLJ25778	-0.319	-0.458	L				
237469_at	---	-0.174	-0.453	L				
240456_at	FLJ11795	-0.053	-0.453	L				
238777_x_at	---	0.107	-0.450	L				
218588_s_at	C5orf3	-0.372	-0.447	L				
230117_at	LOC285878	-0.522	-0.446	B				
222277_at	---	-0.055	-0.446	L				
244436_at	---	-0.217	-0.445	L				
240855_at	---	0.038	-0.444	L				
1553204_at	FLJ30313	-0.345	-0.436	L				
227544_at	C14orf83	0.097	-0.430	B				
220006_at	FLJ12057	-0.042	-0.427	L				
223041_at	CD99L2	-0.149	-0.426	B				
228891_at	LOC349236	-0.271	-0.426	L				
1554466_a_at	MGC13114	0.358	-0.424	B				
228458_at	LOC441150	-0.016	-0.422	B				
216503_at	KIAA1797	-0.463	-0.421	L				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Geneontology		Geneontology	Geneontology	
				Organ	Biological Function	Molecular Function	Cellular Component	Pathway
237583_s_at	LOC440731	0.138	-0.418	L				
243843_at	---	0.017	-0.415	B				
234896_at	---	0.071	-0.415	L				
216483_s_at	C19orf10	-0.162	-0.412	B				
237455_at	---	-0.117	-0.411	B				
231136_at	---	-0.004	-0.411	L				
1554245_x_at	LOC51326	-0.113	-0.409	L				
233481_at	---	-0.101	-0.408	L				
233149_at	---	0.075	-0.404	L				
1566147_a_at	FLJ00310	-0.08	-0.400	L				
1553919_at	C9orf62	-0.073	-0.399	L				
1561034_at	---	0.122	-0.397	L				
233916_at	KIAA1486	-0.066	-0.396	L				
220143_x_at	LUC7L	-0.152	-0.394	B				
222038_s_at	---	-0.31	-0.389	L				
233213_at	---	-0.167	-0.388	L				
236070_at	LOC388963	0.033	-0.386	L				
232848_at	---	-0.093	-0.385	L				
244184_at	---	0.082	-0.383	L				
223523_at	MGC3040	-0.104	-0.382	B				
232589_at	---	-0.121	-0.382	L				
237063_at	---	-0.342	-0.379	L				
233991_at	---	0.111	-0.372	L				
226140_s_at	OTUD1	-0.101	-0.371	L				
240755_at	---	-0.015	-0.371	L				
225577_at	HCG18	0.243	-0.370	L				
230899_at	C21orf18	-0.123	-0.370	L				
217102_at	MAG	0.098	-0.368	B				
1553101_a_at	FLJ20308	-0.389	-0.368	T				
244237_at	FLJ90680	-0.053	-0.367	B				
236574_at	LOC284373	-0.15	-0.362	L				
229178_at	LOC145786	0.12	-0.361	L				
1564763_at	---	-0.117	-0.360	L				
205093_at	PLEKHA6	0.148	-0.358	B				
238298_at	---	-0.032	-0.358	L				
222893_s_at	FLJ13150	0.048	-0.357	L				
235112_at	KIAA1958	-0.26	-0.357	L				
237295_at	---	-0.353	-0.357	T				
218874_s_at	C6orf134	-0.152	-0.354	L				
240895_at	---	-0.103	-0.354	L				
241576_at	---	-0.213	-0.353	L				
1560506_at	---	-0.393	-0.352	L				
221260_s_at	C12orf22	0.109	-0.352	L				
1557610_at	---	0.101	-0.350	L				
224373_s_at	DCOHM	0.123	-0.350	L				
241146_at	---	-0.314	-0.350	L				
1563086_at	---	0.122	-0.349	L				
1564709_at	LOC286238	0.055	-0.349	L				
221080_s_at	FAM31C	0.034	-0.349	L				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Geneontology		Geneontology	Geneontology	
				Organ	Biological Function	Molecular Function	Cellular Component	Pathway
238453_at	C10orf13	-0.107	-0.349	L				
221251_x_at	HMGA1L4	0.122	-0.344	B				
230527_at	---	-0.221	-0.342	T				
1559960_x_at	LOC400547	-0.118	-0.340	B				
1552388_at	FLJ30901	-0.188	-0.340	L				
238999_at	---	-0.265	-0.339	B				
204700_x_at	MGC29875	0.039	-0.339	L				
1564881_at	LOC152578	0.051	-0.336	L				
1569454_a_at	LOC283352	-0.172	-0.336	L				
220218_at	C9orf68	-0.244	-0.333	L				
228790_at	MGC39325	-0.199	-0.333	L				
220173_at	C14orf45	-0.096	-0.332	L				
239408_at	CCM2	-0.092	-0.330	L				
1564392_at	---	-0.132	-0.329	L				
240518_at	FLJ11088	-0.486	-0.329	L				
215472_at	PACRG	0.194	-0.328	B				
229809_at	---	-0.269	-0.327	T				
1555947_at	C9orf10	1.024	-0.326	L				
214077_x_at	MEIS4	-0.339	-0.326	T				
1561543_at	---	0.014	-0.325	L				
230660_at	SERTAD4	-0.189	-0.325	L				
231366_at	---	-0.056	-0.324	L				
232891_at	PTPNS1L2	-0.067	-0.323	L				
234088_at	LOC154761	-0.319	-0.323	L				
226298_at	RUNDC1	-0.196	-0.321	B				
1566597_at	---	-0.086	-0.321	L				
239580_at	---	0.207	-0.321	L				
227524_at	---	0.089	-0.320	L				
239824_s_at	MGC10744	-0.362	-0.320	T				
1554949_at	---	-0.042	-0.317	L				
231643_s_at	CMIP	0.14	-0.316	B				
233568_x_at	CWF19L1	-0.052	-0.315	L				
240946_at	---	-0.025	-0.314	L				
240252_at	---	-0.131	-0.313	B				
1566221_at	---	-0.025	-0.313	L				
237250_at	MBD3L2	-0.208	-0.312	L				
1552456_a_at	C6orf166	-0.114	-0.312	T				
223145_s_at	LOC283484	-0.439	-0.312	T				
1566940_at	KIAA1937	-0.126	-0.311	L				
1557771_at	---	-0.074	-0.310	L				
1568568_x_at	---	-0.013	-0.310	L				
1561224_at	MGC3040	0.033	-0.308	L				
223524_s_at	LOC391705	-0.063	-0.308	L				
1569465_at	LOC440885	0.009	-0.307	L				
239624_at	---	-0.206	-0.307	L				
229470_at	---	-0.028	-0.306	L				
241660_at	---	-0.074	-0.306	L				
242226_at	---	0.113	-0.306	L				
1562278_at	XLHSRF-1	-0.123	-0.305	L				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67%-ARA)	Geneontology		Geneontology		Geneontology	
				Organ	Biological Function	Molecular Function	Cellular Component		Pathway
228078_at	FLJ20308	0.019	-0.304	B					
1557077_a_at	---	-0.266	-0.304	T					
1563064_at	---	0.052	-0.303	B					
229652_s_at	LOC400236	0.037	-0.302	L					
230528_s_at	MGC2752	-0.586	-0.302	T					
208858_s_at	MBC2	-0.039	-0.301	B					
212677_s_at	KIAA0582	-0.417	-0.301	L					
1568402_at	RNU68	-0.07	-0.300	L					
233718_at	LOC89894	-0.003	-0.300	L					
234389_x_at	---	0.235	-0.298	L					
228879_at	---	-0.548	-0.298	T					
1563872_at	LOC284395	-0.167	-0.297	L					
227352_at	FLJ35119	-0.386	-0.297	T					
1567241_at	OR2L1P	0.101	-0.296	L					
1562215_at	---	-0.152	-0.295	B					
1569576_at	FLJ23129	0.037	-0.295	L					
224135_at	NYD-SP11	0.204	-0.295	L					
235752_at	---	-0.408	-0.292	L					
219438_at	FLJ12650	0.097	-0.291	B					
230689_at	---	-0.095	-0.291	B					
1562590_at	FLJ25756	-0.052	-0.291	L					
236991_at	---	0.032	-0.291	L					
229318_at	---	-0.076	-0.289	L					
240198_at	---	-0.185	-0.287	B					
229905_at	MCTP2	0.033	-0.285	L					
234302_s_at	FLJ20308	-0.415	-0.284	T					
220222_at	PRO1905	0.082	-0.281	B					
222848_at	FKSG14	-0.232	-0.281	L					
226272_at	---	-0.212	-0.281	L					
225075_at	PDRG1	0.035	-0.280	L					
229886_at	LRRC27	-0.007	-0.279	B					
220299_at	SPATA6	-0.191	-0.279	L					
232122_s_at	VEPH1	-0.069	-0.278	L					
1558334_a_at	C22orf15	-0.058	-0.277	L					
213237_at	LOC400506	0.204	-0.276	B					
1559544_s_at	---	-0.401	-0.276	L					
232444_at	C6orf204	-0.259	-0.276	L					
241911_at	CDKL3	0.007	-0.276	L					
228805_at	FLJ44216	0.384	-0.275	L					
231921_at	FLJ13096	-0.212	-0.275	L					
234905_at	DKFZP434H116	-0.005	-0.275	T					
201269_s_at	NUDCD3	-0.13	-0.274	B					
218920_at	FLJ10404	-0.187	-0.274	B					
1569428_at	WIBG	0.028	-0.274	L					
1561327_at	C6orf122	-0.215	-0.274	T					
239702_x_at	---	-0.247	-0.274	T					
235836_at	FLJ30594	0.114	-0.272	B					
1561535_at	---	-0.398	-0.272	L					
237992_at	---	-0.134	-0.270	L					

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
236771_at	C6orf159	-0.123	-0.270	T				
217532_x_at	KIAA1935	0.124	-0.269	B				
53991_at	KIAA1277	0.064	-0.269	B				
229580_at	---	-0.123	-0.269	L				
216372_at	---	-0.259	-0.269	T				
236483_at	---	0.316	-0.265	B				
216171_at	---	-0.147	-0.265	L				
220726_at	---	-0.057	-0.264	T				
223526_at	C18orf21	-0.044	-0.263	L				
230521_at	C9orf100	-0.19	-0.262	B				
241153_at	---	-0.24	-0.262	B				
235870_at	LOC339524	0.081	-0.262	L				
221647_s_at	RIC8	0.042	-0.261	B				
1569925_at	---	0.186	-0.261	L				
227420_at	MGC17791	-0.14	-0.261	L				
227710_s_at	---	-0.304	-0.261	T				
230689_at	---	-0.118	-0.261	T				
233963_at	LOC286436	-0.171	-0.259	T				
1558894_a_at	FLJ25393	-0.005	-0.258	L				
226448_at	MGC15887	-0.379	-0.258	L				
235809_at	DKFZp686L181	-0.196	-0.257	B				
1563874_at	FLJ38736	-0.031	-0.257	L				
235211_at	E2IG2	0.069	-0.257	L				
241105_at	---	0.057	-0.257	L				
1565692_at	---	-0.094	-0.256	T				
224881_at	VKORC1L1	0.059	-0.255	B				
233278_at	M-RIP	-0.087	-0.255	B				
1558275_at	Magmas	0.034	-0.254	L				
1560924_at	---	-0.223	-0.250	L				
1568978_s_at	C11orf21	-0.252	-0.250	T				
231477_at	---	-0.033	-0.249	B				
242154_x_at	PPIL5	-0.091	-0.249	B				
231443_at	---	-0.093	-0.248	B				
209889_at	SEC31L2	-0.215	-0.248	L				
1552729_at	MGC16037	-0.06	-0.246	B				
1559970_at	LOC283583	-0.21	-0.246	L				
239770_at	CHR3SYT	0.222	-0.245	L				
241081_at	FLJ38109	-0.137	-0.244	L				
243364_at	AUTS2	-0.008	-0.243	L				
219592_at	MCPH1	0.221	-0.242	L				
231195_at	---	-0.068	-0.242	T				
238744_at	---	-0.107	-0.241	L				
1553910_at	FLJ32833	-0.216	-0.239	L				
1561555_at	---	0.016	-0.239	L				
1562044_at	---	0.175	-0.239	L				
230523_at	---	-0.007	-0.239	L				
223300_s_at	FLJ23518	-0.135	-0.237	B				
1569817_at	---	0.004	-0.237	L				
1570224_at	---	-0.147	-0.237	L				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
243536_x_at	LOC201175	-0.228	-0.236	T				
217082_at	---	0	-0.235	L				
228493_at	AKAP14	-0.39	-0.235	L				
1562682_at	LOC283666	-0.085	-0.234	L				
218860_at	MGC3162	-0.171	-0.234	T				
233259_at	FLJ12057	0.143	-0.233	B				
1559781_at	LOC285423	-0.176	-0.233	L				
243769_at	---	-0.09	-0.232	L				
222261_at	KIAA1609	-0.157	-0.232	T				
1564314_at	LOC219690	-0.035	-0.231	B				
1565978_a_at	FCHO2	-0.026	-0.231	L				
239109_at	---	-0.244	-0.231	T				
1556111_s_at	---	-0.324	-0.230	B				
1566194_at	---	-0.063	-0.230	B				
1561718_at	---	-0.072	-0.230	L				
238931_at	---	0.157	-0.229	B				
217499_x_at	OR7E47P	0.238	-0.229	L				
239105_at	---	0.041	-0.229	L				
231673_at	---	-0.389	-0.228	L				
1563606_a_at	LOC286359	-0.272	-0.228	T				
1554185_at	LOC283887	-0.209	-0.227	B				
239414_at	---	-0.193	-0.227	L				
1566551_at	---	-0.131	-0.227	T				
216838_at	LOC92249	0.029	-0.226	L				
237019_at	---	0.221	-0.226	L				
239759_at	---	0.322	-0.226	L				
239970_at	---	-0.108	-0.226	L				
232177_at	---	0.087	-0.225	L				
230644_at	LRFN5	0.023	-0.224	L				
243011_at	FAM55C	0.035	-0.224	L				
231690_at	---	-0.104	-0.223	T				
225325_at	FLJ20160	-0.121	-0.222	L				
1568666_at	LOC158381	-0.056	-0.221	B				
220032_at	FLJ21986	-0.074	-0.221	T				
209216_at	WDR45	-0.423	-0.220	T				
217380_s_at	---	0.03	-0.219	L				
232435_at	CXorf45	0.145	-0.218	L				
240868_at	DKFZp547A024	-0.014	-0.218	T				
228270_at	DKFZp547K054	-0.148	-0.217	B				
211071_s_at	AF1Q	-0.138	-0.217	L				
219233_s_at	GSDML	-0.186	-0.216	T				
220326_s_at	FLJ10357	0.016	-0.215	L				
238233_at	---	0.02	-0.215	L				
239188_at	C14orf24	-0.179	-0.214	L				
243671_at	---	-0.076	-0.214	L				
238143_at	---	0.154	-0.213	L				
1553423_a_at	FLJ31952	-0.114	-0.213	T				
1559509_at	---	0.106	-0.212	L				
1563015_at	---	-0.138	-0.212	T				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Geneontology	Geneontology	Geneontology	Pathway
				Organ	Biological Function	Molecular Function	Cellular Component	
213242_x_at	KIAA0284	-0.32	-0.212	T				
215110_at	MBL1P1	-0.133	-0.211	B				
244037_at	---	-0.231	-0.211	T				
1563139_at	---	0.017	-0.209	L				
231504_at	LOC130940	-0.072	-0.209	L				
234931_at	AYP1r1	-0.066	-0.209	L				
240628_at	IGSF4	-0.157	-0.209	L				
241767_at	---	0.068	-0.209	T				
234956_at	LOC93444	0.032	-0.208	B				
233641_s_at	C8orf13	-0.198	-0.208	L				
234100_at	---	0.242	-0.208	L				
241422_at	---	-0.025	-0.208	L				
240337_at	---	-0.07	-0.207	L				
1554648_a_at	NIP	-0.015	-0.207	T				
222302_at	---	-0.337	-0.205	L				
1565740_at	---	-0.327	-0.205	T				
226722_at	FAM20C	-0.526	-0.205	T				
240944_at	---	-0.053	-0.205	T				
1567173_at	---	-0.218	-0.204	L				
231039_at	---	-0.091	-0.204	L				
239215_at	LOC401284	-0.048	-0.204	L				
242259_at	FLJ25560	-0.171	-0.204	T				
1560513_at	LOC400568	0.153	-0.203	L				
241139_at	---	-0.061	-0.203	L				
1560517_s_at	---	-0.067	-0.203	T				
1561490_at	AAA1	-0.014	-0.203	T				
220755_s_at	C6orf48	-0.341	-0.202	L				
226056_at	CDGAP	-0.349	-0.202	T				
230042_at	---	0.038	-0.202	T				
231129_at	---	-0.004	-0.202	T				
232569_at	---	-0.187	-0.201	L				
234328_at	---	-0.161	-0.201	T				
241591_at	---	-0.233	-0.201	T				
219164_s_at	C14orf103	0.132	-0.200	B				
1553918_at	C21orf129	0.005	-0.200	T				
1560753_at	---	0.224	-0.200	T				
1561540_at	LOC144920	-0.245	-0.200	T				
1557665_at	---	-0.196	-0.199	B				
228482_at	FLJ36674	0.004	-0.199	L				
236587_at	---	0.286	-0.199	L				
229075_at	---	-0.021	-0.198	B				
1558333_at	C22orf15	0.062	-0.198	L				
1567281_at	---	0.051	-0.198	L				
240775_at	---	0.139	-0.198	L				
1566873_at	---	-0.17	-0.197	L				
238062_at	LOC338328	0.091	-0.197	L				
1560292_a_at	LOC255104	-0.227	-0.197	T				
239764_at	LOC401048	-0.205	-0.197	T				
220749_at	0orf68 /// CCD	0.089	-0.194	L				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Geneontology		Geneontology	Geneontology	
				Organ	Biological Function	Molecular Function	Cellular Component	Pathway
233345_at	FLJ23588	0.123	-0.194	L				
221272_s_at	C1orf21	0.226	-0.193	L				
238302_at	---	0.056	-0.193	L				
226956_at	LOC400924	0.046	-0.192	L				
234612_at	---	0.034	-0.192	L				
1568828_at	---	0.086	-0.191	L				
1561106_at	---	-0.149	-0.190	L				
221591_s_at	FLJ10156	-0.234	-0.190	T				
243387_at	MESP1	-0.134	-0.190	T				
224318_s_at	FLJ10081	0.028	-0.189	B				
237829_at	---	-0.016	-0.189	B				
215496_at	SAMD4	0.045	-0.189	L				
226211_at	MEG3	0.154	-0.189	L				
218097_s_at	CUEDC2	-0.347	-0.189	T				
235132_at	LOC254128	-0.074	-0.189	T				
1563139_at	---	-0.182	-0.188	B				
1566825_at	---	-0.162	-0.188	B				
X-HUMRGEIM10099_	---	0.034	-0.188	B				
228833_s_at	LOC400027	-0.232	-0.188	L				
222694_at	MGC2752	-0.202	-0.188	T				
219346_at	LRFN3	0.137	-0.187	B				
218514_at	FLJ10587	-0.344	-0.187	L				
220755_s_at	C6orf48	-0.267	-0.187	T				
233731_at	---	0.154	-0.186	B				
1569840_at	---	0.141	-0.186	L				
243087_at	NYD-SP29	0.113	-0.186	L				
224875_at	FLJ37562	-0.197	-0.186	T				
230892_at	CGI-26	-0.476	-0.185	L				
239832_at	C9orf42	0.1	-0.185	L				
236714_at	---	-0.085	-0.185	T				
220396_at	PRO2268	0.091	-0.184	L				
235350_at	---	0.102	-0.184	L				
230712_at	FLJ20719	-0.322	-0.183	L				
241992_at	---	-0.11	-0.183	T				
239425_at	---	-0.046	-0.182	L				
227904_at	AZI2	-0.216	-0.181	L				
238834_at	---	-0.435	-0.181	L				
219313_at	KIAA1034	-0.057	-0.181	T				
1568683_at	MGC23284	0.282	-0.180	L				
215252_at	---	-0.042	-0.179	L				
227431_at	RSBN1L	-0.223	-0.179	L				
240289_at	---	0.226	-0.179	T				
234429_at	C9orf130	-0.144	-0.178	B				
1557672_s_at	---	0	-0.178	L				
204985_s_at	MGC2650	-0.381	-0.178	T				
232827_at	---	-0.134	-0.177	L				
243488_at	LOC285513	-0.17	-0.177	T				
1562568_at	---	0.125	-0.176	B				
1552793_at	FLJ37131	0.328	-0.176	L				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
237730_at	LOC197387	-0.4	-0.175	L				
1562693_at	---	-0.213	-0.175	T				
235784_at	---	-0.023	-0.174	T				
207159_x_at	MECT1	0.234	-0.173	B				
211774_s_at	DKFZP564I122	0.027	-0.173	B				
229059_at	ANKRD16	0.066	-0.173	L				
224073_at	FLJ20464	-0.2	-0.173	T				
242698_at	AKAP14	0.1	-0.172	L				
226362_at	---	-0.241	-0.172	T				
222970_at	---	0.011	-0.171	L				
230334_at	---	-0.083	-0.171	T				
243237_at	---	-0.247	-0.171	T				
229238_at	LOC400566	0.243	-0.170	B				
243921_at	---	0.164	-0.169	B				
236509_at	KIAA1598	0.054	-0.169	L				
232818_at	LOC149297	0.028	-0.169	T				
242086_at	SPATA6	-0.226	-0.168	L				
218399_s_at	CDCA4	-0.326	-0.168	T				
224413_s_at	BLP1	-0.188	-0.168	T				
235643_at	C7orf6	0.035	-0.168	T				
242269_at	FLJ42875	0.184	-0.167	L				
215680_at	KIAA1654	-0.29	-0.166	B				
219768_at	B7-H4	0.123	-0.166	L				
227599_at	LOC151963	-0.179	-0.166	T				
1567027_at	SH3GLP2	0.12	-0.165	B				
1564760_at	---	0.141	-0.164	B				
205706_s_at	ANKRD26	-0.217	-0.164	T				
231214_at	---	-0.058	-0.164	T				
1562029_at	---	0.017	-0.163	L				
227455_at	C6orf136	0.53	-0.163	L				
227969_at	LOC400960	-0.239	-0.163	T				
1552878_at	ATOH7	-0.176	-0.162	T				
213330_at	HUMPPA	-0.352	-0.162	T				
227340_s_at	LOC285705	0.484	-0.161	L				
221419_s_at	---	-0.344	-0.161	T				
227349_at	---	-0.21	-0.161	T				
231657_s_at	KFZp434E232	-0.48	-0.161	T				
232326_at	MGC39526	-0.026	-0.161	T				
45714_at	HCFC1R1	-0.26	-0.161	T				
241552_at	---	0.091	-0.159	B				
241985_at	JMY	-0.13	-0.159	T				
229185_at	---	0.31	-0.158	L				
243622_at	LOC146694	-0.328	-0.158	T				
241160_at	---	0.022	-0.157	L				
239708_at	---	-0.091	-0.157	T				
240337_at	---	0.057	-0.157	T				
240987_at	---	-0.165	-0.156	L				
243939_at	---	-0.517	-0.156	L				
243915_at	---	-0.16	-0.156	T				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Geneontology	Geneontology	Geneontology	Pathway
				Organ	Biological Function	Molecular Function	Cellular Component	
229805_at	ZZHHC22	0.113	-0.155	L				
242162_at	FLJ25955	0.117	-0.155	L				
208190_s_at	LISCH7	0.175	-0.154	B				
1555209_at	LOC439951	-0.092	-0.154	T				
52731_at	FLJ20294	-0.419	-0.154	T				
1554017_at	FLJ39378	0.155	-0.153	L				
1566831_at	LOC283104	0.201	-0.153	L				
202279_at	C14orf2	-0.164	-0.153	T				
1566471_at	---	0.236	-0.152	B				
1565882_at	---	0.165	-0.152	L				
220306_at	FAM46C	-0.291	-0.152	L				
244045_at	---	-0.087	-0.152	T				
228752_at	CXorf10	-0.003	-0.151	L				
227955_s_at	---	-0.182	-0.150	L				
1556439_at	---	-0.136	-0.149	L				
1569157_s_at	LOC162993	-0.039	-0.149	T				
215858_at	---	-0.232	-0.149	T				
230286_at	---	0.275	-0.148	B				
1560895_at	---	0.061	-0.148	T				
1552415_a_at	WFDC9	0.084	-0.147	L				
231607_at	---	0.237	-0.147	L				
1562696_at	---	-0.099	-0.147	T				
1554214_at	---	0.069	-0.146	B				
1559506_x_at	FLJ35409	-0.219	-0.146	B				
240492_at	---	-0.14	-0.146	B				
226876_at	MGC45871	-0.485	-0.146	L				
244467_at	LOC440829	0.019	-0.146	T				
244759_x_at	FLJ32096	-0.174	-0.146	T				
1569417_at	LOC133874	-0.358	-0.145	L				
1555151_s_at	TDH	-0.231	-0.145	T				
1552895_a_at	C21orf99	0.037	-0.144	L				
233956_at	---	0.094	-0.144	L				
221946_at	C9orf116	0.01	-0.144	T				
1553197_at	FLJ35775	-0.278	-0.143	B				
1563488_at	KIAA1786	-0.24	-0.143	L				
238484_s_at	---	-0.179	-0.143	L				
244831_at	---	-0.199	-0.143	L				
1552390_a_at	FLJ39553	-0.146	-0.143	T				
1552849_at	LOC130951	0.183	-0.142	L				
1556368_at	LOC90835	0.054	-0.142	T				
1560010_a_at	FLJ32063	-0.16	-0.141	B				
230523_at	---	0.163	-0.141	B				
216644_at	---	0.225	-0.141	L				
243269_s_at	LOC389715	0.061	-0.141	L				
1558827_a_at	C20orf174	0.027	-0.140	L				
222342_at	LOC345667	0.036	-0.140	L				
236627_at	---	0.079	-0.140	T				
1563524_a_at	C14orf85	0.005	-0.139	L				
217835_x_at	C20orf24	-0.21	-0.139	T				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
228875_at	C6orf189	-0.242	-0.138	L				
1559159_at	KIAA0582	0.074	-0.138	T				
1562823_at	---	-0.225	-0.138	T				
1569351_at	FLJ10159	0.057	-0.137	B				
216214_at	---	-0.127	-0.137	L				
243020_at	FAM13A1	-0.022	-0.137	T				
1570600_at	LOC441477	0.096	-0.136	L				
1563477_at	---	0.049	-0.136	T				
1570014_at	FLJ46082	0.032	-0.135	L				
230041_at	---	0.134	-0.134	L				
229113_s_at	FLJ31031	0.26	-0.133	L				
215029_at	---	-0.172	-0.133	T				
1562924_at	LOC340357	0.167	-0.132	L				
223768_at	C21orf122	-0.245	-0.132	T				
243282_at	FLJ10996	0.077	-0.131	L				
216618_at	---	-0.02	-0.130	L				
1566768_at	---	-0.196	-0.130	T				
237174_at	---	-0.217	-0.130	T				
239950_at	---	-0.117	-0.130	T				
238012_at	LOC389815	0.198	-0.129	L				
240697_at	---	0.158	-0.129	L				
227963_at	FLJ35696	-0.242	-0.129	T				
234780_at	BCAS1	-0.253	-0.129	T				
1561331_at	LOC339476	-0.001	-0.127	B				
1569937_at	---	0.066	-0.127	L				
1556896_at	LOC284751	0.125	-0.126	L				
1562731_s_at	MDS2	0.307	-0.126	L				
229231_at	LOC114659	0.265	-0.126	L				
238739_at	---	-0.266	-0.126	T				
226901_at	LOC284018	-0.303	-0.125	L				
1563369_at	FLJ42957	-0.206	-0.125	T				
230220_at	---	-0.037	-0.125	T				
240163_at	LOC283666	0.273	-0.124	L				
1560959_a_at	---	0.03	-0.124	T				
216378_at	---	-0.244	-0.124	T				
216582_at	POM121L2	0.029	-0.123	B				
234658_at	---	0.066	-0.123	T				
1566934_at	TYRO3P	-0.295	-0.122	L				
207063_at	CYorf14	0.093	-0.122	L				
239486_at	---	-0.171	-0.122	L				
1553850_at	C21orf88	0.023	-0.122	T				
236068_s_at	---	-0.244	-0.122	T				
238040_at	---	-0.093	-0.121	L				
219730_at	MED18	0.138	-0.120	T				
1557286_at	---	0.263	-0.119	L				
215380_s_at	C7orf24	-0.329	-0.119	L				
237779_at	---	0.241	-0.119	L				
230491_at	---	0.01	-0.119	T				
241910_x_at	LOC400590	0.095	-0.119	T				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Geneontology	Geneontology	Geneontology	Pathway
				Organ	Biological Function	Molecular Function	Cellular Component		
226093_at	DCP1B	0.022	-0.118	L				
243422_at	---	-0.227	-0.118	T				
1566697_at	---	0.151	-0.117	L				
242228_at	---	-0.003	-0.116	B				
1557535_at	KIAA0992	0.036	-0.116	L				
1559653_at	---	0.009	-0.116	T				
215653_at	---	0.085	-0.115	T				
1557256_a_at	---	0.105	-0.114	L				
236021_at	CCBE1	0.152	-0.113	L				
1553644_at	C14orf49	-0.161	-0.112	L				
237025_at	---	-0.267	-0.112	L				
1566158_s_at	---	0.092	-0.111	T				
231823_s_at	KIAA1295	0.101	-0.110	B				
1561103_at	---	0.192	-0.110	L				
1566821_at	---	0.185	-0.108	L				
217544_at	---	0.16	-0.108	L				
216786_at	LOC159110	-0.031	-0.108	T				
235519_at	LOC138255	0.206	-0.108	T				
240946_at	---	0.127	-0.108	T				
1558253_s_at	---	0	-0.107	L				
226885_at	---	0.085	-0.107	L				
233767_at	---	-0.116	-0.107	T				
1561882_at	---	0.04	-0.106	L				
1566040_at	LOC442146	0.093	-0.105	B				
233804_at	LOC440131	-0.27	-0.105	T				
1555841_at	MGC17337	-0.005	-0.104	L				
222039_at	LOC146909	-0.246	-0.104	T				
1565454_at	XAGE3	0.216	-0.103	B				
236960_at	---	-0.277	-0.102	L				
239038_at	gm117	0.068	-0.102	T				
233048_at	FAM35A	-0.278	-0.101	T				
220268_at	PTD015	0.021	-0.100	L				
232945_at	FLJ32312	-0.166	-0.100	T				
234549_at	---	-0.196	-0.099	B				
1553423_a_at	FLJ31952	-0.1	-0.099	L				
1556901_s_at	LOC149773	0.077	-0.099	L				
1561221_x_at	---	0.147	-0.099	T				
239847_at	---	-0.049	-0.099	T				
243018_at	---	-0.296	-0.097	L				
44120_at	ADCK2	-0.274	-0.097	T				
1564399_a_at	ARMCX4	0.134	-0.096	T				
1561679_at	---	0.22	-0.095	L				
1561480_a_at	---	0.079	-0.095	T				
242025_at	---	-0.08	-0.095	T				
1557486_at	---	-0.141	-0.094	B				
1563685_at	LOC285422	0.29	-0.094	B				
222057_at	MGC3731	0.196	-0.094	L				
231244_at	CAS1	-0.229	-0.094	L				
236069_at	FLJ39005	0.091	-0.094	T				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
1555059_at	---	0.07	-0.092	L				
1557413_a_at	---	0.107	-0.091	L				
1569664_at	FLJ00310	0.085	-0.091	L				
241426_at	KIAA1712	-0.159	-0.091	L				
1564707_x_at	GA	-0.147	-0.091	T				
243022_at	---	-0.166	-0.091	T				
1559444_at	---	-0.285	-0.090	B				
242003_at	LOC157697	-0.176	-0.090	B				
1570206_at	---	-0.137	-0.090	T				
218514_at	FLJ10587	-0.175	-0.088	T				
236059_at	FLJ23342	0.286	-0.088	T				
238818_at	DKFZP434I116	-0.235	-0.088	T				
241569_at	LOC146909	0.082	-0.088	T				
1561966_at	ANKRD28	0.147	-0.087	L				
240996_at	---	-0.4	-0.086	L				
207839_s_at	C9orf127	-0.329	-0.086	T				
1566182_at	---	0.15	-0.085	B				
229295_at	LOC150166	0.142	-0.085	L				
213248_at	LOC221362	0.082	-0.085	T				
214382_at	UNC93A	0.119	-0.085	T				
1566628_at	LRRK1	0.043	-0.084	L				
244889_at	LOC388210	-0.241	-0.084	T				
230860_at	---	-0.132	-0.083	L				
1552455_at	C9orf65	0.131	-0.082	T				
1561519_at	---	0.111	-0.081	L				
217663_at	---	-0.124	-0.079	T				
1569767_at	---	-0.273	-0.078	L				
230537_at	---	0.176	-0.077	L				
1559986_at	---	0.077	-0.077	T				
230092_at	UBXD3	0.163	-0.076	T				
1570470_at	C14orf161	0.108	-0.075	T				
207170_s_at	LETMD1	0.185	-0.074	B				
228839_s_at	LOC439994	0.096	-0.074	B				
1560581_at	---	-0.185	-0.074	T				
220730_at	FLJ12986	0.149	-0.074	T				
1557438_at	---	-0.084	-0.072	T				
235173_at	LOC401093	0.212	-0.072	T				
216273_at	ZNF272	-0.359	-0.071	L				
237662_at	---	-0.383	-0.071	L				
224715_at	WDR34	-0.359	-0.071	T				
236979_at	---	0.222	-0.070	L				
237255_at	LOC440767	0.077	-0.070	T				
1568821_at	HCC-8	-0.117	-0.069	L				
229242_at	---	0.177	-0.069	T				
1556257_at	---	0.129	-0.068	T				
243216_at	---	-0.198	-0.068	T				
232897_at	FLJ20444	-0.269	-0.067	L				
229858_at	---	-0.149	-0.067	T				
235585_at	---	-0.18	-0.067	T				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Geneontology		Geneontology		Geneontology	
				Organ	Biological Function	Molecular Function	Cellular Component		Pathway
236815_at	---	0.439	-0.066	L					
237964_at	---	-0.212	-0.066	L					
229101_at	LOC150166	0.116	-0.065	B					
215132_at	---	0.105	-0.065	L					
216675_at	---	0.147	-0.064	B					
1564475_s_at	LOC285711	-0.215	-0.064	L					
236366_at	LOC440149	0.234	-0.061	T					
217276_x_at	dJ222E13.1	0.282	-0.060	L					
226254_s_at	KIAA1430	-0.329	-0.060	T					
232951_at	---	-0.158	-0.060	T					
236214_at	NYD-SP18	0.261	-0.059	L					
220396_at	PRO2268	0.121	-0.059	T					
231131_at	RP1-32F7.2	-0.153	-0.058	T					
231905_at	C20orf96	0.194	-0.057	B					
238804_at	LOC440998	0.322	-0.057	L					
1553640_at	C8orf21	-0.273	-0.056	B					
228636_at	BHLHB5	-0.337	-0.056	L					
241166_at	TSGA14	-0.256	-0.056	L					
232892_at	C20orf166	0.273	-0.054	B					
243793_at	DJ159A19.3	0.129	-0.054	T					
233352_at	KIBRA	-0.183	-0.053	L					
1559195_at	---	0.285	-0.052	L					
233823_at	KIAA1276	0.26	-0.052	L					
231381_at	HT017	0.12	-0.051	L					
240522_at	---	0.124	-0.051	T					
215675_at	KIAA1655	-0.135	-0.050	T					
220628_s_at	SDK2	-0.233	-0.049	L					
206088_at	LOC440457	-0.384	-0.046	L					
234270_at	---	0.246	-0.045	L					
240772_at	C10orf11	0.189	-0.045	L					
235027_at	---	-0.19	-0.045	T					
214889_at	DKFZP564J102	0.17	-0.044	T					
237023_at	---	0.232	-0.044	T					
1561398_at	---	0.218	-0.043	L					
241300_at	---	0.157	-0.043	T					
1563069_at	---	-0.21	-0.041	L					
236900_x_at	LOC126661	-0.376	-0.041	L					
237509_at	---	0.209	-0.041	T					
238489_at	---	-0.131	-0.041	T					
216828_at	---	-0.222	-0.039	B					
228118_x_at	MGC13114	-0.414	-0.039	L					
232189_at	---	-0.156	-0.039	L					
230569_at	KIAA1430	-0.125	-0.039	T					
240218_at	---	0.159	-0.038	B					
1563254_a_at	---	0.235	-0.038	L					
232253_at	---	0.365	-0.038	L					
1570116_at	---	0.109	-0.038	T					
1557214_at	---	0.197	-0.037	T					
222344_at	C5orf13	-0.141	-0.036	L					

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Organ	Geneontology Biological Function	Geneontology Molecular Function	Geneontology Cellular Component	Pathway
1556395_at	---	0.137	-0.036	T				
236740_at	---	-0.09	-0.035	B				
1554440_at	KIAA0513	0.202	-0.035	L				
231414_at	LOC162993	-0.349	-0.035	L				
241394_at	LOC284120	0.177	-0.035	L				
231466_at	NYD-SP18	-0.219	-0.034	T				
223614_at	DKFZp761D11	-0.315	-0.033	L				
240629_at	---	0.186	-0.033	T				
1568660_a_at	LOC440384	-0.091	-0.032	L				
228096_at	---	0.177	-0.032	T				
231826_at	KIAA1272	0.131	-0.031	T				
231439_at	NSE1	-0.184	-0.030	T				
220344_at	C11orf16	0.213	-0.029	T				
1564379_at	---	0.152	-0.028	B				
1562643_at	---	0.166	-0.028	T				
236046_at	FLJ44896	-0.158	-0.027	L				
1561347_a_at	---	0.145	-0.027	T				
229180_at	KIBRA	-0.355	-0.026	L				
240366_at	---	-0.109	-0.026	T				
241538_at	LOC401583	0.156	-0.026	T				
243531_at	ORAOV1	0.228	-0.026	T				
1558124_at	LOC134492	0.241	-0.024	L				
1562983_at	LOC441025	0.155	-0.024	T				
224274_at	C14orf155	0.131	-0.024	T				
232255_at	LOC401321	-0.146	-0.024	T				
1562190_at	---	-0.15	-0.022	L				
1564358_at	---	-0.179	-0.021	B				
228007_at	C6orf204	-0.249	-0.021	L				
231496_at	FCAMR	0.092	-0.021	L				
1569376_s_at	---	-0.194	-0.021	T				
221242_at	FLJ23022	-0.121	-0.021	T				
227730_at	DYM	-0.204	-0.021	T				
225028_at	---	0.134	-0.020	B				
235559_at	FLJ22374	-0.162	-0.020	T				
227321_at	GATS	-0.236	-0.019	B				
1556770_a_at	LRRC17	0.164	-0.019	T				
214409_at	RFPL3S	0.358	-0.018	B				
231646_at	DPCR1	-0.152	-0.018	L				
1561927_at	C3orf16	0.175	-0.017	L				
243356_at	---	0.479	-0.016	L				
242754_at	---	-0.21	-0.015	T				
239866_at	---	0.232	-0.014	T				
236933_at	LOC388353	-0.331	-0.013	L				
1560982_at	---	0.25	-0.011	T				
240795_at	---	0.156	-0.011	T				
1566805_at	---	0.162	-0.009	T				
237658_at	---	-0.319	-0.008	L				
237945_at	---	-0.185	-0.008	L				
216936_at	---	0.264	-0.006	T				

Affymetrix Probe ID No.	Gene Symbol	Expression change (log2 Values): 1x LCPUFA (L1, 0.33% DHA-0.67% ARA)	Expression change (log2 Values): 3x LCPUFA (L3, 1.00% DHA-0.67% ARA)	Geneontology		Geneontology		Geneontology	
				Organ	Biological Function	Molecular Function	Cellular Component --		Pathway
230650_at	---	-0.12	-0.006	T					
243957_at	---	0.218	-0.006	T					
234216_at	FLJ21408	0.24	-0.005	L					
227086_at	LOC128977	-0.139	-0.004	L					
243492_at	CTMP	0.231	-0.002	L					
230276_at	FAM49A	0.152	-0.001	B					
218659_at	ASXL2	-0.356	-0.001	L					

TABLE 8: Gene List of Up and Downregulated Genes in the Spleen of Baboon (1.00% DHA)

Affy Probe ID	Gene Symbol	Differential Expression (log2 Values)	Biological Process	Molecular Function	Cellular Component	Pathway
239122_at	IL24	0.553	apoptosis/// immune response	cytokine activity	extracellular space	Cytokine-Cytokine Receptor Interaction, JAK-STAT signaling pathway
239093_at	C10orf65	0.551	lysine biosynthesis /// diaminopimelate biosynthesis	---	---	---
203627_at	IGF1R	0.538	regulation of cell cycle /// protein amino acid phosphorylation /// anti-apoptosis /// signal transduction /// positive regulation of cell proliferation /// insulin receptor signaling pathway	receptor activity /// epidermal growth factor receptor activity /// insulin-like growth factor receptor activity /// protein binding /// ATP binding /// transferase activity	integral to membrane	---
226245_at	KCTD1	0.506	potassium ion transport	ion channel activity /// voltage-gated potassium channel activity /// protein binding	voltage-gated potassium channel complex /// membrane	---
209540_at	IGF1	0.491	skeletal development /// DNA replication /// cell motility /// signal transduction /// Ras protein signal transduction /// muscle development /// physiological process /// perception of sound /// positive regulation of cell proliferation /// glycolate metabolism	insulin-like growth factor receptor binding /// hormone activity /// growth factor activity /// prothoracicotrophic hormone activity	extracellular region	---
217562_at	DBCCR1 L	0.487	---	---	---	---
243197_at	---	0.477	---	---	---	---

212624_s_at	CHN1	0.467	intracellular signaling cascade	SH3/SH2 adaptor protein activity /// GTPase activator activity /// diacylglycerol binding	---	---
1559826_a_at	LOC401074	0.465	---	---	---	---
209456_s_at	FBXW11	0.452	Wnt receptor signaling pathway /// protein ubiquitination	ubiquitin-protein ligase activity	ubiquitin ligase complex	---
206917_at	GNA13	0.448	cell motility /// signal transduction /// G-protein coupled receptor protein signaling pathway	GTPase activity /// receptor signaling protein activity /// protein binding /// GTP binding	membrane	G Protein Signaling /// G13 Signaling Pathway
204813_at	MAPK10	0.445	protein amino acid phosphorylation /// signal transduction /// JNK cascade	protein serine/threonine kinase activity /// JUN kinase activity /// MAP kinase activity /// MAP kinase kinase activity /// ATP binding /// transferase activity	---	Apoptosis /// G13 Signaling Pathway /// Integrin-mediated cell adhesion /// MAPK Cascade /// Wnt signaling
234936_s_at	KIAA1345	0.444	---	---	---	---
201200_at	CREG1	0.426	regulation of cell growth /// regulation of transcription from Pol II promoter /// development /// cell proliferation	RNA polymerase II transcription factor activity /// transcription corepressor activity	---	---
205416_s_at	ATXN3	0.426	nucleotide-excision repair /// regulation of transcription, DNA-dependent /// synaptic transmission /// neurogenesis	---	nucleoplasm /// cytoplasm	---
207526_s_at	IL1RL1	0.418	signal transduction	transmembrane receptor activity /// interleukin-1 receptor activity /// receptor signaling protein activity /// protein binding	integral to membrane	---

1561413_at	SPARC	0.412	bone remodeling/// biomineral formation/// cell communication/// development/// enzyme linked receptor protein signaling pathway/// organ development/// organismal physiological process/////ossification/// physiological process/// signal transduction/// skeletal development/// tissue development/// tissue remodeling/// transmembrane receptor protein tyrosine kinase signaling pathway	calcium ion binding/// cation binding/// collagen binding/// copper ion binding/// ion binding/// metal ion binding/// protein binding/// transition metal ion binding	---	---
244032_at	---	0.412	---	---	---	---
1554796_at	DPP6	0.41	proteolysis and peptidolysis	catalytic activity /// dipeptidyl peptidase IV activity	integral to membrane	---
229566_at	LOC440449	0.409	---	---	---	---
224250_s_at	SECISBP2	0.405	protein biosynthesis	RNA binding	nucleus	---
222271_at	---	0.4	---	---	---	---
1554642_at	RNF32	0.398	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
1558279_at	FVT1	0.398	metabolism	oxidoreductase activity	extracellular space	---
209995_s_at	TCL1A	0.397	development	---	microsome	---
1556338_at	UBE1C	0.396	ubiquitin cycle /// apoptosis /// cell cycle	catalytic activity /// ubiquitin activating enzyme activity /// ATP binding /// ligase activity	---	---
239665_at	---	0.396	---	---	---	---

228195_at	MGC13057	0.39	---	---	---	---	---
242899_at	SESN3	0.389	cell cycle arrest	---	nucleus	---	---
1563830_at	KIAA1937	0.385	---	---	---	---	---
229654_at	ZNF44	0.385	regulation of transcription, DNA-dependent	protein binding /// DNA binding /// metal ion binding /// nucleic acid binding /// zinc ion binding	intracellular /// nucleus	---	
1561062_at	---	0.383	---	---	---	---	
1554008_at	OSMR	0.382	cell surface receptor linked signal transduction /// cell proliferation	receptor activity /// oncostatin-M receptor activity	oncostatin-M receptor complex	---	
236920_at	PEPP-2	0.379	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---	
230444_at	---	0.378	---	---	---	---	
1552543_at	STN2	0.377	intracellular protein transport /// endocytosis	---	membrane /// clathrin vesicle coat	---	
221161_at	ASCL3	0.375	regulation of transcription, DNA-dependent	DNA binding	nucleus	---	
229015_at	LOC286367	0.373	---	---	---	---	
1565700_at	---	0.371	---	---	---	---	
241197_at	---	0.371	---	---	---	---	
222956_at	FIGN	0.37	---	ATP binding /// nucleoside-triphosphatase activity /// nucleotide binding	---	---	
235221_at	KIAA0323	0.37	---	---	---	---	

229261_at	SOS1	0.369	Ras protein signal transduction	DNA binding /// Ras guanyl-nucleotide exchange factor activity /// Rho guanyl-nucleotide exchange factor activity /// Rho GTPase activator activity	---		Integrin-mediated cell adhesion
1552910_at	SIGLEC1	0.368	cell adhesion	protein binding /// sugar binding	integral to membrane	---	---
230983_at	BCNP1	0.368	---	---	---	---	---
1558762_at	LOC285989	0.363	---	nucleic acid binding /// zinc ion binding	nucleus	---	---
212133_at	NIPA2	0.362	---	---	---	---	---
235679_at	ENSA	0.358	transport/// response to nutrient	ion channel inhibitor activity/// receptor binding	---	---	---
237349_at	TSHR	0.356	G-protein signaling, coupled to cyclic nucleotide second messenger /// cell-cell signaling /// positive regulation of cell proliferation	thyroid-stimulating hormone receptor activity	integral to plasma membrane	GPCRDB Other /// Peptide GPCRs	
234967_at	IL6ST	0.353	immune response /// cell surface receptor linked signal transduction	receptor activity /// interleukin-6 receptor activity /// oncostatin-M receptor activity	integral to plasma membrane	Ribosomal Proteins	
1557257_at	BCL10	0.352	induction of apoptosis /// regulation of apoptosis /// positive regulation of I-kappaB kinase/NF-kappaB cascade /// negative regulation of cell cycle	signal transducer activity /// protein binding	intracellular	---	
208477_at	KCNC1	0.351	cation transport /// potassium ion transport	voltage-gated potassium channel activity /// protein binding	membrane fraction /// voltage-gated potassium channel complex /// integral to membrane	---	
214474_at	PRKAB2	0.351	fatty acid biosynthesis /// signal transduction	---	---	Fatty Acid Synthesis	

218257_s_at	UGCGL1	0.351	protein amino acid glycosylation	UDP-glucose:glycoprotein glucosyltransferase activity /// transferase activity	soluble fraction /// endoplasmic reticulum	---	
223620_at	GPR34	0.351	G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity /// purinergic nucleotide receptor activity, G-protein coupled	integral to plasma membrane	GPCRDB Class A Rhodopsin-like2	
234518_at	OR51B2	0.351	G-protein coupled receptor protein signaling pathway/// sensory perception/// sensory perception of smell/// signal transduction	olfactory receptor activity	integral to membrane	---	
239718_at	---	0.35	---	---	---	---	
242338_at	DKFZp762C1112	0.349	---	---	---	---	
215973_at	HCG4P6	0.348	---	---	---	---	
234705_at	NCK2	0.346	signal complex formation /// regulation of epidermal growth factor receptor activity /// intracellular signaling cascade /// negative regulation of cell proliferation /// positive regulation of actin filament polymerization /// positive regulation of T-cell proliferation /// T-cell activation	protein binding /// cytoskeletal adaptor activity /// receptor signaling complex scaffold activity	cytoplasm	---	
228538_at	FLJ45880	0.343	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---	
204326_x_at	MT1X	0.34	response to metal ion	metal ion binding	---	---	
1554914_at	PLA2G4D	0.339	phospholipid catabolism	phospholipase activity	---	---	
202428_x_at	DBI	0.339	transport	acyl-CoA binding /// lipid binding /// benzodiazepine receptor binding	---	---	

238357_at	RNPC2	0.339	nuclear mRNA splicing, via spliceosome /// regulation of transcription, DNA-dependent /// mRNA processing	RNA binding	nucleus	mRNA processing
211188_at	CD84	0.338	defense response /// homophilic cell adhesion	---	integral to plasma membrane	---
206594_at	PASK	0.336	protein amino acid phosphorylation /// signal transduction	protein serine/threonine kinase activity /// signal transducer activity /// ATP binding /// transferase activity	---	---
213333_at	MDH2	0.334	glycolysis /// tricarboxylic acid cycle /// malate metabolism	L-lactate dehydrogenase activity /// oxidoreductase activity /// L-malate dehydrogenase activity	mitochondrial matrix	Glycolysis and Gluconeogenesis /// Krebs-TCA Cycle /// Citrate cycle (TCA cycle) /// Pyruvate metabolism /// Glyoxylate and dicarboxylate metabolism /// Carbon fixation /// Reductive carboxylate cycle (CO2 fixation)
217481_x_at	FLJ45455	0.333	---	---	---	---
211137_s_at	ATP2C1	0.332	cation transport /// calcium ion transport /// calcium ion homeostasis /// metabolism /// epidermis development /// proton transport /// positive regulation of I-kappaB kinase/NF-kappaB cascade	magnesium ion binding /// catalytic activity /// signal transducer activity /// calcium-transporting ATPase activity /// ATP binding /// hydrolase activity /// hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	integral to membrane	---

224850_at	ATAD1	0.33	---	nucleotide binding /// ATP binding /// nucleoside-triphosphatase activity	---	---
1552648_a_at	TNFRSF10A	0.329	apoptosis /// induction of apoptosis /// caspase activation /// signal transduction /// activation of NF-kappaB-inducing kinase /// induction of apoptosis via death domain receptors	receptor activity /// death receptor activity /// caspase activator activity /// TRAIL binding	integral to membrane	---
1559119_at	C11orf23	0.328	---	binding	---	---
222938_x_at	ENPP3	0.326	phosphate metabolism /// nucleotide metabolism	nucleic acid binding /// endonuclease activity /// phosphodiesterase I activity /// nucleotide diphosphatase activity /// hydrolase activity	integral to plasma membrane	Purine metabolism /// Starch and sucrose metabolism /// Riboflavin metabolism /// Nicotinate and nicotinamide metabolism /// Pantothenate and CoA biosynthesis
208735_s_at	CTDSP2	0.323	---	phosphoprotein phosphatase activity /// hydrolase activity	soluble fraction /// nucleus	---
226969_at	LOC149448	0.323	---	---	---	---
232637_at	NEDD5	0.323	cytokinesis /// cell cycle	GTPase activity /// GTP binding	contractile ring	---
1552400_at	C15orf27	0.322	---	---	---	---
226833_at	FLJ32499	0.322	---	---	---	---
209856_x_at	ABI2	0.321	actin polymerization and/or depolymerization/// cell migration/// cytoskeleton organization and biogenesis	cytoskeletal adaptor binding/// kinase binding/// SH3/SH2 adaptor binding/// DNA binding	cytoplasm/// cytoskeleton/// filopodium/// lamellipodium/// nucleus	regulation of actin cytoskeleton

213927_at	MAP3K9	0.32	protein amino acid phosphorylation	protein serine/threonine kinase activity /// MAP kinase kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	---	---
234161_at	---	0.32	---	---	---	---
237393_at	---	0.319	---	---	---	---
243872_at	KIAA0261	0.319	---	---	---	---
1557064_s_at	FLJ32731	0.318	---	---	---	---
1562045_at	---	0.318	---	---	---	---
239944_at	BIRC1	0.318	nervous system development /// anti-apoptosis	ATP binding /// nucleoside-triphosphatase activity /// nucleotide binding	intracellular	---
241429_at	---	0.318	---	---	---	---
1570445_at	LOC441117	0.317	---	---	---	---
214762_at	ATP6V1G2	0.317	ATP biosynthesis /// proton transport	hydrogen ion transporter activity /// hydrolase activity	---	Oxidative phosphorylation /// ATP synthesis /// Photosynthesis /// Flagellar assembly /// Type III secretion system
239949_at	FLJ10916	0.317	metabolism	catalytic activity	---	---
243897_at	---	0.317	---	---	---	---
211388_s_at	NCOR2	0.315	regulation of transcription, DNA-dependent	transcription corepressor activity /// DNA binding /// Notch binding /// protein binding	nucleus	---

229443_at	ITPR3	0.314	cation transport /// calcium ion transport	receptor activity /// inositol 1,4,5-triphosphate-sensitive calcium-release channel activity /// calcium channel activity	endoplasmic reticulum /// integral to membrane	---	Calcium regulation in cardiac cells /// Smooth muscle contraction
217814_at	GK001	0.313	---	---	---	---	---
229703_at	DLG1	0.312	G1/S transition checkpoint/// actin filament organization/// cell-cell adhesion/// cortical actin cytoskeleton organization and biogenesis/// endothelial cell proliferation/// establishment and/or maintenance of cell polarity/// negative regulation of progression through mitotic cell cycle/// positive regulation of body size/// positive regulation of developmental growth	cytoskeletal protein binding/// guanylate kinase activity/// phosphoprotein phosphatase activity/// potassium channel regulator activity	basolateral plasma membrane/// cell-cell adherens junction/// endoplasmic reticulum	---	---
230888_at	HSPC049	0.312	---	---	---	---	---

216436_at	PIK3R4	0.311	---	---	---	---	Apoptosis/// B cell receptor signaling pathway/// Focal adhesion /// Insulin signaling /// Jak-STAT signaling pathway/// Phosphatidylinositol signaling system/// Regulation of actin cytoskeleton/// T cell receptor signaling pathway/// Toll-like receptor signaling/// Type II diabetes mellitus
244467_at	LOC440829	0.311	---	---	---	---	---
1569464_at	PPFIBP1	0.31	---	---	---	---	---
219666_at	MS4A6A	0.31	signal transduction	receptor activity	integral to membrane	---	---
204671_s_at	ANKRD6	0.309	---	#VALUE!	---	---	---
234678_at	KRTAP4-3	0.309	---	---	keratin filament	---	---
231517_at	LOC44059	0.308	---	---	---	---	---
226096_at	FNDC5	0.307	---	---	integral to membrane	---	---
229549_at	OPN1SW	0.307	---	calcium ion binding	endoplasmic reticulum /// Golgi apparatus	---	GPCRDB Class A Rhodopsin-like
239610_at	ASB13	0.307	intracellular signaling cascade	---	---	---	---
1556186_s_at	KIAA0090	0.306	---	---	---	---	---
204668_at	RNF24	0.305	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---	

1560877_at	C18orf30	0.304	---	---	integral to membrane	---
232021_at	LOC283464	0.304	carbohydrate biosynthesis	transferase activity, transferring hexosyl groups	---	---
226718_at	AMIGO	0.303	---	---	integral to membrane	---
1555039_a_at	ABCC4	0.302	ion transport	chloride channel activity /// ATP binding /// 15-hydroxyprostaglandin dehydrogenase (NAD+) activity /// ATPase activity /// ATPase activity, coupled to transmembrane movement of substances	integral to membrane	---
211612_s_at	IL13RA1	0.302	cell surface receptor linked signal transduction	receptor activity /// hematopoietin/interferon-class (D200-domain) cytokine receptor activity	plasma membrane /// interleukin-13 receptor complex /// integral to membrane	---
244519_at	ASXL1	0.301	regulation of transcription, DNA-dependent	---	nucleus	---
205184_at	GNG4	0.3	signal transduction /// regulation of G-protein coupled receptor protein signaling pathway	signal transducer activity	heterotrimeric G-protein complex /// plasma membrane	G Protein Signaling /// Calcium regulation in cardiac cells /// Smooth muscle contraction
205228_at	RBMS2	0.3	RNA processing /// regulation of translation	RNA binding	nucleus	---
238517_at	---	0.3	---	---	---	---
241539_at	---	0.3	---	---	---	---
202012_s_at	EXT2	0.299	skeletal development /// glycosaminoglycan biosynthesis /// signal transduction /// negative regulation of cell cycle	transferase activity, transferring glycosyl groups /// N-acetylglucosaminyl-proteoglycan 4-beta-glucuronosyltransferase activity	endoplasmic reticulum membrane /// Golgi apparatus /// integral to membrane	---

217611_at	LOC157697	0.299	---	---	---	---	---
233570_at	TSC1	0.299	cell adhesion /// Rho protein signal transduction /// negative regulation of cell cycle	---	---	---	---
210155_at	MYOC	0.298	visual perception /// morphogenesis	structural molecule activity /// latrotoxin receptor activity	non-muscle myosin /// cilium /// membrane	---	---
239929_at	FLJ32569	0.297	proteolysis and peptidolysis	carboxypeptidase activity /// metallopeptidase activity /// hydrolase activity	---	---	---
244310_at	RORA	0.297	regulation of transcription, DNA dependent/// signal transduction	protein binding/// sequence-specific DNA binding/// steroid hormone receptor activity/// transcription factor activity/// zinc ion binding	nucleus	---	---
1563117_at	LOC388456	0.296	---	---	---	---	---
232589_at	---	0.296	---	---	---	---	---
1558440_at	EFCBP1	0.295	---	---	---	---	---
1563482_at	DPYSL2	0.294	nucleobase, nucleoside, nucleotide and nucleic acid metabolism /// signal transduction /// neurogenesis	dihydropyrimidinase activity /// hydrolase activity	---	---	---
211607_x_at	EGFR	0.293	protein amino acid phosphorylation /// epidermal growth factor receptor signaling pathway /// cell proliferation /// negative regulation of cell cycle	receptor activity /// epidermal growth factor receptor activity /// ATP binding /// transferase activity	endosome /// cytoskeleton /// integral to plasma membrane	---	---
1563121_at	---	0.292	---	---	---	---	---

204241_at	ACOX3	0.292	electron transport /// fatty acid metabolism /// fatty acid beta-oxidation /// bile acid metabolism	acyl-CoA oxidase activity /// oxidoreductase activity	peroxisome	---	---
237030_at	ACPP	0.292	regulation of cell cycle	acid phosphatase activity /// protein tyrosine phosphatase activity /// hydrolase activity	extracellular region	gamma-Hexachlorocyclohexane degradation /// Riboflavin metabolism	---
238195_at	---	0.292	---	---	---	---	---
235210_s_at	RPESP	0.291	---	---	---	---	---
232413_at	PGBD3	0.29	---	---	---	---	---
1569730_at	FLJ40243	0.289	---	binding	---	---	---
219645_at	CASQ1	0.289	muscle development	calcium ion binding	mitochondrial matrix /// smooth endoplasmic reticulum	Calcium regulation in cardiac cells	---
238486_at	FRS2	0.289	transmembrane receptor protein tyrosine phosphatase signaling pathway /// G-protein coupled receptor protein signaling pathway /// fibroblast growth factor receptor signaling pathway	receptor activity /// transmembrane receptor protein tyrosine kinase adaptor protein activity /// insulin receptor binding /// protein binding /// regulator of G-protein signaling activity /// phosphatase activator activity	integral to plasma membrane	---	---
240094_at	DJ971N18.2	0.289	electron transport	electron transporter activity	integral to membrane	---	---
1561389_at	---	0.288	---	---	---	---	---

219956_at	GALNT6	0.288	---	polypeptide N-acetylgalactosaminyltransferase activity /// sugar binding /// transferase activity, transferring glycosyl groups /// manganese ion binding	Golgi apparatus /// integral to membrane		O-Glycan biosynthesis
232685_at	ETV6	0.288	regulation of transcription, DNA-dependent	transcription factor activity	nucleus		Circadian Exercise
237655_at	CEBPD	0.288	regulation of transcription, DNA-dependent /// transcription from Pol II promoter	DNA binding	nucleus	---	
1563814_at	FLJ25143	0.287	---	---	---	---	
227037_at	LOC201164	0.287	metabolism /// lipid catabolism	hydrolase activity	---	---	
211258_s_at	TGFA	0.286	regulation of cell cycle /// cell-cell signaling /// cell proliferation	protein-tyrosine kinase activity /// signal transducer activity /// epidermal growth factor receptor activating ligand activity /// protein binding /// growth factor activity	extracellular space /// soluble fraction /// integral to plasma membrane	---	
226929_at	MTHFR	0.286	amino acid metabolism /// methionine metabolism /// circulation	methylenetetrahydrofolate reductase (NADPH) activity /// oxidoreductase activity	---		One carbon pool by folate
231154_x_at	TINAG	0.286	proteolysis and peptidolysis /// cell adhesion	cysteine-type endopeptidase activity /// protein binding /// cysteine-type peptidase activity	basement membrane	---	
1566469_at	---	0.285	---	---	---	---	

231894_at	SARS	0.285	protein biosynthesis /// seryl-tRNA aminoacylation /// tRNA processing	RNA binding /// serine-tRNA ligase activity /// ATP binding /// ligase activity	soluble fraction /// cytoplasm	Glycine, serine and threonine metabolism /// Aminoacyl-tRNA biosynthesis
232718_at	---	0.285	---	---	---	---
229634_at	FLJ90586	0.283	---	---	---	---
232866_at	FLJ12895	0.283	regulation of transcription, DNA-dependent	nucleic acid binding /// transcription factor activity /// zinc ion binding	nucleus	---
234592_at	---	0.283	---	---	---	---
234712_at	C18orf25	0.283	---	---	---	---
209596_at	DKFZp564I1922	0.282	protein amino acid phosphorylation	vascular endothelial growth factor receptor activity /// ATP binding	---	---
216717_at	FAM48A	0.282	---	---	---	---
219671_at	HPCAL4	0.282	central nervous system development	calcium ion binding	---	---
239987_at	---	0.282	---	---	---	---
1555661_at	OR8D1	0.281	G-protein coupled receptor protein signaling pathway /// perception of smell	olfactory receptor activity	integral to membrane	---
1556753_s_at	HOXC6	0.281	regulation of transcription from RNA polymerase II promoter/// regulation of transcription, DNA-dependent/// development	sequence-specific DNA binding/// transcription corepressor activity/// transcription factor activity	nucleus	---
216482_x_at	ZNF79	0.281	regulation of transcription, DNA-dependent	DNA binding/// Zinc ion binding	nucleus	---
207973_x_at	ACRV1	0.28	development	---	---	---
1553041_at	HTR3C	0.278	ion transport	extracellular ligand-gated ion channel activity /// neurotransmitter receptor activity	integral to membrane /// postsynaptic membrane	---
218244_at	NOL8	0.278	nuclear mRNA splicing, via spliceosome	nucleic acid binding	---	---

1561042_at	EMR3	0.276	neuropeptide signaling pathway	G-protein coupled receptor activity /// calcium ion binding	integral to membrane	GPCRDB Other	
233874_at	KIAA1458	0.276	---	---	---	---	
213063_at	FLJ11806	0.275	---	nucleic acid binding	nucleus	---	
214825_at	---	0.275	---	---	---	---	
226083_at	TMEM70	0.275	---	---	---	---	
226582_at	LOC400043	0.275	---	---	---	---	
230897_at	FLJ20972	0.275	---	---	---	---	
231022_at	---	0.275	---	---	---	---	
232439_at	---	0.274	---	---	---	---	
232682_at	DSU	0.273	---	---	---	---	
1560180_at	CAPN14	0.272	---	---	---	---	
1563157_at	---	0.272	---	---	---	---	
1566277_at	OR5E1P	0.272	G-protein coupled receptor protein signaling pathway /// perception of smell	receptor activity /// olfactory receptor activity	integral to membrane	GPCRDB Other	
204715_at	PANX1	0.272	---	---	gap junction /// integral to membrane	---	
218709_s_at	C20orf9	0.272	---	---	---	---	
231053_at	---	0.272	---	---	---	---	
240110_at	HMGCS2	0.272	acetyl-CoA metabolism /// cholesterol biosynthesis	hydroxymethylglutaryl-CoA synthase activity /// transferase activity	mitochondrion	Synthesis and Degradation of Keton Bodies	
1563528_at	LOC91149	0.271	---	---	---	---	
209569_x_at	D4S234E	0.271	dopamine receptor signaling pathway	dopamine receptor binding	nucleus /// Golgi apparatus /// integral to membrane	---	

221223_x_at	CISH	0.271	regulation of cell growth /// intracellular signaling cascade	---	---	---	---
231321_s_at	PHCA	0.27	ceramide metabolism/// protein biosynthesis	hydrolase activity/// hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides/// structural constituent of ribosome	Golgi membrane/// Golgi stack/// endoplasmic reticulum membrane/// integral to membrane/// intracellular/// ribosome	---	Glycosphingolipid metabolism
1553025_at	GPR126	0.268	neuropeptide signaling pathway	receptor activity /// G-protein coupled receptor activity	membrane /// integral to membrane	---	
210430_x_at	RHD	0.268	---	---	integral to plasma membrane	---	
235811_at	MBNL1	0.268	embryonic development (sensu Mammalia) /// neurogenesis /// muscle development /// embryonic limb morphogenesis /// myoblast differentiation	nucleic acid binding /// double-stranded RNA binding	nucleus /// cytoplasm	---	
1553978_at	MEF2B	0.267	regulation of transcription, DNA-dependent /// transcription from Pol II promoter /// muscle development	transcription factor activity /// transcription coactivator activity	nucleus	---	
233509_at	HERC4	0.267	ubiquitin cycle	ubiquitin-protein ligase activity	intracellular	---	
234562_x_at	CKLFSF8	0.267	chemotaxis	cytokine activity	integral to membrane	---	
205625_s_at	CALB1	0.266	---	calcium ion binding /// protein binding	---	---	
227612_at	ELAVL3	0.266	neurogenesis /// cell differentiation	RNA binding /// mRNA 3'-UTR binding	---	---	
229776_at	SLCO3A1	0.266	ion transport	transporter activity	integral to membrane	---	
231412_at	LOC441366	0.266	---	---	---	---	

1553505_at	FLJ25179	0.265	---	endopeptidase inhibitor activity	---	---	---
215639_at	SH2D3C	0.265	JNK cascade /// small GTPase mediated signal transduction	SH3/SH2 adaptor protein activity /// guanyl-nucleotide exchange factor activity	---	---	---
239044_at	CDA08	0.265	cell-matrix adhesion	---	integrin complex /// integral to membrane	---	---
242387_at	INM01	0.265	---	---	---	---	---
1553558_at	TAS2R41	0.264	G-protein coupled receptor protein signaling pathway /// perception of taste	receptor activity /// G-protein coupled receptor activity	integral to membrane	---	---
242042_s_at	LOC401022	0.264	---	---	---	---	---
217761_at	MTCBP-1	0.263	methionine biosynthesis	---	---	---	---
221497_x_at	EGLN1	0.262	protein metabolism	oxidoreductase activity /// oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen /// oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	cytosol	---	---
231171_at	---	0.262	---	---	---	---	---
237576_x_at	LOC440422	0.262	---	---	---	---	---
213657_s_at	DKFZp547K1113	0.261	---	nucleic acid binding /// zinc ion binding	nucleus	---	---

223756_at	FLJ10081	0.261	---	---	---	---	---
242863_at	---	0.261	---	---	---	---	---
243221_at	FAM20A	0.261	---	---	---	---	---
234618_at	PHTF1	0.259	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---	---
1557406_s_at	LOC283697	0.258	---	---	---	---	---
210871_x_at	SSX2IP	0.258	cell adhesion	protein binding	nucleus	---	---
215969_at	PIGA	0.257	biosynthesis	transferase activity, transferring glycosyl groups /// phosphatidylinositol N-acetylglucosaminyltransferase activity	endoplasmic reticulum membrane /// integral to membrane	---	
239191_at	DKFZp566O084	0.257	metabolism	oxidoreductase activity	---	---	---
1553276_at	ZNF560	0.256	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---	---
219200_at	MGC5297	0.256	apoptosis	protein kinase activity /// ATP binding	---	---	---
228996_at	KIAA2025	0.256	protein ubiquitination	nucleic acid binding /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---	
244140_at	WHSC1	0.256	regulation of transcription, DNA-dependent /// morphogenesis /// protein ubiquitination	DNA binding /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---	
216762_at	ANKRD15	0.255	cell cycle	---	---	---	---

225452_at	PPARBP	0.255	regulation of transcription, DNA-dependent /// transcription initiation from Pol II promoter /// androgen receptor signaling pathway	DNA binding /// receptor activity /// RNA polymerase II transcription mediator activity /// transcriptional activator activity /// ligand-dependent nuclear receptor transcription coactivator activity /// vitamin D receptor binding /// thyroid hormone receptor binding	mediator complex /// nucleus	---	
1568612_at	GABRG2	0.254	ion transport /// chloride transport /// gamma-aminobutyric acid signaling pathway /// synaptic transmission	GABA-A receptor activity /// ion channel activity /// extracellular ligand-gated ion channel activity /// benzodiazepine receptor activity /// neurotransmitter receptor activity	integral to plasma membrane /// integral to membrane /// postsynaptic membrane	---	
205969_at	AADAC	0.254	metabolism	deacetylase activity	endoplasmic reticulum membrane /// microsome /// integral to membrane	---	
218454_at	FLJ22662	0.254	---	---	---	---	
1556460_at	ARHGAP22	0.253	---	---	---	---	
1565358_at	RARA	0.253	regulation of transcription, DNA-dependent /// signal transduction	transcription factor activity /// steroid hormone receptor activity /// retinoic acid receptor activity /// transcription coactivator activity	nucleus		Nuclear Receptors
232488_at	MGC15875	0.253	---	transaminase activity /// pyridoxal phosphate binding	mitochondrion	---	

236532_at	LOC399947	0.253	---	---	---	---	---
1555330_at	GCLC	0.252	cysteine metabolism /// glutamate metabolism /// glutathione biosynthesis /// circulation	nucleic acid binding /// glutamate-cysteine ligase activity /// ligase activity	---	---	Glutamate metabolism /// Glutathione metabolism
234079_at	RGNEF	0.252	intracellular signaling cascade	---	---	---	---
214936_at	LRCH1	0.25	---	---	---	---	---
242685_at	HSPC135	0.25	---	GTP binding	---	---	---
242857_at	STK25	0.25	protein amino acid phosphorylation /// response to oxidative stress /// signal transduction	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	---	---	---
1561887_at	---	0.249	---	---	---	---	---
1562689_at	LOC151484	0.249	---	---	---	---	---
224744_at	IMPA3	0.249	---	inositol or phosphatidylinositol phosphatase activity /// hydrolase activity	---	---	---
234449_at	---	0.249	---	---	---	---	---
1554356_at	SLD5	0.248	---	---	---	---	---
1559578_at	LOC400602	0.248	---	---	---	---	---
206713_at	NTNG1	0.248	axonogenesis	structural molecule activity	extracellular matrix (sensu Metazoa) /// membrane /// anchored to plasma membrane	---	---
227777_at	C10orf18	0.248	---	---	---	---	---
1555274_at	SELI	0.247	phospholipid biosynthesis	transferase activity	integral to membrane	---	---

205873_at	PIGL	0.247	GPI anchor biosynthesis	N-acetylglucosaminylphosphatidylinositol deacetylase activity /// hydrolase activity	endoplasmic reticulum /// integral to membrane	---	---
219877_at	FLJ13842	0.247	---	nucleic acid binding /// zinc ion binding	nucleus	---	---
239009_at	MACF1	0.247	cell cycle arrest	actin binding /// calcium ion binding /// microtubule binding /// actin filament binding	cytoplasm /// cytoskeleton	---	---
1554534_at	DPYD	0.246	electron transport /// 'de novo' pyrimidine base biosynthesis /// uracil catabolism /// thymidine catabolism	dihydroorotate dehydrogenase activity /// dihydroorotate oxidase activity /// electron transporter activity /// iron ion binding /// disulfide oxidoreductase activity /// oxidoreductase activity /// dihydropyrimidine dehydrogenase (NADP+) activity	cytoplasm /// mitochondrion /// membrane	Pyrimidine metabolism /// beta-Alanine metabolism /// Pantothenate and CoA biosynthesis	---
1557241_a_at	SYTL4	0.246	exocytosis/// intracellular protein transport/// transport	Rab GTPase binding/// metal ion binding/// neurexin binding/// phospholipid binding/// transporter activity/// zinc ion binding	extrinsic to plasma membrane/// membrane/// synaptic vesicle	---	---
1564974_at	KRTAP8-1	0.246	---	---	intermediate filament	---	---
221629_x_at	LOC51236	0.246	---	binding	---	---	---

223510_at	NRP2	0.246	angiogenesis /// electron transport /// cell adhesion /// neurogenesis /// axon guidance	receptor activity /// vascular endothelial growth factor receptor activity /// electron transporter activity /// semaphorin receptor activity	membrane fraction /// integral to membrane	---	
226807_at	ZFP1	0.246	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---	
230979_at	BMPR1A	0.246	protein amino acid phosphorylation /// transmembrane receptor protein serine/threonine kinase signaling pathway /// transforming growth factor beta receptor signaling pathway	receptor activity /// transforming growth factor beta receptor activity /// ATP binding /// transferase activity	integral to membrane	Phosphatidylinositol signaling system	
232364_at	FBXO11	0.246	protein ubiquitination/// ubiquitin-dependent protein catabolism	ubiquitin-protein ligase activity/// metal ion binding/// zinc ion binding	ubiquitin ligase complex	---	
207644_at	FOXH1	0.245	regulation of transcription, DNA-dependent /// signal transduction	transcription factor activity /// transcription coactivator activity	nucleus	TGF Beta Signaling Pathway	
218697_at	NCKIPSD	0.245	NLS-bearing substrate-nucleus import /// cytoskeleton organization and biogenesis /// signal transduction	cytoskeletal protein binding	nucleus /// intermediate filament	---	
241208_at	LIM	0.245	heart development	actin binding /// protein kinase C binding /// protein binding /// receptor signaling complex scaffold activity /// actinin binding	membrane fraction /// cytosol	---	
242841_at	---	0.245	---	---	---	---	
1553220_at	ALS2CR13	0.244	---	---	---	---	

220172_at	FLJ13096	0.244	---	---	---	---	---
240450_at	PAPPA	0.244	proteolysis and peptidolysis /// pregnancy /// cell differentiation	metallopeptidase activity /// zinc ion binding /// hydrolase activity	extracellular space /// membrane	---	
1561268_at	---	0.243	---	---	---	---	---
205456_at	CD3E	0.243	protein complex assembly /// signal complex formation /// G-protein coupled receptor protein signaling pathway /// positive regulation of T-cell proliferation /// T-cell activation /// regulation of apoptosis	transmembrane receptor activity /// SH3 domain binding /// protein kinase binding /// receptor signaling complex scaffold activity /// T-cell receptor binding /// protein heterodimerization activity	integral to plasma membrane /// T-cell receptor complex	---	
232476_at	DDEF2	0.243	regulation of GTPase activity	GTPase activator activity/// metal ion binding/// protein binding/// zinc ion binding	---	---	
237809_at	---	0.243	---	---	---	---	---
1559648_at	---	0.242	---	---	---	---	---
1569792_at	MGC50559	0.242	---	S-adenosylmethionine-dependent methyltransferase activity /// transferase activity	---	---	---
243308_at	---	0.242	---	---	---	---	---
1556138_at	COL5A1	0.241	phosphate transport /// cell adhesion	extracellular matrix structural constituent /// heparin binding	collagen /// collagen type V /// cytoplasm	---	
236825_at	BFSP2	0.241	visual perception	structural constituent of cytoskeleton /// structural constituent of eye lens	cytoskeleton /// intermediate filament /// membrane	---	
239584_at	---	0.241	---	---	---	---	---

206429_at	F2RL1	0.24	G-protein coupled receptor protein signaling pathway /// positive regulation of cytosolic calcium ion concentration /// blood coagulation	rhodopsin-like receptor activity /// receptor activity /// receptor binding /// thrombin receptor activity	Golgi apparatus /// integral to plasma membrane	GPCRDB Class A Rhodopsin-like
209910_at	SLC25A16	0.24	transport	binding /// solute:solute antiporter activity	mitochondrion /// mitochondrial inner membrane /// integral to membrane	---
222746_s_at	BSPRY	0.24	---	zinc ion binding	intracellular	---
212576_at	MGRN1	0.239	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
238434_at	SHMT1	0.239	glycine metabolism /// L-serine metabolism /// L-serine catabolism /// one-carbon compound metabolism	glycine hydroxymethyltransferase activity /// transferase activity	cytosol	Glycine, serine and threonine metabolism /// Lysine degradation /// Cyanoamino acid metabolism /// One carbon pool by folate /// Methane metabolism
1554996_at	ZNF479	0.238	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
220880_at	---	0.238	---	---	---	---
1552478_at	IRF6	0.237	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	Apoptosis

202886_s_at	PPP2R1B	0.237	regulation of cell cycle /// inactivation of MAPK /// regulation of DNA replication /// regulation of translation /// protein complex assembly /// protein amino acid dephosphorylation /// ceramide metabolism /// induction of apoptosis /// RNA splicing /// response to organic substance /// second-messenger-mediated signaling /// regulation of Wnt receptor signaling pathway /// regulation of cell adhesion /// negative regulation of cell growth /// regulation of growth /// negative regulation of tyrosine phosphorylation of Stat3 protein /// regulation of transcription /// regulation of cell differentiation	protein phosphatase type 2A activity /// antigen binding /// phosphoprotein phosphatase activity /// protein phosphatase type 2A regulator activity /// protein heterodimerization activity	protein phosphatase type 2A complex /// soluble fraction /// nucleus /// mitochondrion /// cytosol /// microtubule cytoskeleton /// membrane	Glycogen Metabolism
229879_at	ASPH	0.237	muscle contraction /// peptidyl-amino acid modification	peptide-aspartate beta-dioxygenase activity /// binding /// electron transporter activity /// iron ion binding /// calcium ion binding /// structural constituent of muscle /// oxidoreductase activity /// oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	integral to endoplasmic reticulum membrane	---

226978_at	PPARA	0.236	generation of precursor metabolites and energy /// transcription /// regulation of transcription, DNA-dependent /// transcription from Pol II promoter /// lipid metabolism /// fatty acid metabolism	transcription factor activity /// steroid hormone receptor activity /// ligand-dependent nuclear receptor activity	nucleus	Nuclear Receptors
215821_x_at	PSG3	0.235	defense response /// pregnancy	---	extracellular region	---
214085_x_at	GLIPR1	0.234	---	---	integral to membrane/// extracellular region	---
236939_at	LOC401494	0.234	---	---	---	---
1562908_at	LOC339468	0.233	---	---	---	---
1564240_at	---	0.233	---	---	---	---
202507_s_at	SNAP25	0.233	neurotransmitter uptake /// synaptic transmission /// neurotransmitter secretion /// synaptic vesicle docking during exocytosis	---	synaptosome	---
206946_at	HCN4	0.233	cation transport /// potassium ion transport /// sodium ion transport /// muscle contraction /// circulation	voltage-gated potassium channel activity /// cation channel activity /// 3',5'-cAMP binding	membrane fraction /// integral to plasma membrane	---
217617_at	PBX1	0.233	regulation of transcription, DNA-dependent /// transcription from Pol II promoter /// C21-steroid hormone biosynthesis /// sex differentiation /// embryonic development /// hindbrain development /// regulation of transcriptional preinitiation complex formation	transcription factor activity /// protein binding	nucleus	---

222395_s_at	FLJ13855	0.233	ubiquitin cycle	ubiquitin conjugating enzyme activity	---	---
237781_at	HORMAD2	0.232	---	---	---	---
243223_at	---	0.232	---	---	---	---
1553584_at	CXorf36	0.231	---	---	---	---
1556768_at	---	0.231	---	---	---	---
203912_s_at	DNASE1L1	0.231	DNA catabolism	DNA binding /// endonuclease activity /// deoxyribonuclease activity /// hydrolase activity	membrane	---
223292_s_at	MRPS15	0.231	protein biosynthesis	structural constituent of ribosome	mitochondrial small ribosomal subunit /// mitochondrion /// ribosome	---
1558123_at	FLJ35390	0.23	---	---	---	---
210822_at	LOC283345	0.23	---	---	---	---
216708_x_at	IGLJ3	0.23	---	---	---	---
233795_at	ODF3	0.23	---	---	---	---
1554342_s_at	HEL308	0.229	---	nucleic acid binding /// ATP binding /// ATP-dependent helicase activity /// hydrolase activity	nucleus	---
1559535_s_at	---	0.229	---	---	---	---
1562932_at	---	0.229	---	---	---	---

204653_at	TFAP2A	0.229	regulation of transcription, DNA-dependent /// regulation of transcription from Pol II promoter /// signal transduction /// ectoderm development	transcription factor activity /// RNA polymerase II transcription factor activity, enhancer binding /// transcription coactivator activity	nucleus	---
205156_s_at	ACCN2	0.229	ion transport /// sodium ion transport	ion channel activity /// amiloride-sensitive sodium channel activity	integral to membrane	---
231024_at	---	0.229	---	---	---	---
243700_x_at	FAM47A	0.229	---	---	---	---
1564423_at	RGPR	0.228	---	---	---	---
221516_s_at	FLJ20232	0.228	---	---	---	---
236333_at	---	0.228	---	---	---	---
1560896_at	---	0.227	---	---	---	---
218126_at	FLJ10579	0.227	---	binding	---	---
236440_at	---	0.227	---	---	---	---
1568884_at	ZRF1	0.226	protein folding /// regulation of transcription	DNA binding /// heat shock protein binding /// unfolded protein binding	nucleus	---
210904_s_at	IL13RA1	0.226	cell surface receptor linked signal transduction	receptor activity /// hematopoietin/interferon-class (D200-domain) cytokine receptor activity	plasma membrane /// interleukin-13 receptor complex /// integral to membrane	---
211037_s_at	LENG4	0.226	---	receptor activity	---	---
227009_at	---	0.226	---	---	---	---
232148_at	NSMAF	0.226	ceramide metabolism /// signal transduction	receptor signaling protein activity	soluble fraction /// cytoplasm	---
232838_at	KIAA1713	0.226	---	---	---	---

242801_at	WWOX	0.226	metabolism /// steroid metabolism	electron transporter activity /// protein binding /// oxidoreductase activity	---	---
1561217_at	---	0.225	---	---	---	---
1561712_at	FLJ12716	0.225	---	---	---	---
1564729_at	FLJ46266	0.225	---	---	---	---
1570476_at	---	0.224	---	---	---	---
220759_at	FAM12B	0.224	spermatid cell development	nucleic acid binding /// pancreatic ribonuclease activity	extracellular region	---
233901_at	---	0.224	---	---	---	---
1559064_at	NUP153	0.223	transport	DNA binding /// transporter activity /// porin activity	nucleus /// nuclear pore /// integral to membrane /// outer membrane	---
1569474_at	ELL	0.223	regulation of transcription, DNA-dependent /// RNA elongation from Pol II promoter	positive transcription elongation factor activity	nucleus	---
209377_s_at	HMGN3	0.223	---	DNA binding /// thyroid hormone receptor binding	chromatin /// nucleus	---
209738_x_at	PSG9	0.223	pregnancy /// defense response	receptor activity	membrane fraction /// extracellular region	---
1556447_at	LOC285370	0.222	---	---	---	---
1557536_at	WNK2	0.222	protein amino acid phosphorylation /// protein kinase cascade	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	---	---
1559745_at	---	0.222	---	---	---	---
232326_at	MGC39526	0.222	---	---	---	---

233408_at	DEPDC2	0.222	intracellular signaling cascade	guanyl-nucleotide exchange factor activity /// protein binding	---	---
239851_at	TMP21	0.222	ER to Golgi transport /// protein transport	---	membrane fraction /// microsome /// Golgi apparatus /// integral to plasma membrane	mRNA processing
37201_at	ITIH4	0.222	acute-phase response /// hyaluronan metabolism	serine-type endopeptidase inhibitor activity	extracellular region	---
1564021_at	MGC11257	0.221	---	---	---	---
1564783_x_at	OFCC1	0.221	---	---	---	---
206579_at	ZNF192	0.221	regulation of transcription, DNA-dependent	transcription factor activity /// protein binding /// zinc ion binding	nucleus	---
211547_s_at	PAFAH1B1	0.221	establishment of mitotic spindle orientation /// cytokinesis /// lipid metabolism /// cell motility /// microtubule-based process /// mitosis /// signal transduction /// neurogenesis	dynein binding	astral microtubule /// kinetochore /// nuclear membrane /// cytoplasm /// cytoskeleton /// microtubule associated complex /// cell cortex	Wnt signaling /// Glycerophospholipid metabolism
241725_at	E2F7	0.221	regulation of cell cycle /// regulation of transcription, DNA-dependent	transcription factor activity	transcription factor complex	---
1554766_s_at	---	0.22	---	---	---	---
1558914_at	PNAS-4	0.22	---	---	---	---
1564314_at	LOC219690	0.22	---	---	---	---

205542_at	STEAP	0.22	---	channel or pore class transporter activity	early endosome /// integral to plasma membrane /// intercellular junction /// integral to Golgi membrane /// vesicular fraction	---
233610_at	---	0.22	---	---	---	---
234604_at	---	0.22	---	---	---	---
239574_at	ECHDC3	0.22	metabolism	catalytic activity	---	---
239830_at	ETFA	0.22	electron transport	electron carrier activity	mitochondrial matrix	---
241127_at	---	0.22	---	---	---	---
1556924_at	ALS2CR 10	0.219	---	---	---	---
229865_at	FNDC3B	0.219	---	---	---	---
230667_at	---	0.219	---	---	---	---
234256_at	---	0.219	---	---	---	---
239790_s_at	EXOSC2	0.219	rRNA processing	3'-5'-exoribonuclease activity/// 7S RNA binding/// exonuclease activity/// hydrolase activity/// protein binding	cytoplasm/// nucleus/// exosome	---
1556306_at	MLL5	0.218	regulation of transcription, DNA dependent	zinc ion binding/// protein binding	---	---
204563_at	SELL	0.218	cell motility /// cell adhesion	protein binding /// sugar binding	integral to plasma membrane	---
212685_s_at	TBL2	0.218	---	---	---	---
220827_at	CACNA1C	0.218	cation transport /// calcium ion transport /// regulation of heart contraction rate	voltage-gated calcium channel activity /// cation channel activity /// calcium ion binding	voltage-gated calcium channel complex /// integral to membrane	Calcium regulation in cardiac cells
244458_at	ZNF592	0.218	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
1552947_x_at	MGC179 86	0.217	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
1555680_a_at	SMOX	0.217	electron transport	oxidoreductase activity	---	---

1556426_at	HEXA	0.217	carbohydrate metabolism /// glycosphingolipid metabolism	beta-N-acetylhexosaminidase activity /// hydrolase activity, acting on glycosyl bonds	lysosome	N-Glycan degradation /// Aminosugars metabolism /// Glycosaminoglycan degradation /// Globoside metabolism
208540_x_at	S100A11	0.217	negative regulation of DNA transcription /// negative regulation of cell proliferation	calcium ion binding	cytoplasm /// nucleus	---
216746_at	LRCH1	0.217	---	---	---	---
229175_at	SMYD4	0.217	---	binding	---	---
232987_at	---	0.217	---	---	---	---
237913_at	---	0.217	---	---	---	---
226132_s_at	FLJ3143 4	0.216	---	---	---	---
239053_at	WDR39	0.216	positive regulation of cell proliferation /// regulation of transcription from RNA polymerase II promoter	---	nucleus	---
239497_at	EPS15L1	0.216	endocytosis	calcium ion binding	nucleus /// coated pit	---
205525_at	CALD1	0.215	muscle contraction /// muscle development	actin binding /// calmodulin binding /// tropomyosin binding /// myosin binding	cytoskeleton	---
221297_at	GPRC5D	0.215	G-protein coupled receptor protein signaling pathway /// visual perception	sevenless binding /// metabotropic glutamate, GABA-B-like receptor activity	integral to membrane	GPCRDB Class C Metabotropic glutamate pheromone
226387_at	RSBN1L	0.215	---	---	---	---
232116_at	TFCP2L4	0.215	---	---	---	---

202018_s_at	LTF	0.214	transport /// iron ion transport /// iron ion homeostasis /// humoral immune response /// defense response to bacteria	serine-type endopeptidase activity /// ferric iron binding		extracellular space	---
211520_s_at	GRIA1	0.214	ion transport /// potassium ion transport /// signal transduction /// synaptic transmission	receptor activity /// alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor activity /// transporter activity /// ion channel activity /// glutamate-gated ion channel activity /// potassium channel activity /// kainate selective glutamate receptor activity	plasma membrane /// integral to membrane	---	---
213273_at	ODZ4	0.214	---	---	---	---	---
215115_x_at	NTRK3	0.214	neurotrophin binding/// ATP binding/// kinase activity/// nucleotide binding/// protein serine/threonine kinase activity/// protein-tyrosine kinase activity /// receptor activity/// transferase activity/// transmembrane receptor protein tyrosine kinase activity	transmembrane receptor protein tyrosine kinase signaling pathway/// cell differentiation/// nervous system development/// protein amino acid phosphorylation	integral to plasmamembrane	---	---
233259_at	FLJ12057	0.214	---	---	---	---	---
242399_at	FLJ33708	0.214	---	---	---	---	---
243730_at	---	0.214	---	---	---	---	---

203056_s_at	PRDM2	0.213	regulation of transcription, DNA-dependent /// regulation of transcription	DNA binding /// transcription factor activity /// zinc ion binding /// transcription regulator activity /// metal ion binding	nucleus	---	
215934_at	---	0.212	---	---	---	---	
225881_at	SLC35B4	0.212	nucleotide-sugar transport	nucleotide-sugar transporter activity	integral to membrane	---	
226812_at	ZFP91	0.212	regulation of transcription, DNA-dependent	zinc ion binding /// DNA binding	nucleus	---	
229580_at	---	0.212	---	---	---	---	
235294_at	FLJ21168	0.212	---	---	---	---	
239008_at	---	0.212	---	---	---	---	
244702_at	---	0.212	---	---	---	---	
1561776_at	---	0.211	---	---	---	---	
1561895_at	ANK2	0.211	signal transduction /// metabolism	structural constituent of cytoskeleton /// protein binding /// oxidoreductase activity	actin cytoskeleton /// membrane	Ribosomal Proteins	
1568869_at	---	0.211	---	---	---	---	
216675_at	---	0.211	---	---	---	---	
234569_at	---	0.211	---	---	---	---	
240530_at	SLC25A16	0.211	transport	solute:solute antiporter activity	integral to membrane /// mitochondrial inner membrane /// mitochondrion	---	
1552639_at	MGC16635	0.21	---	---	---	---	
1558785_a_at	RGS5	0.21	signal transduction /// regulation of G-protein coupled receptor protein signaling pathway	signal transducer activity /// GTPase activator activity	---	Calcium regulation in cardiac cells /// Smooth muscle contraction	

200831_s_at	SCD	0.21	fatty acid biosynthesis	stearoyl-CoA 9-desaturase activity /// iron ion binding /// oxidoreductase activity	endoplasmic reticulum /// integral to membrane		Fatty Acid Synthesis
208694_at	PRKDC	0.21	double-strand break repair /// DNA recombination /// protein modification	DNA binding /// protein serine/threonine kinase activity /// binding /// transferase activity	nucleus	Cell cycle	---
243402_at	MGC35023	0.21	---	---	---	---	---
1564285_at	LOC164045	0.209	---	---	---	---	---
215443_at	TSHR	0.209	G-protein signaling, coupled to cyclic nucleotide second messenger /// cell-cell signaling /// positive regulation of cell proliferation	thyroid-stimulating hormone receptor activity	integral to plasma membrane	GPCRDB Other /// Peptide GPCRs	---
225116_at	HIPK2	0.209	regulation of cell cycle /// protein amino acid phosphorylation /// induction of apoptosis by intracellular signals /// virus-host interaction /// positive regulation of transforming growth factor beta receptor signaling pathway /// positive regulation of JNK cascade	transcription corepressor activity /// protein serine/threonine kinase activity /// protein binding /// ATP binding /// transferase activity /// virion binding	nucleus /// cytoplasm /// nuclear body	---	
231740_at	KCNJ11	0.209	ion transport /// potassium ion transport	voltage-gated ion channel activity /// potassium channel activity /// ATP-activated inward rectifier potassium channel activity	membrane fraction /// integral to plasma membrane	---	
233566_at	MGC16291	0.209	---	---	---	---	---

1553946_at	DCD	0.208	xenobiotic metabolism /// defense response to bacteria /// defense response to fungi	manganese ion binding	extracellular region	---
1562772_at	DAND5	0.208	---	---	---	---
1562888_at	LOC112937	0.208	carbohydrate metabolism	beta-galactosidase activity	beta-galactosidase complex	---
209785_s_at	PLA2G4C	0.208	---	---	---	---
219504_s_at	FLJ13150	0.208	---	---	---	---
235341_at	DNAJC3	0.208	regulation of translation /// protein folding /// defense response	protein kinase inhibitor activity /// binding /// heat shock protein binding /// unfolded protein binding	cytoplasm	---
237129_at	Cep152	0.208	---	---	---	---
237996_at	---	0.208	---	---	---	---
1553272_at	SLC36A1	0.207	transport /// amino acid transport	amino acid-polyamine transporter activity /// symporter activity	integral to membrane	---
221658_s_at	IL21R	0.207	natural killer cell activation	interleukin-21 receptor activity /// receptor activity /// hematopoietin/interferon-class (D200-domain) cytokine receptor activity	integral to membrane	---
1553004_at	PKD1L1	0.206	---	---	integral to membrane	---
1559063_at	C21orf63	0.206	---	sugar binding	integral to membrane	---
207160_at	IL12A	0.206	---	---	---	cytokine-cytokine receptor interaction/// Jak-STAT signaling pathway/// Toll-like receptor signaling pathway/// Type I diabetes mellitus

215350_at	SYNE1	0.206	nuclear organization and biogenesis /// Golgi organization and biogenesis /// muscle cell differentiation	actin binding /// structural molecule activity /// lamin binding	nuclear membrane /// Golgi apparatus /// cytoskeleton /// integral to membrane /// postsynaptic membrane	---	
233688_at	CSEN	0.206	regulation of transcription from Pol II promoter /// signal transduction	DNA binding /// transcription corepressor activity /// calcium ion binding	nucleus	---	
235668_at	PRDM1	0.206	negative regulation of transcription from RNA polymerase II promoter/// regulation of transcription, DNA-dependent	transcription factor activity/// metal ion binding/// nucleic acid binding/// zinc ion binding	nucleus		
241332_at	---	0.206	---	---	---	---	
1562263_at	LOXL2	0.205	aging/// cell adhesion/// protein modification	copper ion binding/// electron transporter activity/// metal ion binding/// oxidoreductase activity/// protein-lysine 6-oxidase activity/// scavenger receptor activity	extracellular space	Arginine and proline metabolism	
206692_at	KCNJ10	0.205	ion transport /// potassium ion transport	voltage-gated ion channel activity /// potassium channel activity /// ATP binding /// ATP-activated inward rectifier potassium channel activity	integral to plasma membrane	---	
224767_at	RPL37	0.205	protein biosynthesis	structural constituent of ribosome	intracellular /// ribosome	Ribosomal Proteins	
235050_at	SLC2A12	0.205	carbohydrate transport	transporter activity /// sugar porter activity	integral to membrane	---	
242637_at	L3MBTL	0.205	regulation of transcription, DNA-dependent /// chromatin modification	transcription factor activity	nucleus	---	
244561_at	---	0.205	---	---	---	---	

1559133_at	---	0.204	---	---	---	---	---
241419_at	ARHGAP1	0.204	cytoskeleton organization and biogenesis /// signal transduction /// Rho protein signal transduction	SH3/SH2 adaptor protein activity /// Rho GTPase activator activity /// GTP binding	---	---	---
244513_at	MGC33214	0.204	---	---	---	---	---
205161_s_at	PEX11A	0.203	signal transduction /// peroxisome division	---	integral to peroxisomal membrane	---	---
239897_at	BCLAF1	0.203	regulation of transcription, DNA-dependent /// induction of apoptosis	DNA binding /// transcriptional repressor activity	nucleus	---	---
207075_at	CIAS1	0.202	apoptosis /// induction of apoptosis /// inflammatory response /// signal transduction /// perception of sound	---	---	---	---
216832_at	RUNX1T1	0.202	generation of precursor metabolites and energy /// regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---	---
217017_at	OSBPL10	0.202	lipid transport/// steroid metabolism	---	---	---	---
218756_s_at	MGC4172	0.202	metabolism	oxidoreductase activity	---	---	---
233234_at	KCTD16	0.202	potassium ion transport	voltage-gated potassium channel activity /// protein binding	voltage-gated potassium channel complex /// membrane	---	---
239732_x_at	FAM47B /// LOC442444	0.202	---	---	---	---	---
240289_at	---	0.202	---	---	---	---	---
240405_at	CASQ1	0.202	muscle development	calcium ion binding	mitochondrial matrix /// smooth endoplasmic reticulum	---	Calcium regulation in cardiac cells

231333_at	---	0.201	---	---	---	---
239256_at	SDC1	0.201	---	cytoskeletal protein binding	integral to plasma membrane	---
242114_at	LAT1-3TM	0.201	---	---	---	---
1562693_at	---	0.2	---	---	---	---
211162_x_at	SCD	0.2	fatty acid biosynthesis	stearoyl-CoA 9-desaturase activity /// iron ion binding /// oxidoreductase activity	endoplasmic reticulum /// integral to membrane	Fatty Acid Synthesis
232796_at	---	0.2	---	---	---	---
240459_at	YT521	0.2	nuclear mRNA splicing, via spliceosome	---	nucleus	---
1560507_at	DGAT2L3	0.199	---	acyltransferase activity /// transferase activity	---	---
206940_s_at	POU4F1	0.199	regulation of transcription from Pol II promoter /// development /// axonogenesis /// synaptogenesis	transcription factor activity	nucleus	---
208226_x_at	ADAM22	0.199	proteolysis and peptidolysis /// negative regulation of cell adhesion	metalloendopeptidase activity /// integrin binding	integral to membrane	---
214396_s_at	MBD2	0.199	regulation of transcription, DNA-dependent /// negative regulation of transcription	transcription factor activity /// methyl-CpG binding /// transcriptional repressor activity	nucleus	---
240220_at	ELMO2	0.199	phagocytosis /// apoptosis	---	cytoskeleton /// membrane	---
1554312_at	RNF170	0.198	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
1556932_at	---	0.198	---	---	---	---

1557697_at	EPHA5	0.198	protein amino acid phosphorylation /// transmembrane receptor protein tyrosine kinase signaling pathway	protein-tyrosine kinase activity /// receptor activity /// transmembrane-ephrin receptor activity /// ATP binding /// transferase activity	integral to membrane	---
1566448_at	CD6	0.198	immune response /// cell adhesion	scavenger receptor activity /// protein binding	integral to plasma membrane	---
213102_at	ACTR3	0.198	cell motility	structural constituent of cytoskeleton	Arp2/3 protein complex	---
221415_s_at	GJA10	0.198	cell communication	connexon channel activity	connexon complex /// integral to membrane	---
223818_s_at	HBXAP	0.198	regulation of transcription, DNA-dependent /// chromatin modification	DNA binding	nucleus	---
228158_at	LOC440684	0.198	---	---	---	---
230869_at	---	0.198	---	---	---	---
233531_at	MGC9564	0.198	transport	transporter activity	membrane /// integral to membrane	---
1552490_at	LACE1	0.197	---	---	---	---
1569351_at	FLJ10159	0.197	---	---	---	---
213489_at	MAPRE2	0.197	cellular defense response /// signal transduction /// cell proliferation	microtubule binding	---	---
220056_at	IL22RA1	0.197	---	receptor activity /// interferon receptor activity	membrane	---
228490_at	ABHD2	0.197	---	catalytic activity	integral to membrane	---
240443_at	---	0.197	---	---	---	---
240814_at	MGC39584	0.197	---	---	---	---
244418_at	RTN3	0.197	---	---	extracellular space /// endoplasmic reticulum /// integral to membrane	---

208159_x_at	DDX11	0.196	mitotic sister chromatid segregation /// regulation of cell cycle /// S phase of mitotic cell cycle /// G2/M transition of mitotic cell cycle /// nucleobase, nucleoside, nucleotide and nucleic acid metabolism /// nucleotide-excision repair /// positive regulation of cell proliferation /// ATP synthesis coupled proton transport	DNA binding /// ATP-dependent DNA helicase activity /// ATP binding /// hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides /// hydrogen-transporting ATP synthase activity, rotational mechanism /// hydrogen-transporting ATPase activity, rotational mechanism	nucleus /// nucleolus /// proton-transporting two-sector ATPase complex	---
215190_at	GA17	0.196	---	---	---	---
229987_at	USP12	0.196	ubiquitin-dependent protein catabolism /// ubiquitin cycle	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity /// hydrolase activity	---	---
231693_at	FABP1	0.196	organ morphogenesis/// fatty acid metabolism/// transport/// cell-cell signaling	lipid binding/// lipid transporter activity	cytoplasm	---
242803_at	CRIM1	0.196	neurogenesis	serine-type endopeptidase inhibitor activity /// insulin-like growth factor receptor activity	membrane fraction /// integral to membrane	---
1561591_at	KLB	0.195	carbohydrate metabolism	catalytic activity/// cation binding/// glucosidase activity	integral to membrane	---
1562055_at	ZNF91	0.195	regulation of transcription, DNA dependent	transcription factor activity/// zinc ion binding	intracellular/// nucleus	---
1564233_at	FLJ33534	0.195	---	---	---	---
201703_s_at	PPP1R10	0.195	transcription /// protein-nucleus import /// defense response	nucleic acid binding	nucleus	---

223653_x_at	BRUNOL4	0.195	nuclear mRNA splicing, via spliceosome /// germ cell development /// embryonic development /// RNA interference	translation repressor activity, nucleic acid binding /// nucleic acid binding /// BRE binding	nucleus /// ribonucleoprotein complex		mRNA processing
1559485_at	---	0.194	---	---	---	---	---
200603_at	PRKAR1A	0.194	regulation of transcription from Pol II promoter /// protein amino acid phosphorylation /// intracellular signaling cascade	cAMP-dependent protein kinase regulator activity /// 3',5'-cAMP binding	cAMP-dependent protein kinase complex	G Protein Signaling /// Calcium regulation in cardiac cells /// Smooth muscle contraction	
201988_s_at	CREBL2	0.194	transcription /// signal transduction	transcription factor activity	nucleus	---	
221041_s_at	SLC17A5	0.194	transport	transporter activity /// symporter activity	lysosome /// integral to membrane	---	
232338_at	ZNF431	0.194	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---	
236069_at	FLJ39005	0.194	---	---	---	---	
1552312_a_at	MFAP3	0.193	---	extracellular matrix structural constituent	extracellular matrix (sensu Metazoa) /// integral to membrane	---	
204184_s_at	ADRBK2	0.193	protein amino acid phosphorylation /// signal transduction	G-protein coupled receptor kinase activity /// signal transducer activity /// ATP binding /// transferase activity /// beta-adrenergic-receptor kinase activity	---	---	
230572_at	FLJ30277	0.193	---	---	---	---	
1559755_at	C21orf49	0.192	---	---	---	---	
1561917_at	---	0.192	---	---	---	---	

1562839_at	---	0.192	---	---	---	---	---
228610_at	SMBP	0.192	transport	transporter activity/// binding	integral to membrane	---	---
234511_at	C20orf86	0.192	protein modification	---	---	---	---
1561297_at	WARS2	0.191	protein biosynthesis /// tryptophanyl-tRNA aminoacylation	tryptophan-tRNA ligase activity /// ATP binding /// ligase activity	soluble fraction /// mitochondrion	---	Tryptophan metabolism /// Aminoacyl-tRNA biosynthesis
1565868_at	CD44	0.191	cell adhesion /// cell-matrix adhesion /// cell-cell adhesion	receptor activity /// protein binding /// collagen binding /// hyaluronic acid binding	integral to plasma membrane /// membrane /// integral to membrane	---	---
205941_s_at	COL10A1	0.191	skeletal development /// phosphate transport	structural molecule activity	collagen /// cytoplasm	---	---
210399_x_at	FUT6	0.191	protein amino acid glycosylation /// L-fucose catabolism	transferase activity, transferring glycosyl groups /// 3-galactosyl-N-acetylglucosaminide 4-alpha-L-fucosyltransferase activity /// alpha(1,3)-fucosyltransferase activity	extracellular region /// Golgi apparatus /// integral to membrane	---	Blood group glycolipid biosynthesis-lactoseries
214137_at	PTPRJ	0.191	cell-cell signaling/// protein amino acid dephosphorylation/// transmembrane receptor protein tyrosine kinase signaling pathway	transmembrane receptor protein tyrosine phosphatase activity/// hydrolase activity	integral to plasmamembrane	---	Adherens junction
217779_s_at	PNRC2	0.191	---	receptor activity	---	---	---
234848_at	---	0.191	---	---	---	---	---
1558401_at	---	0.19	---	---	---	---	---
206806_at	DGKI	0.19	protein kinase C activation /// intracellular signaling cascade	diacylglycerol kinase activity /// transferase activity	nucleus /// cytoplasm	---	Ribosomal Proteins

1553685_s_at	SP1	0.189	regulation of transcription, DNA-dependent	DNA binding /// RNA polymerase II transcription factor activity /// zinc ion binding /// transcriptional activator activity	nucleus	Smooth muscle contraction
1554840_at	LOC280665	0.189	---	---	---	---
221414_s_at	DEFB126	0.189	proteolysis and peptidolysis /// defense response to bacteria	protease inhibitor activity	extracellular region	---
231695_at	KIAA1463	0.189	metabolism	catalytic activity /// transcription factor binding	nucleus	---
237318_at	SLC43A2	0.189	---	---	---	---
1566485_at	FHIT	0.188	cell cycle /// nucleotide metabolism /// negative regulation of cell cycle	magnesium ion binding /// hydrolase activity /// manganese ion binding /// bis(5'-adenosyl)-triphosphatase activity	cytoplasm	Purine metabolism
214287_s_at	CDC2L5	0.188	development /// positive regulation of cell proliferation/// protein amino acid phosphorylation/// regulation of mitosis	ATP binding/// nucleotide binding/// protein serine/threonine kinase activity/// protein-tyrosine kinase activity/// transferase activity	---	---
216672_s_at	MYT1L	0.188	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
235830_at	---	0.188	---	---	---	---
240237_at	CLCN3	0.188	ion transport /// chloride transport /// regulation of pH /// endosomal lumen acidification	voltage-gated chloride channel activity /// PDZ domain binding /// protein homodimerization activity /// protein heterodimerization activity	early endosome /// late endosome /// Golgi apparatus /// cell surface /// vesicle membrane /// membrane /// integral to membrane	---
1564399_at	ARMCX4	0.187	---	---	---	---

216083_s_at	NEU3	0.187	carbohydrate metabolism /// ganglioside catabolism	exo-alpha-sialidase activity /// hydrolase activity, acting on glycosyl bonds	integral to plasma membrane /// membrane	N-Glycan degradation /// Glycosphingolipid metabolism
216955_at	TAF1	0.187	G1 phase of mitotic cell cycle /// transcription initiation /// regulation of transcription, DNA-dependent /// cell cycle /// autophosphorylation	DNA binding /// histone acetyltransferase activity /// protein serine/threonine kinase activity /// protein binding /// ATP binding /// transferase activity	nucleus /// transcription factor TFIID complex	---
236581_at	---	0.187	---	---	---	---
1556362_at	---	0.186	---	---	---	---
1559587_at	SYMPK	0.186	cell adhesion	protein binding	nucleoplasm /// cytoplasm /// tight junction	---
1564164_at	FLJ20054	0.186	---	---	---	---
217233_at	CHAF1B	0.186	DNA replication-dependent nucleosome assembly/// protein complex assembly/// regulation of transcription-DNA dependent/// cell cycle/// DNA repair	chromatin binding/// histone binding/// unfolded protein binding	chromatin assembly complex/// cytoplasm/// nucleus	---
218820_at	C14orf132	0.186	---	---	integral to membrane	---
228796_at	CPNE4	0.186	---	---	---	---
237209_s_at	NFRKB	0.186	transcription from Pol II promoter /// inflammatory response	specific RNA polymerase II transcription factor activity	nucleus	---
243782_at	---	0.186	---	---	---	---
1561084_at	---	0.185	---	---	---	---
215018_at	KIAA1731	0.185	---	---	---	---

220087_at	BCMO1	0.185	---	beta-carotene 15,15'-monooxygenase activity /// oxidoreductase activity	---		Retinol metabolism
234485_at	LOC340947	0.185	---	---	---		---
206076_at	B7	0.184	---	---	---		---
230152_at	WDR52	0.183	---	---	---		---
243992_at	ZNF198	0.183	regulation of transcription, DNA-dependent	zinc ion binding	nucleus		---
1559507_at	PHACTR1	0.182	---	actin binding/// protein phosphatase inhibitor activity	---		---
1567015_at	CSNK2A1	0.182	Wnt receptor signaling pathway/// protein amino acid phosphorylation	protein binding/// ATP binding/// nucleotide binding/// protein serine/threonine kinase activity/// transferase activity	---		Adherens junction/// Tight junction/// Wnt signaling pathway
222363_at	---	0.182	---	---	---		---
232111_at	---	0.182	---	---	---		---
234025_at	C12orf32	0.182	---	---	---		---
235602_at	TP53INP1	0.182	apoptosis	---	nucleus		---
241204_at	---	0.182	---	---	---		---
1566512_at	GNG4	0.181	regulation of G-protein coupled receptor protein signaling pathway	signal transducer activity	plasma membrane/// heterotrimeric G-protein complex		energy metabolism
218210_at	FN3KRP	0.181	---	kinase activity /// transferase activity	---		---
220970_s_at	KRTAP2-4	0.181	---	---	keratin filament		---
224750_at	FLJ38628	0.181	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex		---
237942_at	SNRK	0.181	---	---	---		---
241244_at	---	0.181	---	---	---		---
1553935_at	MGC2848	0.18	---	---	---		---

216437_at	EPC1	0.18	regulation of transcription, DNA-dependent/// chromatin modification/// regulation of cell growth	transcriptional activator activity/// transcriptional repressor activity	nucleus	---	
242678_at	LPP	0.18	---	zinc ion binding	---	---	
1566970_at	FARP1	0.179	cell adhesion	Rho guanyl-nucleotide exchange factor activity /// cytoskeletal protein binding	cytoplasm /// cytoskeleton /// membrane	---	
224009_x_at	DHRS9	0.179	metabolism /// androgen metabolism /// epithelial cell differentiation /// progesterone metabolism /// retinol metabolism /// 9-cis-retinoic acid biosynthesis	alcohol dehydrogenase activity /// retinol dehydrogenase activity /// oxidoreductase activity /// racemase and epimerase activity /// 3-alpha(17-beta)-hydroxysteroid dehydrogenase (NAD+) activity	microsome /// integral to endoplasmic reticulum membrane	---	
227129_x_at	LOC388312 /// FLJ45445	0.179	---	---	---	---	
235326_at	FLJ12529	0.179	nuclear mRNA splicing, via spliceosome	nucleic acid binding	---	---	
241215_at	---	0.179	---	---	---	---	
1559812_at	---	0.178	---	---	---	---	
1561566_at	LOC285501	0.178	---	---	---	---	
1566124_a_at	FABP6	0.178	lipid metabolism /// transport/// negative regulation of cell proliferation	fatty acid binding/// lipid binding	cytoplasm	---	

215134_at	PI4KII	0.178	phosphatidylinositol biosynthesis	magnesium ion binding /// 1-phosphatidylinositol 4-kinase activity /// protein binding /// kinase activity /// phosphotransferase activity, alcohol group as acceptor	integral to plasma membrane /// lipid raft	---
227233_at	TSPAN2	0.178	cell motility /// cell adhesion /// cell proliferation	---	integral to membrane	---
232763_at	TLN1	0.178	cell motility /// cytoskeletal anchoring	actin binding /// structural constituent of cytoskeleton /// binding	cytoskeleton /// focal adhesion	Integrin-mediated cell adhesion
203622_s_at	LOC56902	0.177	---	RNA binding	---	---
213231_at	DMWD	0.177	meiosis	---	---	---
217556_at	CLCN4	0.177	ion transport /// chloride transport	voltage-gated chloride channel activity	membrane fraction /// integral to plasma membrane	---
225592_at	NRM	0.177	---	---	---	---
237060_at	YTHDF2	0.177	---	---	---	---
1565923_at	SLC17A4	0.176	phosphate metabolism /// transport /// sodium ion transport	transporter activity /// sodium:phosphate symporter activity	membrane fraction /// integral to plasma membrane	---
206945_at	LCT	0.176	carbohydrate metabolism	lactase activity /// glycosylceramidase activity	membrane fraction /// integral to plasma membrane	Galactose metabolism
228809_at	CXorf40	0.176	---	---	---	---
231075_x_at	RAPH1	0.176	signal transduction	---	cytoskeleton	---
1554172_a_at	ZNF261	0.175	development	DNA binding /// zinc ion binding	nucleus	---
1569263_at	CSNK1D	0.175	DNA repair/// protein amino acid phosphorylation/// signal transduction	casein kinase I activity/// ATP binding/// protein serine/threonine kinase activity/// transferase activity/// nucleotide binding	---	circadian rhythm/// gap junction/// hedgehog signaling pathway

215652_at	SDHD	0.175	tricarboxylic acid cycle/// electron transport	electron carrier activity/// heme binding/// iron ion binding/// metal ion binding/// succinate dehydrogenase activity	mitochondrial inner membrane/// integral to membrane/// mitochondrial envelope	Citrate cycle (TCA cycle)/// Oxidative phosphorylation/// Electron Transport Chain/// Oxidative decarboxylation of pyruvate and TCA cycle
1556613_s_at	LOC203107	0.174	---	---	---	---
205067_at	IL1B	0.174	regulation of cell cycle /// apoptosis /// inflammatory response /// signal transduction /// cell-cell signaling /// cell proliferation /// negative regulation of cell proliferation /// antimicrobial humoral response (sensu Vertebrata)	signal transducer activity /// interleukin-1 receptor binding	extracellular space	Smooth muscle contraction
214813_at	ZNF75	0.174	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
235330_at	FLJ33814	0.174	---	---	---	---
242445_at	FGD4	0.173	---	zinc ion binding	---	---
1553281_at	PLCXD2	0.172	intracellular signaling cascade	phospholipase C activity	---	---
1565928_at	MAK10	0.172	---	---	---	---
226947_at	C6orf216	0.172	carbohydrate metabolism	hydrolase activity, hydrolyzing O-glycosyl compounds	---	---
232218_at	TRUB2	0.172	RNA processing	pseudouridylate synthase activity	---	---
235618_at	ZNF507	0.172	---	nucleic acid binding /// zinc ion binding	nucleus	---
238233_at	---	0.172	---	---	---	---

1553459_at	FLJ39660	0.171	---	---	---	---
1560968_at	CDCA2	0.171	---	---	---	---
212695_at	CRY2	0.171	DNA repair	DNA photolyase activity /// lyase activity	---	Circadian Exercise
222916_s_at	HDLBP	0.171	lipid transport /// cholesterol metabolism	nucleic acid binding /// RNA binding /// lipid transporter activity /// lipid binding	nucleus /// plasma membrane	---
223373_s_at	PLA2G12A	0.171	lipid catabolism	calcium ion binding /// hydrolase activity /// calcium-dependent phospholipase A2 activity	extracellular region	---
230992_at	BTNL9	0.171	---	---	integral to membrane	---
235415_at	KIAA0460	0.171	---	---	---	---
211914_x_at	NF1	0.17	Ras protein signal transduction /// negative regulation of cell proliferation /// negative regulation of cell cycle	enzyme inhibitor activity /// Ras GTPase activator activity	cytoplasm	---
213416_at	ITGA4	0.17	cell adhesion/// integrin-mediated signaling pathway	identical protein binding/// calcium ion binding/// receptor activity	integral to membrane/// integrin complex	cell adhesion molecules (CAMs)/// ECM-receptor interaction/// focal adhesion/// hematopoietic cell lineage/// leukocyte transendothelial migration/// regulation of actin cytoskeleton
217539_at	C18orf25	0.17	---	---	---	---
236722_at	AACS	0.17	isoprenoid biosynthesis/// metabolism	acetate-CoA ligase activity/// catalytic activity	---	Butanoate metabolism

239286_at	CDH11	0.17	ossification /// cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	integral to membrane	---
396_f_at	EPOR	0.17	signal transduction /// small GTPase mediated signal transduction	erythropoietin receptor activity /// guanyl-nucleotide exchange factor activity	integral to plasma membrane	---
1568699_at	MGC16028	0.169	---	---	---	---
227547_at	---	0.169	---	---	---	---
219368_at	NAP1L2	0.168	nucleosome assembly	---	nucleus /// chromatin assembly complex	---
227437_at	---	0.168	---	---	---	---
233115_at	DEPDC1B	0.168	intracellular signaling cascade	GTPase activator activity	---	---
236287_at	---	0.168	---	---	---	---
237126_at	MCP	0.168	complement activation, classical pathway	receptor activity	integral to plasma membrane	---
241095_at	---	0.168	---	---	---	---
1552739_s_at	ST7L	0.167	---	binding	---	---
1554594_at	LOC201175	0.167	---	---	---	---
215864_at	INPP4B	0.167	signal transduction	hydrolase activity/// phosphatidylinositol-3,4-bisphosphate 4-phosphatase activity	---	inositol phosphate metabolism/// phosphatidylinositol signaling system
216233_at	CD163	0.167	antimicrobial humoral response (sensu Vertebrata)	scavenger receptor activity	extracellular region /// integral to plasma membrane /// membrane	---
231881_at	CALD1	0.167	muscle contraction /// muscle development	actin binding /// calmodulin binding /// tropomyosin binding /// myosin binding	cytoskeleton	---
239638_at	---	0.167	---	---	---	---
205493_s_at	DPYSL4	0.166	neurogenesis	hydrolase activity	---	---

213823_at	HOXA11	0.166	regulation of transcription, DNA-dependent /// morphogenesis	transcription factor activity	nucleus	---
215679_at	---	0.166	---	---	---	---
241048_at	---	0.166	---	---	---	---
1562094_at	---	0.165	---	---	---	---
202952_s_at	ADAM12	0.165	proteolysis and peptidolysis /// cell adhesion /// myoblast fusion	metalloendopeptidase activity /// protein binding /// zinc ion binding /// hydrolase activity	plasma membrane /// integral to membrane	---
212980_at	AHSA2	0.165	---	---	---	---
224672_x_at	MESDC2	0.165	mesoderm development	---	---	---
231976_at	WINS1	0.165	---	---	---	---
239506_s_at	LOC151300	0.165	---	---	---	---
239513_at	ADORA2A	0.165	cAMP biosynthesis /// neurotransmitter transport /// phagocytosis /// apoptosis /// inflammatory response /// cellular defense response /// G-protein coupled receptor protein signaling pathway /// G-protein signaling, coupled to cAMP nucleotide second messenger /// adenylate cyclase activation /// cell-cell signaling /// central nervous system development /// blood coagulation /// sensory perception /// circulation	rhodopsin-like receptor activity /// A2A adenosine receptor activity, G-protein coupled /// A3 adenosine receptor activity, G-protein coupled /// receptor activity /// gastric inhibitory peptide receptor activity	membrane fraction /// integral to plasma membrane /// integral to membrane	GPCRDB Class A Rhodopsin-like /// Nucleotide GPCRs

241995_at	DGUOK	0.165	nucleobase, nucleoside, nucleotide and nucleic acid metabolism /// guanosine metabolism	deoxyguanosine kinase activity /// ATP binding /// kinase activity /// transferase activity /// phosphotransferase activity, alcohol group as acceptor	mitochondrion	Purine metabolism
243824_at	---	0.165	---	---	---	---
1566524_at	ACTR2	0.164	---	protein binding	cytoskeleton	---
201870_at	TOMM34	0.164	protein folding /// protein-mitochondrial targeting	signal sequence binding /// binding /// unfolded protein binding	mitochondrion /// mitochondrial outer membrane /// integral to membrane	---
214791_at	LOC93349	0.164	---	DNA binding	nucleus	---
234597_at	---	0.164	---	---	---	---
230906_at	GALNT10	0.163	---	polypeptide N-acetylgalactosaminyltransferase activity /// sugar binding /// transferase activity, transferring glycosyl groups /// manganese ion binding	Golgi apparatus /// integral to membrane	O-Glycan biosynthesis
239061_at	FLJ35107	0.163	---	---	---	---
240944_at	---	0.163	---	---	---	---
241007_at	---	0.163	---	---	---	---
242748_at	SREBF2	0.163	regulation of transcription from Pol II promoter /// lipid metabolism /// cholesterol metabolism	DNA binding /// RNA polymerase II transcription factor activity	nucleus /// endoplasmic reticulum /// Golgi apparatus /// integral to membrane	---
206969_at	KRTHA4	0.162	epidermis development	structural molecule activity	intermediate filament	---

220041_at	SMP3	0.162	---	RNA binding /// ribonuclease H activity /// transferase activity, transferring glycosyl groups	---	---
237711_at	LOC283202	0.161	---	---	---	---
1552327_at	ARMCX4	0.16	---	---	---	---
1555163_at	---	0.16	---	---	---	---
1562211_at	ZNF491	0.16	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
1566844_at	PER4	0.16	---	---	---	---
207409_at	LECT2	0.16	skeletal development /// chemotaxis	---	extracellular space /// cytoplasm	---
211182_x_at	RUNX1	0.16	regulation of transcription, DNA-dependent /// development	transcription factor activity /// ATP binding	nucleus	---
220636_at	DNAI2	0.16	---	motor activity	dynein complex	---
235175_at	GBP4	0.16	---	---	---	---
242401_x_at	C20orf26	0.16	---	---	---	---
243172_at	---	0.16	---	---	---	---
1563945_at	LOC284100	0.159	---	---	---	---
218040_at	FLJ10330	0.159	---	---	---	---
221501_x_at	LOC339047	0.159	neuropeptide signaling pathway	---	integral to membrane	---
233045_at	LOC286126	0.159	---	---	---	---
228958_at	ZNF19	0.158	regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	nucleus	---
237678_at	---	0.158	---	---	---	---

1559111_at	---	0.157	---	---	---	---	---
1562777_at	---	0.157	---	---	---	---	---
235132_at	LOC254128	0.157	---	---	---	---	---
236778_at	ATRX	0.157	DNA repair /// DNA methylation /// DNA recombination /// regulation of transcription, DNA-dependent /// chromosome organization and biogenesis (sensu Eukaryota) /// perception of sound	DNA helicase activity /// transcription factor activity /// ATP binding	nucleus /// nuclear heterochromatin	---	---
1558987_at	FLJ40473	0.156	---	---	---	---	---
204714_s_at	F5	0.156	cell adhesion /// blood coagulation	copper ion binding	extracellular region	Blood Clotting Cascade	---
241465_at	C17orf39	0.156	---	---	---	---	---
241770_x_at	SLC22A9	0.156	transport	transporter activity	integral to membrane	---	---
243009_at	INTS4	0.156	snRNA processing	protein binding	integrator complex	---	---
243357_at	NEGR1	0.156	cell adhesion	protein binding	---	---	---
1552836_at	ZNF619	0.155	---	nucleic acid binding /// zinc ion binding	nucleus	---	---
1560905_at	ELAVL2	0.155	nuclear mRNA splicing, via spliceosome /// regulation of transcription, DNA-dependent	RNA binding /// mRNA 3'-UTR binding	---	---	---
204638_at	ACP5	0.155	---	acid phosphatase activity /// hydrolase activity	lysosome /// integral to membrane	gamma-Hexachlorocyclohexane degradation /// Riboflavin metabolism	---
206468_s_at	KIAA0859	0.155	---	S-adenosylmethionine-dependent methyltransferase activity /// transferase activity	---	---	---

1552803_at	FLJ32206	0.154	---	---	---	---	---
1555681_at	---	0.154	---	---	---	---	---
206679_at	APBA1	0.154	protein complex assembly /// intracellular protein transport /// cell adhesion /// synaptic transmission /// neurogenesis /// axon cargo transport	protein binding	synaptic vesicle	---	
244687_at	---	0.154	---	---	---	---	
1565723_at	---	0.153	---	---	---	---	
1569732_at	CCL15	0.153	antimicrobial humoral response (sensu Vertebrata)/// calcium ion homeostasis/// cell-cell signaling/// chemotaxis/// immune response/// signal transduction	chemoattractant activity/// chemokine activity/// heparin binding	extracellular space	Cytokine-cytokine receptor interaction	
202114_at	SNX2	0.153	intracellular protein transport /// endocytosis /// intracellular signaling cascade	protein transporter activity	---	---	
212475_at	KIAA0241	0.153	---	---	---	---	
228441_s_at	PET112L	0.153	protein biosynthesis	translation factor activity, nucleic acid binding /// ligase activity /// glutamyl-tRNA(Gln) amidotransferase activity	mitochondrion	---	
237553_at	---	0.153	---	---	---	---	
244296_at	---	0.153	---	---	---	---	
1569465_at	LOC391705	0.152	---	---	---	---	

214648_at	GPX5	0.152	lipid metabolism /// response to oxidative stress	glutathione peroxidase activity /// electron transporter activity /// oxidoreductase activity	extracellular region	---	
222426_at	MAPKAP1	0.152	---	kinase activity /// Ras interactor activity	---	---	
224256_at	FMNL2	0.152	actin cytoskeleton organization and biogenesis/// cell organization and biogenesis/// regulation of transcription, DNA-dependent	actin binding/// transcription factor activity	nucleus	---	
244752_at	LOC220929	0.152	---	nucleic acid binding /// zinc ion binding	nucleus	---	
1564331_at	LOC162993	0.151	---	---	---	---	
1565894_at	---	0.151	---	---	---	---	
201590_x_at	ANXA2	0.151	skeletal development	phospholipase inhibitor activity /// calcium ion binding /// calcium-dependent phospholipid binding /// cytoskeletal protein binding	soluble fraction /// plasma membrane	Prostaglandin synthesis regulation	
221446_at	ADAM30	0.151	proteolysis and peptidolysis	metalloendopeptidase activity /// zinc ion binding /// hydrolase activity	integral to membrane	---	
241790_at	KLHL7	0.151	---	protein binding	---	---	
243967_at	LAF4	0.151	regulation of transcription, DNA-dependent /// development	DNA binding	nucleus	---	
1558324_a_at	---	0.15	---	---	---	---	

211504_x_at	ROCK2	0.15	cytokinesis /// protein amino acid phosphorylation /// muscle contraction /// intracellular signaling cascade	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// structural molecule activity /// ATP binding /// transferase activity /// diacylglycerol binding	intracellular /// actin cytoskeleton		G13 Signaling Pathway /// Integrin-mediated cell adhesion
211703_s_at	BBP	0.15	---	---	---		---
214932_at	KIDINS220	0.15	carbon utilization by fixation of carbon dioxide	ribulose-bisphosphate carboxylase activity	ribulose bisphosphate carboxylase complex (sensu Magnoliophyta)		---
215811_at	SNCA	0.15	central nervous system development/// anti-apoptosis	protein binding	cytoplasm		Alzheimer's disease/// neurodegenerative Disorders/// Parkinson's disease
1553831_at	APOBEC3D	0.149	metal ion transport	zinc ion binding /// hydrolase activity /// hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines /// metal ion binding	---		---
1555585_a_at	MGC26988	0.149	---	---	---		---
1556084_at	HNRPM	0.149	---	RNA binding /// transmembrane receptor activity	membrane fraction /// nucleus /// integral to plasma membrane /// ribonucleoprotein complex		---
1560496_at	---	0.149	---	---	---		---
204181_s_at	ZNF297B	0.149	regulation of transcription, DNA-dependent	DNA binding /// protein binding /// zinc ion binding	nucleus		---
208798_x_at	GOLGIN-67	0.149	---	---	Golgi apparatus		---

216908_x_at	LOC94431	0.149	---	---	---	---
220459_at	MCM3APAS	0.149	---	---	---	---
237235_at	---	0.149	---	---	---	---
242094_at	---	0.149	---	---	---	---
1562544_at	---	0.148	---	---	---	---
1570222_at	NDST4	0.148	---	sulfotransferase activity /// transferase activity	integral to membrane	---
222588_s_at	FLJ10726	0.148	---	---	---	---
232198_at	MCM8	0.148	---	---	---	---
232877_at	---	0.148	---	---	---	---
237333_at	RBBP4	0.148	---	---	---	---
1555322_at	---	0.147	---	---	---	---
202046_s_at	GRLF1	0.147	regulation of transcription, DNA-dependent /// small GTPase mediated signal transduction /// negative regulation of transcription /// regulation of eye photoreceptor cell development /// negative regulation of cell cycle	DNA binding /// GTPase activator activity /// GTP binding /// transcriptional repressor activity	nucleus	---
203945_at	ARG2	0.147	urea cycle /// arginine catabolism /// nitric oxide biosynthesis	arginase activity /// hydrolase activity /// manganese ion binding	mitochondrion	Urea cycle and metabolism of amino groups /// Arginine and proline metabolism
207646_s_at	CDY1 /// CDY2 /// CDY /// CDY1B	0.147	chromatin assembly or disassembly /// spermatogenesis	chromatin binding	chromatin /// nucleus	---

210427_x_at	ANXA2	0.147	skeletal development	phospholipase inhibitor activity /// calcium ion binding /// calcium-dependent phospholipid binding /// cytoskeletal protein binding	soluble fraction /// plasma membrane		Prostaglandin synthesis regulation
214087_s_at	MYBPC1	0.147	striated muscle contraction /// cell adhesion /// muscle development	actin binding /// protein binding /// structural constituent of muscle	striated muscle thick filament	Striated muscle contraction	
202645_s_at	MEN1	0.146	negative regulation of transcription from Pol II promoter /// regulation of transcription, DNA-dependent	protein binding	nucleus	---	
224084_at	---	0.146	---	---	---	---	---
243689_s_at	MGC72104	0.146	---	---	---	---	---
1559524_at	---	0.145	---	---	---	---	---
209021_x_at	KIAA0652	0.145	---	---	---	---	---
220496_at	CLEC1B	0.145	defense response /// cell surface receptor linked signal transduction	transmembrane receptor activity /// sugar binding	integral to plasma membrane	---	
238377_s_at	---	0.145	---	---	---	---	---
243930_x_at	GLIPR1	0.145	---	---	extracellular region /// integral to membrane	---	
204935_at	PTPN2	0.144	protein amino acid dephosphorylation	protein tyrosine phosphatase activity /// receptor activity /// hydrolase activity	---	---	

207357_s_at	GALNT10	0.144	---	polypeptide N-acetylgalactosaminyltransferase activity /// sugar binding /// transferase activity, transferring glycosyl groups /// manganese ion binding	Golgi apparatus /// integral to membrane	O-Glycan biosynthesis
209195_s_at	ADCY6	0.144	cAMP biosynthesis /// intracellular signaling cascade	magnesium ion binding /// adenylate cyclase activity /// guanylate cyclase activity /// lyase activity	integral to membrane	G Protein Signaling /// Calcium regulation in cardiac cells /// Smooth muscle contraction /// Purine metabolism
214028_x_at	TDRD3	0.144	---	nucleic acid binding	---	---
224015_s_at	MRPS25	0.144	protein biosynthesis	nucleic acid binding /// structural constituent of ribosome	mitochondrion /// mitochondrial small ribosomal subunit	---
238542_at	ULBP2	0.144	antigen presentation /// natural killer cell activation	MHC class I receptor activity	membrane /// MHC class I protein complex	---
220902_at	FLJ12616	0.143	---	---	---	---
1554291_at	KIAA0701	0.142	---	---	---	---
1561336_at	DNASE1L3	0.142	DNA catabolism /// apoptosis	DNA binding /// endonuclease activity /// deoxyribonuclease activity /// calcium ion binding /// hydrolase activity	nucleus	---
1562730_a_at	SGCA	0.142	muscle contraction /// muscle development	calcium ion binding /// protein binding	cytoskeleton /// dystrophin-associated glycoprotein complex /// sarcoglycan complex /// integral to membrane	---
1563324_at	LOC389457	0.142	---	---	---	---
207857_at	LILRA2	0.142	immune response	receptor activity	integral to membrane	---

231179_at	IHPK3	0.142	apoptosis/// DNA repair/// calcium-mediated signaling /// phosphatidylinositol metabolism/// positive regulation of DNA recombination /// protein amino acid phosphorylation /// vesicle-mediated transport	inositol hexakisphosphate kinase activity/// inositol trisphosphate 3-kinase activity /// transferase activity	cytoplasm/// nucleus	---
50277_at	GGA1	0.142	protein complex assembly /// intracellular protein transport /// intra-Golgi transport	---	Golgi stack /// clathrin coat of trans-Golgi network vesicle	---
1567255_at	OR10D1P	0.141	---	---	---	---
203646_at	FDX1	0.141	electron transport /// vitamin metabolism /// steroid metabolism	iron ion binding /// electron carrier activity	mitochondrion	---
226490_at	NHSL1	0.141	---	---	---	---
227221_at	---	0.141	---	---	---	---
221043_at	CHD9	0.14	chromatin assembly or disassembly	ATP binding/// DNA binding/// chromatin binding/// helicase activity	chromatin /// nucleus/// integral to membrane	---
1565282_at	---	0.139	---	---	---	---
235291_s_at	---	0.139	---	---	---	---
237157_at	DKFZp434D0215	0.139	---	---	---	---
1556620_at	ZNF721	0.138	---	zinc ion binding/// nucleic acid binding	intracellular/// nucleus	---
214947_at	FAM105A	0.138	---	---	---	---
229417_at	STAU2	0.138	---	double-stranded RNA binding	intracellular /// nucleus	---
235935_at	C6orf154	0.138	---	---	---	---

240631_at	GPR98	0.138	nervous system development/// cell-cell adhesion/// cell communication/// neuropeptide signaling pathway	G-protein coupled receptor activity/// calcium ion binding	integral to membrane	---	
241331_at	SCAP2	0.138	protein complex assembly /// signal transduction	SH3/SH2 adaptor protein activity ///-kinase activity	---	---	
1554380_at	NEK11	0.137	protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding	---	---	
1566484_at	FHIT	0.137	nucleotide metabolism/// cell cycle/// negative regulation of progression through cell cycle	bis(5'-adenosyl)-triphosphatase activity/// hydrolase activity/// magnesium ion binding	cytoplasm	Purine metabolism	
228267_at	TRIM11	0.137	protein ubiquitination	ligase activity/// metal ion binding/// ubiquitin-protein ligase activity/// zinc ion binding	nucleus/// ubiquitin ligase complex	Tryptophan metabolism	
1559295_at	CREBBP	0.136	regulation of transcription, DNA-dependent/// histone acetylation/// homeostasis/// positive regulation of transcription/// protein complex assembly/// response to hypoxia/// signal transduction	transcription factor activity/// MyoD binding/// acetyltransferase activity/// histone acetyltransferase activity/// protein binding/// signal transducer activity/// transcription coactivator activity/// transferase activity/// zinc ion binding	cytoplasm/// nucleus	adherens junction/// calcium signaling pathway/// cell cycle/// Huntington's disease/// Jak-STAT signaling pathway/// long-term potentiation/// neurodegenerative disorders/// notch signaling pathway/// TGF-beta signaling pathway/// Wnt signaling pathway	
1560906_at	HUMYZ8 2H07	0.136	---	---	---	---	
222597_at	SNAP29	0.136	---	---	---	---	

231433_at	---	0.136	---	---	---	---
1554321_a_at	NFS1	0.135	sulfur amino acid metabolism /// protein complex assembly /// metabolism	transaminase activity /// transferase activity /// cysteine desulfurase activity	nucleus /// mitochondrion /// cytosol	---
222296_at	---	0.135	---	---	---	---
237148_at	AMMECR1	0.135	---	---	---	---
213456_at	SOSTDC1	0.134	---	---	---	---
215713_at	ZFHX1B	0.134	regulation of transcription, DNA-dependent /// neurogenesis /// negative regulation of transcription	transcription factor activity /// zinc ion binding /// transcriptional repressor activity /// phosphatase regulator activity /// SMAD binding	nucleus	TGF Beta Signaling Pathway
221582_at	HIST3H2A	0.134	nucleosome assembly /// chromosome organization and biogenesis (sensu Eukaryota)	DNA binding	nucleosome /// nucleus	---
230285_at	DKFZp313A2432	0.134	---	---	---	---
244167_at	DELGEF	0.134	signal transduction	Ran guanyl-nucleotide exchange factor activity /// protein binding	nucleus /// cytoplasm	---
1566289_at	OR2M4	0.133	G-protein coupled receptor protein signaling pathway /// perception of smell	olfactory receptor activity	integral to membrane	GPCRDB Other
227238_at	MUC15	0.133	---	---	integral to membrane	---
228179_at	HAS3	0.133	carbohydrate metabolism	transferase activity, transferring glycosyl groups /// hyaluronan synthase activity	integral to plasma membrane	---
233902_at	GUCA1C	0.133	signal transduction/// visual perception	calcium sensitive guanylate cyclase activator activity/// calcium ion binding	---	---

238274_at	MYT1L	0.133	regulation of transcription, DNA-dependent/// cell differentiation/// nervous system development	transcription factor activity/// zinc ion binding	nucleus	---
241780_at	CDH11	0.133	ossification /// cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	integral to membrane	---
202066_at	PPFIA1	0.132	---	---	---	---
204440_at	CD83	0.132	defense response /// humoral immune response /// signal transduction	---	integral to plasma membrane	---
215642_at	ZNF518	0.132	---	nucleic acid binding /// zinc ion binding	nucleus	---
219542_at	NEK11	0.132	protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding	---	---
228010_at	PPP2R2C	0.132	signal transduction	phosphoprotein phosphatase activity /// protein phosphatase type 2A regulator activity	protein phosphatase type 2A complex	Glycogen Metabolism
232377_at	NXPH1	0.132	---	---	---	---
242360_at	LDB2	0.132	development	transcription cofactor activity	nucleus	---
210112_at	HPS1	0.131	---	---	---	---
215321_at	RPIB9	0.131	---	---	---	---
217170_at	---	0.131	---	---	---	---
232265_at	ATXN7L1	0.131	---	---	---	---
234790_at	FLJ10986	0.131	carbohydrate metabolism	---	---	---
237888_at	---	0.131	---	---	---	---
238506_at	LOC116064	0.131	---	---	---	---
243025_at	CDA08	0.131	cell-matrix adhesion	---	integrin complex /// integral to membrane	---
1557605_at	---	0.13	---	---	---	---

227971_at	NRK	0.13	protein amino acid phosphorylation	protein serine/threonine kinase activity /// small GTPase regulatory/interacting protein activity /// ATP binding /// transferase activity	---	---
232200_at	HSPA9B	0.13	protein folding	ATP binding /// unfolded protein binding	mitochondrion	---
238580_at	C4orf8	0.13	---	---	---	---
1561086_at	LAF4	0.129	regulation of transcription, DNA-dependent /// development	DNA binding	nucleus	---
201648_at	JAK1	0.129	protein amino acid phosphorylation /// intracellular signaling cascade	protein-tyrosine kinase activity /// Janus kinase activity /// ATP binding /// transferase activity	cytoskeleton	TGF Beta Signaling Pathway
216842_x_at	RBMY1A1 /// RBMY2FP /// RBMY1F /// RBMY1B /// RBMY1D /// RBMY1E /// RBMY1J	0.129	nuclear mRNA splicing, via spliceosome /// RNA processing /// spermatogenesis	nucleic acid binding /// RNA binding	nucleus	---
242843_at	BCAN	0.129	cell adhesion	sugar binding /// hyaluronic acid binding	---	---
210365_at	RUNX1	0.128	regulation of transcription, DNA-dependent /// development	transcription factor activity /// ATP binding	nucleus	---

210799_at	HTR1B	0.128	G-protein signaling, coupled to cyclic nucleotide second messenger /// synaptic transmission	rhodopsin-like receptor activity /// serotonin receptor activity	integral to plasma membrane		GPCRDB Class A Rhodopsin-like /// Monoamine GPCRs
211214_s_at	DAPK1	0.128	protein amino acid phosphorylation /// apoptosis /// signal transduction /// protein kinase cascade /// induction of apoptosis by extracellular signals	protein serine/threonine kinase activity /// calmodulin-dependent protein kinase I activity /// calcium- and calmodulin-dependent protein kinase activity /// calmodulin binding /// ATP binding /// transferase activity	actin cytoskeleton	---	
221895_at	MOSPD2	0.128	---	structural molecule activity	---	---	
225470_at	NUP35	0.128	---	porin activity	integral to membrane /// outer membrane	---	
236634_at	C8orf48	0.128	---	---	---	---	
204205_at	APOBEC3G	0.127	RNA metabolism /// innate immune response /// negative regulation of retroviral genome replication	RNA binding /// cytidine deaminase activity /// zinc ion binding /// hydrolase activity /// protein homodimerization activity	nucleus	---	
215703_at	CFTR	0.127	ion transport /// respiratory gaseous exchange	ion channel activity /// ATP-binding and phosphorylation-dependent chloride channel activity /// channel-conductance-controlling ATPase activity /// protein binding /// ATP binding /// ATPase activity /// PDZ domain binding	membrane fraction /// integral to plasma membrane /// basolateral plasma membrane /// apical plasma membrane	---	

217181_at	IL2	0.127	T cell differentiation/// anti-apoptosis/// antimicrobial humoral response (sensu Vertebrata)/// cell adhesion/// cell-cell signaling/// immune response/// natural killer cell activation/// positive regulation of cell growth/// positive regulation of cell proliferation	cytokine activity/// interleukin-2 receptor binding/// kinase activator activity	extracellular region	Cytokine-cytokine receptor interaction/// Jak-STAT signaling pathway/// T cell receptor signaling pathway/// Type I diabetes mellitus
220180_at	SE57-1	0.127	---	---	---	---
229240_at	ZDHHC21	0.127	---	acyltransferase activity /// transferase activity/// zinc ion binding	integral to membrane	---
1553998_at	DMRTC1	0.126	---	---	---	---
1554578_at	ZNF70	0.126	regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	nucleus	---
1558698_at	ZNF264	0.126	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
208816_x_at	ANXA2P2	0.126	---	---	---	---
213973_at	RRBP1	0.126	protein targeting /// signal transduction /// protein transport	ribosome receptor activity	integral to endoplasmic reticulum membrane	---
217648_at	RWDD3	0.126	---	---	---	---
218648_at	TORC3	0.126	---	---	---	---
233021_at	NDFIP2	0.126	positive regulation of I-kappaB kinase/NF-kappaB cascade	signal transducer activity	---	---
1552752_at	IGSF4D	0.125	---	---	---	---
1553961_s_at	C20orf16	0.125	intracellular signaling cascade /// protein transport	binding	---	---
1560891_at	---	0.125	---	---	---	---

1569688_at	FMO5	0.125	electron transport	monooxygenase activity /// dimethylaniline monooxygenase (N-oxide-forming) activity /// disulfide oxidoreductase activity	microsome /// integral to membrane	---
234593_at	CADPS	0.125	exocytosis	---	cytosol	---
1552738_at	ST7L	0.124	---	binding	---	---
1565132_at	RBMY3AP	0.124	---	---	---	---
1565621_at	---	0.124	---	---	---	---
1566185_at	---	0.124	---	---	---	---
1570479_at	ART1	0.124	protein amino acid ADP-ribosylation	NAD+ ADP-ribosyltransferase activity /// NAD(P)+-protein-arginine ADP-ribosyltransferase activity /// transferase activity, transferring glycosyl groups	integral to plasma membrane	---
225898_at	WDR54	0.124	---	---	---	---
236826_at	C9orf52	0.124	---	binding	---	---
237212_at	---	0.124	---	---	---	---
1555519_at	---	0.123	---	---	---	---
204691_x_at	PLA2G6	0.123	phospholipid metabolism /// lipid catabolism	phospholipase A2 activity /// hydrolase activity	cytoplasm /// membrane	Eicosanoid Synthesis /// Glycerophospholipid metabolism /// Prostaglandin and leukotriene metabolism

214610_at	CYP11B1	0.123	electron transport /// C21-steroid hormone biosynthesis	monooxygenase activity /// steroid 11-beta-monooxygenase activity	mitochondrion /// membrane	C21-Steroid hormone metabolism /// Androgen and estrogen metabolism
223630_at	C7orf13	0.123	metal ion transport	metal ion binding	---	---
234502_at	ARPP-21	0.123	---	nucleic acid binding	---	---
244186_at	C10orf11	0.123	---	---	---	---
1554364_at	PPP2R5C	0.122	signal transduction	phosphoprotein phosphatase activity /// protein phosphatase type 2A regulator activity	protein phosphatase type 2A complex /// nucleus	Wnt signaling /// Glycogen Metabolism
1558794_at	---	0.122	---	---	---	---
239001_at	MGST1	0.122	---	glutathione transferase activity /// transferase activity	mitochondrion /// microsome /// membrane	Glutathione metabolism
240329_at	PTP4A1	0.122	cell cycle/// development/// protein amino acid dephosphorylation	hydrolase activity/// protein tyrosine phosphatase activity	endoplasmic reticulum/// membrane	---
1557504_at	SRP54	0.121	protein targeting /// SRP-dependent cotranslational protein-membrane targeting	nucleotide binding /// RNA binding /// GTP binding /// nucleoside-triphosphatase activity	signal recognition particle (sensu Eukaryota)	---
1564262_at	PROX1	0.121	---	---	---	---
37433_at	PIAS2	0.121	regulation of transcription, DNA-dependent /// ubiquitin cycle /// development	DNA binding /// zinc ion binding	nucleus	---
1555185_x_at	TERF2	0.12	telomerase-dependent telomere maintenance /// cell cycle /// regulation of transcription	telomeric DNA binding	chromosome, telomeric region /// nucleus	---

211426_x_at	GNAQ	0.12	protein amino acid ADP-ribosylation /// signal transduction /// G-protein coupled receptor protein signaling pathway /// phospholipase C activation /// blood coagulation	GTPase activity /// signal transducer activity /// GTP binding	cytoplasm /// heterotrimeric G-protein complex /// plasma membrane	G Protein Signaling /// Calcium regulation in cardiac cells /// Smooth muscle contraction
222184_at	---	0.12	---	---	---	---
201537_s_at	DUSP3	0.119	protein amino acid dephosphorylation	protein tyrosine phosphatase activity /// protein tyrosine/serine/threonine phosphatase activity /// hydrolase activity	---	---
230763_at	LOC128153	0.119	---	---	---	---
231826_at	KIAA1272	0.119	---	---	---	---
1560288_at	---	0.118	---	---	---	---
202444_s_at	SPFH1	0.118	---	---	---	---
218396_at	VPS13C	0.118	---	---	---	---
226771_at	ATP8B2	0.118	cation transport /// metabolism	magnesium ion binding /// catalytic activity /// phospholipid-translocating ATPase activity /// ATP binding /// ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism /// hydrolase activity /// ATPase activity	membrane /// integral to membrane	---
228951_at	FLJ10815	0.118	transport /// amino acid transport	amino acid-polyamine transporter activity	integral to membrane	---

240594_at	CDYL	0.118	chromatin assembly or disassembly /// spermatogenesis /// metabolism	chromatin binding /// catalytic activity /// peptidase activity	chromatin /// nucleus	---
242830_at	LOC388565	0.118	---	---	---	---
203642_s_at	COBLL1	0.117	---	---	---	---
205066_s_at	ENPP1	0.117	generation of precursor metabolites and energy /// phosphate metabolism /// response to nutrients /// nucleotide metabolism	nucleic acid binding /// endonuclease activity /// nucleotide diphosphatase activity /// hydrolase activity	integral to membrane	Purine metabolism /// Starch and sucrose metabolism /// Riboflavin metabolism /// Nicotinate and nicotinamide metabolism /// Pantothenate and CoA biosynthesis
220300_at	RGS3	0.117	inactivation of MAPK /// signal transduction /// regulation of G-protein coupled receptor protein signaling pathway	signal transducer activity /// GTPase activator activity /// protein binding	cytosol	Calcium regulation in cardiac cells /// Smooth muscle contraction
228844_at	SLC13A5	0.117	sodium ion transport	transporter activity	membrane	---
1557753_at	---	0.116	---	---	---	---
1562671_s_at	---	0.116	---	---	---	---
1565752_at	FGD2	0.116	---	zinc ion binding	---	---
1566646_at	LOC149086	0.116	---	---	---	---
209874_x_at	CNNM2	0.116	fatty acid biosynthesis	---	---	---
210692_s_at	SLC43A3	0.116	---	---	---	---

232539_at	SOCS2	0.116	regulation of cell growth /// intracellular signaling cascade /// regulation of signal transduction /// regulation of body size /// positive regulation of neuron differentiation	growth hormone receptor binding /// prolactin receptor binding /// insulin-like growth factor receptor binding		cytoplasm
234910_at	RASAL2	0.116	signal transduction	Ras GTPase activator activity /// GTPase activator activity	---	---
239153_at	FLJ41747	0.116	---	---	---	---
1557599_a_at	SLC26A5	0.115	sensory perception of sound /// sulfate transport /// transport /// regulation of cell shape	motor activity /// sulfate porter activity /// transporter activity		integral to membrane
204327_s_at	ZNF202	0.115	negative regulation of transcription from Pol II promoter /// regulation of transcription, DNA-dependent /// lipid metabolism	transcription factor activity /// specific RNA polymerase II transcription factor activity /// zinc ion binding	nucleus	---
214980_at	UBE3A	0.115	proteolysis and peptidolysis /// ubiquitin-dependent protein catabolism /// ubiquitin cycle /// brain development	ubiquitin conjugating enzyme activity /// ubiquitin-protein ligase activity /// ligase activity	intracellular /// nucleus	---
223295_s_at	LUC7L	0.115	---	---	---	---
224841_x_at	GAS5	0.115	---	---	---	---
226289_at	M11S1	0.115	---	---	integral to plasma membrane	---

231678_s_at	ADH4	0.115	alcohol metabolism /// ethanol oxidation /// aldehyde metabolism	alcohol dehydrogenase activity, zinc-dependent /// electron-transferring-flavoprotein dehydrogenase activity /// zinc ion binding /// oxidoreductase activity	---	Glycolysis / Gluconeogenesis /// Fatty acid metabolism /// Bile acid biosynthesis /// Tyrosine metabolism /// Glycerolipid metabolism
234877_x_at	IGLC1	0.115	---	---	---	---
239733_at	MGC16186	0.115	---	---	---	---
244492_at	SLA	0.115	intracellular signaling cascade	SH3/SH2 adaptor protein activity	---	---
1570224_at	---	0.114	---	---	---	---
233312_at	ROPN1L	0.114	---	---	---	---
1557602_at	LOC201617	0.113	---	---	---	---
1569659_at	HECW1	0.113	---	---	---	---
224174_at	TTTY11	0.113	---	---	---	---
233493_at	OR2A4	0.113	G-protein coupled receptor protein signaling pathway /// perception of smell	olfactory receptor activity	integral to membrane	---
239170_at	ACTR3	0.113	cell motility	structural constituent of cytoskeleton	Arp2/3 protein complex	---
1553636_at	MGC35118	0.112	---	---	---	---
204066_s_at	CENTG2	0.112	---	---	---	---
229011_at	EMP1	0.112	epidermis development /// cell proliferation /// cell death/// cell growth	---	integral to membrane/// membrane fraction	---
239598_s_at	FLJ20481	0.112	metabolism	calcium ion binding /// acyltransferase activity	---	---

1554732_at	MGC2415	0.111	---	---	---	---
1559333_at	SRGAP3	0.111	---	GTPase activator activity	---	---
205649_s_at	FGA	0.111	blood coagulation /// regulation of blood pressure /// positive regulation of cell proliferation	---	extracellular region /// fibrinogen complex /// soluble fraction	Blood Clotting Cascade
211522_s_at	GNRHR	0.111	G-protein coupled receptor protein signaling pathway /// development	rhodopsin-like receptor activity /// gonadotropin-releasing hormone receptor activity	plasma membrane /// integral to membrane	GPCRDB Other /// Peptide GPCRs
213424_at	KIAA0895	0.111	---	---	---	---
220281_at	SLC12A1	0.111	ion transport /// potassium ion transport /// sodium ion transport /// chloride transport /// amino acid transport	transporter activity /// amino acid-polyamine transporter activity /// sodium:potassium:chloride symporter activity /// symporter activity	membrane fraction /// plasma membrane /// membrane /// integral to membrane	---
37145_at	GNLY	0.111	xenobiotic metabolism /// cellular defense response /// defense response to bacteria /// defense response to fungi	---	extracellular space	---
1555864_s_at	PDHA1	0.11	acetyl-CoA metabolism /// glycolysis /// metabolism	pyruvate dehydrogenase (acetyl-transferring) activity /// oxidoreductase activity	mitochondrion	Acetylcholine Synthesis /// Glycolysis and Gluconeogenesis /// Krebs-TCA Cycle /// Glycolysis / Gluconeogenesis /// Valine, leucine and isoleucine biosynthesis /// Pyruvate metabolism /// Butanoate metabolism

1561175_at	LOC283482	0.11	---	---	---	---
1565858_at	LOC388796	0.11	---	---	---	---
1566965_at	DPYD	0.11	electron transport /// 'de novo' pyrimidine base biosynthesis /// uracil catabolism /// thymidine catabolism	dihydroorotate dehydrogenase activity /// dihydroorotate oxidase activity /// electron transporter activity /// iron ion binding /// disulfide oxidoreductase activity /// oxidoreductase activity /// dihydropyrimidine dehydrogenase (NADP+) activity	cytoplasm /// mitochondrion /// membrane	Pyrimidine metabolism /// beta-Alanine metabolism /// Pantothenate and CoA biosynthesis
219007_at	NUP43	0.11	---	porin activity	integral to membrane /// outer membrane	---
220507_s_at	UPB1	0.11	nitrogen compound metabolism	beta-ureidopropionase activity /// hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	---	---
230495_at	LOC150568	0.11	---	---	---	---
233120_at	PHACTR4	0.11	---	---	---	---
234309_at	TTTY7	0.11	---	---	---	---
242052_at	BICD1	0.11	---	---	Golgi apparatus	---
1561853_at	IL23R	0.109	---	receptor activity	---	---
213784_at	RABL4	0.109	small GTPase mediated signal transduction /// protein transport	GTP binding	---	---
234248_at	---	0.109	---	---	---	---
228248_at	AVO3	0.108	---	binding	---	---
242263_at	CGI-100	0.108	intracellular protein transport	protein carrier activity	endoplasmic reticulum /// integral to membrane	---

1555997_s_at	IGFBP5	0.107	regulation of cell growth /// signal transduction	insulin-like growth factor binding	extracellular region	---
1556648_a_at	C10orf40	0.107	---	---	---	---
1556895_a_at	FLJ12442	0.107	---	---	---	---
1563204_at	ACP5	0.107	---	acid phosphatase activity /// hydrolase activity	lysosome /// integral to membrane	gamma-Hexachlorocyclohexane degradation /// Riboflavin metabolism
219265_at	MOBKL2B	0.107	---	---	---	---
244318_at	KIAA0241	0.107	---	---	---	---
1557314_at	FLJ36166	0.106	---	---	---	---
1558641_at	LOC202051	0.106	---	---	---	---
208384_s_at	MID2	0.106	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
239376_at	---	0.106	---	---	---	---
241312_at	---	0.106	---	---	---	---
213503_x_at	ANXA2	0.105	skeletal development	phospholipase inhibitor activity /// calcium ion binding /// calcium-dependent phospholipid binding /// cytoskeletal protein binding	soluble fraction /// plasma membrane	Prostaglandin synthesis regulation
223022_s_at	C6orf55	0.105	---	---	---	---
1561166_a_at	FOXP1	0.104	regulation of transcription, DNA-dependent	nucleic acid binding /// transcription factor activity /// zinc ion binding	nucleus	---
212358_at	CLIPR-59	0.104	---	---	---	---
223853_at	BVES	0.104	---	---	integral to membrane	---

1570596_at	---	0.103	---	---	---	---	---
220703_at	C10orf110	0.103	---	---	---	---	Cholesterol Biosynthesis /// Circadian Exercise
1557700_at	POLH	0.102	DNA replication /// regulation of DNA repair	magnesium ion binding /// damaged DNA binding /// eta DNA polymerase activity /// transferase activity	nucleoplasm	---	---
1566138_at	PTPRN2	0.102	protein amino acid dephosphorylation	protein tyrosine phosphatase activity /// receptor activity /// transmembrane receptor protein tyrosine phosphatase activity /// hydrolase activity	integral to plasma membrane	---	---
1566701_at	VRK3	0.102	protein amino acid phosphorylation	protein serine/threonine kinase activity /// ATP binding /// transferase activity	---	---	---
205931_s_at	CREB5	0.102	transcription from Pol II promoter /// positive regulation of transcription, DNA-dependent	transcription factor activity /// protein binding /// zinc ion binding	nucleus	---	---
216588_at	RPL7 /// LOC388401	0.102	protein biosynthesis	RNA binding /// structural constituent of ribosome /// transcription regulator activity	intracellular /// cytosolic large ribosomal subunit (sensu Eukaryota)	---	Ribosomal Proteins
216953_s_at	WT1	0.102	regulation of transcription; DNA-dependent /// negative regulation of cell cycle	nucleic acid binding /// transcription factor activity /// zinc ion binding	nucleus	---	---
217629_at	---	0.102	---	---	---	---	---
227425_at	REPS2	0.102	epidermal growth factor receptor signaling pathway/// protein complex assembly	calcium ion binding/// protein binding	---	---	---

1554276_at	SART3	0.101	RNA processing	nucleic acid binding	intracellular	---
1557413_at	---	0.101	---	---	---	---
209307_at	SWAP70	0.101	---	calcium ion binding	---	---
212908_at	KIAA0962	0.101	electron transport /// protein folding	electron transporter activity /// heat shock protein binding /// unfolded protein binding	---	---
234499_at	---	0.101	---	---	---	---
234609_at	PRKCE	0.101	protein amino acid phosphorylation /// induction of apoptosis /// intracellular signaling cascade	protein kinase C activity /// signal transducer activity /// ATP binding /// transferase activity /// diacylglycerol binding	membrane fraction	G Protein Signaling /// Wnt signaling /// Calcium regulation in cardiac cells /// Smooth muscle contraction
1562497_at	---	0.1	---	---	---	---
1563057_at	---	0.1	---	---	---	---
203285_s_at	HS2ST1	0.1	---	transferase activity	---	---
204502_at	SAMHD1	0.1	immune response /// signal transduction	catalytic activity /// 3',5'-cyclic-nucleotide phosphodiesterase activity	intracellular	---
228907_at	---	0.1	---	---	---	---
229642_at	ARHGEF7	0.1	signal transduction	guanyl-nucleotide exchange factor activity	---	---
235860_at	KCMF1	0.1	---	nucleic acid binding /// ion channel activity /// zinc ion binding	nucleus	---
240049_at	DLG5	0.1	regulation of cell cycle /// intracellular signaling cascade /// cell-cell adhesion	protein binding /// receptor signaling complex scaffold activity	plasma membrane	---

240603_s_at	MGC16943	0.1	---	exonuclease activity	nucleus	---	
1567182_at	---	0.099	---	---	---	---	
224022_x_at	WNT16	0.099	frizzled-2 signaling pathway /// cell-cell signaling /// development	signal transducer activity /// extracellular matrix structural constituent	extracellular region	Wnt signaling	
224543_at	C9orf13	0.099	---	receptor activity /// calcium ion binding	---	---	
234401_at	---	0.099	---	---	---	---	
1556158_at	DKFZp666G057	0.098	---	---	---	---	
215274_at	SLC12A3	0.098	ion transport /// sodium ion transport /// chloride transport /// amino acid transport	transporter activity /// amino acid-polyamine transporter activity /// symporter activity /// sodium:chloride symporter activity	membrane fraction /// integral to plasma membrane	---	
236652_at	LOC149703	0.098	---	---	---	---	
242555_at	LOC388272	0.098	---	---	---	---	
243884_at	MGC40178	0.098	---	---	---	---	
244368_x_at	SUGT1	0.098	centromere and kinetochore complex maturation/// mitosis/// regulation of progression through cell cycle/// ubiquitin cycle	binding	kinetochore/// ubiquitin ligase complex	---	
1554625_at	BCL6B	0.097	---	nucleic acid binding /// protein binding /// zinc ion binding	nucleus	---	

1555307_at	TTF2	0.097	transcription termination	DNA binding /// Pol II transcription termination factor activity /// helicase activity /// ATP binding /// DNA-dependent ATPase activity	transcription elongation factor complex	---
1560538_at	GTDC1	0.097	---	transferase activity	---	---
1561860_at	---	0.097	---	---	---	---
1570328_s_at	C20orf62	0.097	---	---	---	---
225637_at	FLJ20186	0.097	intracellular signaling cascade /// protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
1556436_at	LOC340414	0.096	---	---	---	---
206808_at	HNRPA3	0.096	---	RNA binding	nucleus /// ribonucleoprotein complex	mRNA processing
206985_at	HSD17B3	0.096	steroid biosynthesis /// sex determination /// metabolism /// male genitalia morphogenesis	estradiol 17-beta-dehydrogenase activity /// oxidoreductase activity	microsome	Steroid Biosynthesis /// Androgen and estrogen metabolism
211544_s_at	GHRHR	0.096	skeletal development /// G-protein coupled receptor protein signaling pathway /// adenylate cyclase activation	receptor activity /// G-protein coupled receptor activity /// growth hormone-releasing hormone receptor activity	plasma membrane /// integral to membrane	GPCRDB Class B Secretin-like /// GPCRDB Other
228666_at	MGC61550	0.096	---	---	---	---
235987_at	PRKXP1	0.096	---	---	---	---
1568592_at	LOC400368	0.095	---	---	---	---
215196_at	LOC91316	0.095	carbohydrate metabolism	hydrolase activity, hydrolyzing O-glycosyl compounds	---	---

219720_s_at	C14orf118	0.095	---	---	---	---
234850_at	MOGAT3	0.095	---	acyltransferase activity /// transferase activity	---	---
225266_at	KIAA0924	0.094	---	nucleic acid binding /// zinc ion binding	nucleus	---
232741_at	GLUD1	0.094	amino acid metabolism /// glutamate catabolism	glutamate dehydrogenase [NAD(P)+] activity /// ATP binding /// GTP binding /// oxidoreductase activity	mitochondrion	Urea cycle and metabolism of amino groups /// Glutamate metabolism /// Arginine and proline metabolism /// D-Glutamine and D-glutamate metabolism /// Nitrogen metabolism
242556_at	HPCAL1	0.094	---	calcium ion binding	---	---
1554076_s_at	MGC17839	0.093	---	---	integral to membrane	---
1556003_a_at	---	0.093	---	---	---	---
1559817_at	OR7A19P	0.093	---	---	---	---
1562280_at	POU2F1	0.093	negative regulation of transcription/// regulation of transcription, DNA-dependent	transcription factor activity/// protein binding	nucleus	---
1562997_at	---	0.093	---	---	---	---
221536_s_at	FLJ11301	0.093	---	GTP binding	---	---
232688_at	BMP2K	0.093	protein amino acid phosphorylation	protein serine/threonine kinase activity /// ATP binding /// transferase activity	nucleus	---
242232_at	LOC149401	0.093	---	---	---	---

1569323_at	PTPRG	0.092	protein amino acid dephosphorylation /// one-carbon compound metabolism /// transmembrane receptor protein tyrosine kinase signaling pathway	carbonate dehydratase activity /// transmembrane receptor protein tyrosine phosphatase activity /// zinc ion binding /// hydrolase activity	integral to plasma membrane	---	
208284_x_at	GGT1	0.092	amino acid metabolism /// glutathione biosynthesis	gamma-glutamyltransferase activity /// acyltransferase activity /// transferase activity	integral to membrane	Eicosanoid Synthesis /// Taurine and hypotaurine metabolism /// Selenoamino acid metabolism /// Cyanoamino acid metabolism /// Glutathione metabolism /// Prostaglandin and leukotriene metabolism	---
223856_at	AKR1CL2	0.092	---	oxidoreductase activity	---	---	---
233366_at	FBXO4	0.092	ubiquitin cycle /// protein ubiquitination	ubiquitin-protein ligase activity	ubiquitin ligase complex	---	---
228820_at	LOC63929	0.091	proteolysis and peptidolysis	peptidase activity /// metalloexopeptidase activity	---	---	---
229816_at	FLJ23129	0.091	---	---	---	---	---
236948_x_at	SFRS11	0.091	nuclear mRNA splicing, via spliceosome /// RNA splicing	RNA binding /// pre-mRNA splicing factor activity	nucleus	---	---
237128_at	FLJ20184	0.091	---	GTPase activator activity	---	---	---
207324_s_at	DSC1	0.09	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	membrane fraction /// cytoskeleton /// integral to plasma membrane /// gap junction /// membrane	---	

207472_at	RARSL	0.09	protein biosynthesis/// arginyl-tRNA aminoacylation	ATP binding/// arginine-tRNA ligase activity	---	---	---
211189_x_at	CD84	0.09	defense response/// homophilic cell adhesion	---	integral to plasma membrane/// plasma membrane	---	---
235909_at	LOC400960	0.09	---	---	---	---	---
1557267_s_at	LOC284952	0.089	---	---	---	---	---
1558722_at	ZNF252	0.089	---	nucleic acid binding /// zinc ion binding	nucleus	---	---
215083_at	PSPC1	0.089	nuclear mRNA splicing, via spliceosome	nucleic acid binding	---	---	---
217642_at	RNF40	0.089	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---	---
227823_at	RGAG4	0.089	---	---	---	---	---
200972_at	TM4SF8	0.088	cell motility /// cell proliferation	---	integral to membrane	---	---
206089_at	NELL1	0.088	cell adhesion /// neurogenesis /// metabolism	structural molecule activity /// calcium ion binding /// kinase activity /// oxidoreductase activity	---	---	---
214233_at	GGA2	0.088	protein complex assembly /// intracellular protein transport /// intra-Golgi transport	protein transporter activity /// ADP-ribosylation factor binding	Golgi stack /// Golgi trans face /// clathrin coat of trans-Golgi network vesicle	---	---
229079_at	EHMT2	0.088	chromatin modification	protein binding/// histone-lysine N-methyltransferase activity/// methyltransferase activity/// transferase activity/// zinc ion binding	nucleus	lysine degradation	
229575_at	---	0.088	---	---	---	---	---
1556267_at	FLJ25056	0.086	---	---	---	---	---

1559462_at	---	0.086	---	---	---	---	---
211840_s_at	PDE4D	0.086	signal transduction /// cyclic nucleotide metabolism	3',5'-cyclic-nucleotide phosphodiesterase activity /// cAMP-specific phosphodiesterase activity /// hydrolase activity	soluble fraction /// insoluble fraction	G Protein Signaling /// Smooth muscle contraction /// Purine metabolism
220522_at	CRB1	0.086	cell adhesion /// establishment and/or maintenance of cell polarity /// cell-cell signaling /// visual perception	structural molecule activity /// calcium ion binding	---	---
234657_at	---	0.086	---	---	---	---
238206_at	LGR7	0.086	signal transduction /// G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity	integral to membrane	GPCRDB Other /// Smooth muscle contraction
1566144_at	---	0.085	---	---	---	---
217397_at	---	0.085	---	---	---	---
232270_at	C9orf3	0.085	proteolysis and peptidolysis	aminopeptidase activity /// membrane alanyl aminopeptidase activity /// metallopeptidase activity	---	---
241581_at	ERBB4	0.085	protein amino acid phosphorylation /// transmembrane receptor protein tyrosine kinase signaling pathway /// development /// cell proliferation	receptor activity /// epidermal growth factor receptor activity /// ATP binding /// transferase activity	integral to plasma membrane	---
1560899_at	ASTN	0.084	cell adhesion /// neuronal cell adhesion /// cell migration	protein binding	integral to membrane	---
1562250_at	SEMA4D	0.084	anti-apoptosis /// immune response /// cell adhesion /// development /// neurogenesis	receptor activity	integral to membrane	---

217033_x_at	NTRK3	0.084	transmembrane receptor protein tyrosine kinase signaling pathway /// protein amino acid phosphorylation /// nervous system development /// cell differentiation	neurotrophin binding /// kinase activity /// ATP binding /// receptor activity /// transferase activity	---	integral to plasma membrane	---
238894_at	RABGAP1L	0.084	---	GTPase activator activity	---		---
1570645_at	---	0.083	---	---	---		---
222663_at	RIOK2	0.083	---	protein serine/threonine kinase activity /// ATP binding /// transferase activity	---		---
225259_at	RAB6B	0.083	intracellular protein transport /// retrograde transport, Golgi to ER /// small GTPase mediated signal transduction	GTPase activity /// GTP binding	Golgi apparatus		---
227706_at	SPIRE2	0.083	---	---	---		---
1555111_at	LOC57821	0.082	---	---	---		---
1566777_at	STRN3	0.082	cell cycle	calmodulin binding	Cytosol /// membrane fraction /// nucleus		---
235526_at	SMAP	0.082	---	---	---		---
242031_at	---	0.082	---	---	---		---
44790_s_at	C13orf18	0.082	---	protein phosphatase inhibitor activity	---		---
1556722_at	FLJ33706	0.081	---	---	---		---
1561437_at	MCHR2	0.081	G-protein coupled receptor protein signaling pathway	receptor activity /// rhodopsin like receptor activity	integral to membrane		Neuroactive ligand-receptor interaction
204631_at	MYH2	0.081	striated muscle contraction /// muscle development	microfilament motor activity /// actin binding /// calmodulin binding /// ATP binding	muscle myosin /// striated muscle thick filament /// myosin		---

2170333_x_at	NTRK3	0.084	transmembrane receptor protein tyrosine kinase signaling pathway /// protein amino acid phosphorylation /// nervous system development /// cell differentiation	neurotrophin binding /// kinase activity /// ATP binding /// receptor activity /// transferase activity	---	integral to plasma membrane	---
238894_at	RABGAP1L	0.084	---	GTPase activator activity	---		---
1570645_at	---	0.083	---	---	---		---
222663_at	RIOK2	0.083	---	protein serine/threonine kinase activity /// ATP binding /// transferase activity	---		---
225259_at	RAB6B	0.083	intracellular protein transport /// retrograde transport, Golgi to ER /// small GTPase mediated signal transduction	GTPase activity /// GTP binding	Golgi apparatus		---
227706_at	SPIRE2	0.083	---	---	---		---
1555111_at	LOC57821	0.082	---	---	---		---
1566777_at	STRN3	0.082	cell cycle	calmodulin binding	Cytosol /// membrane fraction /// nucleus		---
235526_at	SMAP	0.082	---	---	---		---
242031_at	---	0.082	---	---	---		---
44790_s_at	C13orf18	0.082	---	protein phosphatase inhibitor activity	---		---
1556722_at	FLJ33706	0.081	---	---	---		---
1561437_at	MCHR2	0.081	G-protein coupled receptor protein signaling pathway	receptor activity /// rhodopsin like receptor activity	integral to membrane		Neuroactive ligand-receptor interaction
204631_at	MYH2	0.081	striated muscle contraction /// muscle development	microfilament motor activity /// actin binding /// calmodulin binding /// ATP binding	muscle myosin /// striated muscle thick filament /// myosin		---

235173_at	LOC401093	0.081	---	---	---	---	---
240062_at	FAM3C	0.081	---	cytokine activity	extracellular region	---	
237747_at	C10orf45	0.08	---	---	---	---	
1558700_s_at	LOC339324	0.079	---	---	---	---	
207369_at	BRS3	0.079	glucose metabolism /// smooth muscle contraction /// G-protein coupled receptor protein signaling pathway /// response to nutrients /// regulation of blood pressure /// adult feeding behavior	rhodopsin-like receptor activity /// bombesin receptor activity	plasma membrane /// integral to membrane	GPCRDB Class A Rhodopsin-like /// Peptide GPCRs	
220324_at	C6orf155	0.079	---	---	---	---	
242273_at	---	0.079	---	---	---	---	
1566502_at	HYDIN	0.078	---	---	---	---	
203950_s_at	CLCN6	0.078	ion transport /// chloride transport /// regulation of cell volume /// signal transduction	voltage-gated chloride channel activity	membrane fraction /// integral to plasma membrane	---	
231814_at	LOC219612	0.078	---	---	---	---	
234956_at	LOC93444	0.078	---	---	---	---	
241466_at	MTL5	0.078	metal ion homeostasis /// anti-apoptosis /// response to oxidative stress /// spermatogenesis /// response to metal ion	metal ion binding	---	---	
242893_at	TYRP1	0.078	melanin biosynthesis from tyrosine /// metabolism	monooxygenase activity	integral to membrane	---	
1557197_a_at	LGALS3	0.077	---	sugar binding /// IgE binding	extracellular region /// nucleus /// plasma membrane	---	
1559347_at	CNOT4	0.077	---	---	---	---	

1564479_at	UGT2B7	0.077	lipid metabolism	glucuronosyltransferase activity	membrane fraction/// endoplasmic reticulum/// integral to membrane/// microsome		Androgen and estrogen metabolism/// Pentose and glucuronate interconversions/// Porphyrin and chlorophyll metabolism/// Starch and sucrose metabolism
230130_at	SLIT2	0.077	nervous system development /// G-protein coupled receptor protein signaling pathway/// cell differentiation/// chemotaxis /// glial cell migration/// induction of negative chemotaxis/// mesoderm migration/// motor axon guidance/// neuron recognition /// positive regulation of axonogenesis/// sensory perception /// sensory perception of smell/// ureteric bud development	calcium ion binding /// follicle stimulating hormone receptor activity /// receptor binding	extracellular space/// integral to membrane		Axon guidance
232184_at	ALS2	0.077	endosome organization and biogenesis	Ran guanyl-nucleotide exchange factor activity /// Rho guanyl-nucleotide exchange factor activity /// Rab guanyl-nucleotide exchange factor activity	early endosome /// cytosol /// vesicular fraction	---	
206991_s_at	CCR5	0.076	G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity /// receptor activity /// C-C chemokine receptor activity	integral to membrane		GPCRDB Class A Rhodopsin-like /// Peptide GPCRs /// GPCRDB Other
236531_at	---	0.076	---	---	---	---	---

243149_at	EIF4G3	0.076	regulation of translational initiation	RNA cap binding /// translation initiation factor activity	eukaryotic translation initiation factor 4F complex	Translation Factors
1559276_at	KCTD1	0.075	---	---	---	---
1570065_at	LOC400933	0.075	---	---	---	---
204994_at	MX2	0.075	immune response	GTPase activity /// GTP binding	nucleus /// cytoplasm	---
210306_at	L3MBTL	0.074	regulation of transcription, DNA-dependent /// chromatin modification	transcription factor activity	nucleus	---
228554_at	---	0.074	---	---	---	---
228992_at	MED28	0.074	regulation of transcription, DNA-dependent	actin binding	nucleus /// cytoskeleton /// membrane	---
207283_at	DKFZp547I014	0.073	protein biosynthesis	structural constituent of ribosome /// rRNA binding	ribosome	---
219995_s_at	FLJ13841	0.073	---	nucleic acid binding /// zinc ion binding	nucleus	---
1556810_a_at	WASL	0.072	protein complex assembly /// cell motility /// actin polymerization and/or depolymerization	actin binding /// small GTPase regulatory/interacting protein activity	actin cytoskeleton	G13 Signaling Pathway
1557682_a_at	LOC284688	0.072	---	---	---	---
1570425_s_at	LATS1	0.072	G2/M transition of mitotic cell cycle /// sister chromatid segregation /// cytokinesis /// protein amino acid phosphorylation /// cell cycle /// mitosis /// hormone-mediated signaling /// regulation of actin filament polymerization /// negative regulation of cyclin dependent protein kinase activity	magnesium ion binding /// protein serine/threonine kinase activity /// ATP binding /// transferase activity	spindle pole	---

226383_at	FLJ38968	0.072	---	---	---	---	---
1553839_at	DKFZp761B107	0.071	---	---	---	---	---
1562969_at	DNMBP	0.071	intracellular signaling cascade	guanyl-nucleotide exchange factor activity /// protein binding	Golgi apparatus /// cytoskeleton	---	---
207020_at	HSF2BP	0.071	transcription from Pol II promoter /// spermatogenesis	---	---	---	---
210137_s_at	DCTD	0.071	pyrimidine nucleotide metabolism /// nucleotide biosynthesis	dCMP deaminase activity /// zinc ion binding /// hydrolase activity	---	---	Pyrimidine metabolism /// Type II secretion system
232406_at	JAG1	0.071	angiogenesis /// cell fate determination /// cell communication /// Notch signaling pathway /// development /// neurogenesis /// hemopoiesis /// keratinocyte differentiation /// regulation of cell migration /// regulation of cell proliferation /// myoblast differentiation /// endothelial cell differentiation	Notch binding /// structural molecule activity /// calcium ion binding /// growth factor activity	extracellular region /// integral to plasma membrane	---	---
1554237_at	SDCCAG8	0.07	---	---	---	---	---
212917_x_at	RECQL	0.07	DNA repair	DNA binding /// ATP-dependent DNA helicase activity /// ATP binding /// hydrolase activity	nucleus	---	Integrin-mediated cell adhesion /// S1P Signaling
244887_at	RGS13	0.07	signal transduction	signal transducer activity	---	---	---
210736_x_at	DTNA	0.069	striated muscle contraction /// signal transduction /// neuromuscular synaptic transmission	calcium ion binding /// protein binding /// zinc ion binding	synapse	---	---

221399_at	EDA2R	0.069	epidermis development /// morphogenesis of embryonic epithelium /// cell differentiation /// positive regulation of JNK cascade /// activation of NF-kappaB transcription factor	receptor activity /// tumor necrosis factor receptor activity /// protein binding		integral to membrane	---
225789_at	CENTG3	0.069	small GTPase mediated signal transduction /// regulation of GTPase activity	GTPase activator activity /// GTP binding	---	---	---
206127_at	ELK3	0.068	regulation of transcription, DNA-dependent /// regulation of transcription from Pol II promoter /// signal transduction	transcription factor activity /// RNA polymerase II transcription factor activity /// transcription cofactor activity	nucleus	---	---
243125_x_at	---	0.068	---	---	---	---	---
1552258_at	MGC4677	0.067	---	---	---	---	---
1552870_s_at	DKFZp686H1423	0.067	---	---	---	---	---
1554776_at	ZFP42	0.067	---	nucleic acid binding /// zinc ion binding	nucleus	---	---
229823_at	RIMS2	0.067	intracellular protein transport	Rab GTPase binding /// metal ion binding /// protein binding /// zinc ion binding	---	---	---
232939_at	MAML3	0.067	nervous system development /// positive regulation of transcription from RNA polymerase II promoter /// regulation of transcription, DNA-dependent	transcription coactivator activity /// transcription factor activity	nucleus		Notch signaling pathway
239388_at	RNASET2	0.067	RNA catabolism	RNA binding /// endoribonuclease activity /// hydrolase activity	extracellular region	---	---
244474_at	NOL7	0.067	---	---	---	---	---

221101_at	C14orf113	0.066	---	---	---	---	---
235211_at	CHCHD8	0.066	---	---	---	---	---
238179_at	SPG7	0.066	cell adhesion/// nervous system development/// protein catabolism/// proteolysis/// regulation of cell adhesion/// signal transduction	ATP binding/// metal ion binding/// metalloendopeptidase activity/// nucleoside-triphosphatase activity/// nucleotide binding/// unfolded protein binding/// zinc ion binding	extracellular matrix (sensu Metazoa)/// integral to membrane/// mitochondrion	---	---
1556238_at	FLJ22313	0.065	protein modification	---	---	---	---
206532_at	SMARCB1	0.065	DNA integration/// cell cycle/// chromatin remodeling/// negative regulation of progression through cell cycle/// regulation of transcription from RNA polymerase II promoter	protein binding	nucleoplasm	---	---
212183_at	NUDT4	0.065	intracellular signaling cascade /// cyclic nucleotide metabolism /// calcium-mediated signaling /// cyclic-nucleotide-mediated signaling /// regulation of RNA-nucleus export /// intracellular transport	diphosphoinositol-polyphosphate diphosphatase activity /// hydrolase activity	intracellular	---	---
216348_at	RPS17	0.065	protein biosynthesis	RNA binding/// structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukaryota) /// Ribosome	Ribosome	Ribosome
220895_at	USP29	0.065	ubiquitin-dependent protein catabolism /// ubiquitin cycle	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity /// hydrolase activity	---	---	---

226741_at	LOC51234	0.064	---	---	---	---
226967_at	FLJ14768	0.064	---	nucleic acid binding /// zinc ion binding	nucleus	---
1552964_at	C10orf93	0.063	---	---	---	---
1561526_at	---	0.063	---	---	---	---
208463_at	GABRA4	0.063	ion transport /// chloride transport /// gamma-aminobutyric acid signaling pathway /// synaptic transmission	GABA-A receptor activity /// ion channel activity /// extracellular ligand-gated ion channel activity /// benzodiazepine receptor activity /// neurotransmitter receptor activity	integral to plasma membrane /// integral to membrane /// postsynaptic membrane	---
227519_at	PLAC4	0.063	---	---	membrane	---
238643_at	NBL1	0.063	negative regulation of cell cycle	---	---	---
1552678_a_at	USP28	0.062	ubiquitin-dependent protein catabolism /// ubiquitin cycle	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity /// hydrolase activity	---	---
1560619_at	LOC255411	0.062	---	---	---	---
207417_s_at	ZNF177	0.062	negative regulation of transcription from Pol II promoter /// regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
234364_at	IGLC1	0.062	---	---	---	---
242376_at	---	0.062	---	---	---	---
1556180_at	LOC255458	0.061	---	---	---	---
1562079_at	CHIC2	0.061	---	---	membrane	---

1566137_s_at	PTPRN2	0.061	protein amino acid dephosphorylation	transmembrane receptor protein tyrosine phosphatase activity	integral to plasma membrane	Type I diabetes mellitus
221605_s_at	PIPOX	0.061	electron transport /// tetrahydrofolate metabolism	sarcosine oxidase activity /// oxidoreductase activity /// L-pipecolate oxidase activity	peroxisome	---
238810_at	RFX3	0.061	regulation of transcription, DNA-dependent /// negative regulation of transcription	RNA polymerase II transcription factor activity, enhancer binding /// transcriptional repressor activity	nucleus	---
206569_at	IL24	0.06	apoptosis /// immune response	cytokine activity	extracellular region	---
212387_at	TCF4	0.06	regulation of transcription from Pol II promoter	DNA binding /// RNA polymerase II transcription factor activity	nucleus	---
217490_at	---	0.06	---	---	---	---
241594_at	---	0.06	---	---	---	---
241820_at	RIF1	0.06	---	ATP binding /// ATPase activity	---	---
1554637_a_at	CBFA2T2	0.059	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
1566896_at	SPPL3	0.059	---	D-alanyl-D-alanine endopeptidase activity/// peptidase activity	integral to membrane	---
209390_at	TSC1	0.059	cell adhesion /// Rho protein signal transduction /// negative regulation of cell cycle	---	---	---
221066_at	RLN3R1	0.059	G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity /// N-formyl peptide receptor activity	integral to plasma membrane	GPCRDB Other
1556170_at	---	0.058	---	---	---	---

218579_s_at	DHX35	0.058	---	nucleic acid binding /// ATP binding /// ATP-dependent helicase activity /// hydrolase activity	---	---
231434_at	LOC153441	0.058	---	---	---	---
239516_at	LYPLAL1	0.058	---	catalytic activity	---	---
1566861_at	LOC145663	0.057	---	---	---	---
1569072_s_at	ABCB5	0.057	transport	nucleotide binding /// ATP binding /// ATPase activity /// ATPase activity, coupled to transmembrane movement of substances	integral to membrane	---
236953_s_at	LOC387921	0.057	---	---	---	---
238287_at	SLC7A13	0.057	transport /// amino acid transport	amino acid-polyamine transporter activity	integral to membrane	---
241234_at	LOC389025	0.057	---	---	---	---
244578_at	LCP2	0.057	immune response /// transmembrane receptor protein tyrosine kinase signaling pathway /// intracellular signaling cascade	protein binding	---	---
201910_at	FARP1	0.056	cell adhesion	Rho guanyl-nucleotide exchange factor activity /// cytoskeletal protein binding	cytoplasm /// cytoskeleton /// membrane	---
203513_at	FLJ21439	0.056	aromatic compound metabolism	catalytic activity /// ferric iron binding	---	---
238261_at	---	0.056	---	---	---	---

243488_at	LOC285513	0.056	---	---	---	---	---
1552477_a_at	IRF6	0.055	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	Apoptosis	
1559437_at	LOC392084	0.055	---	---	---	---	---
228773_at	---	0.055	---	---	---	---	---
233220_at	GRIN3A	0.054	ion transport /// synaptic transmission	magnesium ion binding /// receptor activity /// ionotropic glutamate receptor activity /// transporter activity /// ion channel activity /// glutamate-gated ion channel activity	membrane /// integral to membrane	---	
236520_at	---	0.054	---	---	---	---	
212848_s_at	C9orf3	0.053	proteolysis and peptidolysis	aminopeptidase activity /// membrane alanyl aminopeptidase activity /// metallopeptidase activity	---	---	
228394_at	STK10	0.053	protein amino acid phosphorylation	protein serine/threonine kinase activity /// ATP binding /// transferase activity	---	---	
1556484_at	FLJ25811	0.052	---	---	extracellular matrix (sensu Metazoa)	---	
1559406_at	ANKRD18A	0.052	---	---	---	---	

1568874_at	NCOA6	0.052	embryonic development (sensu Mammalia) /// DNA replication /// DNA repair /// DNA recombination /// regulation of transcription, DNA-dependent /// transcription initiation from Pol II promoter /// brain development /// heart development /// response to hormone stimulus /// myeloid blood cell differentiation /// estrogen receptor signaling pathway /// glucocorticoid receptor signaling pathway /// positive regulation of transcription from Pol II promoter	chromatin binding /// transcriptional activator activity /// estrogen receptor binding /// ligand-dependent nuclear receptor transcription coactivator activity /// retinoid X receptor binding /// thyroid hormone receptor binding	nucleus /// transcription factor complex	---	
227658_s_at	PLEKHA3	0.052	---	phospholipid binding	membrane	---	
227937_at	LOC339344	0.052	---	DNA binding	nucleus	---	
232467_at	KIRREL	0.052	---	---	integral to membrane	---	
234059_at	CPOX	0.052	heme biosynthesis	coproporphyrinogen oxidase activity /// oxidoreductase activity	mitochondrion	Heme Biosynthesis /// Porphyrin and chlorophyll metabolism	
220669_at	HSHIN1	0.051	---	---	---	---	
235923_at	VTI1A	0.051	intracellular protein transport /// vesicle-mediated transport	protein transporter activity	integral to membrane	---	
205236_x_at	SOD3	0.05	superoxide metabolism	copper, zinc superoxide dismutase activity /// heparin binding /// antioxidant activity /// oxidoreductase activity /// metal ion binding	extracellular matrix (sensu Metazoa) /// soluble fraction	---	
226263_at	C6orf151	0.05	---	---	---	---	

237727_at	C9orf154	0.05	cell communication /// homophilic cell adhesion	calcium ion binding /// sugar binding	membrane /// integral to membrane	---
1570488_at	PCDH9	0.049	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	membrane /// integral to membrane	---
216561_x_at	SOX5	0.049	transcription from RNA polymerase II promoter /// regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
230898_at	KAZALD1	0.049	cell differentiation/// ossification/// regulation of cell growth	insulin-like growth factor binding	extracellular region	---
231233_at	LOC388727	0.049	---	---	---	---
243673_at	RBM41	0.049	---	RNA binding	---	---
1553246_at	FLJ23356	0.048	protein amino acid phosphorylation	protein kinase activity /// ATP binding	---	---
1558900_at	---	0.048	---	---	---	---
1562321_at	PDK4	0.048	glucose metabolism /// protein amino acid phosphorylation	protein kinase activity /// [pyruvate dehydrogenase (lipoamide)] kinase activity /// ATP binding /// transferase activity	mitochondrion	Krebs-TCA Cycle
1564521_x_at	SKB1	0.048	regulation of mitosis /// cell proliferation	methyltransferase activity /// transferase activity	cytoplasm	---
213153_at	KIAA1076	0.048	---	---	---	---
214782_at	CTTN	0.048	---	protein binding	ruffles /// soluble fraction /// cytoplasm /// cytoskeleton /// cell cortex /// lamellipodium	---
240165_at	---	0.047	---	---	---	---
207863_at	ADPRH	0.046	protein modification	magnesium ion binding /// ADP-ribosylarginine hydrolase activity /// hydrolase activity	---	---
221861_at	---	0.045	---	---	---	---

244569_at	LOC157657	0.045	---	---	---	---	---
1569374_at	FLJ43654	0.044	---	---	---	---	---
216898_s_at	COL4A3	0.044	proteolysis and peptidolysis /// phosphate transport /// induction of apoptosis /// caspase activation /// cell adhesion /// cell surface receptor linked signal transduction /// perception of sound /// circulation /// cell proliferation /// negative regulation of cell proliferation /// negative regulation of angiogenesis	serine carboxypeptidase activity /// integrin binding /// extracellular matrix structural constituent /// protein binding /// metalloendopeptidase inhibitor activity	collagen /// collagen type IV /// cytoplasm	---	---
218945_at	MGC26654	0.044	---	---	---	---	---
1553704_x_at	FLJ90396	0.043	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---	---
1557277_a_at	---	0.042	---	---	---	---	---
206379_at	EYA3	0.042	regulation of transcription, DNA-dependent /// development /// visual perception /// metabolism /// morphogenesis	magnesium ion binding /// catalytic activity /// phosphoprotein phosphatase activity /// protein tyrosine phosphatase activity /// hydrolase activity	nucleus	---	---
210839_s_at	ENPP2	0.042	phosphate metabolism /// cell motility /// chemotaxis /// G-protein coupled receptor protein signaling pathway /// nucleotide metabolism	nucleic acid binding /// endonuclease activity /// phosphodiesterase I activity /// nucleotide diphosphatase activity /// transcription factor binding /// hydrolase activity	integral to plasma membrane	---	---

224441_s_at	USP45	0.042	electron transport /// ubiquitin-dependent protein catabolism /// ubiquitin cycle /// transport	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity /// electron transporter activity /// iron ion binding	---	---	---
1563524_at	C14orf85	0.041	---	---	---	---	---
1562507_at	---	0.04	---	---	---	---	---
211587_x_at	CHRNA3	0.04	ion transport /// signal transduction /// synaptic transmission	nicotinic acetylcholine-activated cation-selective channel activity /// transporter activity /// ion channel activity /// extracellular ligand-gated ion channel activity /// acetylcholine receptor activity /// neurotransmitter receptor activity	nicotinic acetylcholine-gated receptor-channel complex /// integral to membrane /// postsynaptic membrane	---	---
203436_at	RPP30	0.039	tRNA processing	ribonuclease P activity /// ribonuclease activity /// hydrolase activity	nucleus /// nucleolar ribonuclease P complex	---	---
1556776_at	ZNF426	0.038	regulation of transcription, DNA-dependent	DNA binding/// metal ion binding/// zinc ion binding	intracellular/// nucleus	---	---
1562532_at	---	0.038	---	---	---	---	---
1569272_at	PIK3C3	0.038	---	inositol or phosphatidylinositol kinase activity /// phosphatidylinositol 3-kinase activity	phosphoinositide 3-kinase complex	---	---
238950_at	---	0.037	---	---	---	---	---

1570133_at	AKAP8L	0.035	---	DEAD/H-box RNA helicase binding/// DNA binding/// metal ion binding/// zinc ion binding	chromosome/// intracellular/// nucleus	---
211610_at	KLF6	0.035	regulation of transcription, DNA-dependent /// cell growth /// B-cell differentiation	nucleic acid binding /// DNA binding /// zinc ion binding /// transcriptional activator activity	nucleus	---
239464_at	---	0.035	---	---	---	---
1557146_a_at	FLJ32252	0.034	---	---	---	---
205663_at	PCBP3	0.034	mRNA metabolism	DNA binding /// RNA binding	nucleus /// ribonucleoprotein complex	---
206983_at	CCR6	0.034	cell motility /// chemotaxis /// humoral immune response /// cellular defense response /// signal transduction /// G-protein coupled receptor protein signaling pathway /// positive regulation of cytosolic calcium ion concentration /// antimicrobial humoral response (sensu Vertebrata)	rhodopsin-like receptor activity /// receptor activity /// C-C chemokine receptor activity	integral to plasma membrane	Peptide GPCRs /// GPCRDB Class A Rhodopsin-like
236977_at	---	0.034	---	---	---	---
213819_s_at	FLOT1	0.033	---	protein binding	integral to membrane/// caveola	Insulin signaling pathway

214917_at	PRKAA1	0.033	activation of MAPK /// response to hypoxia /// protein amino acid phosphorylation /// fatty acid biosynthesis /// cholesterol biosynthesis /// negative regulation of protein biosynthesis /// positive regulation of cholesterol biosynthesis /// positive regulation of gluconeogenesis /// positive regulation of anti-apoptosis /// negative regulation of glucosylceramide biosynthesis /// positive regulation of fatty acid oxidation /// positive regulation of glucose import	protein serine/threonine kinase activity /// cAMP-dependent protein kinase activity /// ATP binding /// transferase activity /// eukaryotic elongation factor-2 kinase activator activity	intracellular	Fatty Acid Synthesis
234767_at	MLSTD2	0.033	---	---	---	---
56919_at	WDR48	0.033	---	---	---	---
1558010_s_at	SLC1A2	0.032	transport /// dicarboxylic acid transport /// synaptic transmission /// L-glutamate transport	L-glutamate transporter activity /// symporter activity /// sodium:dicarboxylate symporter activity	membrane fraction /// integral to membrane	---
214706_at	ZNF200	0.032	regulation of transcription, DNA-dependent	nucleic acid binding /// zinc ion binding	nucleus	---
217340_at	RPL21	0.032	protein biosynthesis	RNA binding/// structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukaryota) /// Ribosome	Ribosome
223533_at	FAD158	0.032	---	---	---	---
1563131_at	---	0.031	---	---	---	---
1569878_at	C10orf21	0.031	regulation of progression through cell cycle	---	---	---

240164_at	MUC4	0.031	cell-matrix adhesion	ErbB-2 class receptor binding /// extracellular matrix structural constituent /// extracellular matrix constituent, lubricant activity	extracellular matrix (sensu Metazoa) /// integral to plasma membrane /// membrane	---
243531_at	ORAOV1	0.031	---	---	---	---
217615_at	LRRC37A	0.03	---	---	---	---
1555246_a_at	SCN1A	0.029	cation transport /// sodium ion transport	voltage-gated sodium channel activity /// cation channel activity	voltage-gated sodium channel complex /// integral to membrane	---
1564194_at	MGC352 95	0.029	signal transduction	receptor activity	integral to membrane	---
203962_s_at	NEBL	0.029	ion transport /// regulation of actin filament length	actin binding /// zinc ion binding /// structural constituent of muscle	cytoskeleton /// actin cytoskeleton	---
213223_at	RPL28	0.029	protein biosynthesis	RNA binding /// structural constituent of ribosome	intracellular /// ribosome /// cytosolic large ribosomal subunit (sensu Eukaryota)	Ribosomal Proteins
225790_at	MSRB3	0.029	protein repair	protein-methionine-R-oxide reductase activity /// zinc ion binding /// oxidoreductase activity	mitochondrion /// endoplasmic reticulum	---
230399_at	NOX1	0.029	proton transport/// FADH2 metabolism/// NADP metabolism/// electron transport/// ion transport	voltage-gated proton channel activity/// iron ion binding/// metal ion binding/// oxidoreductase activity/// superoxide-generating NADPH oxidase activity	integral to membrane	---
1559697_at	---	0.028	---	---	---	---

228585_at	FLJ34077	0.028	---	---	---	---
236107_at	FLJ13855	0.028	ubiquitin cycle	ubiquitin conjugating enzyme activity	---	---
212925_at	C19orf21	0.027	---	---	---	---
238731_at	SETDB2	0.027	chromatin modification	DNA binding /// methyltransferase activity /// zinc ion binding /// transferase activity /// histone-lysine N-methyltransferase activity	nucleus	---
1557567_at	LOC148987	0.026	---	---	---	---
225506_at	KIAA1468	0.026	---	---	---	---
243175_at	URP	0.026	---	hormone activity	extracellular region	---
1552377_s_at	LOC201158	0.025	---	---	integral to membrane	---
1563601_at	MGC43690	0.025	---	---	---	---
243016_at	HSRTSBETA	0.025	metabolism	catalytic activity	---	---
1570411_at	---	0.024	---	---	---	---
222964_at	MGC20741	0.024	ubiquitin-dependent protein catabolism /// ubiquitin cycle	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity /// hydrolase activity	---	---
242933_at	LOC127540	0.024	regulation of transcription, DNA-dependent	DNA binding	chromatin /// nucleus	---
219133_at	FLJ20604	0.022	fatty acid biosynthesis	catalytic activity	---	---

224967_at	UGCG	0.022	glucosylceramide biosynthesis /// glycosphingolipid biosynthesis /// epidermis development	ceramide glucosyltransferase activity /// transferase activity, transferring glycosyl groups	extracellular space /// membrane fraction /// endoplasmic reticulum /// integral to membrane	Glycosphingolipid metabolism
236210_at	DDX31	0.021	---	nucleic acid binding /// ATP binding /// ATP-dependent helicase activity /// hydrolase activity	---	---
1561650_s_at	LOC285692	0.02	---	---	---	---
1569787_at	---	0.02	---	---	---	---
204210_s_at	PCYT1A	0.02	phospholipid biosynthesis /// biosynthesis	choline-phosphate cytidylyltransferase activity /// transferase activity /// nucleotidyltransferase activity	soluble fraction /// membrane	Acetylcholine Synthesis /// Aminophosphonate metabolism /// Glycerophospholipid metabolism
243570_at	KIAA0102	0.02	signal peptide processing	signal peptidase activity	endoplasmic reticulum /// signal peptidase complex /// microsome /// integral to membrane	---
219915_s_at	SLC16A10	0.019	transport	transporter activity	integral to membrane	---
220191_at	GKN1	0.019	regulation of cell cycle /// digestion /// cell proliferation	growth factor activity	---	---
233909_at	STAU2	0.019	---	double-stranded RNA binding	intracellular /// nucleus	---
234832_at	ANTXR1	0.019	---	receptor activity	integral to membrane	---
216352_x_at	PCDHGA3	0.018	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	membrane /// integral to membrane	---
234218_at	---	0.018	---	---	---	---
222576_s_at	EIF2C1	0.017	protein biosynthesis /// regulation of translational initiation	translation initiation factor activity	eukaryotic translation initiation factor 2 complex	---

240824_at	OBFC1	0.017	---	nucleic acid binding	---	---	
244306_at	---	0.017	---	---	---	---	
219783_at	C2orf18	0.016	---	---	---	---	
1559856_s_at	MLL	0.015	regulation of transcription, DNA-dependent /// transcription from Pol II promoter	DNA binding /// transcription factor activity /// RNA polymerase II transcription factor activity /// zinc ion binding	nucleus	---	
1569122_at	LOC400263	0.015	---	---	---	---	
216174_at	HCRP1	0.015	---	---	---	---	
1555317_at	POLK	0.014	mutagenesis /// DNA repair	DNA binding	---	---	
1570352_at	ATM	0.014	DNA repair /// regulation of transcription, DNA-dependent /// meiotic recombination /// signal transduction /// negative regulation of cell cycle	DNA binding /// transcription factor activity /// protein serine/threonine kinase activity /// transferase activity /// phosphotransferase activity, alcohol group as acceptor	intracellular /// nucleus	Cell cycle /// G1 to S cell cycle Reactome /// Ovarian Infertility Genes	
208858_s_at	MBC2	0.014	---	---	---	---	
210840_s_at	IQGAP1	0.014	signal transduction /// small GTPase mediated signal transduction	GTPase inhibitor activity /// Ras GTPase activator activity /// calmodulin binding	actin filament	G13 Signaling Pathway	
221082_s_at	NDRG3	0.013	spermatogenesis /// cell differentiation /// negative regulation of cell growth	catalytic activity	cytoplasm	---	
228775_at	LOC558331	0.013	---	---	---	---	
1559725_at	LOC399924	0.012	---	---	---	---	

205948_at	PTPRT	0.012	protein amino acid dephosphorylation /// transmembrane receptor protein tyrosine kinase signaling pathway	receptor activity /// transmembrane receptor protein tyrosine phosphatase activity /// hydrolase activity	integral to plasma membrane	---
221073_s_at	CARD4	0.012	signal transduction /// regulation of apoptosis /// positive regulation of I-kappaB kinase/NF-kappaB cascade	signal transducer activity /// protein binding /// ATP binding /// caspase activator activity	intracellular	---
235189_at	NARG2	0.012	---	---	---	---
244072_at	FKBP6	0.012	mismatch repair	ATP binding	---	---
200685_at	SFRS11	0.011	nuclear mRNA splicing, via spliceosome /// RNA splicing	RNA binding /// pre-mRNA splicing factor activity	nucleus	---
207785_s_at	RBPSUH	0.011	DNA recombination /// regulation of transcription, DNA-dependent /// transcription from Pol II promoter	recombinase activity /// DNA binding /// RNA polymerase II transcription factor activity	nucleus	---
215052_at	PDZK10	0.011	---	phosphoprotein phosphatase activity /// protein binding	cytoskeleton	---
231042_s_at	CAMK2D	0.011	regulation of cell growth/// protein amino acid phosphorylation	calcium- and calmodulin-dependent protein kinase activity/// ATP binding/// calmodulin binding/// nucleotide binding/// protein serine/threonine kinase activity/// transferase activity	calcium- and calmodulin-dependent protein kinase complex	Calcium signaling pathway/// Wnt signaling pathway

239077_at	GALNAC T-2	0.01	dermatan sulfate proteoglycan biosynthesis, polysaccharide chain biosynthesis /// chondroitin sulfate proteoglycan biosynthesis, polysaccharide chain biosynthesis	protein binding /// acetylgalactosaminyltransferase activity /// transferase activity /// N-acetylgalactosaminyl-proteoglycan 3-beta-glucuronosyltransferase activity	Golgi apparatus /// integral to Golgi membrane	---
239316_at	MGC2477	0.01	---	---	---	---
1553805_at	MGC17310	0.009	---	---	---	---
210601_at	CDH6	0.009	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	integral to membrane	---
233449_at	---	0.009	---	---	---	---
1569406_at	---	0.008	---	---	---	---
218246_at	FLJ12875	0.008	protein ubiquitination /// positive regulation of I-kappaB kinase/NF-kappaB cascade	ubiquitin-protein ligase activity /// signal transducer activity /// zinc ion binding	ubiquitin ligase complex	---
1560810_at	TMEM132D	0.007	---	---	---	---
1561180_at	LRP11	0.007	---	receptor activity	integral to membrane	---
208422_at	MSR1	0.007	phosphate transport /// receptor mediated endocytosis	receptor activity /// scavenger receptor activity /// lipid transporter activity	cytoplasm /// integral to plasma membrane /// membrane	---
224958_at	182-FIP	0.007	---	---	---	---
1556347_at	---	0.006	---	---	---	---
218098_at	ARFGEF2	0.006	exocytosis	guanyl-nucleotide exchange factor activity /// binding	---	---

205479_s_at	PLAU	0.005	proteolysis and peptidolysis /// chemotaxis /// signal transduction /// blood coagulation /// negative regulation of blood coagulation	chymotrypsin activity /// trypsin activity /// plasminogen activator activity /// kinase activity /// hydrolase activity	extracellular space	Wnt signaling /// Blood Clotting Cascade
214685_at	C4orf10	0.005	---	---	---	---
1565111_x_at	OFCC1	0.004	---	---	---	---
210083_at	SEMA7A	0.004	immune response /// development /// neurogenesis	receptor activity	extracellular space /// membrane	---
231607_at	---	0.004	---	---	---	---
243_g_at	MAP4	0.004	negative regulation of microtubule depolymerization	structural molecule activity	microtubule associated complex	---
243937_x_at	LOC255326	0.004	---	---	---	---
215744_at	FUS	0.003	---	DNA binding /// RNA binding /// protein binding /// zinc ion binding	nucleus	mRNA processing
218261_at	AP1M2	0.003	protein targeting /// endocytosis /// vesicle targeting	---	Golgi apparatus /// coated pit /// clathrin vesicle coat	---
1553166_at	CDH24	0.002	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	membrane /// integral to membrane	---
1556502_at	LOC87769	0.002	---	---	---	---
1558813_at	TMED5	0.002	intracellular protein transport	protein carrier activity	endoplasmic reticulum /// integral to membrane	---
219755_at	CBX8	0.002	chromatin assembly or disassembly /// regulation of transcription, DNA-dependent /// chromatin modification	chromatin binding	chromatin /// nucleus	---
230191_at	TTBK1	0.002	protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding	---	---

210576_at	CYP4F8	0.001	electron transport /// prostaglandin metabolism	fatty acid (omega-1)-hydroxylase activity /// unspecific monooxygenase activity	endoplasmic reticulum /// microsome /// membrane	Fatty acid metabolism /// gamma-Hexachlorocyclohexane degradation /// Tryptophan metabolism
222494_at	CHES1	0.001	DNA damage checkpoint /// G2 phase of mitotic cell cycle /// regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
234444_at	CDCP2	0	---	---	---	---
209027_s_at	ABI1	-0.865	---	---	nucleus	---
239062_at	EVER1	-0.699	---	---	integral to membrane	---
205987_at	CD1C	-0.536	antimicrobial humoral response (sensu Vertebrata)	---	integral to plasma membrane	---
225289_at	STAT3	-0.485	negative regulation of transcription from Pol II promoter /// regulation of transcription, DNA-dependent /// cell motility /// acute-phase response /// intracellular signaling cascade /// JAK-STAT cascade /// neurogenesis	transcription factor activity /// signal transducer activity /// hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity /// calcium ion binding	nucleus /// cytoplasm	TGF Beta Signaling Pathway
243906_at	OSTalpha	-0.478	---	---	plasma membrane	---
208433_s_at	LRP8	-0.461	lipid metabolism /// endocytosis /// signal transduction	receptor activity /// transmembrane receptor activity /// calcium ion binding /// apolipoprotein E receptor activity	plasma membrane /// membrane /// integral to membrane	---
209266_s_at	SLC39A8	-0.444	transport /// metal ion transport	metal ion transporter activity	integral to membrane	---
238712_at	---	-0.437	---	---	---	---

216088_s_at	PSMA7	-0.403	ubiquitin-dependent protein catabolism	endopeptidase activity	proteasome core complex (sensu Eukaryota)	Proteasome Degradation /// Proteasome
201105_at	LGALS1	-0.402	apoptosis /// positive regulation of I-kappaB kinase/NF-kappaB cascade	signal transducer activity /// sugar binding	---	---
212858_at	PAQR4	-0.4	---	receptor activity	integral to membrane	---
215344_at	---	-0.395	---	---	---	---
227714_s_at	C9orf86	-0.382	small GTPase mediated signal transduction	GTP binding	---	---
204559_s_at	LSM7	-0.38	nuclear mRNA splicing, via spliceosome	RNA binding /// pre-mRNA splicing factor activity /// U6 snRNA binding	nucleus /// small nucleolar ribonucleoprotein complex	mRNA processing
215259_s_at	IGSF4C	-0.379	---	---	---	---
236186_x_at	IL17RE	-0.365	---	---	---	---
216977_x_at	SNRPA1	-0.362	RNA splicing	RNA binding	snRNP U2	mRNA processing
227505_at	KIAA1276	-0.353	---	---	---	---
212684_at	ZNF3	-0.351	regulation of transcription, DNA-dependent /// cell differentiation /// immune cell activation	nucleic acid binding /// transcription factor activity /// zinc ion binding	nucleus	---
240210_at	FLJ37183	-0.348	---	---	---	---
234342_at	FAM20C	-0.331	---	---	---	---
230902_at	---	-0.33	---	---	---	---
204829_s_at	FOLR2	-0.326	folic acid transport	receptor activity /// folic acid binding	membrane fraction /// membrane	---
217923_at	PEF	-0.324	---	---	---	---
237137_at	---	-0.323	---	---	---	---
202386_s_at	LKAP	-0.322	nuclear mRNA splicing, via spliceosome	nucleic acid binding	---	---

214626_s_at	GANAB	-0.319	carbohydrate metabolism	hydrolase activity, hydrolyzing O-glycosyl compounds /// hydrolase activity	endoplasmic reticulum /// Golgi apparatus	---
206023_at	NMU	-0.316	regulation of smooth muscle contraction /// signal transduction /// neuropeptide signaling pathway /// digestion	receptor binding	---	---
206653_at	POLR3G	-0.316	transcription /// regulation of transcription from Pol III promoter	DNA-directed RNA polymerase activity /// transferase activity	nucleus /// DNA-directed RNA polymerase III complex	---
218415_at	VPS33B	-0.307	vesicle docking during exocytosis /// protein transport /// vesicle-mediated transport	---	membrane	---
232269_x_at	METRN	-0.305	neurogenesis	---	---	---
202607_at	NDST1	-0.302	protein biosynthesis /// protein amino acid deacetylation /// protein amino acid sulfation /// heparan sulfate proteoglycan biosynthesis	structural constituent of ribosome /// [heparan sulfate]-glucosamine N-sulfotransferase activity /// transferase activity	intracellular /// Golgi apparatus /// ribosome /// integral to membrane	---
207756_at	---	-0.299	---	---	---	---
214106_s_at	GMDS	-0.295	carbohydrate metabolism /// leukocyte cell adhesion /// biosynthesis /// 'de novo' GDP-L-fucose biosynthesis	GDP-mannose 4,6-dehydratase activity /// lyase activity	cytoplasm	---

201986_at	THRAP1	-0.287	androgen receptor signaling pathway/// positive regulation of transcription from RNA polymerase II promoter/// regulation of transcription, DNA-dependent /// transcription initiation from RNA polymerase II promoter	RNA polymerase II transcription mediator activity/// ligand-dependent nuclear receptor transcription coactivator activity/// receptor activity/// thyroid hormone receptor binding/// vitamin D receptor binding	mediator complex/// nucleus	---	
231915_at	ZSWIM4	-0.287	---	---	---	---	
242071_x_at	ITGA8	-0.287	cell-matrix adhesion /// integrin-mediated signaling pathway /// cell-cell adhesion	receptor activity /// protein binding	integrin complex /// integral to membrane	---	Integrin-mediated cell adhesion
203082_at	BMS1L	-0.282	ribosome biogenesis	ATP binding	nucleus	---	
205881_at	ZNF74	-0.281	regulation of transcription, DNA-dependent /// development	nucleic acid binding /// DNA binding /// RNA binding /// zinc ion binding	nucleus	---	

217156_at	HADHA	-0.279	lipid metabolism /// fatty acid metabolism	3-hydroxyacyl-CoA dehydrogenase activity /// acetyl-CoA C-acetyltransferase activity /// enoyl-CoA hydratase activity /// long-chain-3-hydroxyacyl-CoA dehydrogenase activity /// lyase activity /// oxidoreductase activity	mitochondrion	Benzoate degradation via CoA ligation /// Butanoate metabolism /// Caprolactam degradation /// Fatty acid elongation in mitochondria /// Fatty acid metabolism /// Limonene and pinene degradation /// Lysine degradation /// Propanoate metabolism /// Tryptophan metabolism /// Valine, leucine and isoleucine degradation /// beta-Alanine metabolism
209731_at	NTHL1	-0.277	carbohydrate metabolism /// base-excision repair /// nucleotide-excision repair, DNA incision, 5'-to lesion	DNA binding /// DNA-(apurinic or apyrimidinic site) lyase activity /// endonuclease activity /// hydrolase activity, acting on glycosyl bonds /// lyase activity /// DNA N-glycosylase activity	nucleus	---
209440_at	PRPS1	-0.276	nucleoside metabolism /// ribonucleoside monophosphate biosynthesis /// nucleotide biosynthesis	magnesium ion binding /// ribose-phosphate diphosphokinase activity /// kinase activity /// transferase activity /// lipoate-protein ligase B activity	---	Pentose phosphate pathway /// Purine metabolism
213008_at	FLJ10719	-0.274	---	---	---	---

1553077_at	SDR-O	-0.273	metabolism	oxidoreductase activity	---	---
225044_at	MGC207 81	-0.272	---	---	---	---
233355_at	LOC2847 39	-0.267	---	---	---	---
215961_at	F12	-0.258	proteolysis and peptidolysis /// blood coagulation /// negative regulation of blood coagulation	coagulation factor Xla activity /// coagulation factor XIIa activity /// chymotrypsin activity /// trypsin activity /// hydrolase activity	extracellular region	Blood Clotting Cascade
224118_at	UBE2B	-0.258	DNA repair /// ubiquitin cycle	ubiquitin conjugating enzyme activity /// ubiquitin-protein ligase activity /// ligase activity	nucleus	Ubiquitin mediated proteolysis
203842_s_at	MAPRE3	-0.254	---	small GTPase regulatory/interacting protein activity	---	---
205085_at	ORC1L	-0.254	DNA replication /// DNA replication initiation	nucleotide binding /// DNA binding /// ATP binding /// nucleoside-triphosphatase activity	nucleus	Cell cycle /// DNA replication Reactome /// G1 to S cell cycle Reactome
1564473_at	LOC1575 70	-0.253	---	---	---	---
201555_at	MCM3	-0.253	DNA replication /// DNA replication initiation /// regulation of transcription, DNA-dependent /// cell cycle	DNA binding /// ATP binding /// DNA-dependent ATPase activity	nucleus /// alpha DNA polymerase:primase complex	Cell cycle/// DNA replication Reactome /// G1 to S cell cycle Reactome
218960_at	TMPRSS 4	-0.253	proteolysis and peptidolysis	chymotrypsin activity /// trypsin activity /// scavenger receptor activity /// peptidase activity /// hydrolase activity	integral to membrane	---
244147_at	KIAA121 7	-0.253	---	---	---	---

241737_x_at	VRK1	-0.251	protein amino acid phosphorylation	protein serine/threonine kinase activity /// ATP binding /// transferase activity	---	---
241012_at	TRBV3-1	-0.25	---	---	---	---
242849_at	SASH1	-0.248	negative regulation of cell cycle	---	---	---
208547_at	HIST1H2BB	-0.246	nucleosome assembly /// chromosome organization and biogenesis (sensu Eukaryota)	DNA binding	nucleosome /// nucleus /// chromosome	---
221454_at	BOK	-0.246	induction of apoptosis /// regulation of apoptosis	---	---	Apoptosis
238842_at	---	-0.246	---	---	---	---
220284_at	DKKL1	-0.242	morphogenesis	signal transducer activity	extracellular space	---
210569_s_at	SIGLEC9	-0.241	cell adhesion /// cell surface receptor linked signal transduction	protein binding /// sugar binding	integral to plasma membrane	---
216630_at	---	-0.241	---	---	---	---
219586_at	FLJ12270	-0.241	---	structural molecule activity	---	---
202178_at	PRKCZ	-0.24	protein amino acid phosphorylation /// anti-apoptosis /// intracellular signaling cascade	protein serine/threonine kinase activity /// atypical protein kinase C activity /// ATP binding /// transferase activity /// diacylglycerol binding	membrane fraction /// cytoplasm /// plasma membrane	G Protein Signaling /// Wnt signaling /// Calcium regulation in cardiac cells /// Smooth muscle contraction /// Phosphatidylinositol signaling system
204724_s_at	COL9A3	-0.24	phosphate transport	structural molecule activity	extracellular matrix (sensu Metazoa) /// collagen type IX /// cytoplasm	---
214250_at	NUMA1	-0.24	mitotic anaphase /// nuclear organization and biogenesis	structural molecule activity	nucleus /// spindle microtubule	---

212128_s_at	DAG1	-0.237	protein complex assembly /// muscle contraction	laminin receptor activity /// calcium ion binding /// protein binding	extracellular matrix (sensu Metazoa) /// membrane fraction /// integral to plasma membrane /// actin cytoskeleton	---
237712_at	---	-0.237	---	---	---	---
231159_at	LOC158813	-0.236	---	---	---	---
219742_at	PRR7	-0.234	---	---	---	---
222638_s_at	C6orf35	-0.234	---	---	---	---
207826_s_at	ID3	-0.232	development	transcription corepressor activity	nucleus	---
225780_at	RSC1A1	-0.232	transport	ion channel inhibitor activity	---	---
212318_at	TNPO3	-0.231	protein transport	receptor activity /// binding	nucleus	---
218594_at	FLJ10359	-0.231	---	binding	---	---
232072_at	ASAHL	-0.231	---	hydrolase activity	---	---
201666_at	TIMP1	-0.23	development /// positive regulation of cell proliferation /// negative regulation of membrane protein ectodomain proteolysis	metalloendopeptidase inhibitor activity	extracellular matrix (sensu Metazoa)	MAPK Cascade /// Matrix Metalloproteinases
203896_s_at	PLCB4	-0.23	lipid metabolism /// intracellular signaling cascade /// lipid catabolism	phosphoinositide phospholipase C activity /// signal transducer activity /// calcium ion binding /// hydrolase activity	---	Inositol phosphate metabolism /// Phosphatidylinositol signaling system
223057_s_at	XPO5	-0.229	---	binding	---	---

210123_s_at	CHRNA7 /// CHRFAM7A	-0.228	activation of MAPK /// ion transport /// signal transduction /// synaptic transmission	nicotinic acetylcholine-activated cation-selective channel activity /// ion channel activity /// extracellular ligand-gated ion channel activity /// acetylcholine receptor activity /// neurotransmitter receptor activity	nicotinic acetylcholine-gated receptor-channel complex /// integral to membrane /// postsynaptic membrane	---
215299_x_at	SULT1A1	-0.228	catecholamine metabolism /// lipid metabolism /// steroid metabolism /// amine metabolism	aryl sulfotransferase activity /// sulfotransferase activity /// transferase activity	---	---
202963_at	RFX5	-0.227	regulation of transcription, DNA-dependent /// transcription from Pol II promoter	transcription factor activity /// transcription coactivator activity	nucleus	---
206659_at	FLJ14082	-0.227	---	---	---	---
1562728_at	LOC147941	-0.225	---	---	---	---
223025_s_at	AP1M1	-0.225	intracellular protein transport /// endocytosis	---	Golgi apparatus /// coated pit /// clathrin vesicle coat	---
236177_s_at	---	-0.225	---	---	---	---
207192_at	DNASE1L2	-0.224	DNA catabolism	DNA binding /// endonuclease activity /// deoxyribonuclease activity /// calcium ion binding /// hydrolase activity	---	---
232693_s_at	ZNF395 /// FBXO16	-0.224	ubiquitin cycle	nucleic acid binding /// zinc ion binding	nucleus	---

240152_at	HDLBP	-0.224	lipid transport /// cholesterol metabolism	nucleic acid binding /// RNA binding /// lipid transporter activity /// lipid binding	nucleus /// plasma membrane	---	
210908_s_at	PFDN5	-0.223	regulation of transcription, DNA-dependent /// protein folding	transcription corepressor activity /// protein binding /// unfolded protein binding	nucleus /// prefoldin complex	---	
235753_at	LOC285944	-0.223	---	---	---	---	
238074_at	MGC43690	-0.222	---	---	---	---	
206560_s_at	MIA	-0.221	cell proliferation	growth factor activity	extracellular space	---	
216048_s_at	RHOBTB3	-0.219	---	GTPase activity /// protein binding	---	---	
232704_s_at	LRRFIP2	-0.217	---	LRR domain binding	---	---	
205388_at	TNNC2	-0.216	regulation of muscle contraction /// muscle development	calcium ion binding	troponin complex	Striated muscle contraction	
242963_at	MGC26963	-0.215	sphingolipid metabolism /// sphingomyelin biosynthesis	kinase activity /// transferase activity /// ceramide cholinephosphotransferase activity	Golgi apparatus /// integral to plasma membrane /// integral to Golgi membrane	---	
240151_at	HAB1	-0.214	---	---	---	---	
241078_at	SLC35E4	-0.214	---	---	---	---	
203606_at	NDUFS6	-0.212	mitochondrial electron transport, NADH to ubiquinone	NADH dehydrogenase activity /// NADH dehydrogenase (ubiquinone) activity /// electron carrier activity /// oxidoreductase activity	mitochondrion	Electron Transport Chain	
1561164_at	---	-0.211	---	---	---	---	

1564215_at	TRIP3	-0.209	regulation of transcription, DNA-dependent	thyroid hormone receptor binding	intracellular	---
238849_at	ACY1	-0.209	proteolysis and peptidolysis /// amino acid metabolism	aminoacylase activity /// metallopeptidase activity /// hydrolase activity	cytosol	Urea cycle and metabolism of amino groups
219092_s_at	C9orf12	-0.208	---	kinase activity	---	---
221706_s_at	MDS032	-0.208	transport	---	endoplasmic reticulum /// Golgi apparatus /// integral to membrane	---
223019_at	C9orf88	-0.208	---	---	---	---
243777_at	RAB7L1	-0.207	intracellular protein transport /// small GTPase mediated signal transduction	GTPase activity /// GTP binding	---	---
233106_at	C14orf82	-0.205	---	---	---	---
244801_at	PSMB7	-0.203	ubiquitin-dependent protein catabolism	endopeptidase activity	proteasome core complex (sensu Eukaryota)	Proteasome Degradation /// Proteasome
229038_at	CWF19L1	-0.201	---	---	---	---
202980_s_at	SIAH1	-0.2	ubiquitin-dependent protein catabolism /// apoptosis /// cell cycle /// development /// spermatogenesis /// protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding /// ligase activity	ubiquitin ligase complex /// nucleus	---
206230_at	LHX1	-0.2	regulation of transcription, DNA-dependent /// neurogenesis	transcription factor activity /// RNA polymerase II transcription factor activity /// zinc ion binding	nucleus	---
203802_x_at	NSUN5	-0.199	---	methyltransferase activity /// transferase activity	---	---
230880_at	KIAA1652	-0.199	---	---	---	---
237581_at	---	-0.199	---	---	---	---

1566932_x_at	TFB2M	-0.197	rRNA modification	rRNA (adenine-N6,N6-)-dimethyltransferase activity /// rRNA methyltransferase activity	---	---		
208445_s_at	BAZ1B	-0.197	transcription /// regulation of transcription, DNA-dependent /// protein ubiquitination	DNA binding /// transcription factor activity /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex /// nucleus	---		
214987_at	GAB1	-0.197	epidermal growth factor receptor signaling pathway /// cell proliferation /// insulin receptor signaling pathway	SH3/SH2 adaptor protein activity /// protein binding	---	---		
216256_at	GRM8	-0.196	G-protein coupled receptor protein signaling pathway /// negative regulation of adenylate cyclase activity /// synaptic transmission /// visual perception /// perception of smell	receptor activity /// metabotropic glutamate, GABA-B-like receptor activity	integral to plasma membrane /// membrane	GPCRDB Class C Metabotropic glutamate pheromone		
1557630_s_at	PPP1R12A	-0.195	regulation of muscle contraction	signal transducer activity	actin cytoskeleton	---		
211632_at	IGHM	-0.195	immune response	antigen binding	membrane fraction	---		
204643_s_at	COVA1	-0.192	nuclear mRNA splicing, via spliceosome /// regulation of cell growth /// electron transport /// ultradian rhythm	nucleic acid binding /// protein disulfide oxidoreductase activity /// oxidoreductase activity	cytosol /// external side of plasma membrane /// membrane	---		
223291_at	MRPS15	-0.192	protein biosynthesis	structural constituent of ribosome	mitochondrial small ribosomal subunit /// mitochondrion/// ribosome	---		
236268_at	SEC22L3	-0.192	ER to Golgi transport /// vesicle-mediated transport	---	endoplasmic reticulum /// integral to membrane	---		
239608_at	LOC254531	-0.192	metabolism /// phospholipid biosynthesis	acyltransferase activity /// transferase activity	integral to membrane	---		
232356_at	KIAA0143	-0.191	---	---	integral to membrane	---		
239869_at	---	-0.19	---	---	---	---		

226138_s_at	PPP1R14B	-0.189	---	protein phosphatase inhibitor activity	---	---	---
224473_x_at	LZTS2	-0.187	cell cycle /// negative regulation of cell cycle	---	cytoplasm /// membrane	---	---
236009_at	---	-0.186	---	---	---	---	---
213019_at	RANBP6	-0.185	protein transport	binding	nucleus	---	---
232257_s_at	DKFZP434N1817	-0.185	---	---	---	---	---
201608_s_at	PWP1	-0.184	transcription	---	nucleus	---	---
1557139_at	DDX11	-0.182	mitotic sister chromatid segregation /// regulation of cell cycle /// S phase of mitotic cell cycle /// G2/M transition of mitotic cell cycle /// nucleobase, nucleoside, nucleotide and nucleic acid metabolism /// nucleotide-excision repair /// positive regulation of cell proliferation /// ATP synthesis coupled proton transport	DNA binding /// ATP-dependent DNA helicase activity /// ATP binding /// hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides /// hydrogen-transporting ATP synthase activity, rotational mechanism /// hydrogen-transporting ATPase activity, rotational mechanism	nucleus /// nucleolus /// proton-transporting two-sector ATPase complex	---	---
202033_s_at	RB1CC1	-0.181	---	kinase activity	---	---	---
211801_x_at	MFN1	-0.181	---	GTPase activity /// GTP binding /// hydrolase activity	mitochondrion /// integral to membrane /// outer membrane	---	---
228371_s_at	PRO0149	-0.181	---	---	---	---	---
1557226_at	LOC374569	-0.18	amino acid metabolism	asparaginase activity	---	---	---
229168_at	COL23A1	-0.18	phosphate transport	structural molecule activity	cytoplasm	---	---

213768_s_at	ASCL1	-0.179	regulation of transcription from Pol II promoter /// neurogenesis /// cell differentiation	transcription factor activity	nucleus	---	
232911_at	KIAA1559	-0.179	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---	
224456_s_at	MGC12982	-0.178	---	---	---	---	
241492_at	---	-0.177	---	---	---	---	
216994_s_at	RUNX2	-0.176	ossification /// regulation of transcription, DNA-dependent	transcription factor activity /// RNA polymerase II transcription factor activity /// ATP binding	nucleus	TGF Beta Signaling Pathway	
203707_at	ZNF263	-0.175	regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	nucleus	---	
212071_s_at	SPTBN1	-0.174	---	actin binding /// structural constituent of cytoskeleton /// calmodulin binding	cytoskeleton /// spectrin /// membrane	---	
230980_x_at	---	-0.174	---	---	---	---	
235986_at	CEPT1	-0.174	lipid metabolism /// phospholipid biosynthesis	ethanolaminephosphotransferase activity /// transferase activity	integral to membrane	---	
1563241_at	PHF12	-0.172	negative regulation of transcription, DNA-dependent	protein binding/// transcriptional repressor activity/// zinc ion binding	nucleus/// transcriptional repressor complex	---	
1569783_at	CYP51A1	-0.172	electron transport /// cholesterol biosynthesis	monooxygenase activity /// sterol 14-demethylase activity	integral to membrane	Cholesterol Biosynthesis /// Fatty acid metabolism /// gamma-Hexachlorocyclohexane degradation /// Tryptophan metabolism	

211817_s_at	KCNJ5	-0.171	ion transport /// potassium ion transport	voltage-gated ion channel activity /// potassium channel activity /// G-protein enhanced inward rectifier potassium channel activity /// G-protein activated inward rectifier potassium channel activity	---	voltage-gated potassium channel complex /// integral to membrane	Calcium regulation in cardiac cells
217990_at	GMPR2	-0.171	nucleotide metabolism	catalytic activity /// GMP reductase activity /// oxidoreductase activity	---		---
218679_s_at	VPS28	-0.171	protein transport	---	---		---
218569_s_at	KBTBD4	-0.17	---	protein binding	---		Electron Transport Chain
234734_s_at	TNRC6A	-0.17	nuclear mRNA splicing, via spliceosome	nucleic acid binding	---		---
220212_s_at	THADA	-0.169	---	receptor activity	---		---
219819_s_at	MRPS28	-0.168	---	RNA binding /// structural constituent of ribosome	mitochondrion /// mitochondrial small ribosomal subunit		---
1557164_a_at	C9orf102	-0.167	---	---	---		---
1568762_at	PDCD6	-0.167	apoptosis /// induction of apoptosis by extracellular signals	calcium ion binding	---		---
214393_at	LOC284062	-0.167	---	---	---		---
1557495_at	---	-0.166	---	---	---		---
221769_at	SSB3	-0.166	intracellular signaling cascade	---	---		---
236993_at	---	-0.166	---	---	---		---
240046_at	FLJ25778	-0.166	---	---	---		---

242011_at	---	-0.166	---	---	---	---
1569062_s_at	IQGAP3	-0.165	small GTPase mediated signal transduction	Ras GTPase activator activity /// calmodulin binding	---	---
221050_s_at	GTPBP2	-0.165	protein biosynthesis	GTP binding	---	---
238304_at	---	-0.165	---	---	---	---
207132_x_at	PFDN5	-0.164	regulation of transcription, DNA-dependent /// protein folding	transcription corepressor activity /// protein binding /// unfolded protein binding	nucleus /// prefoldin complex	---
222223_s_at	IL1F5	-0.164	immune response	interleukin-1 receptor antagonist activity	extracellular region	---
1556439_at	---	-0.162	---	---	---	---
211358_s_at	CIZ1	-0.162	regulation of cell cycle	nucleic acid binding /// zinc ion binding	nucleus	---
227474_at	PAX8	-0.161	GTP biosynthesis /// UTP biosynthesis /// CTP biosynthesis /// regulation of transcription, DNA-dependent /// morphogenesis /// cell differentiation	transcription factor activity /// nucleoside-diphosphate kinase activity /// thyroid-stimulating hormone receptor activity /// ATP binding	nucleus	---
203796_s_at	BCL7A	-0.16	---	actin binding	---	---
211313_s_at	BAZ1B	-0.16	transcription /// regulation of transcription, DNA-dependent /// protein ubiquitination	DNA binding /// transcription factor activity /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex /// nucleus	---
1553227_s_at	WDR9	-0.159	---	---	---	---
1569731_at	SORCS2	-0.159	intracellular protein transport /// neuropeptide signaling pathway	protein binding /// sugar binding /// neuropeptide receptor activity /// protein transporter activity	membrane /// integral to membrane	---
203492_x_at	PIG8	-0.159	---	---	nucleus	---

207635_s_at	KCNH1	-0.159	two-component signal transduction system (phosphorelay) /// cation transport /// potassium ion transport	two-component sensor molecule activity /// voltage-gated potassium channel activity /// calmodulin binding	integral to membrane	---
231763_at	POLR3A	-0.157	transcription /// transcription, DNA-dependent	DNA binding /// DNA-directed RNA polymerase activity /// transferase activity	nucleus /// DNA-directed RNA polymerase III complex	---
1558605_at	---	-0.155	---	---	---	---
209220_at	GPC3	-0.155	morphogenesis	---	extracellular matrix (sensu Metazoa) /// integral to plasma membrane	---
216038_x_at	DAXX	-0.155	regulation of transcription, DNA-dependent /// apoptosis	---	nucleus	Apoptosis
218142_s_at	CRBN	-0.155	ATP-dependent proteolysis	ATP-dependent peptidase activity	mitochondrion	---
224494_x_at	DHRS10	-0.155	metabolism	oxidoreductase activity	---	---
1562657_at	C10orf90	-0.154	---	---	---	---
205221_at	HGD	-0.154	L-phenylalanine catabolism /// tyrosine catabolism	homogentisate 1,2-dioxygenase activity /// oxidoreductase activity	---	Tyrosine metabolism /// Styrene degradation
218868_at	ARP3BETA	-0.154	actin filament polymerization	structural constituent of cytoskeleton /// actin filament binding	actin cytoskeleton	---
222686_s_at	FLJ11151	-0.154	---	hydrolase activity	---	---
236683_at	---	-0.154	---	---	---	---
244245_at	ANKRD9	-0.154	---	---	---	---

205477_s_at	AMBP	-0.153	transport /// cell adhesion /// pregnancy /// anti-inflammatory response /// heme catabolism /// negative regulation of JNK cascade /// negative regulation of immune response	transporter activity /// calcium channel inhibitor activity /// IgA binding /// heme binding /// trypsin inhibitor activity /// plasmin inhibitor activity /// protein homodimerization activity /// calcium oxalate binding	extracellular region /// plasma membrane	---
234867_at	---	-0.152	---	---	---	---
201892_s_at	IMPDH2	-0.151	purine nucleotide biosynthesis /// GMP biosynthesis	IMP dehydrogenase activity /// oxidoreductase activity	---	Purine metabolism
214351_x_at	RPL13	-0.151	protein biosynthesis	RNA binding /// structural constituent of ribosome	intracellular /// cytosolic ribosome (sensu Eukaryota)	Ribosomal Proteins
1557346_a_at	LOC339263	-0.15	---	---	---	---
1561365_at	NRP1	-0.149	angiogenesis /// cell adhesion /// signal transduction /// cell-cell signaling /// neurogenesis /// axon guidance /// positive regulation of cell proliferation	receptor activity /// vascular endothelial growth factor receptor activity	membrane fraction /// integral to membrane	---
235872_at	TERF2	-0.149	telomere maintenance /// cell cycle /// regulation of transcription	telomeric DNA binding	chromosome, telomeric region /// nucleus	---
211319_at	RAE1	-0.148	mRNA export from nucleus/// mitotic spindle assembly	RNA binding/// microtubule binding	cytoplasm/// cytoskeleton/// nuclear outer membrane/// nuclear pore/// nucleus	---
216736_at	TM6SF2	-0.148	---	---	integral to membrane	---

217757_at	A2M	-0.148	intracellular protein transport /// protein homooligomerization	serine-type endopeptidase inhibitor activity /// protein carrier activity /// wide-spectrum protease inhibitor activity /// enzyme binding /// interleukin-8 binding /// interleukin-1 binding /// tumor necrosis factor binding	extracellular region	---	
224482_s_at	RAB11FIP4	-0.148	---	calcium ion binding	---	---	
230148_at	USP34	-0.148	ubiquitin-dependent protein catabolism /// ubiquitin cycle	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity	---	---	
1561121_at	TTC10	-0.145	protein biosynthesis /// excretion	structural constituent of ribosome /// binding	intracellular /// ribosome	---	
212047_s_at	RNF167	-0.145	proteolysis and peptidolysis /// protein ubiquitination	ubiquitin-protein ligase activity /// peptidase activity /// zinc ion binding	ubiquitin ligase complex	---	
224653_at	EIF4EBP2	-0.145	regulation of translation /// negative regulation of protein biosynthesis /// negative regulation of translational initiation	eukaryotic initiation factor 4E binding	---	Translation Factors	
239166_at	MARK3	-0.144	protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	---	---	
201440_at	DDX23	-0.143	RNA splicing	nucleic acid binding /// ATP-dependent RNA helicase activity /// ATP binding /// pre-mRNA splicing factor activity /// hydrolase activity	nucleus	---	

219345_at	CGI-143	-0.143	---	transcription regulator activity	---	---
212348_s_at	AOF2	-0.142	electron transport /// regulation of transcription, DNA-dependent /// chromatin modification	oxidoreductase activity	nucleus	---
1560378_at	GRIK1	-0.141	central nervous system development/// glutamate signaling pathway/// ion transport/// potassium ion transport/// synaptic transmission	kainate selective glutamate receptor activity/// glutamate-gated ion channel activity/// ion channel activity/// potassium channel activity/// receptor activity/// transporter activity	integral to plasma membrane	Neuroactive ligand-receptor interaction
201822_at	TIMM17A	-0.141	protein-mitochondrial targeting	protein translocase activity	mitochondrion /// mitochondrial inner membrane presequence translocase complex /// integral to plasma membrane	---
213111_at	PIP5K3	-0.141	protein folding /// intracellular signaling cascade	ATP binding /// zinc ion binding /// kinase activity /// 1-phosphatidylinositol-4-phosphate 5-kinase activity /// transferase activity /// unfolded protein binding	---	---
1556618_at	ELK4	-0.14	regulation of transcription, DNA-dependent/// transcription from RNA polymerase-II promoter	protein binding/// transcription cofactor activity/// transcription factor activity	nucleus	MAPK signaling pathway
207434_s_at	FXYD2	-0.14	ion transport /// potassium ion transport /// sodium ion transport	transporter activity /// ion channel activity /// sodium:potassium-exchanging ATPase activity	sodium:potassium-exchanging ATPase complex /// membrane /// integral to membrane	Calcium regulation in cardiac cells

221442_at	MC3R	-0.139	G-protein signaling, coupled to cyclic nucleotide second messenger /// G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	rhodopsin-like receptor activity /// melanocyte stimulating hormone receptor activity	integral to plasma membrane	GPCRDB Class A Rhodopsin-like /// Peptide GPCRs
231749_at	TIMM13	-0.138	perception of sound /// protein transport /// mitochondrial inner membrane protein import	zinc ion binding	mitochondrion /// mitochondrial inner membrane presequence translocase complex /// inner membrane /// mitochondrial inner membrane protein insertion complex	---
237623_at	CST3	-0.138	---	cysteine protease inhibitor activity	---	---
204811_s_at	CACNA2D2	-0.137	---	---	membrane	---
209547_s_at	SF4	-0.137	RNA processing	RNA binding	intracellular	mRNA processing
223820_at	RBP5	-0.137	transport	intracellular transporter activity /// lipid binding /// retinol binding	cytoplasm	---
241415_at	RPS6KA3	-0.137	central nervous system development /// protein amino acid phosphorylation /// signal transduction /// skeletal development	ATP binding /// magnesium ion binding /// nucleotide binding /// protein kinase activity /// protein serine/threonine kinase activity /// transferase activity	---	Long-term potentiation /// MAPK signaling pathway /// mTOR signaling pathway
1554934_at	RCBTB1	-0.136	---	protein binding	---	---
208688_x_at	EIF3S9	-0.136	protein biosynthesis /// translational initiation	RNA binding /// translation initiation factor activity	eukaryotic translation initiation factor 3 complex	Translation Factors
226239_at	FLJ90024	-0.136	---	---	---	---

236621_at	RPS27	-0.136	protein biosynthesis /// signal transduction /// cell proliferation	RNA binding /// structural constituent of ribosome /// zinc ion binding	intracellular /// ribosome /// cytosolic small ribosomal subunit (sensu Eukaryota)	Ribosomal Proteins
203033_x_at	FH	-0.135	tricarboxylic acid cycle /// fumarate metabolism /// negative regulation of cell cycle	fumarate hydratase activity /// lyase activity	mitochondrion /// tricarboxylic acid cycle enzyme complex	Krebs-TCA Cycle /// Citrate cycle (TCA cycle) /// Reductive carboxylate cycle (CO2 fixation)
228540_at	QKI	-0.135	---	nucleic acid binding /// RNA binding	---	---
222655_s_at	IMPAD1	-0.134	---	---	---	---
206753_at	RODH-4	-0.133	lipid metabolism /// metabolism	retinol dehydrogenase activity /// electron transporter activity /// oxidoreductase activity	microsome	---
214499_s_at	BCLAF1	-0.133	regulation of transcription, DNA-dependent /// induction of apoptosis	DNA binding /// transcriptional repressor activity	nucleus	---
223719_s_at	RTBDN	-0.132	---	---	---	---
224058_s_at	LOC1581 60	-0.132	metabolism	oxidoreductase activity	---	---
200901_s_at	M6PR	-0.131	transport /// receptor mediated endocytosis /// endosome to lysosome transport	transmembrane receptor activity /// transporter activity	lysosome /// integral to plasma membrane	---
207040_s_at	ST13	-0.13	protein folding	binding /// protein binding, bridging /// unfolded protein binding	cytoplasm	---
221812_at	FBXO42	-0.13	ubiquitin cycle	---	---	---
222986_s_at	SCOTIN	-0.13	positive regulation of I-kappaB kinase/NF-kappaB cascade	DNA binding /// signal transducer activity	nucleus	---
1560915_at	KIAA087 7	-0.129	---	---	---	---

202725_at	POLR2A	-0.129	transcription /// transcription, DNA-dependent /// regulation of transcription, DNA-dependent /// transcription from Pol II promoter	DNA binding /// DNA-directed RNA polymerase activity /// protein binding /// transferase activity	nucleus /// DNA-directed RNA polymerase II, core complex	mRNA processing Reactome /// RNA transcription Reactome /// Purine metabolism /// Pyrimidine metabolism /// RNA polymerase
224986_s_at	PDPK1	-0.129	protein amino acid phosphorylation /// insulin receptor signaling pathway /// actin cytoskeleton organization and biogenesis	protein serine/threonine kinase activity /// 3-phosphoinositide-dependent protein kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	cytoplasm /// plasma membrane	Integrin-mediated cell adhesion
1560412_at	---	-0.128	---	---	---	---
1560728_at	SH3GL2	-0.128	signal transduction /// central nervous system development	protein binding /// lipid binding /// acyltransferase activity /// transferase activity	cytoplasm	---
242417_at	LOC283278	-0.127	---	---	---	---
203294_s_at	LMAN1	-0.126	protein folding /// ER to Golgi transport /// blood coagulation /// protein transport	sugar binding /// mannose binding /// unfolded protein binding	Golgi membrane /// endoplasmic reticulum membrane /// integral to membrane	---
202897_at	PTPNS1	-0.125	---	---	---	---
203648_at	TATDN2	-0.124	---	nuclease activity /// hydrolase activity	---	---
217874_at	SUCLG1	-0.124	tricarboxylic acid cycle /// metabolism	succinate-CoA ligase (GDP-forming) activity /// GTP binding /// ligase activity	mitochondrion	Krebs-TCA Cycle /// Citrate cycle (TCA cycle) /// Propanoate metabolism
233987_at	TFAP2D	-0.123	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---

1561351_at	---	-0.121	---	---	---	---
219478_at	WFDC1	-0.121	negative regulation of cell growth	serine-type endopeptidase inhibitor activity	extracellular space	---
219966_x_at	BANP	-0.121	---	---	nucleus	---
1569712_at	---	-0.12	---	---	---	---
212811_x_at	SLC1A4	-0.12	transport /// dicarboxylic acid transport /// neutral amino acid transport	neutral amino acid transporter activity /// symporter activity /// sodium:dicarboxylate symporter activity	membrane fraction /// integral to plasma membrane	---
226579_at	XRCC3	-0.119	DNA repair/// DNA recombination	ATP binding/// DNA binding/// DNA-dependent ATPase activity/// nucleotide binding	nucleus	---
232247_at	ZNF502	-0.119	regulation of transcription, DNA-dependent	nucleic acid binding /// DNA binding /// zinc ion binding	nucleus	---
229659_s_at	PIGR	-0.118	protein secretion	protein transporter activity/// receptor activity	integral to plasma membrane	---
238661_at	---	-0.118	---	---	---	---
225363_at	PTEN	-0.117	---	---	---	---
233717_x_at	SMO	-0.117	G-protein coupled receptor protein signaling pathway /// development	non-G-protein coupled 7TM receptor activity /// G-protein coupled receptor activity /// protein binding	membrane fraction /// integral to membrane	GPCRDB Other
1562065_at	---	-0.116	---	---	---	---
216806_at	RPSA	-0.116	cell adhesion/// cell surface receptor linked signal transduction/// protein biosynthesis/// regulation of translation	laminin receptor activity/// structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukaryota) /// integrin complex	Prion disease/// Ribosome
223367_at	WBSCR18	-0.116	protein folding	heat shock protein binding /// unfolded protein binding	---	---

1570469_at	---	-0.115	---	---	---	---	---
214004_s_at	VGLL4	-0.115	regulation of transcription, DNA-dependent	---	nucleus	---	---
218713_at	NARG2	-0.115	---	---	---	---	---
237634_at	C1QTNF3	-0.115	phosphate transport	---	cytoplasm	---	---
232660_at	BAD	-0.114	induction of apoptosis /// apoptotic program	protein binding	cytoplasm /// mitochondrial outer membrane	Apoptosis	
224228_s_at	PRDM7	-0.112	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---	
225675_at	C14orf101	-0.112	---	---	integral to membrane	---	
213201_s_at	TNNT1	-0.11	regulation of muscle contraction /// muscle development	tropomyosin binding	---	Striated muscle contraction	
219070_s_at	MOSPD3	-0.11	---	structural molecule activity	integral to membrane	---	
243808_at	CDK6	-0.11	regulation of cell cycle /// G1 phase of mitotic cell cycle /// cytokinesis /// protein amino acid phosphorylation	protein serine/threonine kinase activity /// ATP binding /// transferase activity	---	---	
220577_at	FLJ13373	-0.109	---	---	---	---	
235465_at	FLJ25477	-0.109	---	---	---	---	
1557897_at	---	-0.108	---	---	---	---	
227327_at	SBP1	-0.108	---	---	---	---	
1554652_s_at	LOC37549	-0.107	---	---	---	---	
209862_s_at	PIG8	-0.107	---	---	nucleus	---	

219384_s_at	ADAT1	-0.107	tRNA processing	RNA binding /// tRNA specific adenosine deaminase activity	---	---	---
208021_s_at	RFC1	-0.105	DNA-dependent DNA replication /// regulation of transcription, DNA-dependent /// telomerase-dependent telomere maintenance	nucleotide binding /// DNA binding /// ATP binding /// enzyme activator activity /// nucleoside-triphosphatase activity	nucleus /// DNA replication factor C complex	DNA replication Reactome	
215312_at	---	-0.105	---	---	---	---	---
223908_at	HDAC8	-0.105	regulation of transcription, DNA-dependent /// chromatin modification /// histone deacetylation	histone deacetylase activity /// transcription factor binding /// hydrolase activity	histone deacetylase complex /// nucleus /// cytoplasm	Cell cycle	
220675_s_at	ADPN	-0.103	lipid catabolism /// triacylglycerol biosynthesis /// triacylglycerol catabolism	phospholipase A2 activity /// triacylglycerol lipase activity /// acyltransferase activity /// transferase activity /// hydrolase activity /// nutrient reservoir activity /// mono-olein transacylation activity /// diolein transacylation activity	integral to membrane	---	
227375_at	DKFZP566D1346	-0.103	---	---	---	---	---
234868_s_at	GFRA4	-0.103	---	receptor activity	membrane	---	
227392_at	NISCH	-0.101	intracellular signaling cascade	---	---	---	---
238007_at	ZNF271	-0.101	regulation of transcription, DNA-dependent	DNA binding/// metal ion binding/// zinc ion binding	intracellular/// nucleus	---	
214317_x_at	RPS9	-0.1	protein biosynthesis	RNA binding /// structural constituent of ribosome	intracellular /// cytosolic small ribosomal subunit (sensu Eukaryota)	Ribosomal Proteins	
219719_at	CLST1240	-0.1	---	---	---	---	---

223352_s_at	HLC-8	-0.1	---	---	---	---	---
228670_at	TEP1	-0.1	DNA replication and chromosome cycle /// telomerase-dependent telomere maintenance	telomerase activity /// RNA binding /// protein binding /// ATP binding	chromosome, telomeric region /// telomerase holoenzyme complex	---	
1563950_at	PRG-3	-0.099	---	hydrolase activity	integral to membrane	---	
200609_s_at	WDR1	-0.099	perception of sound	actin binding /// protein binding	cytoskeleton	Hypertrophy model	
43511_s_at	---	-0.099	---	---	---	---	
215206_at	EXT1	-0.098	skeletal development /// glycosaminoglycan biosynthesis /// signal transduction /// negative regulation of cell cycle	transferase activity, transferring glycosyl groups /// N-acetylglucosaminyl-proteoglycan 4-beta-glucuronosyltransferase activity	endoplasmic reticulum membrane /// Golgi apparatus /// integral to membrane	---	
39729_at	PRDX2	-0.097	response to oxidative stress	electron transporter activity /// thioredoxin peroxidase activity /// oxidoreductase activity	cytoplasm	Phenylalanine metabolism /// Prostaglandin and leukotriene metabolism /// Methane metabolism /// Stilbene, coumarine and lignin biosynthesis	
238545_at	ADCY7	-0.096	cAMP biosynthesis/// intracellular signaling cascade	adenylate cyclase activity/// magnesium ion binding	integral to plasma membrane	Calcium signaling pathway /// Gap junction /// Purine metabolism	
239836_at	FLJ10948	-0.095	metabolism	catalytic activity	---	---	
224825_at	DNTTIP1	-0.094	---	---	nucleus	---	
236766_at	C8orf38	-0.094	---	---	---	---	
231580_at	---	-0.092	---	---	---	---	

229034_at	FLJ1015 9	-0.091	---	---	---	---	---
229143_at	CNOT3	-0.091	regulation of transcription, DNA-dependent	protein binding /// transcription regulator activity	nucleus	---	---
237997_s_at	---	-0.091	---	---	---	---	---
208270_s_at	RNPEP	-0.09	proteolysis and peptidolysis /// protein processing	membrane alanyl aminopeptidase activity /// epoxide hydrolase activity /// zinc ion binding /// hydrolase activity /// aminopeptidase B activity	extracellular region /// Golgi apparatus /// plasma membrane	---	---
227408_s_at	SNX25	-0.09	intracellular signaling cascade /// protein transport	signal transducer activity	---	---	---
238236_at	DDEF1	-0.09	regulation of GTPase activity	GTPase activator activity /// metal ion binding /// protein binding /// zinc ion binding	membrane	---	---
202494_at	PPIE	-0.089	protein folding	RNA binding /// peptidyl-prolyl cis-trans isomerase activity /// cyclosporin A binding /// isomerase activity	nucleus	---	---
230254_at	C6orf188	-0.088	---	---	integral to membrane	---	---
222200_s_at	FLJ1027 6	-0.087	---	---	---	---	---

1555940_a_at	PRKCA	-0.086	cell surface receptor linked signal transduction/// induction of apoptosis by extracellular signals/// intracellular signaling cascade/// protein amino acid phosphorylation/// regulation of progression through cell cycle	ATP binding/// calcium ion binding/// diacylglycerol binding/// nucleotide binding/// protein binding/// protein kinase C activity/// transferase activity/// zinc ion binding	membrane fraction	Calcium signaling pathway/// Cholera – infection/// Fc epsilon RI signaling pathway/// Focal adhesion/// Gap junction/// GnRH signaling pathway/// Leukocyte transendothelial migration/// Long-term depression/// Long-term potentiation/// MAPK signaling pathway/// Natural killer cell mediated cytotoxicity/// Pathogenic Escherichia coli infection – EHEC/// Pathogenic Escherichia coli infection – EPEC/// Phosphatidylinositol signaling system/// Tight junction/// VEGF signaling pathway/// Wnt signaling pathway
204968_at	C6orf47	-0.086	---	---	---	---
206299_at	TMEM28	-0.086	---	---	integral to membrane	---
208036_at	OPN1SW	-0.086	signal transduction /// G-protein coupled receptor protein signaling pathway /// visual perception /// phototransduction	receptor activity /// G-protein coupled photoreceptor activity /// blue light photoreceptor activity	integral to plasma membrane	GPCRDB Class A Rhodopsin-like

208280_at	CDRT1	-0.086	---	---	---	---
235739_at	NR4A2	-0.086	regulation of transcription, DNA-dependent /// signal transduction /// antimicrobial humoral response (sensu Vertebrata)	transcription factor activity /// steroid hormone receptor activity /// ligand-dependent nuclear receptor activity	nucleus	Nuclear Receptors
236684_at	RQCD1	-0.086	sex differentiation	---	---	---
1564970_at	SETDB2	-0.085	chromatin modification	DNA binding /// methyltransferase activity /// zinc ion binding /// transferase activity /// histone-lysine N-methyltransferase activity	nucleus	---
208781_x_at	SNX3	-0.085	endocytosis /// intracellular signaling cascade /// protein transport	---	---	---
210193_at	MOBP	-0.085	neurogenesis	---	soluble fraction	---
240850_at	DYRK1A	-0.085	protein amino acid phosphorylation /// neurogenesis	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	nucleus	---
240929_at	---	-0.085	---	---	---	---
243935_at	FRAS1	-0.085	---	structural molecule activity	viral capsid	---
231410_at	---	-0.084	---	---	---	---
209411_s_at	GGA3	-0.083	protein complex assembly /// intracellular protein transport /// intra-Golgi transport	protein transporter activity /// ADP-ribosylation factor binding	Golgi stack /// Golgi trans face /// clathrin coat of trans-Golgi network vesicle	---
215970_at	ZP4	-0.083	fertilization (sensu metazoa)	receptor activity	extracellular matrix (sensu Metazoa)/// integral to membrane	---
1557710_at	---	-0.082	---	---	---	---

224842_at	SMG1	-0.082	mRNA catabolism, nonsense-mediated decay /// autophosphorylation /// phosphoinositide phosphorylation	inositol or phosphatidylinositol kinase activity /// protein serine/threonine kinase activity /// binding /// kinase activity /// phosphotransferase activity, alcohol group as acceptor	cytoplasm	---
1568735_at	DLGAP1	-0.081	cell-cell signaling /// synaptic transmission	---	membrane	---
227736_at	C10orf99	-0.081	---	---	---	---
240399_at	TRIO	-0.081	protein amino acid phosphorylation /// transmembrane receptor protein tyrosine phosphatase signaling pathway	protein serine/threonine kinase activity /// guanyl-nucleotide exchange factor activity /// GTPase activator activity /// ATP binding /// transferase activity	---	---
201533_at	CTNNB1	-0.08	transcription /// regulation of transcription from Pol II promoter /// cell adhesion /// Wnt receptor signaling pathway	signal transducer activity /// structural molecule activity /// protein binding	nucleus /// cytoskeleton /// plasma membrane /// intercellular junction	TGF Beta Signaling Pathway /// Wnt signaling
233382_at	LOC145845	-0.08	---	---	---	---
234899_at	LOC286436	-0.08	---	---	---	---
240359_at	C20orf71	-0.08	---	lipid binding	---	---
223573_s_at	PPP2R2C	-0.079	signal transduction	phosphoprotein phosphatase activity /// protein phosphatase type 2A regulator activity	protein phosphatase type 2A complex	Glycogen Metabolism
226928_x_at	SLC25A37	-0.079	transport	binding	integral to membrane	---

1557631_at	SLC25A4	-0.078	generation of precursor metabolites and energy/// mitochondrial genome maintenance/// mitochondrial transport/// transport	adenine transporter activity	integral to plasma membrane/// mitochondrial inner membrane	---
211870_s_at	PCDHA3	-0.078	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	integral to membrane	---
217950_at	NOSIP	-0.078	---	---	---	---
1554171_at	ZNF261	-0.077	development	DNA binding /// zinc ion binding	nucleus	---
1555938_x_at	VIM	-0.077	---	structural molecule activity /// structural constituent of cytoskeleton /// protein binding	cytoplasm /// intermediate filament	Striated muscle contraction
225337_at	ABHD2	-0.077	---	catalytic activity	integral to membrane	---
239371_at	FOXK2	-0.077	regulation of transcription from RNA polymerase II promoter	RNA polymerase II transcription factor activity/// sequence-specific DNA binding	nucleus	---
232230_at	C10orf75	-0.076	---	---	---	---
234339_s_at	GLTSCR2	-0.076	---	---	nucleus	---
240280_at	ARS2	-0.076	response to arsenic	nucleotide binding	---	---
207348_s_at	LIG3	-0.075	cytokinesis /// DNA replication /// DNA repair /// meiotic recombination /// spermatogenesis	DNA binding /// DNA ligase (ATP) activity /// ATP binding /// ligase activity	nucleus	---
212034_s_at	EXOC7	-0.075	exocytosis /// protein transport	---	exocyst	---
227092_at	---	-0.075	---	---	---	---
242343_x_at	ZNF518	-0.074	---	nucleic acid binding /// zinc ion binding	nucleus	---
1556220_at	---	-0.073	---	---	---	---
1558533_at	LOC124751	-0.073	regulation of transcription, DNA-dependent	nucleic acid binding	intracellular	---

1563223_a_at	FSHPRH1	-0.072	spermatogenesis /// female gamete generation /// sex differentiation	---	---	---
1568675_at	CHRNA10	-0.071	regulation of cell proliferation/// synaptic transmission, cholinergic/// calcium ion transport	receptor binding/// calcium channel activity/// calcium ion binding/// extracellular ligand-gated ion channel activity/// neurotransmitter receptor activity/// nicotinic acetylcholine-activated cation-selective channel activity	integral to membrane/// postsynaptic membrane	---
201642_at	IFNGR2	-0.071	cell surface receptor linked signal transduction /// response to virus /// response to pathogenic bacteria	receptor activity /// hematopoietin/interferon-class (D200-domain) cytokine receptor activity /// interferon-gamma receptor activity	integral to plasma membrane	---
207639_at	FZD9	-0.071	G-protein coupled receptor protein signaling pathway /// frizzled signaling pathway /// development /// neurogenesis	G-protein coupled receptor activity /// Wnt receptor activity	plasma membrane /// integral to membrane	Wnt signaling
211435_at	ZA20D3	-0.071	---	DNA binding /// zinc ion binding	---	---
33322_i_at	SFN	-0.07	regulation of cell cycle /// negative regulation of protein kinase activity /// signal transduction /// cell proliferation	protein kinase C inhibitor activity /// protein domain specific binding	extracellular space /// cytoplasm	Calcium regulation in cardiac cells /// Smooth muscle contraction
238959_at	LOC113251	-0.069	nuclear mRNA splicing, via spliceosome	nucleic acid binding	---	---
211556_at	MAPRE2	-0.068	cellular defense response /// signal transduction /// cell proliferation	microtubule binding	---	---

220844_at	TCEB3B	-0.068	regulation of transcription, DNA-dependent /// defense response	---	nucleus /// integral to membrane	---	
231797_at	SIX4	-0.068	regulation of transcription, DNA-dependent /// morphogenesis	transcription factor activity	nucleus	---	
240561_at	MBNL3	-0.068	development	nucleic acid binding	nucleus	---	
240798_at	CUTL1	-0.068	development/// negative regulation of transcription from RNA polymerase II promoter	RNA polymerase II transcription factor activity/// sequence-specific DNA binding	integral to membrane/// nucleus	---	
1556685_at	---	-0.067	---	---	---	---	
1559503_at	---	-0.067	---	---	---	---	
210805_x_at	RUNX1	-0.067	regulation of transcription, DNA-dependent /// development	transcription factor activity /// ATP binding	nucleus	---	
244839_at	TTN	-0.067	carbohydrate metabolism /// protein amino acid phosphorylation /// striated muscle contraction /// regulation of striated muscle contraction /// response to oxidative stress /// muscle development	peroxidase activity /// protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// hematopoietin/interferon-class (D200-domain) cytokine receptor activity /// structural molecule activity /// calmodulin binding /// ATP binding /// structural constituent of muscle /// cation transporter activity /// myosin binding	cytoskeleton /// membrane /// sarcomere /// Z disc	Striated muscle contraction		
221397_at	TAS2R10	-0.066	G-protein coupled receptor protein signaling pathway /// perception of taste	receptor activity /// G-protein coupled receptor activity /// taste receptor activity	integral to membrane	---	

236284_at	KIAA0146	-0.065	---	---	---	---	---
237397_at	HPN	-0.065	proteolysis and peptidolysis	chymotrypsin activity /// trypsin activity /// scavenger receptor activity /// hydrolase activity	integral to plasma membrane	---	---
1557673_at	---	-0.064	---	---	---	---	---
1562201_x_at	---	-0.063	---	---	---	---	---
239934_x_at	CDC27	-0.063	---	---	---	---	---
1562145_at	---	-0.062	---	---	---	---	---
221813_at	FBXO42	-0.062	ubiquitin cycle	---	---	---	---
226278_at	DKFZp313A2432	-0.062	---	---	---	---	---
237864_at	RAB22A	-0.062	endocytosis /// endosome organization and biogenesis /// small GTPase mediated signal transduction /// protein transport	GTPase activity /// protein binding /// GTP binding	early endosome /// plasma membrane	---	---
231222_at	PACS1	-0.061	---	---	Golgi apparatus	---	---
1568366_at	KIFAP3	-0.06	signal transduction/// microtubule-based process/// protein complex assembly	kinesin binding/// protein binding	endoplasmic reticulum/// kinesin II complex	---	---
201522_x_at	SNRPN /// SNURF	-0.06	mRNA processing	RNA binding /// pre-mRNA splicing factor activity	nucleus /// small nucleolar ribonucleoprotein complex /// nucleus	mRNA processing	
239479_x_at	---	-0.06	---	---	---	---	---
241597_at	RERE	-0.06	development/// regulation of transcription, DNA-dependent	protein binding/// sequence-specific DNA binding/// transcription factor activity/// zinc ion binding	nucleus	Dentatorubropallidoluysian atrophy (DRPLA)	

218866_s_at	POLR3K	-0.059	transcription /// RNA elongation /// regulation of transcription, DNA-dependent /// transcription from Pol III promoter	transcription factor activity /// DNA-directed RNA polymerase activity /// transferase activity	nucleus /// DNA-directed RNA polymerase III complex	RNA transcription Reactome	
210656_at	EED	-0.058	negative regulation of transcription	transcriptional repressor activity	nucleus	---	
238659_at	KIAA0141	-0.058	---	binding	---	---	
1556325_at	FILIP1	-0.057	muscle development	actin binding	cytoskeleton	---	
237272_at	---	-0.057	---	---	---	---	
220784_s_at	UTS2	-0.055	muscle contraction /// synaptic transmission /// regulation of blood pressure	hormone activity	extracellular region /// extracellular space	---	
225261_x_at	TH1L	-0.055	regulation of transcription, DNA-dependent /// negative regulation of transcription	---	nucleus	---	
231363_at	LOC149018	-0.055	---	---	---	---	
238330_s_at	M-RIP	-0.055	---	---	---	---	
240782_at	---	-0.055	---	---	---	---	
241985_at	JMY	-0.055	---	---	---	---	
231264_at	dJ39G22.2	-0.054	---	---	---	---	
204930_s_at	BNIP1	-0.053	apoptosis /// anti-apoptosis	---	integral to membrane	---	
225886_at	DDX5	-0.053	cell growth	RNA binding /// RNA helicase activity /// ATP binding /// ATP-dependent helicase activity	nucleus	---	
1552763_at	MGC26979	-0.052	---	---	---	---	

1566666_at	SUCLG2	-0.052	succinyl-CoA metabolism/// tricarboxylic acid cycle	ATP binding/// succinate-CoA ligase (GDP-forming) activity	mitochondrion	citrate cycle (TCA cycle)/// propanoate metabolism/// oxidative decarboxylation of pyruvate and TCA cycle
208920_at	SRI	-0.052	regulation of action potential /// transport /// intracellular sequestering of iron ion /// regulation of striated muscle contraction /// heart development /// muscle development /// regulation of heart contraction rate	receptor binding /// calcium channel regulator activity /// calcium ion binding	cytoplasm	---
231294_at	SIMP	-0.052	---	---	---	---
243346_at	LMOD3	-0.052	---	tropomyosin binding	cytoskeleton	---
209478_at	STRA13	-0.051	---	---	---	---
228331_at	C11orf31	-0.051	---	---	---	---
232593_at	LOC93082	-0.051	---	---	---	---
242576_x_at	PFAAP5	-0.051	---	---	---	---
1552873_s_at	CXYorf2	-0.05	---	---	---	---
215091_s_at	GTF3A	-0.05	regulation of transcription, DNA-dependent /// transcription from Pol III promoter /// rRNA transcription	DNA binding /// RNA polymerase III transcription factor activity /// RNA binding /// zinc ion binding	nucleus	---
209997_x_at	PCM1	-0.048	electron transport /// transcription	DNA binding /// DNA-directed RNA polymerase activity	pericentriolar material /// nucleus /// cytoplasm	---
242737_at	RAD51L1	-0.048	DNA repair /// meiotic recombination	damaged DNA binding /// ATP binding /// DNA-dependent ATPase activity	nucleus	---

205721_at	GFRA2	-0.046	transmembrane receptor protein tyrosine kinase signaling pathway	receptor activity /// glial cell line-derived neurotrophic factor receptor activity	extrinsic to membrane	---
208291_s_at	TH	-0.046	synaptic transmission /// aromatic amino acid family metabolism /// morphogenesis /// neurotransmitter biosynthesis /// catecholamine biosynthesis	monooxygenase activity /// tyrosine 3-monooxygenase activity /// iron ion binding	---	Biogenic Amine Synthesis /// Tyrosine metabolism
1561058_at	FLI1	-0.045	regulation of transcription, DNA-dependent /// hemostasis /// organogenesis	transcription factor activity	nucleus	---
224487_at	SPON1	-0.045	development/// cell adhesion	protein binding	extracellular matrix (sensu Metazoa)	---
239962_at	EPS15L1	-0.045	endocytosis	calcium ion binding	nucleus /// coated pit	---
243856_at	---	-0.044	---	---	---	---
221433_at	FGF21	-0.043	signal transduction /// cell-cell signaling	growth factor activity	extracellular region /// soluble fraction	---
228383_at	C9orf111	-0.043	---	catalytic activity /// nutrient reservoir activity	---	---
243299_at	VRK2	-0.043	protein amino acid phosphorylation	protein serine/threonine kinase activity /// ATP binding /// transferase activity	integral to membrane	---
213289_at	SATL1	-0.042	---	---	---	---
215120_s_at	SAMD4	-0.042	---	---	---	---
221725_at	WASF2	-0.041	---	---	---	---
226613_at	TBC1D10	-0.041	---	PDZ domain binding	microvillus	---
229032_at	KIAA0789	-0.041	---	sulfotransferase activity	---	---

233161_at	WWOX	-0.041	metabolism /// steroid metabolism	electron transporter activity /// protein binding /// oxidoreductase activity	---	---
204239_s_at	NNAT	-0.04	development /// brain development /// protein-lipoylation	auxiliary transport protein activity	---	---
220887_at	C14orf162	-0.04	---	---	---	---
225927_at	MAP3K1	-0.04	protein amino acid phosphorylation /// protein ubiquitination	magnesium ion binding /// protein serine/threonine kinase activity /// MAP kinase kinase kinase activity /// ubiquitin-protein ligase activity /// ATP binding /// zinc ion binding /// transferase activity	ubiquitin ligase complex	Apoptosis /// MAPK Cascade
224602_at	LOC401152	-0.038	---	---	---	---
201997_s_at	SPEN	-0.037	regulation of transcription, DNA-dependent	DNA binding /// RNA binding	nucleus	---
221693_s_at	MRPS18A	-0.037	protein biosynthesis	structural constituent of ribosome	intracellular /// mitochondrion /// mitochondrial small ribosomal subunit /// ribosome	---
1556060_a_at	KIAA1702	-0.036	phosphoenolpyruvate-dependent sugar phosphotransferase system	sugar porter activity	---	---
230015_at	LOC400621	-0.036	---	---	---	---
235445_at	POTE14	-0.036	---	protein binding	---	---
236127_at	SHARP	-0.036	regulation of transcription, DNA-dependent	DNA binding /// RNA binding	nucleus	---
208725_at	EIF2S2	-0.035	protein biosynthesis /// translational initiation	DNA binding /// RNA binding /// translation initiation factor activity	ribosome /// eukaryotic translation initiation factor 2 complex	Translation Factors

1554986_a_at	SNX19	-0.034	regulation of transcription, DNA-dependent /// intracellular signaling cascade /// protein transport	transcription factor activity	---	---
236014_at	C10orf48	-0.034	---	---	---	---
238494_at	TRAF3IP1	-0.034	---	receptor activity	---	---
207707_s_at	SEC13L1	-0.033	intracellular protein transport	---	---	---
209086_x_at	MCAM	-0.033	cell adhesion /// morphogenesis	protein binding	integral to plasma membrane	---
220032_at	FLJ21986	-0.033	---	---	---	---
206633_at	CHRNA1	-0.031	ion transport /// muscle contraction /// signal transduction /// synaptic transmission	nicotinic acetylcholine-activated cation-selective channel activity /// ion channel activity /// extracellular ligand-gated ion channel activity /// acetylcholine receptor activity	nicotinic acetylcholine-gated receptor-channel complex /// integral to membrane /// postsynaptic membrane	---
217074_at	SMOX	-0.031	electron transport	oxidoreductase activity	---	---
223182_s_at	AGPAT3	-0.031	metabolism /// phospholipid biosynthesis	1-acylglycerol-3-phosphate O-acyltransferase activity /// acyltransferase activity /// transferase activity	integral to membrane	Glycerolipid metabolism /// Glycerophospholipid metabolism
1555612_s_at	G6PC	-0.03	glycogen metabolism /// glycogen biosynthesis /// glucose metabolism /// transport	glucose-6-phosphatase activity /// transporter activity /// sugar porter activity /// hydrolase activity	endoplasmic reticulum /// microsome /// integral to membrane	Glycolysis and Gluconeogenesis /// Glycolysis / Gluconeogenesis /// Galactose metabolism /// Starch and sucrose metabolism
201622_at	SND1	-0.029	regulation of transcription, DNA-dependent	nucleic acid binding /// nuclease activity	nucleus	---

237356_at	ADAMTS 18	-0.029	proteolysis and peptidolysis	metalloendopeptidase activity /// peptidase activity /// hydrolase activity	DNA binding	nucleus	extracellular matrix (sensu Metazoa) /// extracellular matrix	---
212614_at	ARID5B	-0.027	regulation of transcription, DNA-dependent	---	---	---	---	---
222417_s_at	SNX5	-0.026	intracellular signaling cascade	---	---	---	---	---
224679_at	MESDC2	-0.026	mesoderm development	---	---	---	---	---
228565_at	KIAA1804	-0.025	protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	---	---	---	---
201561_s_at	CLSTN1	-0.024	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	---	membrane /// integral to membrane	---	---
212179_at	C6orf111	-0.024	---	---	---	---	---	---
227743_at	MYO15B	-0.024	---	binding	---	cytoskeleton	---	---
1568722_at	TTC7B	-0.023	---	---	---	---	---	---
202249_s_at	WDR42A	-0.023	---	---	---	---	---	---
215175_at	PCNX	-0.023	---	---	---	integral to membrane	---	---

217575_s_at	SOS2	-0.023	small GTPase mediated signal transduction	protein binding/// DNA binding/// guanyl-nucleotide exchange factor activity	---	Dorso-ventral axis formation/// Focal adhesion /// Gap junction /// Insulin signaling pathway /// Jak-STAT signaling pathway /// MAPK signaling pathway /// Natural killer cell mediated cytotoxicity /// Regulation of actin cytoskeleton /// T cell receptor signaling pathway
1561521_at	S100B	-0.022	energy reserve metabolism /// calcium ion homeostasis /// induction of apoptosis /// axonogenesis /// central nervous system development /// learning and/or memory /// cell proliferation /// regulation of cytokine biosynthesis /// positive regulation of complement activation /// astrocyte activation /// hyperphosphorylation /// regulation of long-term neuronal synaptic plasticity	calcium ion binding /// zinc ion binding /// kinase inhibitor activity /// protein homodimerization activity /// S100 beta binding /// S100 alpha binding /// tau protein binding	extracellular region /// nucleus /// cytoplasm	---
209103_s_at	UFD1L	-0.022	ubiquitin-dependent protein catabolism	---	---	---

216894_x_at	CDKN1C	-0.021	regulation of cyclin dependent protein kinase activity /// G1 phase of mitotic cell cycle /// cell cycle /// cell cycle arrest /// negative regulation of cell proliferation /// negative regulation of cell cycle	cyclin-dependent protein kinase inhibitor activity			G1 to S cell cycle Reactome
220166_at	CNNM1	-0.021	fatty acid biosynthesis	---	---	---	---
1553032_at	IL31RA	-0.02	MAPKKK cascade /// anti-apoptosis /// defense response /// transmembrane receptor protein tyrosine kinase signaling pathway /// JAK-STAT cascade /// positive regulation of cell proliferation /// cytokine and chemokine mediated signaling pathway /// macrophage differentiation /// positive regulation of tyrosine phosphorylation of Stat3 protein /// positive regulation of tyrosine phosphorylation of Stat5 protein /// homeostasis /// negative regulation of macrophage activation /// positive regulation of transcription, DNA-dependent	transcription coactivator activity /// receptor activity /// hematopoietin/interferon-class (D200-domain) cytokine receptor activity /// protein kinase binding /// cytokine binding	integral to membrane	---	
225895_at	SYNPO2	-0.02	---	actin binding /// protein binding	nucleus	---	
1566033_at	---	-0.019	---	---	---	---	
207255_at	LEPR	-0.019	energy reserve metabolism /// cell surface receptor linked signal transduction /// development	hematopoietin/interferon-class (D200-domain) cytokine receptor activity	integral to plasma membrane	---	

214075_at	SCIRP10	-0.019	---	---	---	---
1553560_at	VN1R4	-0.016	G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity /// receptor activity /// pheromone receptor activity	integral to membrane	---
1560696_x_at	QTRTD1	-0.016	tRNA processing /// queuosine biosynthesis	queuine tRNA-ribosyltransferase activity /// transferase activity, transferring glycosyl groups	---	---
219550_at	ROBO3	-0.016	chemotaxis /// neurogenesis	receptor activity	integral to membrane	---
222880_at	AKT3	-0.016	protein amino acid phosphorylation /// signal transduction	protein serine/threonine kinase activity /// ATP binding /// transferase activity	---	Integrin-mediated cell adhesion /// S1P Signaling
1557283_at	ZNF519	-0.015	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---

1559638_at	PIK3CD	-0.015	protein amino acid phosphorylation /// signal transduction	inositol or phosphatidylinositol kinase activity /// phosphatidylinositol-4,5-bisphosphate 3-kinase activity /// transferase activity	phosphoinositide 3-kinase complex	Apoptosis /// B cell receptor signaling pathway /// Fc epsilon RI signaling pathway /// Focal adhesion /// Inositol phosphate metabolism /// Insulin signaling pathway /// Jak-STAT signaling pathway /// Leukocyte transendothelial migration /// Natural killer cell mediated cytotoxicity /// Phosphatidylinositol signaling system /// Regulation of actin cytoskeleton /// T cell receptor signaling pathway /// Toll-like receptor signaling pathway /// Type II diabetes mellitus /// VEGF signaling pathway /// mTOR signaling pathway
1562653_at	---	-0.014	---	---	---	---
200009_at	GDI2	-0.014	protein transport /// regulation of GTPase activity	RAB GDP-dissociation inhibitor activity /// GTPase activator activity	---	---
216170_at	CHCHD3	-0.014	---	---	mitochondrion	---
1555110_a_at	KLHL3	-0.013	---	actin binding /// structural molecule activity /// protein binding	cytoskeleton	---

213228_at	PDE8B	-0.013	signal transduction /// cyclic nucleotide metabolism	magnesium ion binding /// 3',5'-cyclic-nucleotide phosphodiesterase activity /// signal transducer activity /// hydrolase activity /// manganese ion binding	---		G Protein Signaling
1555145_at	LOC126731	-0.012	---	---	---		---
1562581_at	LOC254028	-0.012	---	---	---		---
205197_s_at	ATP7A	-0.012	copper ion transport /// metabolism /// mercury ion transport /// metal ion transport	magnesium ion binding /// copper-exporting ATPase activity /// copper ion binding /// ATP binding /// mercury ion transporter activity /// hydrolase activity /// hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances /// metal ion binding /// metal ion transporter activity	Golgi apparatus /// integral to plasma membrane /// membrane		Oxidative phosphorylation
207262_at	APOF	-0.012	lipid metabolism /// lipid transport /// cholesterol metabolism	receptor binding /// lipid transporter activity /// high-density lipoprotein binding /// cholesterol binding	extracellular space		---
1438_at	EPHB3	-0.01	protein amino acid phosphorylation /// signal transduction /// transmembrane receptor protein tyrosine kinase signaling pathway	protein-tyrosine kinase activity /// receptor activity /// ephrin receptor activity /// ATP binding /// transferase activity	integral to plasma membrane /// membrane		---
1554586_at	RHOBTB2	-0.01	small GTPase mediated signal transduction	protein binding /// GTP binding	---		---

203286_at	RNF44	-0.01	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	transcription factor activity	nucleus	ubiquitin ligase complex
217310_s_at	FOXJ3	-0.01	regulation of transcription, DNA-dependent	---	---	---	---
1557044_at	---	-0.008	---	---	---	---	---
201157_s_at	NMT1	-0.008	N-terminal protein myristoylation /// protein-lipoylation	glycylpeptide N-tetradecanoyltransferase activity /// acyltransferase activity /// transferase activity	---	---	---
238342_at	LOC231117	-0.008	---	---	---	---	---
1555461_at	---	-0.007	---	---	---	---	---
205134_s_at	NUFIP1	-0.007	RNA processing	RNA binding /// protein binding /// zinc ion binding	nucleus	---	---
216781_at	KIAA1751	-0.007	---	---	---	---	---
235056_at	ETV6	-0.007	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---	Circadian Exercise
243311_at	DEFB32	-0.007	---	---	---	---	---
223688_s_at	LY6K	-0.006	---	---	---	---	---
1555174_at	---	-0.005	---	---	---	---	---
1557228_at	EHBP1L1	-0.005		---	---	---	---
222352_at	FBXO31	-0.005	ubiquitin cycle	---	---	---	---
229683_s_at	KCTD15	-0.005	---	---	---	---	---
1560913_at	---	-0.004	---	---	---	---	---
214855_s_at	GARNL1	-0.004	---	GTPase activator activity	nucleus	---	---

230101_at	CXCL2	-0.004	inflammatory response/// G-protein coupled receptor protein signaling pathway/// chemotaxis/// sensory perception	chemokine activity	extracellular space/// soluble fraction	Cytokine-cytokine Receptor Interaction
218649_x_at	SDCCAG1	-0.003	---	---	nucleus	---
219042_at	LZTS1	-0.003	cell cycle /// negative regulation of cell cycle	transcription factor activity	cytoplasm /// membrane	---
222143_s_at	FLJ22405	-0.002	protein amino acid dephosphonylation	phosphoprotein phosphatase activity	---	---
224036_s_at	C7orf2	-0.002	---	---	---	---
1555224_at	---	-0.001	---	---	---	---
215260_s_at	TCF3	-0.001	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
231937_at	---	-0.001	---	---	---	---
233584_at	---	-0.001	---	---	---	---
235711_at	PURB	-0.001	---	---	---	---

TABLE 9: Gene List of Up and Downregulated Genes in the Spleen of Baboon (0.33% DHA)

Affy Probe ID	Gene Symbol	Differential Expression (log2 Values)	Biological Process	Molecular Function	Cellular Component	Pathway
230983_at	BCNP1	0.859	---	---	---	---
239122_at	IL24	0.62	apoptosis/// immune response	cytokine activity	extracellular space	Cytokine-Cytokine Receptor Interaction, JAK-STAT signaling pathway
201666_at	TIMP1	0.557	development /// positive regulation of cell proliferation /// negative regulation of membrane protein ectodomain proteolysis	metalloendopeptidase inhibitor activity	extracellular matrix (sensu Metazoa)	MAPK Cascade /// Matrix Metalloproteinases
218454_at	FLJ22662	0.539	---	---	---	---
210839_s_at	ENPP2	0.529	phosphate metabolism /// cell motility /// chemotaxis /// G-protein coupled receptor protein signaling pathway /// nucleotide metabolism	nucleic acid binding /// endonuclease activity /// phosphodiesterase I activity /// nucleotide diphosphatase activity /// transcription factor binding /// hydrolase activity	integral to plasma membrane	---
209540_at	IGF1	0.515	skeletal development /// DNA replication /// cell motility /// signal transduction /// Ras protein signal transduction /// muscle development /// physiological process /// perception of sound /// positive regulation of cell proliferation /// glycolate metabolism	insulin-like growth factor receptor binding /// hormone activity /// growth factor activity /// prothoracicotrophic hormone activity	extracellular region	---

212387_at	TCF4	0.502	regulation of transcription from Pol II promoter	DNA binding /// RNA polymerase II transcription factor activity	nucleus	---
218679_s_at	VPS28	0.499	protein transport	---	---	---
1556325_at	FILIP1	0.494	muscle development	actin binding	cytoskeleton	---
229566_at	LOC440449	0.492	---	---	---	---
214499_s_at	BCLAF1	0.475	regulation of transcription, DNA-dependent /// induction of apoptosis	DNA binding /// transcriptional repressor activity	nucleus	---
209377_s_at	HMGN3	0.455	---	DNA binding /// thyroid hormone receptor binding	chromatin /// nucleus	---
202018_s_at	LTF	0.453	transport /// iron ion transport /// iron ion homeostasis /// humoral immune response /// defense response to bacteria	serine-type endopeptidase activity /// ferric iron binding	extracellular space	---
215091_s_at	GTF3A	0.447	regulation of transcription, DNA-dependent /// transcription from Pol III promoter /// rRNA transcription	DNA binding /// RNA polymerase III transcription factor activity /// RNA binding /// zinc ion binding	nucleus	---
201105_at	LGALS1	0.435	apoptosis /// positive regulation of I-kappaB kinase/NF-kappaB cascade	signal transducer activity /// sugar binding	---	---
208540_x_at	S100A11	0.433	negative regulation of DNA transcription /// negative regulation of cell proliferation	calcium ion binding	cytoplasm/// nucleus	---

225927_at	MAP3K1	0.422	protein amino acid phosphorylation /// protein ubiquitination	magnesium ion binding /// protein serine/threonine kinase activity /// MAP kinase kinase kinase activity /// ubiquitin-protein ligase activity /// ATP binding /// zinc ion binding /// transferase activity	ubiquitin ligase complex	Apoptosis /// MAPK Cascade
208816_x_at	ANXA2P2	0.418	---	---	---	---
201200_at	CREG1	0.414	regulation of cell growth /// regulation of transcription from Pol II promoter /// development /// cell proliferation	RNA polymerase II transcription factor activity /// transcription corepressor activity	---	---
212071_s_at	SPTBN1	0.405		actin binding /// structural constituent of cytoskeleton /// calmodulin binding	cytoskeleton /// spectrin /// membrane	---
219133_at	FLJ20604	0.403	fatty acid biosynthesis	catalytic activity	---	---
218396_at	VPS13C	0.395	---	---	---	---
203513_at	FLJ21439	0.388	aromatic compound metabolism	catalytic activity /// ferric iron binding	---	---
223620_at	GPR34	0.382	G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity /// purinergic nucleotide receptor activity, G-protein coupled	integral to plasma membrane	GPCRDB Class A Rhodopsin-like2
204638_at	ACP5	0.38	---	acid phosphatase activity /// hydrolase activity	lysosome /// integral to membrane	gamma-Hexachlorocyclohexane degradation /// Riboflavin metabolism

217757_at	A2M	0.378	intracellular protein transport /// protein homooligomerization	serine-type endopeptidase inhibitor activity /// protein carrier activity /// wide-spectrum protease inhibitor activity /// enzyme binding /// interleukin-8 binding /// interleukin-1 binding /// tumor necrosis factor binding	extracellular region	---
223295_s_at	LUC7L	0.372	---	---	---	---
227408_s_at	SNX25	0.369	intracellular signaling cascade /// protein transport	signal transducer activity	---	---
200901_s_at	M6PR	0.365	transport /// receptor mediated endocytosis /// endosome to lysosome transport	transmembrane receptor activity /// transporter activity	lysosome /// integral to plasma membrane	---
217562_at	DBCCR1L	0.362	---	---	---	---
210427_x_at	ANXA2	0.359	skeletal development	phospholipase inhibitor activity /// calcium ion binding /// calcium-dependent phospholipid binding /// cytoskeletal protein binding	soluble fraction /// plasma membrane	Prostaglandin synthesis regulation
200972_at	TM4SF8	0.356	cell motility /// cell proliferation	---	integral to membrane	---
224494_x_at	DHRS10	0.356	metabolism	oxidoreductase activity	---	---
233449_at	---	0.356	---	---	---	---
202033_s_at	RB1CC1	0.35	---	kinase activity	---	---
214813_at	ZNF75	0.347	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
242273_at	---	0.346	---	---	---	---

205663_at	PCBP3	0.34	mRNA metabolism	DNA binding /// RNA binding	nucleus /// ribonucleoprotein complex	---
217779_s_at	PNRC2	0.338	---	receptor activity	---	---
204326_x_at	MT1X	0.337	response to metal ion	metal ion binding	---	---
222638_s_at	C6orf35	0.337	---	---	---	---
1556186_s_at	KIAA0090	0.336	---	---	---	---
200685_at	SFRS11	0.335	nuclear mRNA splicing, via spliceosome /// RNA splicing	RNA binding /// pre-mRNA splicing factor activity	nucleus	---
209307_at	SWAP70	0.332	---	calcium ion binding	---	---
220827_at	CACNA1C	0.332	cation transport /// calcium ion transport /// regulation of heart contraction rate	voltage-gated calcium channel activity /// cation channel activity /// calcium ion binding	voltage-gated calcium channel complex /// integral to membrane	Calcium regulation in cardiac cells
224602_at	LOC401152	0.325	---	---	---	---
232148_at	NSMAF	0.325	ceramide metabolism /// signal transduction	receptor signaling protein activity	soluble fraction /// cytoplasm	---
210908_s_at	PFDN5	0.323	regulation of transcription, DNA-dependent /// protein folding	transcription corepressor activity /// protein binding /// unfolded protein binding	nucleus /// prefoldin complex	---
213503_x_at	ANXA2	0.323	skeletal development	phospholipase inhibitor activity /// calcium ion binding /// calcium-dependent phospholipid binding /// cytoskeletal protein binding	soluble fraction /// plasma membrane	Prostaglandin synthesis regulation
1558700_s_at	LOC339324	0.321	---	---	---	---

212624_s_at	CHN1	0.319	intracellular signaling cascade	SH3/SH2 adaptor protein activity /// GTPase activator activity /// diacylglycerol binding	---	---
228951_at	FLJ10815	0.316	transport /// amino acid transport	amino acid-polyamine transporter activity	integral to membrane	---
230980_x_at	---	0.316	---	---	---	---
1570445_a_at	LOC441117	0.315	---	---	---	---
233408_at	DEPDC2	0.315	intracellular signaling cascade	guanyl-nucleotide exchange factor activity /// protein binding	---	---
219007_at	NUP43	0.313	---	porin activity	integral to membrane /// outer membrane	---
207417_s_at	ZNF177	0.312	negative regulation of transcription from Pol II promoter /// regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
222417_s_at	SNX5	0.312	intracellular signaling cascade	---	---	---
234734_s_at	TNRC6A	0.312	nuclear mRNA splicing, via spliceosome	nucleic acid binding	---	---
226383_at	FLJ38968	0.311	---	---	---	---
208694_at	PRKDC	0.31	double-strand break repair /// DNA recombination /// protein modification	DNA binding /// protein serine/threonine kinase activity /// binding /// transferase activity	nucleus	Cell cycle
224967_at	UGCG	0.31	glucosylceramide biosynthesis /// glycosphingolipid biosynthesis /// epidermis development	ceramide glucosyltransferase activity /// transferase activity, transferring glycosyl groups	extracellular space /// membrane fraction /// endoplasmic reticulum /// integral to membrane	Glycosphingolipid metabolism

201648_at	JAK1	0.308	protein amino acid phosphorylation /// intracellular signaling cascade	protein-tyrosine kinase activity /// Janus kinase activity /// ATP binding /// transferase activity	cytoskeleton	TGF Beta Signaling Pathway
212179_at	C6orf111	0.306	---	---	---	---
214825_at	---	0.306	---	---	---	---
218579_s_at	DHX35	0.306	---	nucleic acid binding /// ATP binding /// ATP-dependent helicase activity /// hydrolase activity	---	---
226132_s_at	FLJ31434	0.304	---	---	---	---
231517_at	LOC440590	0.303	---	---	---	---
216894_x_at	CDKN1C	0.3	regulation of cyclin dependent protein kinase activity /// G1 phase of mitotic cell cycle /// cell cycle /// cell cycle arrest /// negative regulation of cell proliferation /// negative regulation of cell cycle	cyclin-dependent protein kinase inhibitor activity	nucleus	G1 to S cell cycle Reactome
234339_s_at	GLTSCR2	0.299	---	---	nucleus	---
200009_at	GDI2	0.298	protein transport /// regulation of GTPase activity	RAB GDP-dissociation inhibitor activity /// GTPase activator activity	---	---
220507_s_at	UPB1	0.298	nitrogen compound metabolism	beta-ureidopropionase activity /// hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	---	---
222588_s_at	FLJ10726	0.298	---	---	---	---

214980_at	UBE3A	0.297	proteolysis and peptidolysis /// ubiquitin-dependent protein catabolism /// ubiquitin cycle /// brain development	ubiquitin conjugating enzyme activity /// ubiquitin-protein ligase activity /// ligase activity	intracellular /// nucleus	---
214250_at	NUMA1	0.294	mitotic anaphase /// nuclear organization and biogenesis	structural molecule activity	nucleus /// spindle microtubule	---
225266_at	KIAA0924	0.294	---	nucleic acid binding /// zinc ion binding	nucleus	---
200603_at	PRKAR1A	0.293	regulation of transcription from Pol II promoter /// protein amino acid phosphorylation /// intracellular signaling cascade	cAMP-dependent protein kinase regulator activity /// 3',5'-cAMP binding	cAMP-dependent protein kinase complex	G Protein Signaling /// Calcium regulation in cardiac cells /// Smooth muscle contraction
37145_at	GNLY	0.292	xenobiotic metabolism /// cellular defense response /// defense response to bacteria /// defense response to fungi	---	extracellular space	---
213111_at	PIP5K3	0.291	protein folding /// intracellular signaling cascade	ATP binding /// zinc ion binding /// kinase activity /// 1-phosphatidylinositol-4-phosphate 5-kinase activity /// transferase activity /// unfolded protein binding	---	---
204968_at	C6orf47	0.289	---	---	---	---
225898_at	WDR54	0.286	---	---	---	---

201590_x_at	ANXA2	0.285	skeletal development	phospholipase inhibitor activity /// calcium ion binding /// calcium-dependent phospholipid binding /// cytoskeletal protein binding	soluble fraction /// plasma membrane	Prostaglandin synthesis regulation
1554766_s_at	---	0.284	---	---	---	---
216348_at	RPS17	0.283	protein biosynthesis	RNA binding/// structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukaryota) /// Ribosome	Ribosome
222686_s_at	FLJ11151	0.282	---	hydrolase activity	---	---
225780_at	RSC1A1	0.282	transport	ion channel inhibitor activity	---	---
238712_at	---	0.282	---	---	---	---
206983_at	CCR6	0.281	cell motility /// chemotaxis /// humoral immune response /// cellular defense response /// signal transduction /// G-protein coupled receptor protein signaling pathway /// positive regulation of cytosolic calcium ion concentration /// antimicrobial humoral response (sensu Vertebrata)	rhodopsin-like receptor activity /// receptor activity /// C-C chemokine receptor activity	integral to plasma membrane	Peptide GPCRs /// GPCRDB Class A Rhodopsin-like
214855_s_at	GARNL1	0.281	---	GTPase activator activity	nucleus	---
230444_at	---	0.281	---	---	---	---
207857_at	LILRA2	0.28	immune response	receptor activity	integral to membrane	---

226978_at	PPARA	0.279	generation of precursor metabolites and energy /// transcription /// regulation of transcription, DNA-dependent /// transcription from Pol II promoter /// lipid metabolism /// fatty acid metabolism	transcription factor activity /// steroid hormone receptor activity /// ligand-dependent nuclear receptor activity	nucleus	Nuclear Receptors
1565282_at	---	0.276	---	---	---	---
225363_at	PTEN	0.276	---	---	---	---
213231_at	DMWD	0.275	meiosis	---	---	---
205197_s_at	ATP7A	0.273	copper ion transport /// metabolism /// mercury ion transport /// metal ion transport	magnesium ion binding /// copper-exporting ATPase activity /// copper ion binding /// ATP binding /// mercury ion transporter activity /// hydrolase activity /// hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances /// metal ion binding /// metal ion transporter activity	Golgi apparatus /// integral to plasma membrane /// membrane	Oxidative phosphorylation
213102_at	ACTR3	0.273	cell motility	structural constituent of cytoskeleton	Arp2/3 protein complex	---
225637_at	FLJ20186	0.273	intracellular signaling cascade /// protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---

201533_at	CTNNB1	0.271	transcription /// regulation of transcription from Pol II promoter /// cell adhesion /// Wnt receptor signaling pathway	signal transducer activity /// structural molecule activity /// protein binding	nucleus /// cytoskeleton /// plasma membrane /// intercellular junction	TGF Beta Signaling Pathway /// Wnt signaling	
218866_s_at	POLR3K	0.271	transcription /// RNA elongation /// regulation of transcription, DNA-dependent /// transcription from Pol III promoter	transcription factor activity /// DNA-directed RNA polymerase activity /// transferase activity	nucleus /// DNA-directed RNA polymerase III complex	RNA transcription Reactome	
225675_at	C14orf101	0.271	---	---	integral to membrane	---	
227706_at	SPIRE2	0.271	---	---	---	---	
230148_at	USP34	0.271	ubiquitin-dependent protein catabolism /// ubiquitin cycle	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity	---	---	
208858_s_at	MBC2	0.27	---	---	---	---	
228538_at	FLJ45880	0.269	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---	
208781_x_at	SNX3	0.268	endocytosis /// intracellular signaling cascade /// protein transport	---	---	---	
226741_at	LOC51234	0.268	---	---	---	---	
44790_s_at	C13orf18	0.268	---	protein phosphatase inhibitor activity	---	---	

202725_at	POLR2A	0.267	transcription /// transcription, DNA-dependent /// regulation of transcription, DNA-dependent /// transcription from Pol II promoter	DNA binding /// DNA-directed RNA polymerase activity /// protein binding /// transferase activity	nucleus /// DNA-directed RNA polymerase II, core complex	mRNA processing Reactome /// RNA transcription Reactome /// Purine metabolism /// Pyrimidine metabolism /// RNA polymerase
211703_s_at	BBP	0.267	---	---	---	---
230130_at	SLIT2	0.267	nervous system development /// G-protein coupled receptor protein signaling pathway /// cell differentiation /// chemotaxis /// glial cell migration /// induction of negative chemotaxis /// mesoderm migration /// motor axon guidance /// neuron recognition /// positive regulation of axonogenesis /// sensory perception /// sensory perception of smell /// ureteric bud development	calcium ion binding /// follicle stimulating hormone receptor activity /// receptor binding	extracellular space /// integral to membrane	Axon guidance
209390_at	TSC1	0.266	cell adhesion /// Rho protein signal transduction /// negative regulation of cell cycle	---	---	---
201157_s_at	NMT1	0.264	N-terminal protein myristoylation /// protein-lipoylation	glycylpeptide N-tetradecanoyltransferase activity /// acyltransferase activity /// transferase activity	---	---

202114_at	SNX2	0.264	intracellular protein transport /// endocytosis /// intracellular signaling cascade	protein transporter activity	---	---
239316_at	MGC2477	0.264	---	---	---	---
207785_s_at	RBPSUH	0.263	DNA recombination /// regulation of transcription, DNA-dependent /// transcription from Pol II promoter	recombinase activity /// DNA binding /// RNA polymerase II transcription factor activity	nucleus	---
212848_s_at	C9orf3	0.263	proteolysis and peptidolysis	aminopeptidase activity /// membrane alanyl aminopeptidase activity /// metallopeptidase activity	---	---
205477_s_at	AMBP	0.261	transport /// cell adhesion /// pregnancy /// anti-inflammatory response /// heme catabolism /// negative regulation of JNK cascade /// negative regulation of immune response	transporter activity /// calcium channel inhibitor activity /// IgA binding /// heme binding /// trypsin inhibitor activity /// plasmin inhibitor activity /// protein homodimerization activity /// calcium oxalate binding	extracellular region /// plasma membrane	---

226771_at	ATP8B2	0.261	cation transport /// metabolism	magnesium ion binding /// catalytic activity /// phospholipid-translocating ATPase activity /// ATP binding /// ATPase activity /// ATP coupled to transmembrane movement of ions, phosphorylative mechanism /// hydrolase activity /// ATPase activity	membrane /// integral to membrane	---
212917_x_at	RECQL	0.26	DNA repair	DNA binding /// ATP-dependent DNA helicase activity /// ATP binding /// hydrolase activity	nucleus	---
1561650_s_at	LOC285692	0.259	---	---	---	---
214004_s_at	VGLL4	0.257	regulation of transcription, DNA-dependent	---	nucleus	---
218244_at	NOL8	0.257	nuclear mRNA splicing, via spliceosome	nucleic acid binding	---	---
210840_s_at	IQGAP1	0.256	signal transduction /// small GTPase mediated signal transduction	GTPase inhibitor activity /// Ras GTPase activator activity /// calmodulin binding	actin filament	G13 Signaling Pathway
224986_s_at	PDPK1	0.256	protein amino acid phosphorylation /// insulin receptor signaling pathway /// actin cytoskeleton organization and biogenesis	protein serine/threonine kinase activity /// 3-phosphoinositide-dependent protein kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	cytoplasm /// plasma membrane	Integrin-mediated cell adhesion
215679_at	---	0.254	---	---	---	---

202386_s_at	LKAP	0.252	nuclear mRNA splicing, via spliceosome	nucleic acid binding	---	---
221861_at	---	0.252	---	---	---	---
203950_s_at	CLCN6	0.25	ion transport /// chloride transport /// regulation of cell volume /// signal transduction	voltage-gated chloride channel activity	membrane fraction /// integral to plasma membrane	---
207040_s_at	ST13	0.25	protein folding	binding /// protein binding, bridging /// unfolded protein binding	cytoplasm	---
218648_at	TORC3	0.25	---	---	---	---
1558123_at	FLJ35390	0.249	---	---	---	---
224841_x_at	GAS5	0.248	---	---	---	---
234364_at	IGLC1	0.248	---	---	---	---
231179_at	IHPK3	0.246	apoptosis/// DNA repair/// calcium-mediated signaling /// phosphatidylinositol metabolism/// positive regulation of DNA recombination /// protein amino acid phosphorylation /// vesicle-mediated transport	inositol hexakisphosphate kinase activity/// inositol trisphosphate 3-kinase activity /// transferase activity	cytoplasm/// nucleus	---
215744_at	FUS	0.245	---	DNA binding /// RNA binding /// protein binding /// zinc ion binding	nucleus	mRNA processing
242737_at	RAD51L1	0.244	DNA repair /// meiotic recombination	damaged DNA binding /// ATP binding /// DNA-dependent ATPase activity	nucleus	---

228441_s_at	PET112L	0.243	protein biosynthesis	translation factor activity, nucleic acid binding /// ligase activity /// glutamyl-tRNA(Gln) amidotransferase activity	mitochondrion	---
200609_s_at	WDR1	0.242	perception of sound	actin binding /// protein binding	cytoskeleton	Hypertrophy model
201910_at	FARP1	0.242	cell adhesion	Rho guanyl-nucleotide exchange factor activity /// cytoskeletal protein binding	cytoplasm /// cytoskeleton /// membrane	---
214932_at	KIDINS220	0.241	carbon utilization by fixation of carbon dioxide	ribulose-bisphosphate carboxylase activity	ribulose bisphosphate carboxylase complex (sensu Magnoliophyta)	---
1559437_at	LOC392084	0.24	---	---	---	---
203627_at	IGF1R	0.239	regulation of cell cycle /// protein amino acid phosphorylation /// anti-apoptosis /// signal transduction /// positive regulation of cell proliferation /// insulin receptor signaling pathway	receptor activity /// epidermal growth factor receptor activity /// insulin-like growth factor receptor activity /// protein binding /// ATP binding /// transferase activity	integral to membrane	---
227823_at	RGAG4	0.239	---	---	---	---
219384_s_at	ADAT1	0.238	tRNA processing	RNA binding /// tRNA specific adenosine deaminase activity	---	---
234936_s_at	KIAA1345	0.238	---	---	---	---
244467_at	LOC440829	0.238	---	---	---	---
228394_at	STK10	0.237	protein amino acid phosphorylation	protein serine/threonine kinase activity /// ATP binding /// transferase activity	---	---

202507_s_at	SNAP25	0.236	neurotransmitter uptake /// synaptic transmission /// neurotransmitter secretion /// synaptic vesicle docking during exocytosis	---	synaptosome	---
207132_x_at	PFDN5	0.236	regulation of transcription, DNA-dependent /// protein folding	transcription corepressor activity /// protein binding /// unfolded protein binding	nucleus /// prefoldin complex	---
33322_i_at	SFN	0.236	regulation of cell cycle /// negative regulation of protein kinase activity /// signal transduction /// cell proliferation	protein kinase C inhibitor activity /// protein domain specific binding	extracellular space /// cytoplasm	Calcium regulation in cardiac cells /// Smooth muscle contraction
210137_s_at	DCTD	0.235	pyrimidine nucleotide metabolism /// nucleotide biosynthesis	dCMP deaminase activity /// zinc ion binding /// hydrolase activity	---	Pyrimidine metabolism /// Type II secretion system
212614_at	ARID5B	0.234	regulation of transcription, DNA-dependent	DNA binding	nucleus	---
209195_s_at	ADCY6	0.233	cAMP biosynthesis /// intracellular signaling cascade	magnesium ion binding /// adenylate cyclase activity /// guanylate cyclase activity /// lyase activity	integral to membrane	G Protein Signaling /// Calcium regulation in cardiac cells /// Smooth muscle contraction /// Purine metabolism
224744_at	IMPA3	0.232	---	inositol or phosphatidylinositol phosphatase activity /// hydrolase activity	---	---
203842_s_at	MAPRE3	0.23	---	small GTPase regulatory/interacting protein activity	---	---

218098_at	ARFGEF2	0.23	exocytosis	guanyl-nucleotide exchange factor activity /// binding	---	---
201522_x_at	SNRPN /// SNURF	0.229	mRNA processing	RNA binding /// pre-mRNA splicing factor activity	nucleus /// small nucleolar ribonucleoprotein complex /// nucleus	mRNA processing
234609_at	PRKCE	0.228	protein amino acid phosphorylation /// induction of apoptosis /// intracellular signaling cascade	protein kinase C activity /// signal transducer activity /// ATP binding /// transferase activity /// diacylglycerol binding	membrane fraction	G Protein Signaling /// Wnt signaling /// Calcium regulation in cardiac cells /// Smooth muscle contraction
201642_at	IFNGR2	0.226	cell surface receptor linked signal transduction /// response to virus /// response to pathogenic bacteria	receptor activity /// hematopoietin/interferon-class (D200-domain) cytokine receptor activity /// interferon-gamma receptor activity	integral to plasma membrane	---
202012_s_at	EXT2	0.225	skeletal development /// glycosaminoglycan biosynthesis /// signal transduction /// negative regulation of cell cycle	transferase activity, transferring glycosyl groups /// N-acetylglucosaminyl-proteoglycan 4-beta-glucuronosyltransferase activity	endoplasmic reticulum membrane /// Golgi apparatus /// integral to membrane	---
208270_s_at	RNPEP	0.225	proteolysis and peptidolysis /// protein processing	membrane alanyl aminopeptidase activity /// epoxide hydrolase activity /// zinc ion binding /// hydrolase activity /// aminopeptidase B activity	extracellular region /// Golgi apparatus /// plasma membrane	---
242576_x_at	PFAAP5	0.225	---	---	---	---

210576_at	CYP4F8	0.224	electron transport /// prostaglandin metabolism	fatty acid (omega-1)-hydroxylase activity /// unspecific monooxygenase activity	endoplasmic reticulum /// microsome /// membrane	Fatty acid metabolism /// gamma-Hexachlorocyclohexane degradation /// Tryptophan metabolism
221223_x_at	CISH	0.224	regulation of cell growth /// intracellular signaling cascade	---	---	---
215052_at	PDZK10	0.222	---	phosphoprotein phosphatase activity /// protein binding	cytoskeleton	---
217874_at	SUCLG1	0.222	tricarboxylic acid cycle /// metabolism	succinate-CoA ligase (GDP-forming) activity /// GTP binding /// ligase activity	mitochondrion	Krebs-TCA Cycle /// Citrate cycle (TCA cycle) /// Propanoate metabolism
202066_at	PPFIA1	0.221	---	---	---	---
218649_x_at	SDCCAG1	0.22	---	---	nucleus	---
205479_s_at	PLAU	0.219	proteolysis and peptidolysis /// chemotaxis /// signal transduction /// blood coagulation /// negative regulation of blood coagulation	chymotrypsin activity /// trypsin activity /// plasminogen activator activity /// kinase activity /// hydrolase activity	extracellular space	Wnt signaling /// Blood Clotting Cascade
218945_at	MGC2654	0.219	---	---	---	---
219550_at	ROBO3	0.219	chemotaxis /// neurogenesis	receptor activity	integral to membrane	---
232111_at	---	0.219	---	---	---	---
213063_at	FLJ11806	0.218	---	nucleic acid binding	nucleus	---
219719_at	CLST11240	0.218	---	---	---	---
1552947_x_at	MGC17986	0.216	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---

1560696_x_at	QTRTD1	0.216	tRNA processing /// queuosine biosynthesis	queuine tRNA-ribosyltransferase activity /// transferase activity, transferring glycosyl groups	---	---
203285_s_at	HS2ST1	0.216	---	transferase activity	---	---
224487_at	SPON1	0.216	development/// cell adhesion	protein binding	extracellular matrix (sensu Metazoa)	---
201622_at	SND1	0.215	regulation of transcription, DNA-dependent	nucleic acid binding /// nuclease activity	nucleus	---
209411_s_at	GGA3	0.215	protein complex assembly /// intracellular protein transport /// intra-Golgi transport	protein transporter activity /// ADP-ribosylation factor binding	Golgi stack /// Golgi trans face /// clathrin coat of trans-Golgi network vesicle	---
237318_at	SLC43A2	0.215	---	---	---	---
1552803_a_at	FLJ32206	0.214	---	---	---	---
220212_s_at	THADA	0.214	---	receptor activity	---	---
201892_s_at	IMPDH2	0.213	purine nucleotide biosynthesis /// GMP biosynthesis	IMP dehydrogenase activity /// oxidoreductase activity	---	Purine metabolism
212576_at	MGRN1	0.213	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
227612_at	ELAVL3	0.213	neurogenesis /// cell differentiation	RNA binding /// mRNA 3'-UTR binding	---	---
202428_x_at	DBI	0.212	transport	acyl-CoA binding /// lipid binding /// benzodiazepine receptor binding	---	---
212034_s_at	EXOC7	0.212	exocytosis /// protein transport	---	exocyst	---

219042_at	LZTS1	0.212	cell cycle /// negative regulation of cell cycle	transcription factor activity	cytoplasm /// membrane	---
231410_at	---	0.211	---	---	---	---
203286_at	RNF44	0.21	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
222916_s_at	HDLBP	0.21	lipid transport /// cholesterol metabolism	nucleic acid binding /// RNA binding /// lipid transporter activity /// lipid binding	nucleus /// plasma membrane	---
203082_at	BMS1L	0.209	ribosome biogenesis	ATP binding	nucleus	---
216953_s_at	WT1	0.209	regulation of transcription, DNA-dependent /// negative regulation of cell cycle	nucleic acid binding /// transcription factor activity /// zinc ion binding	nucleus	---
225470_at	NUP35	0.209	---	porin activity	integral to membrane /// outer membrane	---
234485_at	LOC340947	0.209	---	---	---	---
211358_s_at	CIZ1	0.208	regulation of cell cycle	nucleic acid binding /// zinc ion binding	nucleus	---
207283_at	DKFZp547I014	0.207	protein biosynthesis	structural constituent of ribosome /// rRNA binding	ribosome	---
1563131_at	---	0.206	---	---	---	---
201561_s_at	CLSTN1	0.206	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	membrane /// integral to membrane	---
221725_at	WASF2	0.206	---	---	---	---
234592_at	---	0.206	---	---	---	---
217074_at	SMOX	0.204	electron transport	oxidoreductase activity	---	---
209103_s_at	UFD1L	0.203	ubiquitin-dependent protein catabolism	---	---	---

233717_x_at	SMO	0.203	G-protein coupled receptor protein signaling pathway /// development	non-G-protein coupled 7TM receptor protein coupled receptor activity /// protein binding	membrane fraction /// integral to membrane		GPCRDB Other
242343_x_at	ZNF518	0.203	---	nucleic acid binding /// zinc ion binding	nucleus	---	
240062_at	FAM3C	0.202	---	cytokine activity	extracellular region	---	
208021_s_at	RFC1	0.201	DNA-dependent DNA replication /// regulation of transcription, DNA-dependent /// telomerase-dependent telomere maintenance	nucleotide binding /// DNA binding /// ATP binding /// enzyme activator activity /// nucleoside-triphosphatase activity	nucleus /// DNA replication factor C complex		DNA replication Reactome
209731_at	NTHL1	0.201	carbohydrate metabolism /// base-excision repair /// nucleotide-excision repair, DNA incision, 5'- to lesion	DNA binding /// DNA-(apurinic or apyrimidinic site) lyase activity /// endonuclease activity /// hydrolase activity, acting on glycosyl bonds /// lyase activity /// DNA N-glycosylase activity	nucleus	---	
1553704_x_at	FLJ90396	0.2	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---	
217990_at	GMPR2	0.199	nucleotide metabolism	catalytic activity /// GMP reductase activity /// oxidoreductase activity	---	---	
221536_s_at	FLJ11301	0.199	---	GTP binding	---	---	
208725_at	EIF2S2	0.198	protein biosynthesis /// translational initiation	DNA binding /// RNA binding /// translation initiation factor activity	ribosome /// eukaryotic translation initiation factor 2 complex	---	Translation Factors
1556502_at	LOC87769	0.197	---	---	---	---	
238330_s_at	M-RIP	0.197	---	---	---	---	

1570133_at	AKAP8L	0.195	---	DEAD/H-box RNA helicase binding/// DNA binding/// metal ion binding/// zinc ion binding	chromosome/// intracellular/// nucleus	---
212047_s_at	RNF167	0.195	proteolysis and peptidolysis /// protein ubiquitination	ubiquitin-protein ligase activity /// peptidase activity /// zinc ion binding	ubiquitin ligase complex	---
224679_at	MESDC2	0.195	mesoderm development	---	---	---
204811_s_at	CACNA2D2	0.194	---	---	membrane	---
238342_at	LOC23117	0.194	---	---	---	---
1553227_s_at	WDR9	0.193	---	---	---	---
204563_at	SELL	0.191	cell motility /// cell adhesion	protein binding /// sugar binding	integral to plasma membrane	---
224842_at	SMG1	0.191	mRNA catabolism, nonsense-mediated decay /// autophosphorylation /// phosphoinositide phosphorylation	inositol or phosphatidylinositol kinase activity /// protein serine/threonine kinase activity /// binding /// kinase activity /// phosphotransferase activity, alcohol group as acceptor	cytoplasm	---
202897_at	PTPNS1	0.19	---	---	---	---
206946_at	HCN4	0.19	cation transport /// potassium ion transport /// sodium ion transport /// muscle contraction /// circulation	voltage-gated potassium channel activity /// cation channel activity /// 3',5'-cAMP binding	membrane fraction /// integral to plasma membrane	---
204631_at	MYH2	0.189	striated muscle contraction /// muscle development	microfilament motor activity /// actin binding /// calmodulin binding /// ATP binding	muscle myosin /// striated muscle thick filament /// myosin	---
218040_at	FLJ10330	0.189	---	---	---	---

219504_s_at	FLJ13150	0.189	---	---	---	---	---
238659_at	KIAA0141	0.189	---	binding	---	---	---
226613_at	TBC1D10	0.188	---	PDZ domain binding	microvillus	---	---
1555274_a_at	SELI	0.187	phospholipid biosynthesis	transferase activity	integral to membrane	---	
1568722_at	TTC7B	0.187	---	---	---	---	
207826_s_at	ID3	0.187	development	transcription corepressor activity	nucleus	---	
242685_at	HSPC135	0.187	---	GTP binding	---	---	
203646_at	FDX1	0.186	electron transport /// vitamin metabolism /// steroid metabolism	iron ion binding /// electron carrier activity	mitochondrion	---	
43511_s_at	---	0.186	---	---	---	---	
230906_at	GALNT10	0.185	---	polypeptide N-acetylgalactosaminyltransferase activity /// sugar binding /// transferase activity, transferring glycosyl groups /// manganese ion binding	Golgi apparatus /// integral to membrane	O-Glycan biosynthesis	
244245_at	ANKRD9	0.185	---	---	---	---	
218210_at	FN3KRP	0.184	---	kinase activity /// transferase activity	---	---	
226947_at	C6orf216	0.184	carbohydrate metabolism	hydrolase activity, hydrolyzing O-glycosyl compounds	---	---	
231678_s_at	ADH4	0.184	alcohol metabolism /// ethanol oxidation /// aldehyde metabolism	alcohol dehydrogenase activity, zinc-dependent /// electron-transferring-flavoprotein dehydrogenase activity /// zinc ion binding /// oxidoreductase activity	---		Glycolysis / Gluconeogenesis /// Fatty acid metabolism /// Bile acid biosynthesis /// Tyrosine metabolism /// Glycerolipid metabolism

216806_at	RPSA	0.183	cell adhesion/// cell surface receptor linked signal transduction/// protein biosynthesis/// regulation of translation	laminin receptor activity/// structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukaryota) /// integrin complex	Prion disease/// Ribosome
225789_at	CENTG3	0.181	small GTPase mediated signal transduction /// regulation of GTPase activity	GTPase activator activity /// GTP binding	---	---
233120_at	PHACTR4	0.18	---	---	---	---
244752_at	LOC220929	0.18	---	nucleic acid binding /// zinc ion binding	nucleus	---
1553272_at	SLC36A1	0.179	transport /// amino acid transport	amino acid-polyamine transporter activity /// symporter activity	integral to membrane	---
222494_at	CHES1	0.179	DNA damage checkpoint /// G2 phase of mitotic cell cycle /// regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
243808_at	CDK6	0.179	regulation of cell cycle /// G1 phase of mitotic cell cycle /// cytokinesis /// protein amino acid phosphorylation	protein serine/threonine kinase activity /// ATP binding /// transferase activity	---	---
238731_at	SETDB2	0.178	chromatin modification	DNA binding /// methyltransferase activity /// zinc ion binding /// transferase activity /// histone-lysine N-methyltransferase activity	nucleus	---

222986_s_at	SCOTIN	0.177	positive regulation of I-kappaB kinase/NF-kappaB cascade	DNA binding /// signal transducer activity	nucleus	---
232693_s_at	ZNF395 /// FBXO16	0.177	ubiquitin cycle	nucleic acid binding /// zinc ion binding	nucleus	---
1555519_at	---	0.176	---	---	---	---
203606_at	NDUFS6	0.176	mitochondrial electron transport, NADH to ubiquinone	NADH dehydrogenase activity /// NADH dehydrogenase (ubiquinone) activity /// electron carrier activity /// oxidoreductase activity	mitochondrion	Electron Transport Chain
226387_at	RSBN1L	0.175	---	---	---	---
242338_at	DKFZp762C1112	0.175	---	---	---	---
209266_s_at	SLC39A8	0.174	transport /// metal ion transport	metal ion transporter activity	integral to membrane	---
1555224_at	---	0.173	---	---	---	---
202980_s_at	SIAH1	0.173	ubiquitin-dependent protein catabolism /// apoptosis /// cell cycle /// development /// spermatogenesis /// protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding /// ligase activity	ubiquitin ligase complex /// nucleus	---
223182_s_at	AGPAT3	0.173	metabolism /// phospholipid biosynthesis	1-acylglycerol-3-phosphate O-acyltransferase activity /// acyltransferase activity /// transferase activity	integral to membrane	Glycerolipid metabolism /// Glycerophospholipid metabolism
209995_s_at	TCL1A	0.172	development	---	microsome	---
212358_at	CLIPR-59	0.172	---	---	---	---

216588_at	RPL7 /// LOC388401	0.172	protein biosynthesis	RNA binding /// structural constituent of ribosome /// transcription regulator activity	intracellular /// cytosolic large ribosomal subunit (sensu Eukaryota)	Ribosomal Proteins
222143_s_at	FLJ22405	0.172	protein amino acid dephosphorylation	phosphoprotein phosphatase activity	---	---
224482_s_at	RAB11FIP4	0.172	---	calcium ion binding	---	---
207707_s_at	SEC13L1	0.171	intracellular protein transport	---	---	---
241539_at	---	0.171	---	---	---	---
1561175_at	LOC283482	0.17	---	---	---	---
202178_at	PRKCZ	0.17	protein amino acid phosphorylation /// anti-apoptosis /// intracellular signaling cascade	protein serine/threonine kinase activity /// atypical protein kinase C activity /// ATP binding /// transferase activity /// diacylglycerol binding	membrane fraction /// cytoplasm /// plasma membrane	G Protein Signaling /// Wnt signaling /// Calcium regulation in cardiac cells /// Smooth muscle contraction /// Phosphatidylinositol signaling system
204813_at	MAPK10	0.17	protein amino acid phosphorylation /// signal transduction /// JNK cascade	protein serine/threonine kinase activity /// JUN kinase activity /// MAP kinase activity /// MAP kinase kinase activity /// ATP binding /// transferase activity	---	Apoptosis /// G13 Signaling Pathway /// Integrin-mediated cell adhesion /// MAPK Cascade /// Wnt signaling
1553505_at	FLJ25179	0.169	---	endopeptidase inhibitor activity	---	---
215274_at	SLC12A3	0.169	ion transport /// sodium ion transport /// chloride transport /// amino acid transport	transporter activity /// amino acid-polyamine transporter activity /// symporter activity /// sodium:chloride symporter activity	membrane fraction /// integral to plasma membrane	---

233021_at	NDFIP2	0.168	positive regulation of I-kappaB kinase/NF-kappaB cascade	signal transducer activity	---	---	---
201608_s_at	PWP1	0.167	transcription	---	nucleus	---	
225886_at	DDX5	0.167	cell growth	RNA binding /// RNA helicase activity /// ATP binding /// ATP-dependent helicase activity	nucleus	---	
232356_at	KIAA0143	0.167	---	---	integral to membrane	---	
1553246_a_at	FLJ23356	0.165	protein amino acid phosphorylation	protein kinase activity /// ATP binding	---	---	
1554237_at	SDCCAG8	0.165	---	---	---	Integrin-mediated cell adhesion /// S1P Signaling	
1555864_s_at	PDHA1	0.165	acetyl-CoA metabolism /// glycolysis /// metabolism	pyruvate dehydrogenase (acetyl-transferring) activity /// oxidoreductase activity	mitochondrion	Acetylcholine Synthesis /// Glycolysis and Gluconeogenesis /// Krebs-TCA Cycle /// Glycolysis / Gluconeogenesis /// Valine, leucine and isoleucine biosynthesis /// Pyruvate metabolism /// Butanoate metabolism	
213153_at	KIAA1076	0.165	---	---	---	---	
221454_at	BOK	0.165	induction of apoptosis /// regulation of apoptosis	---	---	Apoptosis	
201440_at	DDX23	0.164	RNA splicing	nucleic acid binding /// ATP-dependent RNA helicase activity /// ATP binding /// pre-mRNA splicing factor activity /// hydrolase activity	nucleus	---	
236684_at	RQCD1	0.164	sex differentiation	---	---	---	

201555_at	MCM3	0.163	DNA replication /// DNA replication initiation /// regulation of transcription, DNA-dependent /// cell cycle	DNA binding /// ATP binding /// DNA-dependent ATPase activity	nucleus /// alpha DNA polymerase:primase complex	Cell cycle/// DNA replication Reactome /// G1 to S cell cycle Reactome
217340_at	RPL21	0.163	protein biosynthesis	RNA binding/// structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukaryota) /// Ribosome	Ribosome
229634_at	FLJ90586	0.163	---	---	---	---
243346_at	LMOD3	0.163	---	tropomyosin binding	cytoskeleton	---
1553978_at	MEF2B	0.162	regulation of transcription, DNA-dependent /// transcription from Pol II promoter /// muscle development	transcription factor activity /// transcription coactivator activity	nucleus	---
228666_at	MGC61550	0.162	---	---	---	---
243673_at	RBM41	0.162	---	RNA binding	---	---
224015_s_at	MRPS25	0.161	protein biosynthesis	nucleic acid binding /// structural constituent of ribosome	mitochondrion /// mitochondrial small ribosomal subunit	---
238842_at	---	0.161	---	---	---	---
1559587_at	SYMPK	0.16	cell adhesion	protein binding	nucleoplasm /// cytoplasm /// tight junction	---
210123_s_at	CHRNA7 /// CHRFAM7A	0.16	activation of MAPK /// ion transport /// signal transduction /// synaptic transmission	nicotinic acetylcholine-activated cation-selective channel activity /// ion channel activity /// extracellular ligand-gated ion channel activity /// acetylcholine receptor activity /// neurotransmitter receptor activity	nicotinic acetylcholine-gated receptor-channel complex /// integral to membrane /// postsynaptic membrane	---

211632_at	IGHM	0.16	immune response	antigen binding	membrane fraction	---
222655_s_at	IMPAD1	0.16	---	---	---	---
1554171_at	ZNF261	0.159	development	DNA binding /// zinc ion binding	nucleus	---
1564974_at	KRTAP8-1	0.159	---	---	intermediate filament	---
212695_at	CRY2	0.159	DNA repair	DNA photolyase activity /// lyase activity	---	Circadian Exercise
225261_x_at	TH1L	0.159	regulation of transcription, DNA-dependent /// negative regulation of transcription	---	nucleus	---
209862_s_at	PIG8	0.158	---	---	nucleus	---
239718_at	---	0.158	---	---	---	---
56919_at	WDR48	0.158	---	---	---	---
1556158_at	DKFZp666G057	0.157	---	---	---	---
225506_at	KIAA1468	0.157	---	---	---	---
234678_at	KRTAP4-3	0.157	---	---	keratin filament	---
1569406_at	---	0.156	---	---	---	---
219966_x_at	BANP	0.156	---	---	nucleus	---
208445_s_at	BAZ1B	0.155	transcription /// regulation of transcription, DNA-dependent /// protein ubiquitination	DNA binding /// transcription factor activity /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex /// nucleus	---
1561389_at	---	0.154	---	---	---	---
201997_s_at	SPEN	0.154	regulation of transcription, DNA-dependent	DNA binding /// RNA binding	nucleus	---

210822_at	LOC283345	0.154	---	---	---	---
1559064_at	NUP153	0.153	transport	DNA binding /// transporter activity /// porin activity	nucleus /// nuclear pore /// integral to membrane /// outer membrane	---
1562653_at	---	0.153	---	---	---	---
233161_at	WWOX	0.153	metabolism /// steroid metabolism	electron transporter activity /// protein binding /// oxidoreductase activity	---	---
1554996_at	ZNF479	0.152	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
231222_at	PACS1	0.152	---	---	Golgi apparatus	---
243906_at	OSTalpha	0.152	---	---	plasma membrane	---
211388_s_at	NCOR2	0.151	regulation of transcription, DNA-dependent	transcription corepressor activity/// DNA binding/// Notch binding/// protein binding	nucleus	---
217950_at	NOSIP	0.151	---	---	---	---
237996_at	---	0.151	---	---	---	---
240944_at	---	0.151	---	---	---	---
218142_s_at	CRBN	0.15	ATP-dependent proteolysis	ATP-dependent peptidase activity	mitochondrion	---
221415_s_at	GJA10	0.15	cell communication	connexon channel activity	connexon complex /// integral to membrane	---
209220_at	GPC3	0.149	morphogenesis	---	extracellular matrix (sensu Metazoa) /// integral to plasma membrane	---
217814_at	GK001	0.149	---	---	---	---
215321_at	RPIB9	0.148	---	---	---	---
1557267_s_at	LOC284952	0.147	---	---	---	---
225337_at	ABHD2	0.147	---	catalytic activity	integral to membrane	---

232682_at	DSU	0.147	---	---	---	---	---
242031_at	---	0.147	---	---	---	---	---
210430_x_at	RHD	0.146	---	---	integral to plasma membrane	---	---
220087_at	BCMO1	0.146	---	beta-carotene 15,15'-monooxygenase activity /// oxidoreductase activity	---	Retinol metabolism	
229703_at	DLG1	0.146	G1/S transition checkpoint/// actin filament organization/// cell-cell adhesion/// cortical actin cytoskeleton organization and biogenesis/// endothelial cell proliferation/// establishment and/or maintenance of cell polarity/// negative regulation of progression through mitotic cell cycle/// positive regulation of body size/// positive regulation of developmental growth	cytoskeletal protein binding/// guanylate kinase activity/// phosphoprotein phosphatase activity/// potassium channel regulator activity	basolateral plasma membrane/// cell-cell adherens junction/// endoplasmic reticulum	---		
209547_s_at	SF4	0.145	RNA processing	RNA binding	intracellular	mRNA processing	
238950_at	---	0.145	---	---	---	---	
241127_at	---	0.145	---	---	---	---	
236953_s_at	LOC387921	0.144	---	---	---	---	
206560_s_at	MIA	0.143	cell proliferation	growth factor activity	extracellular space	---	
224825_at	DNTTIP1	0.143	---	---	nucleus	---	

1556436_at	LOC340414	0.142	---	---	---	---	---
1561180_at	LRP11	0.142	---	receptor activity		integral to membrane	---
244368_x_at	SUGT1	0.142	centromere and kinetochore complex maturation/// mitosis/// regulation of progression through cell cycle/// ubiquitin cycle	binding	kinetochore/// ubiquitin ligase complex	---	---
1564970_at	SETDB2	0.141	chromatin modification	DNA binding /// methyltransferase activity /// zinc ion binding /// transferase activity /// histone-lysine N-methyltransferase activity	nucleus	---	---
204559_s_at	LSM7	0.141	nuclear mRNA splicing, via spliceosome	RNA binding /// pre-mRNA splicing factor activity /// U6 snRNA binding	nucleus /// small nucleolar ribonucleoprotein complex	mRNA processing	---
214317_x_at	RPS9	0.141	protein biosynthesis	RNA binding /// structural constituent of ribosome	intracellular /// cytosolic small ribosomal subunit (sensu Eukaryota)	Ribosomal Proteins	---
229683_s_at	KCTD15	0.141	---	---	---	---	---
1552400_at	C15orf27	0.14	---	---	---	---	---
1570476_at	---	0.14	---	---	---	---	---
202249_s_at	WDR42A	0.14	---	---	---	---	---

202494_at	PPIE	0.14	protein folding	RNA binding /// peptidyl-prolyl cis-trans isomerase activity /// cyclosporin A binding /// isomerase activity	nucleus	---
203033_x_at	FH	0.14	tricarboxylic acid cycle /// fumarate metabolism /// negative regulation of cell cycle	fumarate hydratase activity /// lyase activity	mitochondrion /// tricarboxylic acid cycle enzyme complex	Krebs-TCA Cycle /// Citrate cycle (TCA cycle) /// Reductive carboxylate cycle (CO2 fixation)
228383_at	C9orf111	0.14	---	catalytic activity /// nutrient reservoir activity	---	---
232072_at	ASAHL	0.14	---	hydrolase activity	---	---
203707_at	ZNF263	0.139	regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	nucleus	---
1569464_at	PPFIBP1	0.138	---	---	---	---
241415_at	RPS6KA3	0.138	central nervous system development /// protein amino acid phosphorylation /// signal transduction /// skeletal development	ATP binding /// magnesium ion binding /// nucleotide binding /// protein kinase activity /// protein serine/threonine kinase activity /// transferase activity	---	Long-term potentiation /// MAPK signaling pathway /// mTOR signaling pathway
212980_at	AHSA2	0.137	---	---	---	---
220844_at	TCEB3B	0.136	regulation of transcription, DNA-dependent /// defense response	---	nucleus /// integral to membrane	---
1570222_at	NDST4	0.135	---	sulfotransferase activity /// transferase activity	integral to membrane	---

208291_s_at	TH	0.135	synaptic transmission /// aromatic amino acid family metabolism /// morphogenesis /// neurotransmitter biosynthesis /// catecholamine biosynthesis	monooxygenase activity /// tyrosine 3-monooxygenase activity /// iron ion binding	---	Biogenic Amine Synthesis /// Tyrosine metabolism
222426_at	MAPKAP1	0.135	---	kinase activity /// Ras interactor activity	---	---
239574_at	ECHDC3	0.135	metabolism	catalytic activity	---	---
211137_s_at	ATP2C1	0.134	cation transport /// calcium ion transport /// calcium ion homeostasis /// metabolism /// epidermis development /// proton transport /// positive regulation of I-kappaB kinase/NF-kappaB cascade	magnesium ion binding /// catalytic activity /// signal transducer activity /// calcium-transporting ATPase activity /// ATP binding /// hydrolase activity /// hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	integral to membrane	---
215299_x_at	SULT1A1	0.134	catecholamine metabolism /// lipid metabolism /// steroid metabolism /// amine metabolism	aryl sulfotransferase activity /// sulfotransferase activity /// transferase activity	---	---
1562932_at	---	0.132	---	---	---	---
1564314_at	LOC219690	0.131	---	---	---	---
216977_x_at	SNRPA1	0.131	RNA splicing	RNA binding	snRNP U2	mRNA processing
237888_at	---	0.131	---	---	---	---
206076_at	B7	0.13	---	---	---	---
218126_at	FLJ10579	0.13	---	binding	---	---

218257_s_at	UGCGL1	0.13	protein amino acid glycosylation	UDP-glucose:glycoprotein glucosyltransferase activity /// transferase activity	soluble fraction /// endoplasmic reticulum	---	
223820_at	RBP5	0.13	transport	intracellular transporter activity /// lipid binding /// retinol binding	cytoplasm	---	
1561413_at	SPARC	0.129	bone remodeling/// biomineral formation/// cell communication/// development/// enzyme linked receptor protein signaling pathway/// organ development/// organismal physiological process/// ossification/// physiological process/// signal transduction/// skeletal development/// tissue development/// tissue remodeling/// transmembrane receptor protein tyrosine kinase signaling pathway	calcium ion binding/// cation binding/// collagen binding/// copper ion binding/// ion binding/// metal ion binding/// protein binding/// transition metal ion binding	---	---	
231915_at	ZSWIM4	0.129	---	---	---	---	
207756_at	---	0.128	---	---	---	---	
216708_x_at	IGLJ3	0.128	---	---	---	---	
219345_at	CGI-143	0.128	---	transcription regulator activity	---	---	
238849_at	ACY1	0.128	proteolysis and peptidolysis /// amino acid metabolism	aminoacylase activity /// metallopeptidase activity /// hydrolase activity	cytosol	Urea cycle and metabolism of amino groups	

243777_at	RAB7L1	0.128	intracellular protein transport /// small GTPase mediated signal transduction	GTPase activity /// GTP binding	---	---
1565700_at	---	0.125	---	---	---	---
214762_at	ATP6V1G2	0.125	ATP biosynthesis /// proton transport	hydrogen ion transporter activity /// hydrolase activity	---	Oxidative phosphorylation /// ATP synthesis /// Photosynthesis /// Flagellar assembly /// Type III secretion system
239093_at	C10orf65	0.125	lysine biosynthesis /// diaminopimelate biosynthesis	---	---	---
232987_at	---	0.124	---	---	---	---
218709_s_at	C20orf9	0.123	---	---	---	---
230399_at	NOX1	0.123	proton transport/// FADH2 metabolism/// NADP metabolism/// electron transport/// ion transport	voltage-gated proton channel activity/// iron ion binding/// metal ion binding/// oxidoreductase activity/// superoxide-generating NADPH oxidase activity	integral to membrane	---
37201_at	ITIH4	0.123	acute-phase response /// hyaluronan metabolism	serine-type endopeptidase inhibitor activity	extracellular region	---
1555307_at	TTF2	0.122	transcription termination	DNA binding /// Pol II transcription termination factor activity /// helicase activity /// ATP binding /// DNA-dependent ATPase activity	transcription elongation factor complex	---
212685_s_at	TBL2	0.122	---	---	---	---

223653_x_at	BRUNOL4	0.122	nuclear mRNA splicing, via spliceosome /// germ cell development /// embryonic development /// RNA interference	translation repressor activity, nucleic acid binding /// nucleic acid binding /// BRE binding	nucleus /// ribonucleoprotein complex	mRNA processing
1560288_at	---	0.121	---	---	---	---
212348_s_at	AOF2	0.121	electron transport /// regulation of transcription, DNA-dependent /// chromatin modification	oxidoreductase activity	nucleus	---
218868_at	ARP3BETA	0.121	actin filament polymerization	structural constituent of cytoskeleton /// actin filament binding	actin cytoskeleton	---
224036_s_at	C7orf2	0.121	---	---	---	---
202607_at	NDST1	0.12	protein biosynthesis /// protein amino acid deacetylation /// protein amino acid sulfation /// heparan sulfate proteoglycan biosynthesis	structural constituent of ribosome /// [heparan sulfate]-glucosamine N-sulfotransferase activity /// transferase activity	intracellular /// Golgi apparatus /// ribosome /// integral to membrane	---
243175_at	URP	0.12	---	hormone activity	extracellular region	---
222200_s_at	FLJ10276	0.119	---	---	---	---
1554934_at	RCBTB1	0.118	---	protein binding	---	---
1557277_at	---	0.118	---	---	---	---

205416_s_at	ATXN3	0.118	nucleotide-excision repair /// regulation of transcription, DNA-dependent /// synaptic transmission /// neurogenesis	---	nucleoplasm /// cytoplasm	---
208280_at	CDRT1	0.117	---	---	---	---
219956_at	GALNT6	0.117	---	polypeptide N-acetylgalactosaminyltransferase activity /// sugar binding /// transferase activity, transferring glycosyl groups /// manganese ion binding	Golgi apparatus /// integral to membrane	O-Glycan biosynthesis
222352_at	FBXO31	0.117	ubiquitin cycle	---	---	---
231580_at	---	0.117	---	---	---	---
1557314_at	FLJ36166	0.116	---	---	---	---
1557504_at	SRP54	0.116	protein targeting /// SRP-dependent cotranslational protein-membrane targeting	nucleotide binding /// RNA binding /// GTP binding /// nucleoside-triphosphatase activity	signal recognition particle (sensu Eukaryota)	---
203802_x_at	NSUN5	0.116	---	methyltransferase activity /// transferase activity	---	---
1559745_at	---	0.115	---	---	---	---
214351_x_at	RPL13	0.115	protein biosynthesis	RNA binding /// structural constituent of ribosome	intracellular /// cytosolic ribosome (sensu Eukaryota)	Ribosomal Proteins
232338_at	ZNF431	0.114	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
239479_x_at	---	0.114	---	---	---	---

240110_at	HMGCS2	0.114	acetyl-CoA metabolism /// cholesterol biosynthesis	hydroxymethylglutaryl-CoA synthase activity /// transferase activity	mitochondrion	Synthesis and Degradation of Keton Bodies
207644_at	FOXH1	0.113	regulation of transcription, DNA-dependent /// signal transduction	transcription factor activity /// transcription coactivator activity	nucleus	TGF Beta Signaling Pathway
221050_s_at	GTPBP2	0.113	protein biosynthesis	GTP binding	---	---
221433_at	FGF21	0.113	signal transduction /// cell signaling	growth factor activity	extracellular region /// soluble fraction	---
239153_at	FLJ41747	0.113	---	---	---	---
221066_at	RLN3R1	0.112	G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity /// N-formyl peptide receptor activity	integral to plasma membrane	GPCRDB Other
50277_at	GGA1	0.112	protein complex assembly /// intracellular protein transport /// intra-Golgi transport	protein transporter activity	Golgi stack /// clathrin coat of trans-Golgi network vesicle	---
238206_at	LGR7	0.111	signal transduction /// G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity	integral to membrane	GPCRDB Other /// Smooth muscle contraction
205969_at	AADAC	0.11	metabolism	deacetylase activity	endoplasmic reticulum membrane /// microsome /// integral to membrane	---
223019_at	C9orf88	0.11	---	---	---	---
1561268_at	---	0.109	---	---	---	---
218756_s_at	MGC4172	0.109	metabolism	oxidoreductase activity	---	---
236014_at	C10orf48	0.109	---	---	---	---
214085_x_at	GLIPR1	0.108	---	---	integral to membrane/// extracellular region	---

232364_at	FBXO11	0.108	protein ubiquitination/// ubiquitin-dependent protein catabolism	ubiquitin-protein ligase activity/// metal ion binding/// zinc ion binding	nucleus	ubiquitin ligase complex	---
239053_at	WDR39	0.108	positive regulation of cell proliferation/// regulation of transcription from RNA polymerase II promoter	---	---	---	---
240280_at	ARS2	0.108	response to arsenic	nucleotide binding	---	---	---
1557064_s_at	FLJ32731	0.107	---	---	---	---	---
227009_at	---	0.107	---	---	---	---	---
242556_at	HPCAL1	0.107	---	calcium ion binding	---	---	---
228331_at	C11orf31	0.106	---	---	---	---	---
234604_at	---	0.106	---	---	---	---	---
213273_at	ODZ4	0.105	---	---	---	---	---
226579_at	XRCC3	0.105	DNA repair/// DNA recombination	ATP binding/// DNA binding/// DNA-dependent ATPase activity/// nucleotide binding	nucleus	---	---
230979_at	BMPR1A	0.105	protein amino acid phosphorylation /// transmembrane receptor protein serine/threonine kinase signaling pathway /// transforming growth factor beta receptor signaling pathway	receptor activity /// transforming growth factor beta receptor activity /// ATP binding /// transferase activity	integral to membrane	Phosphatidylinositol signaling system	---
232377_at	NXPH1	0.105	---	---	---	---	---

238434_at	SHMT1	0.105	glycine metabolism /// L-serine metabolism /// L-serine catabolism /// one-carbon compound metabolism	glycine hydroxymethyltransferase activity /// transferase activity	cytosol	Glycine, serine and threonine metabolism /// Lysine degradation /// Cyanoamino acid metabolism /// One carbon pool by folate /// Methane metabolism
202963_at	RFX5	0.104	regulation of transcription, DNA-dependent /// transcription from Pol II promoter	transcription factor activity /// transcription coactivator activity	nucleus	---
203896_s_at	PLCB4	0.104	lipid metabolism /// intracellular signaling cascade /// lipid catabolism	phosphoinositide phospholipase C activity /// signal transducer activity /// calcium ion binding /// hydrolase activity	---	Inositol phosphate metabolism /// Phosphatidylinositol signaling system
242893_at	TYRP1	0.104	melanin biosynthesis from tyrosine /// metabolism	monooxygenase activity	integral to membrane	---
220675_s_at	ADPN	0.103	lipid catabolism /// triacylglycerol biosynthesis /// triacylglycerol catabolism	phospholipase A2 activity /// triacylglycerol lipase activity /// acyltransferase activity /// transferase activity /// hydrolase activity /// nutrient reservoir activity /// mono-olein transacylation activity /// diolein transacylation activity	integral to membrane	---
224653_at	EIF4EBP2	0.103	regulation of translation /// negative regulation of protein biosynthesis /// negative regulation of translational initiation	eukaryotic initiation factor 4E binding	---	Translation Factors

224850_at	ATAD1	0.103	---	nucleotide binding /// ATP binding /// nucleoside-triphosphatase activity	---	---
1557599_a_at	SLC26A5	0.102	sensory perception of sound /// sulfate transport /// transport /// regulation of cell shape	motor activity /// sulfate porter activity /// transporter activity	integral to membrane	---
233610_at	---	0.102	---	---	---	---
234597_at	---	0.102	---	---	---	---
238517_at	---	0.102	---	---	---	---
240814_at	MGC39584	0.102	---	---	---	---
1569712_at	---	0.101	---	---	---	---
207160_at	IL12A	0.101	---	---	---	cytokine-cytokine receptor interaction /// Jak-STAT signaling pathway /// Toll-like receptor signaling pathway /// Type I diabetes mellitus
1560507_at	DGAT2L3	0.1	---	acyltransferase activity /// transferase activity	---	---
216717_at	FAM48A	0.1	---	---	---	---
220459_at	MCM3APAS	0.1	---	---	---	---
234342_at	FAM20C	0.1	---	---	---	---
203642_s_at	COBLL1	0.099	---	---	---	---
221414_s_at	DEFB126	0.099	proteolysis and peptidolysis /// defense response to bacteria	protease inhibitor activity	extracellular region	---
239790_s_at	EXOSC2	0.099	rRNA processing	3'-5'-exoribonuclease activity /// 7S RNA binding /// exonuclease activity /// hydrolase activity /// protein binding	cytoplasm /// nucleus /// exosome	---

1559133_at	---	0.098	---	---	---	---
242830_at	LOC388565	0.098	---	---	---	---
201822_at	TIMM17A	0.097	protein-mitochondrial targeting	protein translocase activity	mitochondrion /// mitochondrial inner membrane presequence translocase complex /// integral to plasma membrane	---
239062_at	EVER1	0.097	---	---	integral to membrane	---
242399_at	FLJ33708	0.097	---	---	---	---
39729_at	PRDX2	0.097	response to oxidative stress	electron transporter activity /// thioredoxin peroxidase activity /// oxidoreductase activity	cytoplasm	Phenylalanine metabolism /// Prostaglandin and leukotriene metabolism /// Methane metabolism /// Stilbene, coumarine and lignin biosynthesis
240094_at	DJ971N18.2	0.096	electron transport	electron transporter activity	integral to membrane	---
241332_at	---	0.096	---	---	---	---
1559119_at	C11orf23	0.095	---	binding	---	---
1559648_at	---	0.095	---	---	---	---
206594_at	PASK	0.095	protein amino acid phosphorylation /// signal transduction	protein serine/threonine kinase activity /// signal transducer activity /// ATP binding /// transferase activity	---	---

230101_at	CXCL2	0.095	inflammatory response/// G-protein coupled receptor protein signaling pathway/// chemotaxis/// sensory perception	chemokine activity	extracellular space/// soluble fraction		Cytokine-cytokine Receptor Interaction
234868_s_at	GFRA4	0.095	---	receptor activity	membrane	---	
227392_at	NISCH	0.093	intracellular signaling cascade	---	---	---	
1554914_at	PLA2G4D	0.092	phospholipid catabolism	phospholipase activity	---	---	
1562045_at	---	0.092	---	---	---	---	
232247_at	ZNF502	0.092	regulation of transcription, DNA-dependent	nucleic acid binding /// DNA binding /// zinc ion binding	nucleus	---	
242401_x_at	C20orf26	0.092	---	---	---	---	
1563157_at	---	0.091	---	---	---	---	
218594_at	FLJ10359	0.091	---	binding	---	---	
236127_at	SHARP	0.091	regulation of transcription, DNA-dependent	DNA binding /// RNA binding	nucleus	---	
1563121_at	---	0.09	---	---	---	---	
1569792_a_at	MGC50559	0.09	---	S-adenosylmethionine-dependent methyltransferase activity /// transferase activity	---	---	
215190_at	GA17	0.09	---	---	---	---	
232488_at	MGC15875	0.09	---	transaminase activity /// pyridoxal phosphate binding	mitochondrion	---	

236177_s_at	---	0.09	---	---	---	---
244032_at	---	0.09	---	---	---	---
235175_at	GBP4	0.089	---	---	---	---
207262_at	APOF	0.088	lipid metabolism /// lipid transport /// cholesterol metabolism	receptor binding /// lipid transporter activity /// high-density lipoprotein binding /// cholesterol binding	extracellular space	---
226278_at	DKFZp313A2432	0.088	---	---	---	---
1568735_at	DLGAP1	0.086	cell-cell signaling /// synaptic transmission	---	membrane	---
212684_at	ZNF3	0.086	regulation of transcription, DNA-dependent /// cell differentiation /// immune cell activation	nucleic acid binding /// transcription factor activity /// zinc ion binding	nucleus	---
212133_at	NIPA2	0.085	---	---	---	---
234569_at	---	0.085	---	---	---	---
1553935_at	MGC2848	0.084	---	---	---	---
1567182_at	---	0.084	---	---	---	---
210569_s_at	SIGLEC9	0.084	cell adhesion /// cell surface receptor linked signal transduction	protein binding /// sugar binding	integral to plasma membrane	---
236069_at	FLJ39005	0.083	---	---	---	---
239665_at	---	0.083	---	---	---	---
239836_at	FLJ10948	0.083	metabolism	catalytic activity	---	---
243221_at	FAM20A	0.082	---	---	---	---
219092_s_at	C9orf12	0.081	---	kinase activity	---	---
235132_at	LOC254128	0.081	---	---	---	---
1554356_at	SLD5	0.08	---	---	---	---

220902_at	FLJ12616	0.08	---	---	---	---	---
1556932_at	---	0.079	---	---	---	---	---
1557536_at	WNK2	0.079	protein amino acid phosphorylation /// protein kinase cascade	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	---	---	---
242387_at	INM01	0.079	---	---	---	---	---
236634_at	C8orf48	0.078	---	---	---	---	---
219877_at	FLJ13842	0.077	---	nucleic acid binding /// zinc ion binding	nucleus	---	---
230888_at	HSPC049	0.077	---	---	---	---	---
237576_x_at	LOC44042 2	0.077	---	---	---	---	---
221693_s_at	MRPS18A	0.076	protein biosynthesis	structural constituent of ribosome	intracellular /// mitochondrion /// mitochondrial small ribosomal subunit /// ribosome	---	---
221769_at	SSB3	0.076	intracellular signaling cascade	---	---	---	---
232269_x_at	METRN	0.076	neurogenesis	---	---	---	---
213823_at	HOXA11	0.075	regulation of transcription, DNA-dependent /// morphogenesis	transcription factor activity	nucleus	---	---
231797_at	SIX4	0.075	regulation of transcription, DNA-dependent /// morphogenesis	transcription factor activity	nucleus	---	---
232704_s_at	LRRFIP2	0.075	---	LRR domain binding	---	---	---
239191_at	DKFZp566O084	0.075	metabolism	oxidoreductase activity	---	---	---
239987_at	---	0.075	---	---	---	---	---

1562094_at	---	0.074	---	---	---	---
209440_at	PRPS1	0.073	nucleoside metabolism /// ribonucleoside monophosphate biosynthesis /// nucleotide biosynthesis	magnesium ion binding /// ribose-phosphate diphosphokinase activity /// kinase activity /// transferase activity /// lipoate-protein ligase B activity	---	Pentose phosphate pathway /// Purine metabolism
211817_s_at	KCNJ5	0.072	ion transport /// potassium ion transport	voltage-gated ion channel activity /// potassium channel activity /// G-protein enhanced inward rectifier potassium channel activity /// G-protein activated inward rectifier potassium channel activity	voltage-gated potassium channel complex /// integral to membrane	Calcium regulation in cardiac cells
1564331_at	LOC162993	0.071	---	---	---	---
227327_at	SBP1	0.071	---	---	---	---
232198_at	MCM8	0.07	---	---	---	---
240210_at	FLJ37183	0.07	---	---	---	---
244310_at	RORA	0.07	regulation of transcription, DNA dependent/// signal transduction	protein binding/// sequence specific DNA binding/// steroid hormone receptor activity/// transcription factor activity/// zinc ion binding	nucleus	---
218713_at	NARG2	0.069	---	---	---	---
226239_at	FLJ90024	0.069	---	---	---	---
234161_at	---	0.069	---	---	---	---
236284_at	KIAA0146	0.069	---	---	---	---
205161_s_at	PEX11A	0.068	signal transduction /// peroxisome division	---	integral to peroxisomal membrane	---

232476_at	DDEF2	0.068	regulation of GTPase activity	GTPase activator activity/// metal ion binding/// protein binding/// zinc ion binding	---	---
234256_at	---	0.068	---	---	---	---
1561566_at	LOC285501	0.067	---	---	---	---
215443_at	TSHR	0.067	G-protein signaling, coupled to cyclic nucleotide second messenger /// cell-cell signaling /// positive regulation of cell proliferation	thyroid-stimulating hormone receptor activity	integral to plasma membrane	GPCRDB Other /// Peptide GPCRs
226138_s_at	PPP1R14B	0.067	---	protein phosphatase inhibitor activity	---	---
231894_at	SARS	0.067	protein biosynthesis /// seryl-tRNA aminoacylation /// tRNA processing	RNA binding /// serine-tRNA ligase activity /// ATP binding /// ligase activity	soluble fraction /// cytoplasm	Glycine, serine and threonine metabolism /// Aminoacyl-tRNA biosynthesis
234712_at	C18orf25	0.067	---	---	---	---
240443_at	---	0.067	---	---	---	---
219666_at	MS4A6A	0.066	signal transduction	receptor activity	integral to membrane	---
1566932_x_at	TFB2M	0.065	rRNA modification	rRNA (adenine-N6,N6-)-dimethyltransferase activity /// rRNA methyltransferase activity	---	---
203648_at	TATDN2	0.065	---	nuclease activity /// hydrolase activity	---	---
233901_at	---	0.065	---	---	---	---
242417_at	LOC283278	0.065	---	---	---	---
242899_at	SESN3	0.065	cell cycle arrest	---	nucleus	---
1558914_at	PNAS-4	0.064	---	---	---	---

201986_at	THRAP1	0.064	androgen receptor signaling pathway/// positive regulation of transcription from RNA polymerase II promoter/// regulation of transcription, DNA-dependent /// transcription initiation from RNA polymerase II promoter	RNA polymerase II transcription mediator activity/// ligand-dependent nuclear receptor transcription coactivator activity/// receptor activity/// thyroid hormone receptor binding/// vitamin D receptor binding	mediator complex/// nucleus	---
219671_at	HPCAL4	0.064	central nervous system development	calcium ion binding	---	---
205221_at	HGD	0.063	L-phenylalanine catabolism /// tyrosine catabolism	homogentisate 1,2-dioxygenase activity /// oxidoreductase activity	---	Tyrosine metabolism /// Styrene degradation
205873_at	PIGL	0.063	GPI anchor biosynthesis	N-acetylglucosaminylphosphatidylinositol deacetylase activity /// hydrolase activity	endoplasmic reticulum /// integral to membrane	---
213333_at	MDH2	0.063	glycolysis /// tricarboxylic acid cycle /// malate metabolism	L-lactate dehydrogenase activity /// oxidoreductase activity /// L-malate dehydrogenase activity	mitochondrial matrix	Glycolysis and Gluconeogenesis /// Krebs-TCA Cycle /// Citrate cycle (TCA cycle) /// Pyruvate metabolism /// Glyoxylate and dicarboxylate metabolism /// Carbon fixation /// Reductive carboxylate cycle (CO2 fixation)
214474_at	PRKAB2	0.063	fatty acid biosynthesis /// signal transduction	---	---	Fatty Acid Synthesis
237712_at	---	0.063	---	---	---	---

1565868_at	CD44	0.062	cell adhesion /// cell-matrix adhesion /// cell-cell adhesion	receptor activity /// protein binding /// collagen binding /// hyaluronic acid binding	integral to plasma membrane /// membrane /// integral to membrane	---
219200_at	MGC5297	0.062	apoptosis	protein kinase activity /// ATP binding	---	---
232660_at	BAD	0.061	induction of apoptosis /// apoptotic program	protein binding	cytoplasm /// mitochondrial outer membrane	Apoptosis
1558279_at	FVT1	0.06	metabolism	oxidoreductase activity	extracellular space	---
237030_at	ACPP	0.06	regulation of cell cycle	acid phosphatase activity /// protein tyrosine phosphatase activity /// hydrolase activity	extracellular region	gamma-Hexachlorocyclohexane degradation /// Riboflavin metabolism
201870_at	TOMM34	0.059	protein folding /// protein-mitochondrial targeting	signal sequence binding /// unfolded protein binding	mitochonidrion /// mitochondrial outer membrane /// integral to membrane	---
223856_at	AKR1CL2	0.059	---	oxidoreductase activity	---	---
225881_at	SLC35B4	0.059	nucleotide-sugar transport	nucleotide-sugar transporter activity	integral to membrane	---
235221_at	KIAA0323	0.059	---	---	---	---
236920_at	PEPP-2	0.059	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
216233_at	CD163	0.058	antimicrobial humoral response (sensu Vertebrata)	scavenger receptor activity	extracellular region /// integral to plasma membrane /// membrane	---
231233_at	LOC388727	0.058	---	---	---	---
232866_at	FLJ12895	0.058	regulation of transcription, DNA-dependent	nucleic acid binding /// transcription factor activity /// zinc ion binding	nucleus	---

232877_at	---	0.058	---	---	---	---	---
235291_s_at	---	0.058	---	---	---	---	---
239962_at	EPS15L1	0.058	endocytosis	calcium ion binding	nucleus /// coated pit	---	---
241215_at	---	0.058	---	---	---	---	---
1556618_at	ELK4	0.057	regulation of transcription, DNA-dependent /// transcription from RNA polymerase II promoter	protein binding /// transcription cofactor activity /// transcription factor activity	nucleus	---	MAPK signaling pathway
215703_at	CFTR	0.057	ion transport /// respiratory gaseous exchange	ion channel activity /// ATP-binding and phosphorylation-dependent chloride channel activity /// channel-conductance-controlling ATPase activity /// protein binding /// ATP binding /// ATPase activity /// PDZ domain binding	membrane fraction /// integral to plasma membrane /// basolateral plasma membrane /// apical plasma membrane	---	
235830_at	---	0.057	---	---	---	---	---
203912_s_at	DNASE1L1	0.056	DNA catabolism	DNA binding /// endonuclease activity /// deoxyribonuclease activity /// hydrolase activity	membrane	---	
215018_at	KIAA1731	0.056	---	---	---	---	---
241204_at	---	0.056	---	---	---	---	---
224750_at	FLJ38628	0.055	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---	
230869_at	---	0.055	---	---	---	---	---
233045_at	LOC286126	0.055	---	---	---	---	---

235679_at	ENSA	0.054	transport/// response to nutrient	ion channel inhibitor activity/// receptor binding	---	---
242801_at	WWOX	0.054	metabolism /// steroid metabolism	electron transporter activity /// protein binding /// oxidoreductase activity	---	---
242803_at	CRIM1	0.054	neurogenesis	serine-type endopeptidase inhibitor activity /// insulin-like growth factor receptor activity	membrane fraction /// integral to membrane	---
1558440_at	EFCBP1	0.053	---	---	---	---
222746_s_at	BSPRY	0.053	---	zinc ion binding	intracellular	---
232230_at	C10orf75	0.053	---	---	---	---
241737_x_at	VRK1	0.053	protein amino acid phosphorylation	protein serine/threonine kinase activity /// ATP binding /// transferase activity	---	---
1568366_at	KIFAP3	0.052	signal transduction/// microtubule-based process/// protein complex assembly	kinesin binding/// protein binding	endoplasmic reticulum/// kinesin II complex	---
223908_at	HDAC8	0.052	regulation of transcription, DNA-dependent /// chromatin modification /// histone deacetylation	histone deacetylase activity /// transcription factor binding /// hydrolase activity	histone deacetylase complex /// nucleus /// cytoplasm	Cell cycle
1554578_at	ZNF70	0.051	regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	nucleus	---
236186_x_at	IL17RE	0.051	---	---	---	---
1564240_at	---	0.05	---	---	---	---

238377_s_at	---	0.05	---	---	---	---
239934_x_at	CDC27	0.05	---	---	---	---
242841_at	---	0.05	---	---	---	---
1561776_at	---	0.049	---	---	---	---
216088_s_at	PSMA7	0.049	ubiquitin-dependent protein catabolism	endopeptidase activity	proteasome core complex (sensu Eukaryota)	Proteasome Degradation /// Proteasome
218569_s_at	KBTBD4	0.049	---	protein binding	---	Electron Transport Chain
228195_at	MGC13057	0.049	---	---	---	---
229143_at	CNOT3	0.049	regulation of transcription, DNA-dependent	protein binding /// transcription regulator activity	nucleus	---
234618_at	PHTF1	0.049	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
225044_at	MGC20781	0.048	---	---	---	---
244418_at	RTN3	0.048	---	---	extracellular space /// endoplasmic reticulum /// integral to membrane	---
217611_at	LOC157697	0.047	---	---	---	---
229549_at	OPN1SW	0.047	---	calcium ion binding	endoplasmic reticulum /// Golgi apparatus	GPCRDB Class A Rhodopsin-like
234511_at	C20orf86	0.047	protein modification	---	---	---
1555938_x_at	VIM	0.046	---	structural molecule activity /// structural constituent of cytoskeleton /// protein binding	cytoplasm /// intermediate filament	Striated muscle contraction

207434_s_at	FXYD2	0.045	ion transport /// potassium ion transport /// sodium ion transport	transporter activity /// ion channel activity /// sodium:potassium-exchanging ATPase activity	sodium:potassium-exchanging ATPase complex /// membrane /// integral to membrane	Calcium regulation in cardiac cells
1556220_at	---	0.044	---	---	---	---
222938_x_at	ENPP3	0.044	phosphate metabolism /// nucleotide metabolism	nucleic acid binding /// endonuclease activity /// phosphodiesterase I activity /// nucleotide diphosphatase activity /// hydrolase activity	integral to plasma membrane	Purine metabolism /// Starch and sucrose metabolism /// Riboflavin metabolism /// Nicotinate and nicotinamide metabolism /// Pantothenate and CoA biosynthesis
238357_at	RNPC2	0.044	nuclear mRNA splicing, via spliceosome /// regulation of transcription, DNA-dependent /// mRNA processing	RNA binding	nucleus	mRNA processing
240459_at	YT521	0.044	nuclear mRNA splicing, via spliceosome	---	nucleus	---
1562201_x_at	---	0.043	---	---	---	---
227971_at	NRK	0.042	protein amino acid phosphorylation	protein serine/threonine kinase activity /// small GTPase regulatory/interacting protein activity /// ATP binding /// transferase activity	---	---
234967_at	IL6ST	0.042	immune response /// cell surface receptor linked signal transduction	receptor activity /// interleukin-6 receptor activity /// oncostatin-M receptor activity	integral to plasma membrane	Ribosomal Proteins
221812_at	FBXO42	0.041	ubiquitin cycle	---	---	---

224118_at	UBE2B	0.041	DNA repair /// ubiquitin cycle	ubiquitin conjugating enzyme activity /// ubiquitin-protein ligase activity /// ligase activity	nucleus	Ubiquitin mediated proteolysis
235294_at	FLJ21168	0.041	---	---	---	---
1566970_at	FARP1	0.04	cell adhesion	Rho guanyl-nucleotide exchange factor activity /// cytoskeletal protein binding	cytoplasm /// cytoskeleton /// membrane	---
1553558_at	TAS2R41	0.039	G-protein coupled receptor protein signaling pathway /// perception of taste	receptor activity /// G-protein coupled receptor activity	integral to membrane	---
1555111_at	LOC57821	0.039	---	---	---	---
1553685_s_at	SP1	0.038	regulation of transcription, DNA-dependent	DNA binding /// RNA polymerase II transcription factor activity /// zinc ion binding /// transcriptional activator activity	nucleus	Smooth muscle contraction
208226_x_at	ADAM22	0.038	proteolysis and peptidolysis /// negative regulation of cell adhesion	metalloendopeptidase activity /// integrin binding	integral to membrane	---
1560538_at	GTDC1	0.037	---	transferase activity	---	---
1564729_at	FLJ46266	0.037	---	---	---	---
214936_at	LRCH1	0.037	---	---	---	---
216736_at	TM6SF2	0.037	---	---	integral to membrane	---
232326_at	MGC39526	0.037	---	---	---	---

239166_at	MARK3	0.036	protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	---	---
241429_at	---	0.035	---	---	---	---
212318_at	TNPO3	0.034	protein transport	receptor activity /// binding	nucleus	---
229659_s_at	PIGR	0.034	protein secretion	protein transporter activity/// receptor activity	integral to plasma membrane	---
231321_s_at	PHCA	0.034	ceramide metabolism/// protein biosynthesis	hydrolase activity/// hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides/// structural constituent of ribosome	Golgi membrane/// Golgi stack/// endoplasmic reticulum membrane/// integral to membrane/// intracellular/// ribosome	Glycosphingolipid metabolism
241419_at	ARHGAP1	0.034	cytoskeleton organization and biogenesis /// signal transduction /// Rho protein signal transduction	SH3/SH2 adaptor protein activity /// Rho GTPase activator activity /// GTP binding	---	---
1556460_a_at	ARHGAP2	0.033	---	---	---	---
205625_s_at	CALB1	0.033	---	calcium ion binding /// protein binding	---	---
216482_x_at	ZNF79	0.033	regulation of transcription, DNA-dependent	DNA binding/// Zinc ion binding	nucleus	---

221442_at	MC3R	0.033	G-protein signaling, coupled to cyclic nucleotide second messenger /// G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	rhodopsin-like receptor activity /// melanocyte stimulating hormone receptor activity	integral to plasma membrane	GPCRDB Class A Rhodopsin-like /// Peptide GPCRs
221629_x_at	LOC51236	0.033	---	binding	---	---
1559578_at	LOC400602	0.032	---	---	---	---
242849_at	SASH1	0.032	negative regulation of cell cycle	---	---	---
1555330_at	GCLC	0.031	cysteine metabolism /// glutamate metabolism /// glutathione biosynthesis /// circulation	nucleic acid binding /// glutamate-cysteine ligase activity /// ligase activity	---	Glutamate metabolism /// Glutathione metabolism
1565923_at	SLC17A4	0.031	phosphate metabolism /// transport /// sodium ion transport	transporter activity /// sodium:phosphate symporter activity	membrane fraction /// integral to plasma membrane	---
214393_at	LOC284062	0.031	---	---	---	---
217556_at	CLCN4	0.031	ion transport /// chloride transport	voltage-gated chloride channel activity	membrane fraction /// integral to plasma membrane	---
218697_at	NCKIPSD	0.031	NLS-bearing substrate-nucleus import /// cytoskeleton organization and biogenesis /// signal transduction	cytoskeletal protein binding	nucleus /// intermediate filament	---

244140_at	WHSC1	0.031	regulation of transcription, DNA-dependent /// morphogenesis /// protein ubiquitination	DNA binding /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
232218_at	TRUB2	0.03	RNA processing	pseudouridylate synthase activity	---	---
233688_at	CSEN	0.03	regulation of transcription from Pol II promoter /// signal transduction	DNA binding /// transcription corepressor activity /// calcium ion binding	nucleus	---
234025_at	C12orf32	0.03	---	---	---	---
234850_at	MOGAT3	0.03	---	acyltransferase activity /// transferase activity	---	---
1566485_at	FHIT	0.028	cell cycle /// nucleotide metabolism /// negative regulation of cell cycle	magnesium ion binding /// hydrolase activity /// manganese ion binding /// bis(5'-adenosyl)-triphosphatase activity	cytoplasm	Purine metabolism
227375_at	DKFZP566D1346	0.028	---	---	---	---
1553004_at	PKD1L1	0.027	---	---	integral to membrane	---
220300_at	RGS3	0.027	inactivation of MAPK /// signal transduction /// regulation of G-protein coupled receptor protein signaling pathway	signal transducer activity /// GTPase activator activity /// protein binding	cytosol	Calcium regulation in cardiac cells /// Smooth muscle contraction
1554342_s_at	HEL308	0.026	---	nucleic acid binding /// ATP binding /// ATP-dependent helicase activity /// hydrolase activity	nucleus	---

1557241_a_at	SYTL4	0.026	exocytosis/// intracellular protein transport/// transport	Rab GTPase binding/// metal ion binding/// neurexin binding/// phospholipid binding/// transporter activity/// zinc ion binding	extrinsic to plasma membrane/// membrane/// synaptic vesicle	---
1554380_at	NEK11	0.025	protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding	---	---
1565132_at	RBMY3AP	0.025	---	---	---	---
236939_at	LOC401494	0.025	---	---	---	---
239733_at	MGC16186	0.025	---	---	---	---
1554796_at	DPP6	0.024	proteolysis and peptidolysis	catalytic activity /// dipeptidyl-peptidase IV activity	integral to membrane	---
204643_s_at	COVA1	0.024	nuclear mRNA splicing, via spliceosome /// regulation of cell growth /// electron transport /// ultradian rhythm	nucleic acid binding /// protein disulfide oxidoreductase activity /// oxidoreductase activity	cytosol /// external side of plasma membrane /// membrane	---
214791_at	LOC93349	0.024	---	DNA binding	nucleus	---
227714_s_at	C9orf86	0.024	small GTPase mediated signal transduction	GTP binding	---	---
243884_at	MGC40178	0.024	---	---	---	---
239944_at	BIRC1	0.023	nervous system development/// anti-apoptosis	ATP binding/// nucleoside-triphosphatase activity/// nucleotide binding	intracellular	---
243782_at	---	0.023	---	---	---	---
1563830_a_at	KIAA1937	0.022	---	---	---	---

234562_x_at	CKLFSF8	0.022	chemotaxis	cytokine activity	integral to membrane	---
236440_at	---	0.022	---	---	---	---
1555039_a_at	ABCC4	0.021	ion transport	chloride channel activity /// ATP binding /// 15-hydroxyprostaglandin dehydrogenase (NAD+) activity /// ATPase activity, coupled to transmembrane movement of substances	integral to membrane	---
220056_at	IL22RA1	0.021	---	receptor activity /// interferon receptor activity	membrane	---
236825_at	BFSP2	0.021	visual perception	structural constituent of cytoskeleton /// structural constituent of eye lens	cytoskeleton /// intermediate filament /// membrane	---
243149_at	EIF4G3	0.021	regulation of translational initiation	RNA cap binding /// translation initiation factor activity	eukaryotic translation initiation factor 4F complex	Translation Factors
214287_s_at	CDC2L5	0.02	development /// positive regulation of cell proliferation/// protein amino acid phosphorylation/// regulation of mitosis	ATP binding/// nucleotide binding/// protein serine/threonine kinase activity/// protein-tyrosine kinase activity/// transferase activity	---	---
229417_at	STAU2	0.02	---	double-stranded RNA binding	intracellular /// nucleus	---
236287_at	---	0.019	---	---	---	---
241725_at	E2F7	0.019	regulation of cell cycle /// regulation of transcription, DNA-dependent	transcription factor activity	transcription factor complex	---
243016_at	HSRTSBETA	0.019	metabolism	catalytic activity	---	---

1568884_at	ZRF1	0.018	protein folding /// regulation of transcription	DNA binding /// heat shock protein binding /// unfolded protein binding	nucleus	---	
201703_s_at	PPP1R10	0.018	transcription /// protein-nucleus import /// defense response	nucleic acid binding	nucleus	---	
206969_at	KRTHA4	0.018	epidermis development	structural molecule activity	intermediate filament	---	
215134_at	PI4KII	0.018	phosphatidylinositol biosynthesis	magnesium ion binding /// 1-phosphatidylinositol 4-kinase activity /// protein binding /// kinase activity /// phosphotransferase activity, alcohol group as acceptor	integral to plasma membrane /// lipid raft	---	
215350_at	SYNE1	0.018	nuclear organization and biogenesis /// Golgi organization and biogenesis /// muscle cell differentiation	actin binding /// structural molecule activity /// lamin binding	nuclear membrane /// Golgi apparatus /// cytoskeleton /// integral to membrane /// postsynaptic membrane	---	
217539_at	C18orf25	0.018	---	---	---	---	
231412_at	LOC441366	0.018	---	---	---	---	
1559535_s_at	---	0.017	---	---	---	---	

229879_at	ASPH	0.017	muscle contraction /// peptidyl-amino acid modification	peptide-aspartate beta-dioxygenase activity /// binding /// electron transporter activity /// iron ion binding /// calcium ion binding /// structural constituent of muscle /// oxidoreductase activity /// oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	integral to endoplasmic reticulum membrane	---
235050_at	SLC2A12	0.017	carbohydrate transport	transporter activity /// sugar porter activity	integral to membrane	---
242748_at	SREBF2	0.017	regulation of transcription from Pol II promoter /// lipid metabolism /// cholesterol metabolism	DNA binding /// RNA polymerase II transcription factor activity	nucleus /// endoplasmic reticulum /// Golgi apparatus /// integral to membrane	---
224767_at	RPL37	0.016	protein biosynthesis	structural constituent of ribosome	intracellular /// ribosome	Ribosomal Proteins
239830_at	ETFA	0.016	electron transport	electron carrier activity	mitochondrial matrix	---
1559063_at	C21orf63	0.015	---	sugar binding	integral to membrane	---
213657_s_at	DKFZp547K1113	0.015	---	nucleic acid binding /// zinc ion binding	nucleus	---

216436_at	PIK3R4	0.015	---	---	---	Apoptosis/// B cell receptor signaling pathway/// Focal adhesion /// Insulin signaling /// Jak-STAT signaling pathway/// Phosphatidylinositol signaling system/// Regulation of actin cytoskeleton/// T cell receptor signaling pathway/// Toll-like receptor signaling/// Type II diabetes mellitus
227547_at	---	0.015	---	---	---	---
240237_at	CLCN3	0.015	ion transport /// chloride transport /// regulation of pH /// endosomal lumen acidification	voltage-gated chloride channel activity /// PDZ domain binding /// protein homodimerization activity /// protein heterodimerization activity	early endosome /// late endosome /// Golgi apparatus /// cell surface /// vesicle membrane /// membrane /// integral to membrane	---
1560896_at	---	0.014	---	---	---	---
1561062_at	---	0.014	---	---	---	---
1563814_at	FLJ25143	0.014	---	---	---	---
203622_s_at	LOC56902	0.014	---	RNA binding	---	---
207075_at	CIAS1	0.014	apoptosis /// induction of apoptosis /// inflammatory response /// signal transduction /// perception of sound	---	---	---
211188_at	CD84	0.014	defense response /// homophilic cell adhesion	---	integral to plasma membrane	---

211319_at	RAE1	0.014	mRNA export from nucleus/// mitotic spindle assembly	RNA binding/// microtubule binding	cytoplasm/// cytoskeleton/// nuclear outer membrane/// nuclear pore/// nucleus	---
226096_at	FNDC5	0.014	---	---	integral to membrane	---
236532_at	LOC399947	0.014	---	---	---	---
239044_at	CDA08	0.014	cell-matrix adhesion	---	integrin complex /// integral to membrane	---
242071_x_at	ITGA8	0.014	cell-matrix adhesion /// integrin-mediated signaling pathway /// cell-cell adhesion	receptor activity /// protein binding	integrin complex /// integral to membrane	Integrin-mediated cell adhesion
1552478_a_at	IRF6	0.013	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	Apoptosis
1557406_s_at	LOC28369 7	0.013	---	---	---	---
237997_s_at	---	0.013	---	---	---	---
244561_at	---	0.013	---	---	---	---
1568612_at	GABRG2	0.012	ion transport /// chloride transport /// gamma-aminobutyric acid signaling pathway /// synaptic transmission	GABA-A receptor activity /// ion channel activity /// extracellular ligand-gated ion channel activity /// benzodiazepine receptor activity /// neurotransmitter receptor activity	integral to plasma membrane /// integral to membrane /// postsynaptic membrane	---
211607_x_at	EGFR	0.012	protein amino acid phosphorylation /// epidermal growth factor receptor signaling pathway /// cell proliferation /// negative regulation of cell cycle	receptor activity /// epidermal growth factor receptor activity /// ATP binding /// transferase activity	endosome /// cytoskeleton /// integral to plasma membrane	---

1558762_at	LOC285989	0.011	---	nucleic acid binding /// zinc ion binding	nucleus	---
214396_s_at	MBD2	0.011	regulation of transcription, DNA-dependent /// negative regulation of transcription	transcription factor activity /// methyl-CpG binding /// transcriptional repressor activity	nucleus	---
232589_at	---	0.011	---	---	---	---
241197_at	---	0.011	---	---	---	---
1568869_at	---	0.01	---	---	---	---
232021_at	LOC283464	0.01	carbohydrate biosynthesis	transferase activity, transferring hexosyl groups	---	---
227233_at	TSPAN2	0.009	cell motility /// cell adhesion /// cell proliferation	---	integral to membrane	---
241465_at	C17orf39	0.009	---	---	---	---
215821_x_at	PSG3	0.008	defense response /// pregnancy	---	extracellular region	---
232413_at	PGBD3	0.008	---	---	---	---
214626_s_at	GANAB	0.007	carbohydrate metabolism	hydrolase activity, hydrolyzing O-glycosyl compounds /// hydrolase activity	endoplasmic reticulum /// Golgi apparatus	---
220970_s_at	KRTAP2-4	0.007	---	---	keratin filament	---
1559111_a_at	---	0.006	---	---	---	---
1566277_at	OR5E1P	0.006	G-protein coupled receptor protein signaling pathway /// perception of smell	receptor activity /// olfactory receptor activity	integral to membrane	GPCRDB Other
1568699_at	MGC16028	0.006	---	---	---	---

209596_at	DKFZp564I1922	0.006	protein amino acid phosphorylation	vascular endothelial growth factor receptor activity /// ATP binding	---	---
216672_s_at	MYT1L	0.006	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
1554312_at	RNF170	0.005	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
1562997_at	---	0.005	---	---	---	---
206808_at	HNRPA3	0.005	---	RNA binding	nucleus /// ribonucleoprotein complex	mRNA processing
221297_at	GPRC5D	0.005	G-protein coupled receptor protein signaling pathway /// visual perception	seweless binding /// metabotropic glutamate, GABA-B-like receptor activity	integral to membrane	GPCRDB Class C Metabotropic glutamate pheromone
235618_at	ZNF507	0.005	---	nucleic acid binding /// zinc ion binding	nucleus	---
239610_at	ASB13	0.005	intracellular signaling cascade	---	---	---
1561084_at	---	0.004	---	---	---	---
213019_at	RANBP6	0.004	protein transport	binding	nucleus	---
217923_at	PEF	0.004	---	calcium ion binding	---	---
1569474_at	ELL	0.003	regulation of transcription, DNA-dependent /// RNA elongation from Pol II promoter	positive transcription elongation factor activity	nucleus	---
205525_at	CALD1	0.003	muscle contraction /// muscle development	actin binding /// calmodulin binding /// tropomyosin binding /// myosin binding	cytoskeleton	---
231333_at	---	0.003	---	---	---	---

237655_at	CEBPD	0.003	regulation of transcription, DNA-dependent /// transcription from Pol II promoter	DNA binding	nucleus	---
1554364_at	PPP2R5C	0.002	signal transduction	phosphoprotein phosphatase activity /// protein phosphatase type 2A regulator activity	protein phosphatase type 2A complex /// nucleus	Wnt signaling /// Glycogen Metabolism
1564399_at	ARMCX4	0.001	---	---	---	---
1566469_at	---	0.001	---	---	---	---
1569323_at	PTPRG	0.001	protein amino acid dephosphorylation /// one-carbon compound metabolism /// transmembrane receptor protein tyrosine signaling pathway	carbonate dehydratase activity /// transmembrane receptor protein tyrosine phosphatase activity /// zinc ion binding /// hydrolase activity	integral to plasma membrane	---
229575_at	---	0.001	---	---	---	---
204935_at	PTPN2	0	protein amino acid dephosphorylation	protein tyrosine phosphatase activity /// receptor activity /// hydrolase activity	---	---
213927_at	MAP3K9	0	protein amino acid phosphorylation	protein serine/threonine kinase activity /// MAP kinase kinase kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	---	---
220496_at	CLEC1B	0	defense response /// cell surface receptor linked signal transduction	transmembrane receptor activity /// sugar binding	integral to plasma membrane	---

1555997_s_at	IGFBP5	-0.489	regulation of cell growth /// signal transduction	insulin-like growth factor binding	extracellular region	---
239869_at	---	-0.464	---	---	---	---
1557673_at	---	-0.448	---	---	---	---
223533_at	FAD158	-0.446	---	---	---	---
237137_at	---	-0.433	---	---	---	---
243_g_at	MAP4	-0.428	negative regulation of microtubule depolymerization	structural molecule activity	microtubule associated complex	---
235189_at	NARG2	-0.427	---	---	---	---
206023_at	NMU	-0.417	regulation of smooth muscle contraction /// signal transduction /// neuropeptide signaling pathway /// digestion	receptor binding	---	---
216048_s_at	RHOBTB3	-0.415	---	GTPase activity /// protein binding	---	---
1554986_a_at	SNX19	-0.403	regulation of transcription, DNA-dependent /// intracellular signaling cascade /// protein transport	transcription factor activity	---	---
235465_at	FLJ25477	-0.403	---	---	---	---
1564479_a_at	UGT2B7	-0.395	lipid metabolism	glucuronosyltransferase activity	membrane fraction /// endoplasmic reticulum /// integral to membrane /// microsome	Androgen and estrogen metabolism /// Pentose and glucuronate interconversions /// Porphyrin and chlorophyll metabolism /// Starch and sucrose metabolism
210904_s_at	IL13RA1	-0.393	cell surface receptor linked signal transduction	receptor activity /// hematopoietin/interferon-class (D200-domain) cytokine receptor activity	plasma membrane /// interleukin-13 receptor complex /// integral to membrane	---

225289_at	STAT3	-0.383	negative regulation of transcription from Pol II promoter /// regulation of transcription, DNA-dependent /// cell motility /// acute-phase response /// intracellular signaling cascade /// JAK-STAT cascade /// neurogenesis	transcription factor activity /// signal transducer activity /// hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity /// calcium ion binding	nucleus /// cytoplasm	TGF Beta Signaling Pathway
210805_x_at	RUNX1	-0.382	regulation of transcription, DNA-dependent /// development	transcription factor activity /// ATP binding	nucleus	---
223853_at	BVES	-0.38	---	---	integral to membrane	---
222880_at	AKT3	-0.375	protein amino acid phosphorylation /// signal transduction	protein serine/threonine kinase activity /// ATP binding /// transferase activity	---	Integrin-mediated cell adhesion /// S1P Signaling
224456_s_at	MGC12982	-0.375	---	---	---	---
215970_at	ZP4	-0.374	fertilization (sensu metazoa)	receptor activity	extracellular matrix (sensu Metazoa)/// integral to membrane	---
203796_s_at	BCL7A	-0.37	---	actin binding	---	---
209456_s_at	FBXW11	-0.361	Wnt receptor signaling pathway /// protein ubiquitination	ubiquitin-protein ligase activity	ubiquitin ligase complex	---
209997_x_at	PCM1	-0.36	electron transport /// transcription	DNA binding /// DNA-directed RNA polymerase activity	pericentriolar material /// nucleus /// cytoplasm	---
1562728_at	LOC147941	-0.359	---	---	---	---

205948_at	PTPRT	-0.359	protein amino acid dephosphorylation /// transmembrane receptor protein tyrosine kinase signaling pathway	receptor activity /// transmembrane receptor protein tyrosine phosphatase activity /// hydrolase activity	integral to plasma membrane	---
211612_s_at	IL13RA1	-0.358	cell surface receptor linked signal transduction	receptor activity /// hematopoietin/interferon-class (D200-domain) cytokine receptor activity	plasma membrane /// interleukin-13 receptor complex /// integral to membrane	---
240798_at	CUTL1	-0.358	development/// negative regulation of transcription from RNA polymerase II promoter	RNA polymerase II transcription factor activity/// sequence-specific DNA binding	integral to membrane/// nucleus	---
211189_x_at	CD84	-0.354	defense response/// homophilic cell adhesion	---	integral to plasma membrane/// plasma membrane	---
230254_at	C6orf188	-0.354	---	---	integral to membrane	---
242933_at	LOC127540	-0.351	regulation of transcription, DNA-dependent	DNA binding	chromatin /// nucleus	---
1559347_at	CNOT4	-0.345	---	---	---	---
213768_s_at	ASCL1	-0.344	regulation of transcription from Pol II promoter /// neurogenesis /// cell differentiation	transcription factor activity	nucleus	---
1563324_at	LOC389457	-0.34	---	---	---	---
201537_s_at	DUSP3	-0.339	protein amino acid dephosphorylation	protein tyrosine phosphatase activity /// protein tyrosine/serine/threonine phosphatase activity /// hydrolase activity	---	---
237581_at	---	-0.339	---	---	---	---

203056_s_at	PRDM2	-0.338	regulation of transcription, DNA-dependent /// regulation of transcription	DNA binding /// transcription factor activity /// zinc ion binding /// transcription regulator activity /// metal ion binding	nucleus	---
1561526_at	---	-0.333	---	---	---	---
235056_at	ETV6	-0.333	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	Circadian Exercise
239371_at	FOXK2	-0.332	regulation of transcription from RNA polymerase II promoter	RNA polymerase II transcription factor activity/// sequence-specific DNA binding	nucleus	---
1560412_at	---	-0.33	---	---	---	---
221813_at	FBXO42	-0.33	ubiquitin cycle	---	---	---
241331_at	SCAP2	-0.329	protein complex assembly /// signal transduction	SH3/SH2 adaptor protein activity /// kinase activity	---	---
215961_at	F12	-0.328	proteolysis and peptidolysis /// blood coagulation /// negative regulation of blood coagulation	coagulation factor Xia activity /// coagulation factor XIIa activity /// chymotrypsin activity /// trypsin activity /// hydrolase activity	extracellular region	Blood Clotting Cascade
211544_s_at	GHRHR	-0.326	skeletal development /// G-protein coupled receptor protein signaling pathway /// adenylate cyclase activation	receptor activity /// G-protein coupled receptor activity /// growth hormone-releasing hormone receptor activity	plasma membrane /// integral to membrane	GPCRDB Class B Secretin-like /// GPCRDB Other
217310_s_at	FOXJ3	-0.323	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---

1554732_at	MGC24125	-0.322	---	---	---	---
205236_x_at	SOD3	-0.322	superoxide metabolism	copper, zinc superoxide dismutase activity /// heparin binding /// antioxidant activity /// oxidoreductase activity /// metal ion binding	extracellular matrix (sensu Metazoa) /// soluble fraction	---
1563950_at	PRG-3	-0.319	---	hydrolase activity	integral to membrane	---
233584_at	---	-0.319	---	---	---	---
239584_at	---	-0.319	---	---	---	---
211610_at	KLF6	-0.318	regulation of transcription, DNA-dependent /// cell growth /// B-cell differentiation	nucleic acid binding /// DNA binding /// zinc ion binding /// transcriptional activator activity	nucleus	---
223291_at	MRPS15	-0.317	protein biosynthesis	structural constituent of ribosome	mitochondrial small ribosomal subunit /// mitochondrion /// ribosome	---
205456_at	CD3E	-0.313	protein complex assembly /// signal complex formation /// G-protein coupled receptor protein signaling pathway /// positive regulation of T-cell proliferation /// T-cell activation /// regulation of apoptosis	transmembrane receptor activity /// SH3 domain binding /// protein kinase binding /// receptor signaling complex scaffold activity /// T-cell receptor binding /// protein heterodimerization activity	integral to plasma membrane /// T-cell receptor complex	---
204994_at	MX2	-0.312	immune response	GTPase activity /// GTP binding	nucleus /// cytoplasm	---
210692_s_at	SLC43A3	-0.312	---	---	---	---
209086_x_at	MCAM	-0.307	cell adhesion /// morphogenesis	protein binding	integral to plasma membrane	---

242011_at	---	-0.307	---	---	---	---
233220_at	GRIN3A	-0.305	ion transport /// synaptic transmission	magnesium ion binding /// receptor activity /// ionotropic glutamate receptor activity /// transporter activity /// ion channel activity /// glutamate-gated ion channel activity	membrane /// integral to membrane	---
1555612_s_at	G6PC	-0.302	glycogen metabolism /// glycogen biosynthesis /// glucose metabolism /// transport	glucose-6-phosphatase activity /// transporter activity /// sugar porter activity /// hydrolase activity	endoplasmic reticulum /// microsome /// integral to membrane	Glycolysis and Gluconeogenesis /// Glycolysis / Gluconeogenesis /// Galactose metabolism /// Starch and sucrose metabolism
219915_s_at	SLC16A10	-0.302	transport	transporter activity	integral to membrane	---
233382_at	LOC145845	-0.3	---	---	---	---
236977_at	---	-0.295	---	---	---	---
222184_at	---	-0.294	---	---	---	---
238959_at	LOC113251	-0.294	nuclear mRNA splicing, via spliceosome	nucleic acid binding	---	---
206753_at	RODH-4	-0.293	lipid metabolism /// metabolism	retinol dehydrogenase activity /// electron transporter activity /// oxidoreductase activity	microsome	---
236993_at	---	-0.293	---	---	---	---
228248_at	AVO3	-0.292	---	binding	---	---
219478_at	WFDC1	-0.291	negative regulation of cell growth	serine-type endopeptidase inhibitor activity	extracellular space	---
223818_s_at	HBXAP	-0.29	regulation of transcription, DNA-dependent /// chromatin modification	DNA binding	nucleus	---

229032_at	KIAA0789	-0.29	---	sulfotransferase activity	---	---
208433_s_at	LRP8	-0.289	lipid metabolism /// endocytosis /// signal transduction	receptor activity /// transmembrane receptor activity /// calcium ion binding /// apolipoprotein E receptor activity	plasma membrane /// membrane /// integral to membrane	---
238494_at	TRAF3IP1	-0.289	---	receptor activity	---	---
204930_s_at	BNIP1	-0.287	apoptosis /// anti-apoptosis	---	integral to membrane	---
241492_at	---	-0.286	---	---	---	---
1557710_at	---	-0.285	---	---	---	---
231937_at	---	-0.285	---	---	---	---
215811_at	SNCA	-0.283	central nervous system development/// anti-apoptosis	protein binding	cytoplasm	Alzheimer's disease/// neurodegenerative Disorders/// Parkinson's disease
224250_s_at	SECISBP2	-0.283	protein biosynthesis	RNA binding	nucleus	---
241012_at	TRBV3-1	-0.283	---	---	---	---
244801_at	PSMB7	-0.283	ubiquitin-dependent protein catabolism	endopeptidase activity	proteasome core complex (sensu Eukaryota)	Proteasome Degradation /// Proteasome
1569731_at	SORCS2	-0.281	intracellular protein transport /// neuropeptide signaling pathway	protein binding /// sugar binding /// neuropeptide receptor activity /// protein transporter activity	membrane /// integral to membrane	---
237809_at	---	-0.279	---	---	---	---
244519_at	ASXL1	-0.279	regulation of transcription, DNA-dependent	---	nucleus	---
240561_at	MBNL3	-0.278	development	nucleic acid binding	nucleus	---

232270_at	C9orf3	-0.277	proteolysis and peptidolysis	aminopeptidase activity /// membrane alanyl aminopeptidase activity /// metallopeptidase activity	---	---
215206_at	EXT1	-0.276	skeletal development /// glycosaminoglycan biosynthesis /// signal transduction /// negative regulation of cell cycle	transferase activity, transferring glycosyl groups /// N-acetylglucosaminyl-proteoglycan 4-beta-glucuronosyltransferase activity	endoplasmic reticulum membrane /// Golgi apparatus /// integral to membrane	---
1556685_at	---	-0.274	---	---	---	---
236766_at	C8orf38	-0.274	---	---	---	---
211214_s_at	DAPK1	-0.273	protein amino acid phosphorylation /// apoptosis /// signal transduction /// protein kinase cascade /// induction of apoptosis by extracellular signals	protein serine/threonine kinase activity /// calmodulin-dependent protein kinase I activity /// calcium- and calmodulin-dependent protein kinase activity /// calmodulin binding /// ATP binding /// transferase activity	actin cytoskeleton	---
211870_s_at	PCDHA3	-0.273	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	integral to membrane	---
205388_at	TNNC2	-0.272	regulation of muscle contraction /// muscle development	calcium ion binding	troponin complex	Striated muscle contraction
222576_s_at	EIF2C1	-0.272	protein biosynthesis /// regulation of translational initiation	translation initiation factor activity	eukaryotic translation initiation factor 2 complex	---

205721_at	GFRA2	-0.27	transmembrane receptor protein tyrosine kinase signaling pathway	receptor activity /// glial cell line-derived neurotrophic factor receptor activity	extrinsic to membrane	---	
242360_at	LDB2	-0.269	development	transcription cofactor activity	nucleus	---	
1569732_at	CCL15	-0.268	antimicrobial humoral response (sensu Vertebrata)/// calcium ion homeostasis/// cell-cell signaling/// chemotaxis/// immune response/// signal transduction	chemoattractant activity/// chemokine activity/// heparin binding	extracellular space	Cytokine-cytokine receptor interaction	
220032_at	FLJ21986	-0.268	---	---	---	---	
230015_at	LOC400621	-0.268	---	---	---	---	
1561164_at	---	-0.264	---	---	---	---	
240152_at	HDLBP	-0.264	lipid transport /// cholesterol metabolism	nucleic acid binding /// RNA binding /// lipid transporter activity /// lipid binding	nucleus /// plasma membrane	---	
1555174_at	---	-0.263	---	---	---	---	
202444_s_at	SPFH1	-0.263	---	---	---	---	
235711_at	PURB	-0.263	---	---	---	---	
223573_s_at	PPP2R2C	-0.262	signal transduction	phosphoprotein phosphatase activity /// protein phosphatase type 2A regulator activity	protein phosphatase type 2A complex	Glycogen Metabolism	

206429_at	F2RL1	-0.261	G-protein coupled receptor protein signaling pathway /// positive regulation of cytosolic calcium ion concentration /// blood coagulation	rhodopsin-like receptor activity /// receptor activity /// receptor binding /// thrombin receptor activity	Golgi apparatus /// integral to plasma membrane	GPCRDB Class A Rhodopsin-like
238261_at	---	-0.261	---	---	---	---
219070_s_at	MOSPD3	-0.26	---	structural molecule activity	integral to membrane	---
235330_at	FLJ33814	-0.26	---	---	---	---
234309_at	TTTY7	-0.259	---	---	---	---
1557164_a_at	C9orf102	-0.257	---	---	---	---
232265_at	ATXN7L1	-0.257	---	---	---	---
1569878_at	C10orf21	-0.256	regulation of progression through cell cycle	---	---	---
227474_at	PAX8	-0.256	GTP biosynthesis /// UTP biosynthesis /// CTP biosynthesis /// regulation of transcription, DNA-dependent /// morphogenesis /// cell differentiation	transcription factor activity /// nucleoside-diphosphate kinase activity /// thyroid-stimulating hormone receptor activity /// ATP binding	nucleus	---
1557700_at	POLH	-0.255	DNA replication /// regulation of DNA repair	magnesium ion binding /// damaged DNA binding /// eta DNA polymerase activity /// transferase activity	nucleoplasm	---
206917_at	GNA13	-0.255	cell motility /// signal transduction /// G-protein coupled receptor protein signaling pathway	GTPase activity /// receptor signaling protein activity /// protein binding /// GTP binding	membrane	G Protein Signaling /// G13 Signaling Pathway

218246_at	FLJ12875	-0.254	protein ubiquitination /// positive regulation of I-kappaB kinase/NF-kappaB cascade	ubiquitin-protein ligase activity /// signal transducer activity /// zinc ion binding		---
237356_at	ADAMTS18	-0.254	proteolysis and peptidolysis	metalloendopeptidase activity /// peptidase activity /// hydrolase activity	extracellular matrix (sensu Metazoa) /// extracellular matrix	---
1556180_at	LOC255458	-0.253	---	---	---	---
1556267_at	FLJ25056	-0.253	---	---	---	---
211435_at	ZA20D3	-0.253	---	DNA binding /// zinc ion binding	---	---
221082_s_at	NDRG3	-0.25	spermatogenesis /// cell differentiation /// negative regulation of cell growth	catalytic activity	cytoplasm	---
241820_at	RIF1	-0.25	---	ATP binding /// ATPase activity	---	---
209027_s_at	ABI1	-0.248	---	---	nucleus	---
214233_at	GGA2	-0.248	protein complex assembly /// intracellular protein transport /// intra-Golgi transport	protein transporter activity /// ADP-ribosylation factor binding	Golgi stack /// Golgi trans face /// clathrin coat of trans-Golgi network vesicle	---
228610_at	SMBP	-0.248	transport	transporter activity/// binding	integral to membrane	---
234502_at	ARPP-21	-0.248	---	nucleic acid binding	---	---
1560810_at	TMEM132D	-0.246	---	---	---	---
1562657_at	C10orf90	-0.246	---	---	---	---

1570352_at	ATM	-0.246	DNA repair /// regulation of transcription, DNA-dependent /// meiotic recombination /// signal transduction /// negative regulation of cell cycle	DNA binding /// transcription factor activity /// protein serine/threonine kinase activity /// transferase activity /// phosphotransferase activity, alcohol group as acceptor	intracellular /// nucleus	Cell cycle /// G1 to S cell cycle Reactome /// Ovarian Infertility Genes
221895_at	MOSPD2	-0.246	---	structural molecule activity	---	---
227505_at	KIAA1276	-0.246	---	---	---	---
243689_s_at	MGC72104	-0.246	---	---	---	---
1564215_at	TRIP3	-0.245	regulation of transcription, DNA-dependent	thyroid hormone receptor binding	intracellular	---
229168_at	COL23A1	-0.245	phosphate transport	structural molecule activity	cytoplasm	---
220191_at	GKN1	-0.244	regulation of cell cycle /// digestion /// cell proliferation	growth factor activity	---	---
227736_at	C10orf99	-0.244	---	---	---	---
1555585_a_at	MGC26988	-0.243	---	---	---	---
235445_at	POTE14	-0.243	---	protein binding	---	---
1557897_at	---	-0.242	---	---	---	---
207348_s_at	LIG3	-0.242	cytokinesis /// DNA replication /// DNA repair /// meiotic recombination /// spermatogenesis	DNA binding /// DNA ligase (ATP) activity /// ATP binding /// ligase activity	nucleus	---

219755_at	CBX8	-0.241	chromatin assembly or disassembly /// regulation of transcription, DNA-dependent /// chromatin modification	chromatin binding	chromatin /// nucleus	---
231814_at	LOC219612	-0.241	---	---	---	---
237235_at	---	-0.241	---	---	---	---
238007_at	ZNF271	-0.241	regulation of transcription, DNA-dependent	DNA binding/// metal ion binding/// zinc ion binding	intracellular/// nucleus	---
235739_at	NR4A2	-0.24	regulation of transcription, DNA-dependent /// signal transduction /// antimicrobial humoral response (sensu Vertebrata)	transcription factor activity /// steroid hormone receptor activity /// ligand-dependent nuclear receptor activity	nucleus	Nuclear Receptors
1562581_at	LOC254028	-0.239	---	---	---	---
238236_at	DDEF1	-0.239	regulation of GTPase activity	GTPase activator activity/// metal ion binding/// protein binding/// zinc ion binding	membrane	---
234867_at	---	-0.238	---	---	---	---
241985_at	JMY	-0.238	---	---	---	---
1554652_s_at	LOC375449	-0.236	---	protein serine/threonine kinase activity /// kinase activity	---	---
218960_at	TMPRSS4	-0.236	proteolysis and peptidolysis	chymotrypsin activity /// trypsin activity /// scavenger receptor activity /// peptidase activity /// hydrolase activity	integral to membrane	---

224058_s_at	LOC158160	-0.236	metabolism	oxidoreductase activity	---	---
1560891_a_at	---	-0.235	---	---	---	---
204327_s_at	ZNF202	-0.235	negative regulation of transcription from Pol II promoter /// regulation of transcription, DNA-dependent /// lipid metabolism	transcription factor activity /// specific RNA polymerase II transcription factor activity /// zinc ion binding	nucleus	---
214075_at	SCIRP10	-0.235	---	---	---	---
223352_s_at	HLC-8	-0.235	---	---	---	---
1570488_at	PCDH9	-0.234	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	membrane /// integral to membrane	---
210656_at	EED	-0.234	negative regulation of transcription	transcriptional repressor activity	nucleus	---
223367_at	WBSCR18	-0.234	protein folding	heat shock protein binding /// unfolded protein binding	---	---
234767_at	MLSTD2	-0.234	---	---	---	---
236621_at	RPS27	-0.234	protein biosynthesis /// signal transduction /// cell proliferation	RNA binding /// structural constituent of ribosome /// zinc ion binding	intracellular /// ribosome /// cytosolic small ribosomal subunit (sensu Eukaryota)	Ribosomal Proteins
240782_at	---	-0.233	---	---	---	---
1557682_a_at	LOC284688	-0.232	---	---	---	---
228773_at	---	-0.232	---	---	---	---
235860_at	KCMF1	-0.232	---	nucleic acid binding /// ion channel activity /// zinc ion binding	nucleus	---
241312_at	---	-0.232	---	---	---	---
1565752_at	FGD2	-0.231	---	zinc ion binding	---	---

231881_at	CALD1	-0.229	muscle contraction /// muscle development	actin binding /// calmodulin binding /// tropomyosin binding /// myosin binding	cytoskeleton	---	
1553961_s_at	C20orf161	-0.228	intracellular signaling cascade /// protein transport	binding	---	---	
239170_at	ACTR3	-0.228	cell motility	structural constituent of cytoskeleton	Arp2/3 protein complex	---	
1553166_at	CDH24	-0.227	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	membrane /// integral to membrane	---	
1563223_a_at	FSHPRH1	-0.227	spermatogenesis /// female gamete generation /// sex differentiation	---	---	---	
1563524_a_at	C14orf85	-0.227	---	---	---	---	
208735_s_at	CTDSP2	-0.227	---	phosphoprotein phosphatase activity /// hydrolase activity	soluble fraction /// nucleus	---	
215120_s_at	SAMD4	-0.227	---	---	---	---	
222223_s_at	IL1F5	-0.227	immune response	interleukin-1 receptor antagonist activity	extracellular region	---	
223025_s_at	AP1M1	-0.227	intracellular protein transport /// endocytosis	---	Golgi apparatus /// coated pit /// clathrin vesicle coat	---	
221516_s_at	FLJ20232	-0.226	---	---	---	---	
206991_s_at	CCR5	-0.225	G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity /// receptor activity /// C-C chemokine receptor activity	integral to membrane	GPCRDB Class A Rhodopsin-like /// Peptide GPCRs /// GPCRDB Other	

1552678_a_at	USP28	-0.224	ubiquitin-dependent protein catabolism /// ubiquitin cycle	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity /// hydrolase activity	---	---
217615_at	LRRC37A	-0.224	---	---	---	---
225790_at	MSRB3	-0.224	protein repair	protein-methionine-R-oxide reductase activity /// zinc ion binding /// oxidoreductase activity	mitochondrion /// endoplasmic reticulum	---
232593_at	LOC93082	-0.224	---	---	---	---
244492_at	SLA	-0.224	intracellular signaling cascade	SH3/SH2 adaptor protein activity	---	---
237397_at	HPN	-0.223	proteolysis and peptidolysis	chymotrypsin activity /// trypsin activity /// scavenger receptor activity /// hydrolase activity	integral to plasma membrane	---
237623_at	CST3	-0.223	---	cysteine protease inhibitor activity	---	---
1568675_at	CHRNA10	-0.222	regulation of cell proliferation/// synaptic transmission, cholinergic/// calcium ion transport	receptor binding/// calcium channel activity/// calcium ion binding/// extracellular ligand-gated ion channel activity/// neurotransmitter receptor activity/// nicotinic acetylcholine-activated cation-selective channel activity	integral to membrane/// postsynaptic membrane	---
236652_at	LOC149703	-0.222	---	---	---	---

242963_at	MGC26963	-0.222	sphingolipid metabolism /// sphingomyelin biosynthesis	kinase activity /// transferase activity /// ceramide cholinephosphotransferase activity	Golgi apparatus /// integral to plasma membrane /// integral to Golgi membrane	---
238661_at	---	-0.219	---	---	---	---
239077_at	GALNACT-2	-0.219	dermatan sulfate proteoglycan biosynthesis, polysaccharide chain biosynthesis /// chondroitin sulfate proteoglycan biosynthesis, polysaccharide chain biosynthesis	protein binding /// acetylgalactosaminyltransferase activity /// transferase activity /// N-acetylgalactosaminyl-proteoglycan 3-beta-glucuronosyltransferase activity	Golgi apparatus /// integral to Golgi membrane	---
214685_at	C4orf10	-0.218	---	---	---	---
230902_at	---	-0.218	---	---	---	---
1556347_at	---	-0.217	---	---	---	---
230191_at	TTBK1	-0.217	protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding	---	---
1555110_a_at	KLHL3	-0.216	---	actin binding /// structural molecule activity /// protein binding	cytoskeleton	---
1564473_at	LOC157570	-0.214	---	---	---	---
1565858_at	LOC388796	-0.214	---	---	---	---
202645_s_at	MEN1	-0.214	negative regulation of transcription from Pol II promoter /// regulation of transcription, DNA-dependent	protein binding	nucleus	---

216352_x_at	PCDHGA3	-0.214	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	membrane /// integral to membrane	---
227658_s_at	PLEKHA3	-0.214	---	phospholipid binding	membrane	---
1555246_a_at	SCN1A	-0.213	cation transport /// sodium ion transport	voltage-gated sodium channel activity /// cation channel activity	voltage-gated sodium channel complex /// integral to membrane	---
1562280_at	POU2F1	-0.213	negative regulation of transcription/// regulation of transcription, DNA-dependent	transcription factor activity/// protein binding	nucleus	---
227743_at	MYO15B	-0.213	---	binding	cytoskeleton	---
234899_at	LOC286436	-0.213	---	---	---	---
235872_at	TERF2	-0.213	telomerase-dependent telomere maintenance /// cell cycle /// regulation of transcription	telomeric DNA binding	chromosome, telomeric region /// nucleus	---
216994_s_at	RUNX2	-0.212	ossification /// regulation of transcription, DNA-dependent	transcription factor activity /// RNA polymerase II transcription factor activity /// ATP binding	nucleus	TGF Beta Signaling Pathway
235986_at	CEPT1	-0.212	lipid metabolism /// phospholipid biosynthesis	ethanolaminephosphotransferase activity /// transferase activity	integral to membrane	---
1554321_a_at	NFS1	-0.211	sulfur amino acid metabolism /// protein complex assembly /// metabolism	transaminase activity /// transferase activity /// cysteine desulfurase activity	nucleus /// mitochondrion /// cytosol	---
215260_s_at	TCF3	-0.211	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---

1554586_a_at	RHOBTB2	-0.21	small GTPase mediated signal transduction	protein binding /// GTP binding	---	---
212811_x_at	SLC1A4	-0.21	transport /// dicarboxylic acid transport /// neutral amino acid transport	neutral amino acid transporter activity /// symporter activity /// sodium:dicarboxylate symporter activity	membrane fraction /// integral to plasma membrane	---
231607_at	---	-0.21	---	---	---	---
234657_at	---	-0.21	---	---	---	---
207639_at	FZD9	-0.209	G-protein coupled receptor protein signaling pathway /// frizzled signaling pathway /// development /// neurogenesis	G-protein coupled receptor activity /// Wnt receptor activity	plasma membrane /// integral to membrane	Wnt signaling
231264_at	dJ39G22.2	-0.209	---	---	---	---
235526_at	SMAP	-0.209	---	---	---	---
1559406_at	ANKRD18A	-0.208	---	---	---	---
206633_at	CHRNA1	-0.207	ion transport /// muscle contraction /// signal transduction /// synaptic transmission	nicotinic acetylcholine-activated cation-selective channel activity /// ion channel activity /// extracellular ligand-gated ion channel activity /// acetylcholine receptor activity	nicotinic acetylcholine-gated receptor-channel complex /// integral to membrane /// postsynaptic membrane	---
1563601_at	MGC43690	-0.206	---	---	---	---
207863_at	ADPRH	-0.206	protein modification	magnesium ion binding /// ADP-ribosylarginine hydrolase activity /// hydrolase activity	---	---
213819_s_at	FLOT1	-0.206	---	protein binding	integral to membrane/// caveola	Insulin signaling pathway

226969_at	LOC149448	-0.206	---	---	---	---	---
1552873_s_at	CXYorf2	-0.205	---	---	---	---	---
224256_at	FMNL2	-0.205	actin cytoskeleton organization and biogenesis/// cell organization and biogenesis/// regulation of transcription, DNA-dependent	actin binding/// transcription factor activity	nucleus	---	---
1562065_at	---	-0.204	---	---	---	---	---
242637_at	L3MBTL	-0.204	regulation of transcription, DNA-dependent /// chromatin modification	transcription factor activity	nucleus	---	---
209478_at	STRA13	-0.203	---	---	---	---	---
237913_at	---	-0.203	---	---	---	---	---
240164_at	MUC4	-0.203	cell-matrix adhesion	ErbB-2 class receptor binding /// extracellular matrix structural constituent /// extracellular matrix consituent, lubricant activity	extracellular matrix (sensu Metazoa) /// integral to plasma membrane /// membrane	---	---
1560378_at	GRIK1	-0.202	central nervous system development/// glutamate signaling pathway/// ion transport/// potassium ion transport/// synaptic transmission	kainate selective glutamate receptor activity/// glutamate-gated ion channel activity/// ion channel activity/// potassium channel activity/// receptor activity/// transporter activity	integral to plasma membrane	Neuroactive ligand-receptor interaction	

237349_at	TSHR	-0.202	G-protein signaling, coupled to cyclic nucleotide second messenger /// cell-cell signaling /// positive regulation of cell proliferation	thyroid-stimulating hormone receptor activity	integral to plasma membrane	GPCRDB Other /// Peptide GPCRs
242376_at	---	-0.202	---	---	---	---
1562532_at	---	-0.201	---	---	---	---
204602_at	SAMHD1	-0.201	immune response /// signal transduction	catalytic activity /// 3',5'-cyclic-nucleotide phosphodiesterase activity	intracellular	---
219783_at	C2orf18	-0.2	---	---	---	---
220887_at	C14orf162	-0.2	---	---	---	---
229816_at	FLJ23129	-0.2	---	---	---	---

1553032_at	IL31RA	-0.199	MAPKKK cascade /// anti-apoptosis /// defense response /// transmembrane receptor protein tyrosine kinase signaling pathway /// JAK-STAT cascade /// positive regulation of cell proliferation /// cytokine and chemokine mediated signaling pathway /// macrophage differentiation /// positive regulation of tyrosine phosphorylation of Stat3 protein /// positive regulation of tyrosine phosphorylation of Stat5 protein /// homeostasis /// negative regulation of macrophage activation /// positive regulation of transcription, DNA-dependent	transcription coactivator activity /// receptor activity /// hematopoietin/interferon-class (D200-domain) cytokine receptor activity /// protein kinase binding /// cytokine binding	integral to membrane	---
1555145_at	LOC126731	-0.199	---	---	---	---
207646_s_at	CDY1 /// CDY2 /// CDY /// CDY1B	-0.199	chromatin assembly or disassembly /// spermatogenesis	chromatin binding	chromatin /// nucleus	---
225895_at	SYNPO2	-0.199	---	actin binding /// protein binding	nucleus	---

229011_at	EMP1	-0.199	epidermis development /// cell proliferation /// cell death/// cell growth	---		integral to membrane/// membrane fraction	---
207020_at	HSF2BP	-0.198	transcription from Pol II promoter /// spermatogenesis	---	---		---
224958_at	182-FIP	-0.198	---	---	---	---	---
226928_x_at	SLC25A37	-0.198	transport	binding	integral to membrane		---
236778_at	ATRX	-0.198	DNA repair /// DNA methylation /// DNA recombination /// regulation of transcription, DNA-dependent /// chromosome organization and biogenesis (sensu Eukaryota) /// perception of sound	DNA helicase activity /// transcription factor activity /// ATP binding	nucleus /// nuclear heterochromatin		---
1566033_at	---	-0.197	---	---	---		---
204714_s_at	F5	-0.197	cell adhesion /// blood coagulation	copper ion binding	extracellular region		Blood Clotting Cascade
214987_at	GAB1	-0.197	epidermal growth factor receptor signaling pathway /// cell proliferation /// insulin receptor signaling pathway	SH3/SH2 adaptor protein activity /// protein binding	---		---
1558533_at	LOC124751	-0.196	regulation of transcription, DNA-dependent	nucleic acid binding	intracellular		---
213008_at	FLJ10719	-0.196	---	---	---		---
215642_at	ZNF518	-0.196	---	nucleic acid binding /// zinc ion binding	nucleus		---

228820_at	LOC63929	-0.196	proteolysis and peptidolysis	peptidase activity /// metalloexopeptidase activity	---	---
239009_at	MACF1	-0.195	cell cycle arrest	actin binding /// calcium ion binding /// microtubule binding /// actin filament binding	cytoplasm /// cytoskeleton	---
225452_at	PPARBP	-0.194	regulation of transcription, DNA-dependent /// transcription initiation from Pol II promoter /// androgen receptor signaling pathway	DNA binding /// receptor activity /// RNA polymerase II transcription mediator activity /// transcriptional activator activity /// ligand-dependent nuclear receptor transcription coactivator activity /// vitamin D receptor binding /// thyroid hormone receptor binding	mediator complex /// nucleus	---
229034_at	FLJ10159	-0.194	---	---	---	---
238179_at	SPG7	-0.194	cell adhesion/// nervous system development/// protein catabolism/// proteolysis/// regulation of cell adhesion/// signal transduction	ATP binding/// metal ion binding/// metalloendopeptidase activity/// nucleoside-triphosphatase activity/// nucleotide binding/// unfolded protein binding/// zinc ion binding	extracellular matrix (sensu Metazoa)/// integral to membrane/// mitochondrion	---
1558987_at	FLJ40473	-0.193	---	---	---	---
222597_at	SNAP29	-0.193	---	---	---	---
234832_at	ANTXR1	-0.193	---	receptor activity	integral to membrane	---

244839_at	TTN	-0.193	carbohydrate metabolism /// protein amino acid phosphorylation /// striated muscle contraction /// regulation of striated muscle contraction /// response to oxidative stress /// muscle development	peroxidase activity /// protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// hematopoietin/interferon-class (D200-domain) cytokine receptor activity /// structural molecule activity /// calmodulin binding /// ATP binding /// structural constituent of muscle /// cation transporter activity /// myosin binding	cytoskeleton /// membrane /// sarcomere /// Z disc	Striated muscle contraction
206127_at	ELK3	-0.192	regulation of transcription, DNA-dependent /// regulation of transcription from Pol II promoter /// signal transduction	transcription factor activity /// RNA polymerase II transcription factor activity /// transcription cofactor activity	nucleus	---
208422_at	MSR1	-0.192	phosphate transport /// receptor mediated endocytosis	receptor activity /// scavenger receptor activity /// lipid transporter activity	cytoplasm /// integral to plasma membrane /// membrane	---
221397_at	TAS2R10	-0.192	G-protein coupled receptor protein signaling pathway /// perception of taste	receptor activity /// G-protein coupled receptor activity /// taste receptor activity	integral to membrane	---
234218_at	---	-0.192	---	---	---	---
234593_at	CADPS	-0.192	exocytosis	---	cytosol	---

239513_at	ADORA2A	-0.192	cAMP biosynthesis /// neurotransmitter transport /// phagocytosis /// apoptosis /// inflammatory response /// cellular defense response /// G-protein coupled receptor protein signaling pathway /// G-protein signaling, coupled to cAMP nucleotide second messenger /// adenylate cyclase activation /// cell-cell signaling /// central nervous system development /// blood coagulation /// sensory perception /// circulation	rhodopsin-like receptor activity /// A2A adenosine receptor activity, G-protein coupled /// A3 adenosine receptor activity, G-protein coupled /// receptor activity /// gastric inhibitory peptide receptor activity	membrane fraction /// integral to plasma membrane /// integral to membrane	GPCRDB Class A Rhodopsin-like /// Nucleotide GPCRs
1561058_at	FLI1	-0.191	regulation of transcription, DNA-dependent /// hemostasis /// organogenesis	transcription factor activity	nucleus	---	
1566701_at	VRK3	-0.191	protein amino acid phosphorylation	protein serine/threonine kinase activity /// ATP binding /// transferase activity	---	---	

211426_x_at	GNAQ	-0.19	protein amino acid ADP-ribosylation /// signal transduction /// G-protein coupled receptor protein signaling pathway /// phospholipase C activation /// blood coagulation	GTPase activity /// signal transducer activity /// GTP binding	cytoplasm /// heterotrimeric G-protein complex /// plasma membrane	G Protein Signaling /// Calcium regulation in cardiac cells /// Smooth muscle contraction
221399_at	EDA2R	-0.19	epidermis development /// morphogenesis of embryonic epithelium /// cell differentiation /// positive regulation of JNK cascade /// activation of NF-kappaB transcription factor	receptor activity /// tumor necrosis factor receptor activity /// protein binding	integral to membrane	---
231024_at	---	-0.19	---	---	---	---
1569374_at	FLJ43654	-0.189	---	---	---	---
205085_at	ORC1L	-0.189	DNA replication /// DNA replication initiation	nucleotide binding /// DNA binding /// ATP binding /// nucleoside-triphosphatase activity	nucleus	Cell cycle /// DNA replication Reactome /// G1 to S cell cycle Reactome
223057_s_at	XPO5	-0.189	---	binding	---	---
230898_at	KAZALD1	-0.189	cell differentiation/// ossification/// regulation of cell growth	insulin-like growth factor binding	extracellular region	---
231826_at	KIAA1272	-0.189	---	---	---	---
238304_at	---	-0.189	---	---	---	---
243531_at	ORAOV1	-0.189	---	---	---	---

1438_at	EPHB3	-0.188	protein amino acid phosphorylation /// signal transduction /// transmembrane receptor protein tyrosine kinase signaling pathway	protein-tyrosine kinase activity /// receptor activity /// ephrin receptor activity /// ATP binding /// transferase activity	integral to plasma membrane /// membrane	---
1552836_at	ZNF619	-0.188	---	nucleic acid binding /// zinc ion binding	nucleus	---
229038_at	CWF19L1	-0.188	---	---	---	---
1560913_at	---	-0.187	---	---	---	---
1566524_at	ACTR2	-0.187	---	protein binding	cytoskeleton	---
206692_at	KCNJ10	-0.187	ion transport /// potassium ion transport	voltage-gated ion channel activity /// potassium channel activity /// ATP binding /// ATP-activated inward rectifier potassium channel activity	integral to plasma membrane	---
1561853_at	IL23R	-0.186	---	receptor activity	---	---
1562263_at	LOXL2	-0.186	aging/// cell adhesion/// protein modification	copper ion binding/// electron transporter activity/// metal ion binding/// oxidoreductase activity/// protein-lysine 6-oxidase activity/// scavenger receptor activity	extracellular space	Arginine and proline metabolism
205931_s_at	CREB5	-0.185	transcription from Pol II promoter /// positive regulation of transcription, DNA-dependent	transcription factor activity /// protein binding /// zinc ion binding	nucleus	---

241234_at	LOC389025	-0.185	---	---	---	---	---
231695_at	KIAA1463	-0.184	metabolism	catalytic activity /// transcription factor binding	nucleus	---	
240359_at	C20orf71	-0.184	---	lipid binding	---	---	
244296_at	---	-0.184	---	---	---	---	
1566138_at	PTPRN2	-0.183	protein amino acid dephosphorylation	protein tyrosine phosphatase activity /// receptor activity /// transmembrane receptor protein tyrosine phosphatase activity /// hydrolase activity	integral to plasma membrane	---	
210799_at	HTR1B	-0.183	G-protein signaling, coupled to cyclic nucleotide second messenger /// synaptic transmission	rhodopsin-like receptor activity /// serotonin receptor activity	integral to plasma membrane	GPCRDB Class A Rhodopsin-like /// Monoamine GPCRs	
211914_x_at	NF1	-0.183	Ras protein signal transduction /// negative regulation of cell proliferation /// negative regulation of cell cycle	enzyme inhibitor activity /// Ras GTPase activator activity	cytoplasm	---	
220577_at	FLJ13373	-0.183	---	---	---	---	
231022_at	---	-0.183	---	---	---	---	
239464_at	---	-0.183	---	---	---	---	
240824_at	OBFC1	-0.183	---	nucleic acid binding	---	---	
213223_at	RPL28	-0.182	protein biosynthesis	RNA binding /// structural constituent of ribosome	intracellular /// ribosome /// cytosolic large ribosomal subunit (sensu Eukaryota)	---	Ribosomal Proteins
220669_at	HSHIN1	-0.182	---	---	---	---	

240329_at	PTP4A1	-0.182	cell cycle/// development/// protein amino acid dephosphorylation	hydrolase activity/// protein tyrosine phosphatase activity	endoplasmic reticulum/// membrane	---	
217617_at	PBX1	-0.181	regulation of transcription, DNA-dependent /// transcription from Pol II promoter /// C21-steroid hormone biosynthesis /// sex differentiation /// embryonic development /// hindbrain development /// regulation of transcriptional preinitiation complex formation	transcription factor activity /// protein binding	nucleus	---	
220166_at	CNNM1	-0.181	fatty acid biosynthesis	---	---	---	
228540_at	QKI	-0.18	---	nucleic acid binding /// RNA binding	---	---	

1559638_at	PIK3CD	-0.179	protein amino acid phosphorylation/// signal transduction	inositol or phosphatidylinositol kinase activity/// phosphatidylinositol-4,5-bisphosphate 3-kinase activity/// transferase activity	phosphoinositide 3-kinase complex	Apoptosis/// B cell receptor signaling pathway/// Fc epsilon RI signaling pathway/// Focal adhesion/// Inositol phosphate metabolism/// Insulin signaling pathway/// Jak-STAT signaling pathway/// Leukocyte transendothelial migration/// Natural killer cell mediated cytotoxicity/// Phosphatidylinositol signaling system/// Regulation of actin cytoskeleton/// T cell receptor signaling pathway/// Toll-like receptor signaling pathway/// Type II diabetes mellitus/// VEGF signaling pathway/// mTOR signaling pathway
212908_at	KIAA0962	-0.179	electron transport /// protein folding	electron transporter activity /// heat shock protein binding /// unfolded protein binding	---	---
227221_at	---	-0.179	---	---	---	---
238545_at	ADCY7	-0.179	cAMP biosynthesis/// intracellular signaling cascade	adenylate cyclase activity/// magnesium ion binding	integral to plasma membrane	Calcium signaling pathway /// Gap junction /// Purine metabolism
226083_at	TMEM70	-0.178	---	---	---	---
233312_at	ROPN1L	-0.178	---	---	---	---
233909_at	STAU2	-0.178	---	double-stranded RNA binding	intracellular /// nucleus	---

1553805_at	MGC17310	-0.177	---	---	---	---
204239_s_at	NNAT	-0.177	development /// brain development /// protein-lipoylation	auxiliary transport protein activity	---	---
210601_at	CDH6	-0.177	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	integral to membrane	---
241597_at	RERE	-0.177	development/// regulation of transcription, DNA-dependent	protein binding/// sequence specific DNA binding/// transcription factor activity/// zinc ion binding	nucleus	Dentatorubropallidoluysian atrophy (DRPLA)
211587_x_at	CHRNA3	-0.176	ion transport /// signal transduction /// synaptic transmission	nicotinic acetylcholine-activated cation-selective channel activity /// transporter activity /// ion channel activity /// extracellular ligand-gated ion channel activity /// acetylcholine receptor activity /// neurotransmitter receptor activity	nicotinic acetylcholine-gated receptor-channel complex /// integral to membrane /// postsynaptic membrane	---
227519_at	PLAC4	-0.176	---	---	membrane	---
1566777_at	STRN3	-0.175	cell cycle	calmodulin binding	Cytosol/// membrane fraction/// nucleus	---
204440_at	CD83	-0.175	defense response /// humoral immune response /// signal transduction	---	integral to plasma membrane	---
228809_at	CXorf40	-0.175	---	---	---	---
235211_at	CHCHD8	-0.175	---	---	---	---
1562772_a_at	DAND5	-0.174	---	---	---	---

204724_s_at	COL9A3	-0.174	phosphate transport	structural molecule activity	extracellular matrix (sensu Metazoa) /// collagen type IX /// cytoplasm	---
213201_s_at	TNNT1	-0.174	regulation of muscle contraction /// muscle development	tropomyosin binding	---	Striated muscle contraction
215083_at	PSPC1	-0.174	nuclear mRNA splicing, via spliceosome	nucleic acid binding	---	---
237553_at	---	-0.174	---	---	---	---
1557146_a_at	FLJ32252	-0.173	---	---	---	---
211313_s_at	BAZ1B	-0.173	transcription /// regulation of transcription, DNA-dependent /// protein ubiquitination	DNA binding /// transcription factor activity /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex /// nucleus	---
215175_at	PCNX	-0.173	---	---	integral to membrane	---
228775_at	LOC55831	-0.173	---	---	---	---
231159_at	LOC158813	-0.173	---	---	---	---
239929_at	FLJ32569	-0.173	proteolysis and peptidolysis	carboxypeptidase activity /// metallopeptidase activity /// hydrolase activity	---	---
243937_x_at	LOC25326	-0.173	---	---	---	---
1553839_at	DKFZp761B107	-0.172	---	---	---	---
1556484_at	FLJ25811	-0.172	---	---	extracellular matrix (sensu Metazoa)	---

208463_at	GABRA4	-0.172	ion transport /// chloride transport /// gamma-aminobutyric acid signaling pathway /// synaptic transmission	GABA-A receptor activity /// ion channel activity /// extracellular ligand-gated ion channel activity /// benzodiazepine receptor activity /// neurotransmitter receptor activity	integral to plasma membrane /// integral to membrane /// postsynaptic membrane	---
229642_at	ARHGEF7	-0.172	signal transduction	guanyl-nucleotide exchange factor activity	---	---
1558641_at	LOC202051	-0.171	---	---	---	---
1565111_x_at	OFCC1	-0.171	---	---	---	---
206468_s_at	KIAA0859	-0.171	---	S-adenosylmethionine-dependent methyltransferase activity /// transferase activity	---	---
240405_at	CASQ1	-0.17	muscle development	calcium ion binding	mitochondrial matrix /// smooth endoplasmic reticulum	Calcium regulation in cardiac cells
243488_at	LOC286513	-0.17	---	---	---	---
1553077_at	SDR-O	-0.169	metabolism	oxidoreductase activity	---	---
1559856_s_at	MLL	-0.169	regulation of transcription, DNA-dependent /// transcription from Pol II promoter	DNA binding /// transcription factor activity /// RNA polymerase II transcription factor activity /// zinc ion binding	nucleus	---
204181_s_at	ZNF297B	-0.169	regulation of transcription, DNA-dependent	DNA binding /// protein binding /// zinc ion binding	nucleus	---

207409_at	LECT2	-0.169	skeletal development /// chemotaxis	---	extracellular space /// cytoplasm	---
1552752_at	IGSF4D	-0.168	---	---	---	---
228179_at	HAS3	-0.168	carbohydrate metabolism	transferase activity, transferring glycosyl groups /// hyaluronan synthase activity	integral to plasma membrane	---
230763_at	LOC128153	-0.168	---	---	---	---
238894_at	RABGAP1L	-0.168	---	GTPase activator activity	---	---
1559812_at	---	-0.167	---	---	---	---
206653_at	POLR3G	-0.167	transcription /// regulation of transcription from Pol III promoter	DNA-directed RNA polymerase activity /// transferase activity	nucleus /// DNA-directed RNA polymerase III complex	---
208920_at	SRI	-0.167	regulation of action potential /// transport /// intracellular sequestering of iron ion /// regulation of striated muscle contraction /// heart development /// muscle development /// regulation of heart contraction rate	receptor binding /// calcium channel regulator activity /// calcium ion binding	cytoplasm	---
226967_at	FLJ14768	-0.167	---	nucleic acid binding /// zinc ion binding	nucleus	---
244306_at	---	-0.167	---	---	---	---
1553025_at	GPR126	-0.166	neuropeptide signaling pathway	receptor activity /// G-protein coupled receptor activity	membrane /// integral to membrane	---
1562507_at	---	-0.166	---	---	---	---

204066_s_at	CENTG2	-0.166	---	---	---	---
215934_at	---	-0.166	---	---	---	---
224543_at	C9orf13	-0.166	---	receptor activity /// calcium ion binding	---	---
232184_at	ALS2	-0.166	endosome organization and biogenesis	Ran guanyl-nucleotide exchange factor activity /// Rho guanyl-nucleotide exchange factor activity /// Rab guanyl-nucleotide exchange factor activity	early endosome /// cytosol /// vesicular fraction	---
1553560_at	VN1R4	-0.165	G-protein coupled receptor protein signaling pathway	rhodopsin-like receptor activity /// receptor activity /// pheromone receptor activity	integral to membrane	---
1556895_at	FLJ12442	-0.165	---	---	---	---
1562544_at	---	-0.165	---	---	---	---
216781_at	KIAA1751	-0.165	---	---	---	---
219542_at	NEK11	-0.165	protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding	---	---
243872_at	KIAA0261	-0.165	---	---	---	---
1556722_at	FLJ33706	-0.164	---	---	---	---
1562671_s_at	---	-0.164	---	---	---	---
204715_at	PANX1	-0.164	---	---	gap junction /// integral to membrane	---
213289_at	SATL1	-0.164	---	---	---	---
214782_at	CTTN	-0.164	---	protein binding	ruffles /// soluble fraction /// cytoplasm /// cytoskeleton /// cell cortex /// lamellipodium	---

227129_x_at	LOC388312 /// FLJ45445	-0.164	---	---	---	---	---
240399_at	TRIO	-0.164	protein amino acid phosphorylation /// transmembrane receptor protein tyrosine phosphatase signaling pathway	protein serine/threonine kinase activity /// guanyl-nucleotide exchange factor activity /// GTPase activator activity /// ATP binding /// transferase activity	---	---	---
1552258_at	MGC4677	-0.163	---	---	---	---	---
202046_s_at	GRLF1	-0.163	regulation of transcription, DNA-dependent /// small GTPase mediated signal transduction /// negative regulation of transcription /// regulation of eye photoreceptor cell development /// negative regulation of cell cycle	DNA binding /// GTPase activator activity /// GTP binding /// transcriptional repressor activity	nucleus	---	---
215652_at	SDHD	-0.163	tricarboxylic acid cycle/// electron transport	electron carrier activity/// heme binding/// iron ion binding/// metal ion binding/// succinate dehydrogenase activity	mitochondrial inner membrane/// integral to membrane/// mitochondrial envelope	Citrate cycle (TCA cycle)/// Oxidative phosphorylation/// Electron Transport Chain/// Oxidative decarboxylation of pyruvate and TCA cycle	
225259_at	RAB6B	-0.163	intracellular protein transport /// retrograde transport, Golgi to ER /// small GTPase mediated signal transduction	GTPase activity /// GTP binding	Golgi apparatus	---	

232467_at	KIRREL	-0.163	---	---	integral to membrane	---
232539_at	SOCS2	-0.163	regulation of cell growth /// intracellular signaling cascade /// regulation of signal transduction /// regulation of body size /// positive regulation of neuron differentiation	growth hormone receptor binding /// prolactin receptor binding /// insulin-like growth factor receptor binding	cytoplasm	---
234444_at	CDCP2	-0.163	---	---	---	---
235909_at	LOC400960	-0.163	---	---	---	---
1566666_at	SUCLG2	-0.162	succinyl-CoA metabolism/// tricarboxylic acid cycle	ATP binding/// succinate-CoA ligase (GDP-forming) activity	mitochondrion	citrate cycle (TCA cycle)/// propanoate metabolism/// oxidative decarboxylation of pyruvate and TCA cycle
223719_s_at	RTBDN	-0.162	---	---	---	---
214947_at	FAM105A	-0.161	---	---	---	---
215344_at	---	-0.161	---	---	---	---
221501_x_at	LOC339047	-0.161	neuropeptide signaling pathway	---	integral to membrane	---
221605_s_at	PIPOX	-0.161	electron transport /// tetrahydrofolate metabolism	sarcosine oxidase activity /// oxidoreductase activity /// L-pipecolate oxidase activity	peroxisome	---
1554076_s_at	MGC17839	-0.16	---	---	integral to membrane	---
1557228_at	EHBP1L1	-0.16	---	---	---	---
216170_at	CHCHD3	-0.159	---	---	mitochondrion	---
1554637_a_at	CBFA2T2	-0.158	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---

211522_s_at	GNRHR	-0.158	G-protein coupled receptor protein signaling pathway /// development	rhodopsin-like receptor activity /// gonadotropin-releasing hormone receptor activity	plasma membrane /// integral to membrane	GPCRDB Other /// Peptide GPCRs
214706_at	ZNF200	-0.158	regulation of transcription, DNA-dependent	nucleic acid binding /// zinc ion binding	nucleus	---
217575_s_at	SOS2	-0.158	small GTPase mediated signal transduction	protein binding /// DNA binding /// guanyl-nucleotide exchange factor activity	---	Dorso-ventral axis formation /// Focal adhesion /// Gap junction /// Insulin signaling pathway /// Jak-STAT signaling pathway /// MAPK signaling pathway /// Natural killer cell mediated cytotoxicity /// Regulation of actin cytoskeleton /// T cell receptor signaling pathway
228992_at	MED28	-0.158	regulation of transcription, DNA-dependent	actin binding	nucleus /// cytoskeleton /// membrane	---
242232_at	LOC149401	-0.158	---	---	---	---
244474_at	NOL7	-0.158	---	---	---	---
232741_at	GLUD1	-0.157	amino acid metabolism /// glutamate catabolism	glutamate dehydrogenase [NAD(P)+] activity /// ATP binding /// GTP binding /// oxidoreductase activity	mitochondrion	Urea cycle and metabolism of amino groups /// Glutamate metabolism /// Arginine and proline metabolism /// D-Glutamine and D-glutamate metabolism /// Nitrogen metabolism
237272_at	---	-0.157	---	---	---	---
237678_at	---	-0.157	---	---	---	---

2107 36_x_ at	DTNA	-0.156	striated muscle contraction /// signal transduction /// neuromuscular synaptic transmission	calcium ion binding /// protein binding /// zinc ion binding	synapse	---
2344 99_at	---	-0.156	---	---	---	---
1552 477_a _at	IRF6	-0.155	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	Apoptosis
1556 426_at	HEXA	-0.155	carbohydrate metabolism /// glycosphingolipid metabolism	beta-N-acetylhexosaminidase activity /// hydrolase activity, acting on glycosyl bonds	lysosome	N-Glycan degradation /// Aminosugars metabolism /// Glycosaminoglycan degradation /// Globoside metabolism
2069 40_s_ at	POU4F1	-0.155	regulation of transcription from Pol II promoter /// development /// axonogenesis /// synaptogenesis	transcription factor activity	nucleus	---
2124 75_at	KIAA0241	-0.155	---	---	---	---
2197 42_at	PRR7	-0.155	---	---	---	---
2288 44_at	SLC13A5	-0.155	sodium ion transport	transporter activity	membrane	---
2210 73_s_ at	CARD4	-0.154	signal transduction /// regulation of apoptosis /// positive regulation of I-kappaB kinase/NF-kappaB cascade	signal transducer activity /// protein binding /// ATP binding /// caspase activator activity	intracellular	---
2312 94_at	SIMP	-0.154	---	---	---	---
2414 66_at	MTL5	-0.154	metal ion homeostasis /// anti-apoptosis /// response to oxidative stress /// spermatogenesis /// response to metal ion	metal ion binding	---	---
2433 57_at	NEGR1	-0.154	cell adhesion	protein binding	---	---

1560905_at	ELAVL2	-0.153	nuclear mRNA splicing, via spliceosome /// regulation of transcription, DNA-dependent	RNA binding /// mRNA 3'-UTR binding	---	---	
203945_at	ARG2	-0.153	urea cycle /// arginine catabolism /// nitric oxide biosynthesis	arginase activity /// hydrolase activity /// manganese ion binding	mitochondrion	Urea cycle and metabolism of amino groups /// Arginine and proline metabolism	
232911_at	KIAA1559	-0.153	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---	
232939_at	MAML3	-0.153	nervous system development/// positive regulation of transcription from RNA polymerase II promoter/// regulation of transcription, DNA-dependent	transcription coactivator activity/// transcription factor activity	nucleus	Notch signaling pathway	
243308_at	---	-0.153	---	---	---	---	
1559276_at	KCTD1	-0.152	---	---	---	---	
205134_s_at	NUFIP1	-0.152	RNA processing	RNA binding /// protein binding /// zinc ion binding	nucleus	---	
219645_at	CASQ1	-0.152	muscle development	calcium ion binding	mitochondrial matrix /// smooth endoplasmic reticulum	Calcium regulation in cardiac cells	
1552377_s_at	LOC201158	-0.151	---	---	integral to membrane	---	
1566484_at	FHIT	-0.151	nucleotide metabolism/// cell cycle/// negative regulation of progression through cell cycle	bis(5'-adenosyl)-triphosphatase activity/// hydrolase activity/// magnesium ion binding	cytoplasm	Purine metabolism	

211520_s_at	GRIA1	-0.151	ion transport /// potassium ion transport /// signal transduction /// synaptic transmission	receptor activity /// alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor activity /// transporter activity /// ion channel activity /// glutamate-gated ion channel activity /// potassium channel activity /// kainate selective glutamate receptor activity	plasma membrane /// integral to membrane	---
216174_at	HCRP1	-0.151	---	---	---	---
226490_at	NHSL1	-0.151	---	---	---	---
228371_s_at	PRO0149	-0.151	---	---	---	---
206579_at	ZNF192	-0.15	regulation of transcription, DNA-dependent	transcription factor activity /// protein binding /// zinc ion binding	nucleus	---
207357_s_at	GALNT10	-0.15	---	polypeptide N-acetylgalactosaminyltransferase activity /// sugar binding /// transferase activity, transferring glycosyl groups /// manganese ion binding	Golgi apparatus /// integral to membrane	O-Glycan biosynthesis
208036_at	OPN1SW	-0.15	signal transduction /// G-protein coupled receptor protein signaling pathway /// visual perception /// phototransduction	receptor activity /// G-protein coupled photoreceptor activity /// blue light photoreceptor activity	integral to plasma membrane	GPCRDB Class A Rhodopsin-like
235173_at	LOC401093	-0.15	---	---	---	---
241048_at	---	-0.15	---	---	---	---

244072_at	FKBP6	-0.15	mismatch repair	---	---	---
1552870_s_at	DKFZp686H1423	-0.149	---	---	---	---
1557139_at	DDX11	-0.149	mitotic sister chromatid segregation /// regulation of cell cycle /// S phase of mitotic cell cycle /// G2/M transition of mitotic cell cycle /// nucleobase, nucleoside, nucleotide and nucleic acid metabolism /// nucleotide-excision repair /// positive regulation of cell proliferation /// ATP synthesis coupled proton transport	DNA binding /// ATP-dependent DNA helicase activity /// ATP binding /// hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides /// hydrogen-transporting ATP synthase activity, rotational mechanism /// hydrogen-transporting ATPase activity, rotational mechanism	nucleus /// nucleolus /// proton-transporting two-sector ATPase complex	---
1563241_at	PHF12	-0.149	negative regulation of transcription, DNA-dependent	protein binding /// transcriptional repressor activity /// zinc ion binding	nucleus /// transcriptional repressor complex	---
228554_at	---	-0.149	---	---	---	---
228585_at	FLJ34077	-0.149	---	---	---	---
234449_at	---	-0.149	---	---	---	---
238274_at	MYT1L	-0.149	regulation of transcription, DNA-dependent /// cell differentiation /// nervous system development	transcription factor activity /// zinc ion binding	nucleus	---
238810_at	RFX3	-0.149	regulation of transcription, DNA-dependent /// negative regulation of transcription	RNA polymerase II transcription factor activity, enhancer binding /// transcriptional repressor activity	nucleus	---

222395_s_at	FLJ13855	-0.148	ubiquitin cycle	ubiquitin conjugating enzyme activity	---	---
228958_at	ZNF19	-0.148	regulation of transcription, DNA-dependent	transcription factor activity /// zinc ion binding	nucleus	---
237864_at	RAB22A	-0.148	endocytosis /// endosome organization and biogenesis /// small GTPase mediated signal transduction /// protein transport	GTPase activity /// protein binding /// GTP binding	early endosome /// plasma membrane	---
238643_at	NBL1	-0.148	negative regulation of cell cycle	---	---	---
1554276_at	SART3	-0.147	RNA processing	nucleic acid binding	intracellular	---
206659_at	FLJ14082	-0.147	---	---	---	---
206299_at	TMEM28	-0.146	---	---	integral to membrane	---
243025_at	CDA08	-0.146	cell-matrix adhesion	---	integrin complex /// integral to membrane	---
1552543_a_at	STN2	-0.145	intracellular protein transport /// endocytosis	---	membrane /// clathrin vesicle coat	---
1554291_at	KIAA0701	-0.145	---	---	---	---
1555680_a_at	SMOX	-0.145	electron transport	oxidoreductase activity	---	---
212183_at	NUDT4	-0.145	intracellular signaling cascade /// cyclic nucleotide metabolism /// calcium-mediated signaling /// cyclic-nucleotide-mediated signaling /// regulation of RNA-nucleus export /// intracellular transport	diphosphoinositol-polyphosphate diphosphatase activity /// hydrolase activity	intracellular	---

239388_at	RNASET2	-0.145	RNA catabolism	RNA binding /// endoribonuclease activity /// hydrolase activity	extracellular region	---
396_f_at	EPOR	-0.145	signal transduction /// small GTPase mediated signal transduction	erythropoietin receptor activity /// guanyl-nucleotide exchange factor activity	integral to plasma membrane	---
1566861_at	LOC145663	-0.144	---	---	---	---
207255_at	LEPR	-0.144	energy reserve metabolism /// cell surface receptor linked signal transduction /// development	hematopoietin/interferon-class (D200-domain) cytokine receptor activity	integral to plasma membrane	---
220324_at	C6orf155	-0.144	---	---	---	---
226929_at	MTHFR	-0.144	amino acid metabolism /// methionine metabolism /// circulation	methylenetetrahydrofolate reductase (NADPH) activity /// oxidoreductase activity	---	One carbon pool by folate
241581_at	ERBB4	-0.144	protein amino acid phosphorylation /// transmembrane receptor protein tyrosine kinase signaling pathway /// development /// cell proliferation	receptor activity /// epidermal growth factor receptor activity /// ATP binding /// transferase activity	integral to plasma membrane	---
1562777_at	---	-0.143	---	---	---	---
211840_s_at	PDE4D	-0.143	signal transduction /// cyclic nucleotide metabolism	3',5'-cyclic-nucleotide phosphodiesterase activity /// cAMP-specific phosphodiesterase activity /// hydrolase activity	soluble fraction /// insoluble fraction	G Protein Signaling /// Smooth muscle contraction /// Purine metabolism

1569072_s_at	ABCB5	-0.142	transport	nucleotide binding /// ATP binding /// ATPase activity /// ATPase activity, coupled to transmembrane movement of substances	integral to membrane	---
1556170_at	---	-0.141	---	---	---	---
1560968_at	CDCA2	-0.141	---	---	---	---
1566896_at	SPPL3	-0.141	---	D-alanyl-D-alanine endopeptidase activity/// peptidase activity	integral to membrane	---
1570411_at	---	-0.141	---	---	---	---
212858_at	PAQR4	-0.141	---	receptor activity	integral to membrane	---
220703_at	C10orf110	-0.141	---	---	---	Cholesterol Biosynthesis /// Circadian Exercise
242678_at	LPP	-0.141	---	zinc ion binding	---	---

1561521_at	S100B	-0.14	energy reserve metabolism /// calcium ion homeostasis /// induction of apoptosis /// axonogenesis /// central nervous system development /// learning and/or memory /// cell proliferation /// regulation of cytokine biosynthesis /// positive regulation of complement activation /// astrocyte activation /// hyperphosphorylation /// regulation of long-term neuronal synaptic plasticity	calcium ion binding /// zinc ion binding /// kinase inhibitor activity /// protein homodimerization activity /// S100 beta binding /// S100 alpha binding /// tau protein binding	extracellular region /// nucleus /// cytoplasm	---
223022_s_at	C6orf55	-0.14	---	---	---	---
229175_at	SMYD4	-0.14	---	binding	---	---
206569_at	IL24	-0.139	apoptosis /// immune response	cytokine activity	extracellular region	---
214648_at	GPX5	-0.139	lipid metabolism /// response to oxidative stress	glutathione peroxidase activity /// electron transporter activity /// oxidoreductase activity	extracellular region	---
237942_at	SNRK	-0.139	---	---	---	---
239061_at	FLJ35107	-0.139	---	---	---	---
240289_at	---	-0.139	---	---	---	---
208798_x_at	GOLGIN-67	-0.138	---	---	Golgi apparatus	---
216038_x_at	DAXX	-0.138	regulation of transcription, DNA-dependent /// apoptosis	---	nucleus	Apoptosis

216908_x_at	LOC94431	-0.138	---	---	---	---
1553998_at	DMRTC1	-0.137	---	---	---	---
1555681_at	---	-0.137	---	---	---	---
1557346_at	LOC339263	-0.137	---	---	---	---
1561042_at	EMR3	-0.137	neuropeptide signaling pathway	G-protein coupled receptor activity /// calcium ion binding	integral to membrane	GPCRDB Other
204829_s_at	FOLR2	-0.137	folic acid transport	receptor activity /// folic acid binding	membrane fraction /// membrane	---
228267_at	TRIM11	-0.137	protein ubiquitination	ligase activity/// metal ion binding/// ubiquitin-protein ligase activity/// zinc ion binding	nucleus/// ubiquitin ligase complex	Tryptophan metabolism
241780_at	CDH11	-0.137	ossification /// cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	integral to membrane	---
1557567_at	LOC148987	-0.136	---	---	---	---
1570328_s_at	C20orf62	-0.136	---	---	---	---
238287_at	SLC7A13	-0.136	transport /// amino acid transport	amino acid-polyamine transporter activity	integral to membrane	---
1559697_at	---	-0.135	---	---	---	---
208384_s_at	MID2	-0.135	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
220895_at	USP29	-0.135	ubiquitin-dependent protein catabolism /// ubiquitin cycle	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity /// hydrolase activity	---	---

244569_at	LOC157657	-0.135	---	---	---	---
1555940_a_at	PRKCA	-0.134	cell surface receptor linked signal transduction/// induction of apoptosis by extracellular signals/// intracellular signaling cascade/// protein amino acid phosphorylation/// regulation of progression through cell cycle	ATP binding/// calcium ion binding/// diacylglycerol binding/// nucleotide binding/// protein binding/// protein kinase C activity/// transferase activity/// zinc ion binding	membrane fraction	Calcium signaling pathway/// Cholera – Infection/// Fc epsilon RI signaling pathway/// Focal adhesion/// Gap junction/// GnRH signaling pathway/// Leukocyte transendothelial migration/// Long-term depression/// Long-term potentiation/// MAPK signaling pathway/// Natural killer cell mediated cytotoxicity/// Pathogenic Escherichia coli infection – EHEC/// Pathogenic Escherichia coli infection – EPEC/// Phosphatidylinositol signaling system/// Tight junction/// VEGF signaling pathway/// Wnt signaling pathway
1562145_at	---	-0.134	---	---	---	---
1564783_x_at	OFCC1	-0.134	---	---	---	---
1565723_at	---	-0.134	---	---	---	---

215115_x_at	NTRK3	-0.134	neurotrophin binding /// ATP binding /// kinase activity /// nucleotide binding /// protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// receptor activity /// transferase activity /// transmembrane receptor protein tyrosine kinase activity	transmembrane receptor protein tyrosine kinase signaling pathway /// cell differentiation /// nervous system development /// protein amino acid phosphorylation	integral to plasmamembrane	---
231749_at	TIMM13	-0.134	perception of sound /// protein transport /// mitochondrial inner membrane protein import	zinc ion binding	mitochondrion /// mitochondrial inner membrane presequence translocase complex /// inner membrane /// mitochondrial inner membrane protein insertion complex	---
233902_at	GUCA1C	-0.134	signal transduction /// visual perception	calcium sensitive guanylate cyclase activator activity /// calcium ion binding	---	---
233987_at	TFAP2D	-0.134	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
1560619_at	LOC255411	-0.133	---	---	---	---
217170_at	---	-0.133	---	---	---	---
1557044_at	---	-0.132	---	---	---	---
1557283_a_at	ZNF519	-0.132	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---

206679_at	APBA1	-0.132	protein complex assembly /// intracellular protein transport /// cell adhesion /// synaptic transmission /// neurogenesis /// axon cargo transport	protein binding	synaptic vesicle	---
225116_at	HIPK2	-0.132	regulation of cell cycle /// protein amino acid phosphorylation /// induction of apoptosis by intracellular signals /// virus-host interaction /// positive regulation of transforming growth factor beta receptor signaling pathway /// positive regulation of JNK cascade	transcription corepressor activity /// protein serine/threonine kinase activity /// protein binding /// ATP binding /// transferase activity /// virion binding	nucleus /// cytoplasm /// nuclear body	---
236210_at	DDX31	-0.132	---	nucleic acid binding /// ATP binding /// ATP-dependent helicase activity /// hydrolase activity	---	---
1558813_at	TMED5	-0.131	intracellular protein transport	protein carrier activity	endoplasmic reticulum /// integral to membrane	---

1568874_at	NCOA6	-0.131	embryonic development (sensu Mammalia) /// DNA replication /// DNA repair /// DNA recombination /// regulation of transcription, DNA-dependent /// transcription initiation from Pol II promoter /// brain development /// heart development /// response to hormone stimulus /// myeloid blood cell differentiation /// estrogen receptor signaling pathway /// glucocorticoid receptor signaling pathway /// positive regulation of transcription from Pol II promoter	chromatin binding /// transcriptional activator activity /// estrogen receptor binding /// ligand-dependent nuclear receptor transcription coactivator activity /// retinoid X receptor binding /// thyroid hormone receptor binding	nucleus /// transcription factor complex	---
203436_at	RPP30	-0.131	tRNA processing	ribonuclease P activity /// ribonuclease activity /// hydrolase activity	nucleus /// nucleolar ribonuclease P complex	---
209738_x_at	PSG9	-0.131	pregnancy/// defense response	receptor activity	membrane fraction/// extracellular region	---
226582_at	LOC400043	-0.131	---	---	---	---
235923_at	VTI1A	-0.131	intracellular protein transport /// vesicle-mediated transport	protein transporter activity	integral to membrane	---
236520_at	---	-0.131	---	---	---	---
243967_at	LAF4	-0.131	regulation of transcription, DNA-dependent /// development	DNA binding	nucleus	---

1557605_a_at	---	-0.13	---	---	---	---
1558722_at	ZNF252	-0.13	---	nucleic acid binding /// zinc ion binding	nucleus	---
242052_at	BICD1	-0.13	---	---	Golgi apparatus	---
1553220_at	ALS2CR13	-0.129	---	---	---	---
211801_x_at	MFN1	-0.129	---	GTPase activity /// GTP binding /// hydrolase activity	mitochondrion /// integral to membrane /// outer membrane	---
231363_at	LOC149018	-0.129	---	---	---	---
232257_s_at	DKFZP434N1817	-0.129	---	---	---	---
221101_at	C14orf113	-0.128	---	---	---	---
1556060_a_at	KIAA1702	-0.127	phosphoenolpyruvate-dependent sugar phosphotransferase system	sugar porter activity	---	---
1569272_at	PIK3C3	-0.127	---	inositol or phosphatidylinositol kinase activity /// phosphatidylinositol 3-kinase activity	phosphoinositide 3-kinase complex	---
217642_at	RNF40	-0.127	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
221161_at	ASCL3	-0.127	regulation of transcription, DNA-dependent	DNA binding	nucleus	---
223688_s_at	LY6K	-0.127	---	---	---	---
1555185_x_at	TERF2	-0.126	telomerase-dependent telomere maintenance /// cell cycle /// regulation of transcription	telomeric DNA binding	chromosome, telomeric region /// nucleus	---

211504_x_at	ROCK2	-0.126	cytokinesis /// protein amino acid phosphorylation /// muscle contraction /// intracellular signaling cascade	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// structural molecule activity /// ATP binding /// transferase activity /// diacylglycerol binding	intracellular /// actin cytoskeleton	G13 Signaling Pathway /// Integrin-mediated cell adhesion
227937_at	LOC339344	-0.126	---	DNA binding	nucleus	---
235987_at	PRKXP1	-0.126	---	---	---	---
237209_s_at	NFRKB	-0.126	transcription from Pol II promoter /// inflammatory response	specific RNA polymerase II transcription factor activity	nucleus	---
240850_at	DYRK1A	-0.125	protein amino acid phosphorylation /// neurogenesis	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	nucleus	---
1561365_at	NRP1	-0.124	angiogenesis /// cell adhesion /// signal transduction /// cell-cell signaling /// neurogenesis /// axon guidance /// positive regulation of cell proliferation	receptor activity /// vascular endothelial growth factor receptor activity	membrane fraction /// integral to membrane	---
1561591_at	KLB	-0.124	carbohydrate metabolism	catalytic activity /// cation binding /// glucosidase activity	integral to membrane	---
1562079_at	CHIC2	-0.124	---	---	membrane	---

1570425_s_at	LATS1	-0.124	G2/M transition of mitotic cell cycle /// sister chromatid segregation /// cytokinesis /// protein amino acid phosphorylation /// cell cycle /// mitosis /// hormone-mediated signaling /// regulation of actin filament polymerization /// negative regulation of cyclin dependent protein kinase activity	magnesium ion binding /// protein serine/threonine kinase activity /// ATP binding /// transferase activity	spindle pole	---
206532_at	SMARCB1	-0.124	DNA integration/// cell cycle/// chromatin remodeling/// negative regulation of progression through cell cycle/// regulation of transcription from RNA polymerase II promoter	protein binding	nucleoplasm	---
207324_s_at	DSC1	-0.124	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	membrane fraction /// cytoskeleton /// integral to plasma membrane /// gap junction /// membrane	---
226289_at	M11S1	-0.124	---	---	integral to plasma membrane	---
242555_at	LOC388272	-0.124	---	---	---	---
244186_at	C10orf11	-0.124	---	---	---	---
244887_at	RGS13	-0.124	signal transduction	signal transducer activity	---	---

1560728_at	SH3GL2	-0.123	signal transduction /// central nervous system development	protein binding /// lipid binding /// acyltransferase activity /// transferase activity	cytoplasm	---
1562211_at	ZNF491	-0.123	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
205493_s_at	DPYSL4	-0.123	neurogenesis	hydrolase activity	---	---
209021_x_at	KIAA0652	-0.123	---	---	---	---
1566646_at	LOC149086	-0.122	---	---	---	---
211556_at	MAPRE2	-0.122	cellular defense response /// signal transduction /// cell proliferation	microtubule binding	---	---
217397_at	---	-0.122	---	---	---	---
210083_at	SEMA7A	-0.121	immune response /// development /// neurogenesis	receptor activity	extracellular space /// membrane	---
224228_s_at	PRDM7	-0.121	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
234948_at	---	-0.121	---	---	---	---
1559725_at	LOC399924	-0.12	---	---	---	---
1562730_a_at	SGCA	-0.12	muscle contraction /// muscle development	calcium ion binding /// protein binding	cytoskeleton /// dystrophin-associated glycoprotein complex /// sarcoglycan complex /// integral to membrane	---
217490_at	---	-0.12	---	---	---	---
1554625_at	BCL6B	-0.119	---	nucleic acid binding /// protein binding /// zinc ion binding	nucleus	---

1556648_at	C10orf40	-0.119	---	---	---	---
1559333_at	SRGAP3	-0.119	---	GTPase activator activity	---	---
232406_at	JAG1	-0.119	angiogenesis /// cell fate determination /// cell communication /// Notch signaling pathway /// development /// neurogenesis /// hemopoiesis /// keratinocyte differentiation /// regulation of cell migration /// regulation of cell proliferation /// myoblast differentiation /// endothelial cell differentiation	Notch binding /// structural molecule activity /// calcium ion binding /// growth factor activity	extracellular region /// integral to plasma membrane	---
233493_at	OR2A4	-0.119	G-protein coupled receptor protein signaling pathway /// perception of smell	olfactory receptor activity	integral to membrane	---
1552739_s_at	ST7L	-0.118	---	binding	---	---
203294_s_at	LMAN1	-0.118	protein folding /// ER to Golgi transport /// blood coagulation /// protein transport	sugar binding /// mannose binding /// unfolded protein binding	Golgi membrane /// endoplasmic reticulum membrane /// integral to membrane	---
213973_at	RRBP1	-0.118	protein targeting /// signal transduction /// protein transport	ribosome receptor activity	integral to endoplasmic reticulum membrane	---
233115_at	DEPDC1B	-0.118	intracellular signaling cascade	GTPase activator activity	---	---
236009_at	---	-0.118	---	---	---	---

1552763_at	MGC26979	-0.117	---	---	---	---
1556439_at	---	-0.117	---	---	---	---
228490_at	ABHD2	-0.117	---	catalytic activity	integral to membrane	---
236333_at	---	-0.117	---	---	---	---
218261_at	AP1M2	-0.116	protein targeting /// endocytosis /// vesicle targeting	---	Golgi apparatus /// coated pit /// clathrin vesicle coat	---
223510_at	NRP2	-0.116	angiogenesis /// electron transport /// cell adhesion /// neurogenesis /// axon guidance	receptor activity /// vascular endothelial growth factor receptor activity /// electron transporter activity /// semaphorin receptor activity	membrane fraction /// integral to membrane	---
228565_at	KIAA1804	-0.116	protein amino acid phosphorylation	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	---	---
237727_at	C9orf154	-0.116	cell communication /// homophilic cell adhesion	calcium ion binding /// sugar binding	membrane /// integral to membrane	---
240594_at	CDYL	-0.116	chromatin assembly or disassembly /// spermatogenesis /// metabolism	chromatin binding /// catalytic activity /// peptidase activity	chromatin /// nucleus	---
241078_at	SLC35E4	-0.116	---	---	---	---
244578_at	LCP2	-0.116	immune response /// transmembrane receptor protein tyrosine kinase signaling pathway /// intracellular signaling cascade	protein binding	---	---

1569787_at	---	-0.115	---	---	---	---	---
203962_s_at	NEBL	-0.115	ion transport /// regulation of actin filament length	actin binding /// zinc ion binding /// structural constituent of muscle	cytoskeleton /// actin cytoskeleton	---	
204210_s_at	PCYT1A	-0.115	phospholipid biosynthesis /// biosynthesis	cytidylyltransferase activity /// transferase activity /// nucleotidyltransferase activity	choline-phosphate membrane soluble fraction ///	Acetylcholine Synthesis /// Aminophosphonate metabolism /// Glycerophospholipid metabolism	
235341_at	DNAJC3	-0.115	regulation of translation /// protein folding /// defense response	protein kinase inhibitor activity /// binding /// heat shock protein binding /// unfolded protein binding	cytoplasm	---	
237128_at	FLJ20184	-0.115	---	GTPase activator activity	---	---	
212925_at	C19orf21	-0.114	---	---	---	---	
220180_at	SE57-1	-0.114	---	---	---	---	
224009_x_at	DHRS9	-0.114	metabolism /// androgen metabolism /// epithelial cell differentiation /// progesterone metabolism /// retinol metabolism /// 9-cis-retinoic acid biosynthesis	alcohol dehydrogenase activity /// retinol dehydrogenase activity /// oxidoreductase activity /// racemase and epimerase activity /// 3-alpha(17-beta)-hydroxysteroid dehydrogenase (NAD+) activity	microsome /// integral to endoplasmic reticulum membrane	---	
229079_at	EHMT2	-0.114	chromatin modification	protein binding/// histone-lysine N-methyltransferase activity/// methyltransferase activity/// transferase activity/// zinc ion binding	nucleus	lysine degradation	

237129_at	Cep152	-0.114	---	---	---	---
239506_s_at	LOC151300	-0.114	---	---	---	---
1559503_a_at	---	-0.113	---	---	---	---
1562908_at	LOC339468	-0.113	---	---	---	---
206806_at	DGKI	-0.113	protein kinase C activation /// intracellular signaling cascade	diacylglycerol kinase activity /// transferase activity	nucleus /// cytoplasm	Ribosomal Proteins
224441_s_at	USP45	-0.113	electron transport /// ubiquitin-dependent protein catabolism /// ubiquitin cycle /// transport	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity /// electron transporter activity /// iron ion binding	---	---
242445_at	FGD4	-0.113	---	zinc ion binding	---	---
1555317_at	POLK	-0.112	mutagenesis /// DNA repair	DNA binding	---	---
1559817_at	OR7A19P	-0.112	---	---	---	---
1564164_at	FLJ20054	-0.112	---	---	---	---
208688_x_at	EIF3S9	-0.112	protein biosynthesis /// translational initiation	RNA binding /// translation initiation factor activity	eukaryotic translation initiation factor 3 complex	Translation Factors
210306_at	L3MBTL	-0.112	regulation of transcription, DNA-dependent /// chromatin modification	transcription factor activity	nucleus	---
234401_at	---	-0.112	---	---	---	---
237333_at	RBBP4	-0.112	---	---	---	---
1566137_s_at	PTPRN2	-0.111	protein amino acid dephosphorylation	transmembrane receptor protein tyrosine phosphatase activity	integral to plasma membrane	Type I diabetes mellitus

205066_s_at	ENPP1	-0.111	generation of precursor metabolites and energy /// phosphate metabolism /// response to nutrients /// nucleotide metabolism	nucleic acid binding /// endonuclease activity /// nucleotide diphosphatase activity /// hydrolase activity	integral to membrane	Purine metabolism /// Starch and sucrose metabolism /// Riboflavin metabolism /// Nicotinate and nicotinamide metabolism /// Pantothenate and CoA biosynthesis
1561860_at	---	-0.11	---	---	---	---
1570224_at	---	-0.11	---	---	---	---
231433_at	---	-0.11	---	---	---	---
231763_at	POLR3A	-0.11	transcription /// transcription, DNA-dependent	DNA binding /// DNA-directed RNA polymerase activity /// transferase activity	nucleus /// DNA-directed RNA polymerase III complex	---
1558698_at	ZNF264	-0.109	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
204668_at	RNF24	-0.109	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
222296_at	---	-0.109	---	---	---	---
234790_at	FLJ10986	-0.109	carbohydrate metabolism	---	---	---
244702_at	---	-0.109	---	---	---	---
1569062_s_at	IQGAP3	-0.108	small GTPase mediated signal transduction	Ras GTPase activator activity /// calmodulin binding	---	---
205987_at	CD1C	-0.108	antimicrobial humoral response (sensu Vertebrata)	---	integral to plasma membrane	---

216842_x_at	RBMY1A1 /// RBMY2FP /// RBMY1F /// RBMY1B /// RBMY1D /// RBMY1E /// RBMY1J	-0.108	nuclear mRNA splicing, via spliceosome /// RNA processing /// spermatogenesis	nucleic acid binding /// RNA binding	nucleus	---
1565894_at	---	-0.107	---	---	---	---
1566185_at	---	-0.107	---	---	---	---
1566289_at	OR2M4	-0.107	G-protein coupled receptor protein signaling pathway /// perception of smell	olfactory receptor activity	integral to membrane	GPCRDB Other
1570469_at	---	-0.107	---	---	---	---
206945_at	LCT	-0.107	carbohydrate metabolism	lactase activity /// glycosylceramidase activity	membrane fraction /// integral to plasma membrane	Galactose metabolism
232763_at	TLN1	-0.107	cell motility /// cytoskeletal anchoring	actin binding /// structural constituent of cytoskeleton /// binding	cytoskeleton /// focal adhesion	Integrin-mediated cell adhesion
236531_at	---	-0.107	---	---	---	---
1562055_at	ZNF91	-0.106	regulation of transcription, DNA dependent	transcription factor activity/// zinc ion binding	intracellular/// nucleus	---
1569730_at	FLJ40243	-0.106	---	binding	---	---

211258_s_at	TGFA	-0.106	regulation of cell cycle /// cell-cell signaling /// cell proliferation	protein-tyrosine kinase activity /// signal transducer activity /// epidermal growth factor receptor activating ligand activity /// protein binding /// growth factor activity	extracellular space /// soluble fraction /// integral to plasma membrane	---	
231434_at	LOC153441	-0.106	---	---	---	---	
237212_at	---	-0.106	---	---	---	---	
1552964_at	C10orf93	-0.105	---	---	---	---	
1555163_at	---	-0.105	---	---	---	---	
1562689_at	LOC151484	-0.105	---	---	---	---	
215259_s_at	IGSF4C	-0.105	---	---	---	---	
239598_s_at	FLJ20481	-0.105	metabolism	calcium ion binding /// acyltransferase activity	---	---	
243935_at	FRAS1	-0.105	---	structural molecule activity	viral capsid	---	
1553281_at	PLCXD2	-0.104	intracellular signaling cascade	phospholipase C activity	---	---	
206379_at	EYA3	-0.104	regulation of transcription, DNA-dependent /// development /// visual perception /// metabolism /// morphogenesis	magnesium ion binding /// catalytic activity /// phosphoprotein phosphatase activity /// protein tyrosine phosphatase activity /// hydrolase activity	nucleus	---	
230992_at	BTNL9	-0.104	---	---	integral to membrane	---	
232838_at	KIAA1713	-0.104	---	---	---	---	
1556362_at	---	-0.103	---	---	---	---	

1556810_a_at	WASL	-0.103	protein complex assembly /// cell motility /// actin polymerization and/or depolymerization	actin binding /// small GTPase regulatory/interacting protein activity	actin cytoskeleton	G13 Signaling Pathway
1567015_at	CSNK2A1	-0.103	Wnt receptor signaling pathway/// protein amino acid phosphorylation	protein binding/// ATP binding/// nucleotide binding/// protein serine/threonine kinase activity/// transferase activity	---	Adherens junction/// Tight junction/// Wnt signaling pathway
210193_at	MOBP	-0.103	neurogenesis	---	soluble fraction	---
243197_at	---	-0.103	---	---	---	---
1556084_at	HNRPM	-0.102	---	RNA binding /// transmembrane receptor activity	membrane fraction /// nucleus /// integral to plasma membrane /// ribonucleoprotein complex	---
1560899_at	ASTN	-0.102	cell adhesion /// neuronal cell adhesion /// cell migration	protein binding	integral to membrane	---
213228_at	PDE8B	-0.102	signal transduction /// cyclic nucleotide metabolism	magnesium ion binding /// 3',5'-cyclic-nucleotide phosphodiesterase activity /// signal transducer activity /// hydrolase activity /// manganese ion binding	---	G Protein Signaling
235668_at	PRDM1	-0.102	negative regulation of transcription from RNA polymerase II promoter/// regulation of transcription, DNA-dependent	transcription factor activity/// metal ion binding/// nucleic acid binding/// zinc ion binding	nucleus	
236722_at	AACS	-0.102	isoprenoid biosynthesis/// metabolism	acetate-CoA ligase activity/// catalytic activity	---	Butanoate metabolism

237157_at	DKFZp434D0215	-0.102	---	---	---	---
1557226_at	LOC374569	-0.101	amino acid metabolism	asparaginase activity	---	---
205649_s_at	FGA	-0.101	blood coagulation /// regulation of blood pressure /// positive regulation of cell proliferation	---	extracellular region /// fibrinogen complex /// soluble fraction	Blood Clotting Cascade
212128_s_at	DAG1	-0.101	protein complex assembly /// muscle contraction	laminin receptor activity /// calcium ion binding /// protein binding	extracellular matrix (sensu Metazoa) /// membrane fraction /// integral to plasma membrane /// actin cytoskeleton	---
227092_at	---	-0.101	---	---	---	---
229987_at	USP12	-0.1	ubiquitin-dependent protein catabolism /// ubiquitin cycle	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity /// hydrolase activity	---	---
232200_at	HSPA9B	-0.1	protein folding	ATP binding /// unfolded protein binding	mitochondrion	---
1558010_s_at	SLC1A2	-0.099	transport /// dicarboxylic acid transport /// synaptic transmission /// L-glutamate transport	L-glutamate transporter activity /// symporter activity /// sodium:dicarboxylate symporter activity	membrane fraction /// integral to membrane	---
238074_at	MGC43690	-0.099	---	---	---	---
244458_at	ZNF592	-0.099	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---

202886_s_at	PPP2R1B	-0.098	regulation of cell cycle /// inactivation of MAPK /// regulation of DNA replication /// regulation of translation /// protein complex assembly /// protein amino acid dephosphorylation /// ceramide metabolism /// induction of apoptosis /// RNA splicing /// response to organic substance /// second-messenger-mediated signaling /// regulation of Wnt receptor signaling pathway /// regulation of cell adhesion /// negative regulation of cell growth /// regulation of growth /// negative regulation of tyrosine phosphorylation of Stat3 protein /// regulation of transcription /// regulation of cell differentiation	protein phosphatase type 2A activity /// antigen binding /// phosphoprotein phosphatase activity /// binding /// protein binding /// protein phosphatase type 2A regulator activity /// protein heterodimerization activity	protein phosphatase type 2A complex /// soluble fraction /// nucleus /// mitochondrion /// cytosol /// microtubule /// cytoskeleton /// membrane	Glycogen Metabolism
235811_at	MBNL1	-0.098	embryonic development (sensu Mammalia) /// neurogenesis /// muscle development /// embryonic limb morphogenesis /// myoblast differentiation	nucleic acid binding /// double-stranded RNA binding	nucleus /// cytoplasm	—

1554172_at	ZNF261	-0.097	development	DNA binding /// zinc ion binding	nucleus	---
1561166_at	FOXP1	-0.097	regulation of transcription, DNA-dependent	nucleic acid binding /// transcription factor activity /// zinc ion binding	nucleus	---
216561_x_at	SOX5	-0.097	transcription from RNA polymerase II promoter /// regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---
234910_at	RASAL2	-0.097	signal transduction	Ras GTPase activator activity/// GTPase activator activity	---	---
239001_at	MGST1	-0.097	---	glutathione transferase activity /// transferase activity	mitochondrion /// microsome /// membrane	Glutathione metabolism
1568592_at	LOC400368	-0.096	---	---	---	---
232796_at	---	-0.096	---	---	---	---
240151_at	HAB1	-0.096	---	---	---	---
207635_s_at	KCNH1	-0.095	two-component signal transduction system (phosphorelay) /// cation transport /// potassium ion transport	two-component sensor molecule activity /// voltage-gated potassium channel activity /// calmodulin binding	integral to membrane	---
224672_x_at	MESDC2	-0.095	mesoderm development	---	---	---
233234_at	KCTD16	-0.095	potassium ion transport	voltage-gated potassium channel activity /// protein binding	voltage-gated potassium channel complex /// membrane	---
233259_at	FLJ12057	-0.095	---	---	---	---
1564262_at	PROX1	-0.094	---	---	---	---
227238_at	MUC15	-0.094	---	---	integral to membrane	---

1556306_at	MLL5	-0.093	regulation of transcription, DNA dependent	zinc ion binding/// protein binding	---	---
216437_at	EPC1	-0.093	regulation of transcription, DNA-dependent/// chromatin modification/// regulation of cell growth	transcriptional activator activity/// transcriptional repressor activity	nucleus	---
221041_s_at	SLC17A5	-0.093	transport	transporter activity /// symporter activity	lysosome /// integral to membrane	---
233566_at	MGC16291	-0.093	---	---	---	---
1569122_at	LOC400263	-0.092	---	---	---	---
208284_x_at	GGT1	-0.092	amino acid metabolism /// glutathione biosynthesis	gamma-glutamyltransferase activity /// acyltransferase activity /// transferase activity	integral to membrane	Eicosanoid Synthesis /// Taurine and hypotaurine metabolism /// Selenoamino acid metabolism /// Cyanoamino acid metabolism /// Glutathione metabolism /// Prostaglandin and leukotriene metabolism
228907_at	---	-0.092	---	---	---	---
229823_at	RIMS2	-0.092	intracellular protein transport	Rab GTPase binding/// metal ion binding/// protein binding/// zinc ion binding	---	---
232688_at	BMP2K	-0.092	protein amino acid phosphorylation	protein serine/threonine kinase activity /// ATP binding /// transferase activity	nucleus	---
237747_at	C10orf45	-0.092	---	---	---	---
237393_at	---	-0.091	---	---	---	---

238542_at	ULBP2	-0.091	antigen presentation /// natural killer cell activation	MHC class I receptor activity	membrane /// MHC class I protein complex	---	
1562497_at	---	-0.09	---	---	---	---	
214137_at	PTPRJ	-0.09	cell-cell signaling /// protein amino acid dephosphorylation /// transmembrane receptor protein tyrosine kinase signaling pathway	transmembrane receptor protein tyrosine phosphatase activity /// hydrolase activity	integral to plasmamembrane	---	Adherens junction
216832_at	RUNX1T1	-0.09	generation of precursor metabolites and energy /// regulation of transcription, DNA-dependent	transcription factor activity	nucleus	---	
232116_at	TFCP2L4	-0.09	---	---	---	---	
233106_at	C14orf82	-0.09	---	---	---	---	
1566144_at	---	-0.089	---	---	---	---	
1566844_at	PER4	-0.089	---	---	---	---	
1570596_at	---	-0.089	---	---	---	---	
221043_at	CHD9	-0.089	chromatin assembly or disassembly	ATP binding /// DNA binding /// chromatin binding /// helicase activity	chromatin /// nucleus /// integral to membrane	---	
234518_at	OR51B2	-0.089	G-protein coupled receptor protein signaling pathway /// sensory perception /// sensory perception of smell /// signal transduction	olfactory receptor activity	integral to membrane	---	
242094_at	---	-0.089	---	---	---	---	

206089_at	NELL1	-0.088	cell adhesion /// neurogenesis /// metabolism	structural molecule activity /// calcium ion binding /// kinase activity /// oxidoreductase activity	---	---
209874_x_at	CNNM2	-0.088	fatty acid biosynthesis	---	---	---
211162_x_at	SCD	-0.088	fatty acid biosynthesis	stearoyl-CoA 9-desaturase activity /// iron ion binding /// oxidoreductase activity	endoplasmic reticulum /// integral to membrane	Fatty Acid Synthesis
220522_at	CRB1	-0.088	cell adhesion /// establishment and/or maintenance of cell polarity /// cell-cell signaling /// visual perception	structural molecule activity /// calcium ion binding	---	---
242263_at	CGI-100	-0.088	intracellular protein transport	protein carrier activity	endoplasmic reticulum /// integral to membrane	---
1562321_at	PDK4	-0.087	glucose metabolism /// protein amino acid phosphorylation	protein kinase activity /// [pyruvate dehydrogenase (lipoamide)] kinase activity /// ATP binding /// transferase activity	mitochondrion	Krebs-TCA Cycle
213784_at	RABL4	-0.087	small GTPase mediated signal transduction /// protein transport	GTP binding	---	---
1556753_s_at	HOXC6	-0.086	regulation of transcription from RNA polymerase II promoter/// regulation of transcription, DNA-dependent/// development	sequence-specific DNA binding/// transcription corepressor activity/// transcription factor activity	nucleus	---

1556768_at	---	-0.086	---	---	---	---	---
1560877_at	C18orf30	-0.086	---	---	integral to membrane	---	---
1565621_at	---	-0.086	---	---	---	---	---
230495_at	LOC150568	-0.086	---	---	---	---	---
234059_at	CPOX	-0.086	heme biosynthesis	coproporphyrinogen oxidase activity /// oxidoreductase activity	mitochondrion	Heme Biosynthesis /// Porphyrin and chlorophyll metabolism	---
241208_at	LIM	-0.086	heart development	actin binding /// protein kinase C binding /// protein binding /// receptor signaling complex scaffold activity /// actinin binding	membrane fraction /// cytosol	---	---
1556776_at	ZNF426	-0.085	regulation of transcription, DNA-dependent	DNA binding/// metal ion binding/// zinc ion binding	intracellular/// nucleus	---	---
1570645_at	---	-0.085	---	---	---	---	---
217017_at	OSBPL10	-0.085	lipid transport/// steroid metabolism	---	---	---	---
1564194_at	MGC35295	-0.084	signal transduction	receptor activity	integral to membrane	---	---
221582_at	HIST3H2A	-0.084	nucleosome assembly /// chromosome organization and biogenesis (sensu Eukaryota)	DNA binding	nucleosome /// nucleus	---	---
235935_at	C6orf154	-0.084	---	---	---	---	---

241995_at	DGUOK	-0.084	nucleobase, nucleoside, nucleotide and nucleic acid metabolism /// guanosine metabolism	deoxyguanosine kinase activity /// ATP binding /// kinase activity /// transferase activity /// phosphotransferase activity, alcohol group as acceptor	mitochondrion	Purine metabolism
1563057_at	---	-0.083	---	---	---	---
211037_s_at	LENG4	-0.083	---	receptor activity	---	---
219995_s_at	FLJ13841	-0.083	---	nucleic acid binding /// zinc ion binding	nucleus	---
236107_at	FLJ13855	-0.083	ubiquitin cycle	ubiquitin conjugating enzyme activity	---	---
1564423_at	RGPR	-0.082	---	---	---	---
1566502_at	HYDIN	-0.082	---	---	---	---
229580_at	---	-0.082	---	---	---	---
1559295_at	CREBBP	-0.081	regulation of transcription, DNA-dependent /// histone acetylation /// homeostasis /// positive regulation of transcription /// protein complex assembly /// response to hypoxia /// signal transduction	transcription factor activity /// MyoD binding /// acetyltransferase activity /// histone acetyltransferase activity /// protein binding /// signal transducer activity /// transcription coactivator activity /// transferase activity /// zinc ion binding	cytoplasm /// nucleus	adherens junction /// calcium signaling pathway /// cell cycle /// Huntington's disease /// Jak-STAT signaling pathway /// long-term potentiation /// neurodegenerative disorders /// notch signaling pathway /// TGF-beta signaling pathway /// Wnt signaling pathway
227437_at	---	-0.081	---	---	---	---

228996_at	KIAA2025	-0.081	protein ubiquitination	nucleic acid binding /// ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---	
240049_at	DLG5	-0.081	regulation of cell cycle /// intracellular signaling cascade /// cell-cell adhesion	protein binding /// receptor signaling complex scaffold activity	plasma membrane	---	
1553041_at	HTR3C	-0.08	ion transport	extracellular ligand-gated ion channel activity /// neurotransmitter receptor activity	integral to membrane /// postsynaptic membrane	---	
1557753_at	---	-0.08	---	---	---	---	
1564521_x_at	SKB1	-0.08	regulation of mitosis /// cell proliferation	methyltransferase activity /// transferase activity	cytoplasm	---	
1565928_at	MAK10	-0.08	---	---	---	---	
223630_at	C7orf13	-0.08	metal ion transport	metal ion binding	---	---	
237060_at	YTHDF2	-0.08	---	---	---	---	
239286_at	CDH11	-0.08	ossification /// cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	integral to membrane	---	
240631_at	GPR98	-0.08	nervous system development/// cell-cell adhesion/// cell communication/// neuropeptide signaling pathway	G-protein coupled receptor activity/// calcium ion binding	integral to membrane	---	
1559507_at	PHACTR1	-0.079	---	actin binding/// protein phosphatase inhibitor activity	---	---	

214106_s_at	GMDS	-0.079	carbohydrate metabolism /// leukocyte cell adhesion /// biosynthesis /// 'de novo' GDP-L-fucose biosynthesis	GDP-mannose 4,6-dehydratase activity /// lyase activity	cytoplasm	---
215713_at	ZFHX1B	-0.079	regulation of transcription, DNA-dependent /// neurogenesis /// negative regulation of transcription	transcription factor activity /// zinc ion binding /// transcriptional repressor activity /// phosphatase regulator activity /// SMAD binding	nucleus	TGF Beta Signaling Pathway
227425_at	REPS2	-0.079	epidermal growth factor receptor signaling pathway/// protein complex assembly	calcium ion binding/// protein binding	---	---
242843_at	BCAN	-0.079	cell adhesion	sugar binding /// hyaluronic acid binding	---	---
217156_at	HADHA	-0.078	lipid metabolism /// fatty acid metabolism	3-hydroxyacyl-CoA dehydrogenase activity/// acetyl-CoA C-acetyltransferase activity/// enoyl-CoA hydratase activity/// long-chain-3-hydroxyacyl-CoA dehydrogenase activity/// lyase activity/// oxidoreductase activity	mitochondrion	Benzoate degradation via CoA ligation/// Butanoate metabolism/// Caprolactam degradation /// Fatty acid elongation in mitochondria/// Fatty acid metabolism/// Limonene and pinene degradation /// Lysine degradation/// Propanoate metabolism/// Tryptophan metabolism/// Valine, leucine and isoleucine degradation/// beta-Alanine metabolism

221658_s_at	IL21R	-0.078	natural killer cell activation	interleukin-21 receptor activity /// receptor activity /// hematopoietin/interferon class (D200-domain) cytokine receptor activity	integral to membrane	---
231154_x_at	TINAG	-0.078	proteolysis and peptidolysis /// cell adhesion	cysteine-type endopeptidase activity /// protein binding /// cysteine-type peptidase activity	basement membrane	---
240165_at	---	-0.078	---	---	---	---
243992_at	ZNF198	-0.078	regulation of transcription, DNA-dependent	zinc ion binding	nucleus	---
204653_at	TFAP2A	-0.077	regulation of transcription, DNA-dependent /// regulation of transcription from Pol II promoter /// signal transduction /// ectoderm development	transcription factor activity /// RNA polymerase II transcription factor activity, enhancer binding /// transcription coactivator activity	nucleus	---
207472_at	RARSL	-0.077	protein biosynthesis/// arginyl-tRNA aminoacylation	ATP binding/// arginine-tRNA ligase activity	---	---
227777_at	C10orf18	-0.077	---	---	---	---
231042_s_at	CAMK2D	-0.077	regulation of cell growth/// protein amino acid phosphorylation	calcium- and calmodulin-dependent protein kinase activity/// ATP binding/// calmodulin binding/// nucleotide binding/// protein serine/threonine kinase activity/// transferase activity	calcium- and calmodulin-dependent protein kinase complex	Calcium signaling pathway/// Wnt signaling pathway
236683_at	---	-0.077	---	---	---	---
1560915_at	KIAA0877	-0.076	---	---	---	---

205941_s_at	COL10A1	-0.076	skeletal development /// phosphate transport	structural molecule activity	collagen /// cytoplasm	---	
210399_x_at	FUT6	-0.076	protein amino acid glycosylation /// L-fucose catabolism	transferase activity, transferring glycosyl groups /// 3-galactosyl-N-acetylglucosaminide 4-alpha-L-fucosyltransferase activity /// alpha(1,3)-fucosyltransferase activity	extracellular region /// Golgi apparatus /// integral to membrane	Blood group glycolipid biosynthesis-lactoseries	
1555461_at	---	-0.075	---	---	---	---	
1557697_at	EPHA5	-0.075	protein amino acid phosphorylation /// transmembrane receptor protein tyrosine kinase signaling pathway	protein-tyrosine kinase activity /// receptor activity /// transmembrane-ephrin receptor activity /// ATP binding /// transferase activity	integral to membrane	---	
1569659_at	HECW1	-0.075	---	---	---	---	
1570479_at	ART1	-0.075	protein amino acid ADP-ribosylation	NAD+ ADP-ribosyltransferase activity /// NAD(P)+-protein-arginine ADP-ribosyltransferase activity /// transferase activity, transferring glycosyl groups	integral to plasma membrane	---	
204691_x_at	PLA2G6	-0.075	phospholipid metabolism /// lipid catabolism	phospholipase A2 activity /// hydrolase activity	cytoplasm /// membrane	Eicosanoid Synthesis /// Glycerophospholipid metabolism /// Prostaglandin and leukotriene metabolism	
224473_x_at	LZTS2	-0.075	cell cycle /// negative regulation of cell cycle	---	cytoplasm /// membrane	---	

243730_at	---	-0.075	---	---	---	---
1557630_s_at	PPP1R12A	-0.074	regulation of muscle contraction	signal transducer activity	actin cytoskeleton	---
1564233_at	FLJ33534	-0.074	---	---	---	---
215639_at	SH2D3C	-0.074	JNK cascade /// small GTPase mediated signal transduction	SH3/SH2 adaptor protein activity /// guanyl-nucleotide exchange factor activity	---	---
227037_at	LOC201164	-0.074	metabolism /// lipid catabolism	hydrolase activity	---	---
1556620_at	ZNF721	-0.073	---	zinc ion binding/// nucleic acid binding	intracellular/// nucleus	---
1561086_at	LAF4	-0.073	regulation of transcription, DNA-dependent /// development	DNA binding	nucleus	---
1561887_at	---	-0.073	---	---	---	---
217629_at	---	-0.073	---	---	---	---
231053_at	---	-0.073	---	---	---	---
244167_at	DELGEF	-0.073	signal transduction	Ran guanyl-nucleotide exchange factor activity /// protein binding	nucleus /// cytoplasm	---
1562839_at	---	-0.072	---	---	---	---
208547_at	HIST1H2BB	-0.072	nucleosome assembly /// chromosome organization and biogenesis (sensu Eukaryota)	DNA binding	nucleosome /// nucleus /// chromosome	---
222956_at	FIGN	-0.072	---	ATP binding/// nucleoside-triphosphatase activity/// nucleotide binding	---	---
228158_at	LOC440684	-0.072	---	---	---	---

237781_at	HORMAD2	-0.072	---	---	---	---
244687_at	---	-0.072	---	---	---	---
207369_at	BRS3	-0.071	glucose metabolism /// smooth muscle contraction /// G-protein coupled receptor protein signaling pathway /// response to nutrients /// regulation of blood pressure /// adult feeding behavior	rhodopsin-like receptor activity /// bombesin receptor activity	plasma membrane /// integral to membrane	GPCRDB Class A Rhodopsin-like /// Peptide GPCRs
216898_s_at	COL4A3	-0.071	proteolysis and peptidolysis /// phosphate transport /// induction of apoptosis /// caspase activation /// cell adhesion /// cell surface receptor linked signal transduction /// perception of sound /// circulation /// cell proliferation /// negative regulation of cell proliferation /// negative regulation of angiogenesis	serine carboxypeptidase activity /// integrin binding /// extracellular matrix structural constituent /// protein binding /// metalloendopeptidase inhibitor activity	collagen /// collagen type IV /// cytoplasm	---
220784_s_at	UTS2	-0.071	muscle contraction /// synaptic transmission /// regulation of blood pressure	hormone activity	extracellular region /// extracellular space	---
222271_at	---	-0.071	---	---	---	---
226245_at	KCTD1	-0.071	potassium ion transport	ion channel activity /// voltage-gated potassium channel activity /// protein binding	voltage-gated potassium channel complex /// membrane	---
241244_at	---	-0.071	---	---	---	---

206713_at	NTNG1	-0.07	axonogenesis	structural molecule activity	extracellular matrix (sensu Metazoa) /// membrane /// anchored to plasma membrane	---
213456_at	SOSTDC1	-0.07	---	---	---	---
220636_at	DNAI2	-0.07	---	motor activity	dynein complex	---
230572_at	FLJ30277	-0.07	---	---	---	---
237148_at	AMMECR1	-0.07	---	---	---	---
1553276_at	ZNF560	-0.069	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
1553584_at	CXorf36	-0.069	---	---	---	---
206985_at	HSD17B3	-0.069	steroid biosynthesis /// sex determination /// metabolism /// male genitalia morphogenesis	estradiol 17-beta-dehydrogenase activity /// oxidoreductase activity	microsome	Steroid Biosynthesis /// Androgen and estrogen metabolism
229654_at	ZNF44	-0.069	regulation of transcription, DNA-dependent	protein binding /// DNA binding /// metal ion binding /// nucleic acid binding /// zinc ion binding	intracellular /// nucleus	---
231740_at	KCNJ11	-0.069	ion transport /// potassium ion transport	voltage-gated ion channel activity /// potassium channel activity /// ATP-activated inward rectifier potassium channel activity	membrane fraction /// integral to plasma membrane	---
234877_x_at	IGLC1	-0.069	---	---	---	---
1561437_at	MCHR2	-0.068	G-protein coupled receptor protein signaling pathway	receptor activity /// rhodopsin-like receptor activity	integral to membrane	Neuroactive ligand-receptor interaction

1566512_at	GNG4	-0.068	regulation of G-protein coupled receptor protein signaling pathway	signal transducer activity	plasma membrane/// heterotrimeric G-protein complex	energy metabolism	
226812_at	ZFP91	-0.068	regulation of transcription, DNA-dependent	zinc ion binding/// DNA binding	nucleus	---	
233355_at	LOC284739	-0.068	---	---	---	---	
1557413_a_at	---	-0.067	---	---	---	---	
1561917_at	---	-0.067	---	---	---	---	
1566124_a_at	FABP6	-0.067	lipid metabolism /// transport/// negative regulation of cell proliferation	fatty acid binding/// lipid binding	cytoplasm	---	
220281_at	SLC12A1	-0.067	ion transport /// potassium ion transport /// sodium ion transport /// chloride transport /// amino acid transport	transporter activity /// amino acid-polyamine transporter activity /// sodium:potassium:chloride symporter activity /// symporter activity	membrane fraction /// plasma membrane /// membrane /// integral to membrane	---	
228670_at	TEP1	-0.067	DNA replication and chromosome cycle /// telomerase-dependent telomere maintenance	telomerase activity /// RNA binding /// protein binding /// ATP binding	chromosome, telomeric region /// telomerase holoenzyme complex	---	
235602_at	TP53INP1	-0.067	apoptosis	---	nucleus	---	
239638_at	---	-0.067	---	---	---	---	
223292_s_at	MRPS15	-0.066	protein biosynthesis	structural constituent of ribosome	mitochondrial small ribosomal subunit /// mitochondrion/// ribosome	---	
234956_at	LOC93444	-0.066	---	---	---	---	

217233_at	CHAF1B	-0.065	DNA replication-dependent nucleosome assembly/// protein complex assembly/// regulation of transcription, DNA dependent/// cell cycle/// DNA repair	chromatin binding/// histone binding/// unfolded protein binding	chromatin assembly complex/// cytoplasm/// nucleus	---
219720_s_at	C14orf118	-0.065	---	---	---	---
223373_s_at	PLA2G12A	-0.065	lipid catabolism	calcium ion binding /// hydrolase activity /// calcium-dependent phospholipase A2 activity	extracellular region	---
243299_at	VRK2	-0.065	protein amino acid phosphorylation	protein serine/threonine kinase activity /// ATP binding /// transferase activity	integral to membrane	---
200831_s_at	SCD	-0.064	fatty acid biosynthesis	stearoyl-CoA 9-desaturase activity /// iron ion binding /// oxidoreductase activity	endoplasmic reticulum /// integral to membrane	Fatty Acid Synthesis
201988_s_at	CREBL2	-0.064	transcription /// signal transduction	transcription factor activity	nucleus	---
216955_at	TAF1	-0.064	G1 phase of mitotic cell cycle /// transcription initiation /// regulation of transcription, DNA-dependent /// cell cycle /// autophosphorylation	DNA binding /// histone acetyltransferase activity /// protein serine/threonine kinase activity /// protein binding /// ATP binding /// transferase activity	nucleus /// transcription factor TFIID complex	---
239851_at	TMP21	-0.064	ER to Golgi transport /// protein transport	---	membrane fraction /// microsome /// Golgi apparatus /// integral to plasma membrane	mRNA processing

229261_at	SOS1	-0.063	Ras protein signal transduction	DNA binding /// Ras guanyl-nucleotide exchange factor activity /// Rho guanyl-nucleotide exchange factor activity /// Rho GTPase activator activity	---	Integrin-mediated cell adhesion
233795_at	ODF3	-0.063	---	---	---	---
235210_s_at	RPESP	-0.063	---	---	---	---
241095_at	---	-0.063	---	---	---	---
242863_at	---	-0.063	---	---	---	---
1560496_at	---	-0.062	---	---	---	---
1561336_at	DNASE1L3	-0.062	DNA catabolism /// apoptosis	DNA binding /// endonuclease activity /// deoxyribonuclease activity /// calcium ion binding /// hydrolase activity	nucleus	---
1561351_at	---	-0.062	---	---	---	---
1564021_at	MGC11257	-0.062	---	---	---	---
1564285_at	LOC164045	-0.062	---	---	---	---
226807_at	ZFP1	-0.062	regulation of transcription, DNA-dependent	DNA binding /// zinc ion binding	nucleus	---
228796_at	CPNE4	-0.062	---	---	---	---

238486_at	FRS2	-0.062	transmembrane receptor protein tyrosine phosphatase signaling pathway /// G-protein coupled receptor protein signaling pathway /// fibroblast growth factor receptor signaling pathway	receptor activity /// transmembrane receptor protein tyrosine kinase adaptor protein activity /// insulin receptor binding /// protein binding /// regulator of G-protein signaling activity /// phosphatase activator activity	integral to plasma membrane	---	
1558794_at	---	-0.061	---	---	---	---	
207526_s_at	IL1RL1	-0.061	signal transduction	transmembrane receptor activity /// interleukin-1 receptor activity /// receptor signaling protein activity /// protein binding	integral to membrane	---	
216256_at	GRM8	-0.061	G-protein coupled receptor protein signaling pathway /// negative regulation of adenylate cyclase activity /// synaptic transmission /// visual perception /// perception of smell	receptor activity /// metabotropic glutamate, GABA-B-like receptor activity	integral to plasma membrane /// membrane	GPCRDB Class C Metabotropic glutamate pheromone	
230285_at	DKFZp313A2432	-0.061	---	---	---	---	
241594_at	---	-0.061	---	---	---	---	
243570_at	KIAA0102	-0.061	signal peptide processing	signal peptidase activity	endoplasmic reticulum /// signal peptidase complex /// microsome /// integral to membrane	---	

217033_x_at	NTRK3	-0.06	transmembrane receptor protein tyrosine kinase signaling pathway /// protein amino acid phosphorylation/// nervous system development/// cell differentiation	neurotrophin binding/// kinase activity/// ATP binding/// receptor activity/// transferase activity	integral to plasma membrane	---	
235753_at	LOC285944	-0.06	---	---	---	---	---
1553636_at	MGC35118	-0.059	---	---	---	---	---
1569351_at	FLJ10159	-0.059	---	---	---	---	---
216083_s_at	NEU3	-0.059	carbohydrate metabolism /// ganglioside catabolism	exo-alpha-sialidase activity /// hydrolase activity, acting on glycosyl bonds	integral to plasma membrane /// membrane	N-Glycan degradation /// Glycosphingolipid metabolism	
217481_x_at	FLJ45455	-0.059	---	---	---	---	---
217761_at	MTCBP-1	-0.059	methionine biosynthesis	---	---	---	---
220284_at	DKKL1	-0.059	morphogenesis	signal transducer activity	extracellular space	---	
232637_at	NEDD5	-0.059	cytokinesis /// cell cycle	GTPase activity /// GTP binding	contractile ring	---	
37433_at	PIAS2	-0.059	regulation of transcription, DNA-dependent /// ubiquitin cycle /// development	DNA binding /// zinc ion binding	nucleus	---	
1561297_at	WARS2	-0.058	protein biosynthesis /// tryptophanyl-tRNA aminoacylation	tryptophan-tRNA ligase activity /// ATP binding /// ligase activity	soluble fraction /// mitochondrion	Tryptophan metabolism /// Aminoacyl-tRNA biosynthesis	
226263_at	C6orf151	-0.058	---	---	---	---	---
238580_at	C4orf8	-0.058	---	---	---	---	---
244147_at	KIAA1217	-0.058	---	---	---	---	---

1555661_at	OR8D1	-0.057	G-protein coupled receptor protein signaling pathway /// perception of smell	olfactory receptor activity	integral to membrane	---
1558785_a_at	RGS5	-0.057	signal transduction /// regulation of G-protein coupled receptor protein signaling pathway	signal transducer activity /// GTPase activator activity	---	Calcium regulation in cardiac cells /// Smooth muscle contraction
1565358_at	RARA	-0.057	regulation of transcription, DNA-dependent /// signal transduction	transcription factor activity /// steroid hormone receptor activity /// retinoic acid receptor activity /// transcription coactivator activity	nucleus	Nuclear Receptors
210365_at	RUNX1	-0.057	regulation of transcription, DNA-dependent /// development	transcription factor activity /// ATP binding	nucleus	---
234248_at	---	-0.057	---	---	---	---
1556003_a_at	---	-0.056	---	---	---	---
205228_at	RBMS2	-0.056	RNA processing /// regulation of translation	RNA binding	nucleus	---
216675_at	---	-0.056	---	---	---	---
233570_at	TSC1	-0.056	cell adhesion /// Rho protein signal transduction /// negative regulation of cell cycle	---	---	---
210871_x_at	SSX2IP	-0.055	cell adhesion	protein binding	nucleus	---
242042_s_at	LOC401022	-0.055	---	---	---	---
1558605_at	---	-0.054	---	---	---	---

1562969_at	DNMBP	-0.054	intracellular signaling cascade	guanyl-nucleotide exchange factor activity /// protein binding	Golgi apparatus /// cytoskeleton	---
213489_at	MAPRE2	-0.054	cellular defense response /// signal transduction /// cell proliferation	microtubule binding	---	---
217648_at	RWDD3	-0.054	---	---	---	---
221497_x_at	EGLN1	-0.054	protein metabolism	oxidoreductase activity /// oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen /// oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	cytosol	---
213424_at	KIAA0895	-0.053	---	---	---	---
221446_at	ADAM30	-0.053	proteolysis and peptidolysis	metalloendopeptidase activity /// zinc ion binding /// hydrolase activity	integral to membrane	---
237711_at	LOC283202	-0.053	---	---	---	---
240603_s_at	MGC16943	-0.053	---	exonuclease activity	nucleus	---
1568762_at	PDCD6	-0.052	apoptosis /// induction of apoptosis by extracellular signals	calcium ion binding	---	---

214610_at	CYP11B1	-0.052	electron transport /// C21-steroid hormone biosynthesis	monooxygenase activity /// steroid 11-beta-monooxygenase activity	mitochondrion /// membrane	C21-Steroid hormone metabolism /// Androgen and estrogen metabolism
214917_at	PRKAA1	-0.052	activation of MAPK /// response to hypoxia /// protein amino acid phosphorylation /// fatty acid biosynthesis /// cholesterol biosynthesis /// negative regulation of protein biosynthesis /// positive regulation of cholesterol biosynthesis /// positive regulation of gluconeogenesis /// positive regulation of anti-apoptosis /// negative regulation of glucosylceramide biosynthesis /// positive regulation of fatty acid oxidation /// positive regulation of glucose import	protein serine/threonine kinase activity /// cAMP-dependent protein kinase activity /// ATP binding /// transferase activity /// eukaryotic elongation factor-2 kinase activator activity	intracellular	Fatty Acid Synthesis
218415_at	VPS33B	-0.052	vesicle docking during exocytosis /// protein transport /// vesicle-mediated transport	---	membrane	---
237126_at	MCP	-0.052	complement activation, classical pathway	---	receptor activity	integral to plasma membrane	---
238195_at	---	-0.052	---	---	---	---	---
1553459_at	FLJ39660	-0.051	---	---	---	---	---
216630_at	---	-0.051	---	---	---	---	---
231171_at	---	-0.051	---	---	---	---	---

243009_at	INTS4	-0.051	snRNA processing	protein binding	integrator complex	---
1552327_at	ARMCX4	-0.05	---	---	---	---
1558900_at	---	-0.05	---	---	---	---
243897_at	---	-0.05	---	---	---	---
1552738_a_at	ST7L	-0.049	---	binding	---	---
207973_x_at	ACRV1	-0.049	development	---	---	---
1558324_a_at	---	-0.048	---	---	---	---
1563528_at	LOC91149	-0.048	---	---	---	---
206230_at	LHX1	-0.048	regulation of transcription, DNA-dependent /// neurogenesis	transcription factor activity /// RNA polymerase II transcription factor activity /// zinc ion binding	nucleus	---
219586_at	FLJ12270	-0.048	---	structural molecule activity	---	---
1569263_at	CSNK1D	-0.047	DNA repair/// protein amino acid phosphorylation/// signal transduction	casein kinase I activity/// ATP binding/// protein serinr/threonine kinase activity/// transferase activity/// nucleotide binding	---	circadian rhythm/// gap junction/// hedgehog signaling pathway
202952_s_at	ADAM12	-0.047	proteolysis and peptidolysis /// cell adhesion /// myoblast fusion	metalloendopeptidase activity /// protein binding /// zinc ion binding /// hydrolase activity	plasma membrane /// integral to membrane	---

215969_at	PIGA	-0.047	biosynthesis	transferase activity, transferring glycosyl groups /// phosphatidylinositol N-acetylglucosaminyltransferase activity	endoplasmic reticulum membrane /// integral to membrane	---
221706_s_at	MDS032	-0.047	transport	---	endoplasmic reticulum /// Golgi apparatus /// integral to membrane	---
231075_x_at	RAPH1	-0.046	signal transduction	---	cytoskeleton	---
1561217_at	---	-0.045	---	---	---	---
214028_x_at	TDRD3	-0.045	---	nucleic acid binding	---	---
243125_x_at	---	-0.045	---	---	---	---
1563482_at	DPYSL2	-0.044	nucleobase, nucleoside, nucleotide and nucleic acid metabolism /// signal transduction /// neurogenesis	dihydropyrimidinase activity /// hydrolase activity	---	---
220759_at	FAM12B	-0.044	spermatid cell development	nucleic acid binding /// pancreatic ribonuclease activity	extracellular region	---
243930_x_at	GLIPR1	-0.044	---	---	extracellular region /// integral to membrane	---
1559755_at	C21orf49	-0.043	---	---	---	---
1561712_at	FLJ12716	-0.043	---	---	---	---

211547_s_at	PAFAH1B1	-0.043	establishment of mitotic spindle orientation /// cytokinesis /// lipid metabolism /// cell motility /// microtubule-based process /// mitosis /// signal transduction /// neurogenesis	dynein binding	astral microtubule /// kinetochore /// nuclear membrane /// cytoplasm /// cytoskeleton /// microtubule associated complex /// cell cortex	Wnt signaling /// Glycerophospholipid metabolism
1559524_at	---	-0.042	---	---	---	---
217181_at	IL2	-0.042	T cell differentiation/// anti-apoptosis/// antimicrobial humoral response (sensu Vertebrata)/// cell adhesion/// cell-cell signaling/// immune response/// natural killer cell activation/// positive regulation of cell growth/// positive regulation of cell proliferation	cytokine activity/// interleukin-2 receptor binding/// kinase activator activity	extracellular region	Cytokine-cytokine receptor interaction/// Jak-STAT signaling pathway/// T cell receptor signaling pathway/// Type I diabetes mellitus
235415_at	KIAA0460	-0.042	---	---	---	---
236826_at	C9orf52	-0.042	---	binding	---	---
244318_at	KIAA0241	-0.042	---	---	---	---
239516_at	LYPLAL1	-0.041	---	catalytic activity	---	---
1552312_a_at	MFAP3	-0.04	---	extracellular matrix structural constituent	extracellular matrix (sensu Metazoa) /// integral to membrane	---

1554534_at	DPYD	-0.04	electron transport /// 'de novo' pyrimidine base biosynthesis /// uracil catabolism /// thymidine catabolism	dihydroorotate dehydrogenase activity /// dihydroorotate oxidase activity /// electron transporter activity /// iron ion binding /// disulfide oxidoreductase activity /// oxidoreductase activity /// dihydropyrimidine dehydrogenase (NADP+) activity	cytoplasm /// mitochondrion /// membrane	Pyrimidine metabolism /// beta-Alanine metabolism /// Pantothenate and CoA biosynthesis	
1554776_at	ZFP42	-0.04	---	nucleic acid binding /// zinc ion binding	nucleus	---	
207192_at	DNASE1L2	-0.04	DNA catabolism	DNA binding /// endonuclease activity /// deoxyribonuclease activity /// calcium ion binding /// hydrolase activity	---	---	
222964_at	MGC20741	-0.04	ubiquitin-dependent protein catabolism /// ubiquitin cycle	cysteine-type endopeptidase activity /// ubiquitin thiolesterase activity /// hydrolase activity	---	---	
224022_x_at	WNT16	-0.04	frizzled-2 signaling pathway /// cell-cell signaling /// development	signal transducer activity /// extracellular matrix structural constituent	extracellular region	Wnt signaling	
1562693_at	---	-0.039	---	---	---	---	
205184_at	GNG4	-0.039	signal transduction /// regulation of G-protein coupled receptor protein signaling pathway	signal transducer activity	heterotrimeric G-protein complex /// plasma membrane	G Protein Signaling /// Calcium regulation in cardiac cells /// Smooth muscle contraction	

225592_at	NRM	-0.039	---	---	---	---
226833_at	FLJ32499	-0.039	---	---	---	---
1556447_at	LOC285370	-0.038	---	---	---	---
1563204_at	ACP5	-0.038	---	acid phosphatase activity /// hydrolase activity	lysosome /// integral to membrane	gamma-Hexachlorocyclohexane degradation /// Riboflavin metabolism
216762_at	ANKRD15	-0.038	cell cycle	---	---	---
218820_at	C14orf132	-0.038	---	---	integral to membrane	---
232718_at	---	-0.038	---	---	---	---
239376_at	---	-0.038	---	---	---	---
1569688_at	FMO5	-0.037	electron transport	monooxygenase activity /// dimethylaniline monooxygenase (N-oxide-forming) activity /// disulfide oxidoreductase activity	microsome /// integral to membrane	---
229240_at	ZDHHC21	-0.037	---	acyltransferase activity /// transferase activity/// zinc ion binding	integral to membrane	---
1554642_at	RNF32	-0.036	protein ubiquitination	ubiquitin-protein ligase activity /// zinc ion binding	ubiquitin ligase complex	---
1556924_at	ALS2CR10	-0.036	---	---	---	---
205156_s_at	ACCN2	-0.036	ion transport /// sodium ion transport	ion channel activity /// amiloride-sensitive sodium channel activity	integral to membrane	---
238233_at	---	-0.036	---	---	---	---
1556338_at	UBE1C	-0.035	ubiquitin cycle /// apoptosis /// cell cycle	catalytic activity /// ubiquitin activating enzyme activity /// ATP binding /// ligase activity	---	---

1569783_at	CYP51A1	-0.035	electron transport /// cholesterol biosynthesis	monooxygenase activity /// sterol 14-demethylase activity	integral to membrane	Cholesterol Biosynthesis /// Fatty acid metabolism /// gamma-Hexachlorocyclohexane degradation /// Tryptophan metabolism
209785_s_at	PLA2G4C	-0.035	---	---	---	---
239256_at	SDC1	-0.035	---	cytoskeletal protein binding	integral to plasma membrane	---
204241_at	ACOX3	-0.034	electron transport /// fatty acid metabolism /// fatty acid beta-oxidation /// bile acid metabolism	acyl-CoA oxidase activity /// oxidoreductase activity	peroxisome	---
243824_at	---	-0.034	---	---	---	---
1559462_at	---	-0.033	---	---	---	---
1566448_at	CD6	-0.033	immune response /// cell adhesion	scavenger receptor activity /// protein binding	integral to plasma membrane	---
220172_at	FLJ13096	-0.033	---	---	---	---
240450_at	PAPPA	-0.032	proteolysis and peptidolysis /// pregnancy /// cell differentiation	metallopeptidase activity /// zinc ion binding /// hydrolase activity	extracellular space /// membrane	---
241790_at	KLHL7	-0.032	---	protein binding	---	---

1566965_at	DPYD	-0.031	electron transport /// 'de novo' pyrimidine base biosynthesis /// uracil catabolism /// thymidine catabolism	dihydroorotate dehydrogenase activity /// dihydroorotate oxidase activity /// electron transporter activity /// iron ion binding /// disulfide oxidoreductase activity /// oxidoreductase activity /// dihydropyrimidine dehydrogenase (NADP+) activity	cytoplasm /// mitochondrion /// membrane	Pyrimidine metabolism /// beta-Alanine metabolism /// Pantothenate and CoA biosynthesis
1567255_at	OR10D1P	-0.031	---	---	---	---
219368_at	NAP1L2	-0.031	nucleosome assembly	---	nucleus /// chromatin assembly complex	---
239497_at	EPS15L1	-0.031	endocytosis	calcium ion binding	nucleus /// coated pit	---
1552648_a_at	TNFRSF10A	-0.03	apoptosis /// induction of apoptosis /// caspase activation /// signal transduction /// activation of NF-kappaB-inducing kinase /// induction of apoptosis via death domain receptors	receptor activity /// death receptor activity /// caspase activator activity /// TRAIL binding	integral to membrane	---
204671_s_at	ANKRD6	-0.029	---	---	---	---
242857_at	STK25	-0.029	protein amino acid phosphorylation /// response to oxidative stress /// signal transduction	protein serine/threonine kinase activity /// protein-tyrosine kinase activity /// ATP binding /// transferase activity	---	---
1557197_a_at	LGALS3	-0.028	---	sugar binding /// IgE binding	extracellular region /// nucleus /// plasma membrane	---

222663_at	RIOK2	-0.028	---	protein serine/threonine kinase activity /// ATP binding /// transferase activity	---	---
1561121_at	TTC10	-0.027	protein biosynthesis /// excretion	structural constituent of ribosome /// binding	intracellular /// ribosome	---
1562888_at	LOC112937	-0.027	carbohydrate metabolism	beta-galactosidase activity	beta-galactosidase complex	---
228010_at	PPP2R2C	-0.027	signal transduction	phosphoprotein phosphatase activity /// protein phosphatase type 2A regulator activity	protein phosphatase type 2A complex	Glycogen Metabolism
1554840_at	LOC280665	-0.026	---	---	---	---
211182_x_at	RUNX1	-0.026	regulation of transcription, DNA-dependent /// development	transcription factor activity /// ATP binding	nucleus	---
215973_at	HCG4P6	-0.026	---	---	---	---
1553946_at	DCD	-0.025	xenobiotic metabolism /// defense response to bacteria /// defense response to fungi	manganese ion binding	extracellular region	---
1556138_a_at	COL5A1	-0.024	phosphate transport /// cell adhesion	extracellular matrix structural constituent /// heparin binding	collagen /// collagen type V /// cytoplasm	---
209569_x_at	D4S234E	-0.024	dopamine receptor signaling pathway	dopamine receptor binding	nucleus /// Golgi apparatus /// integral to membrane	---
216746_at	LRCH1	-0.024	---	---	---	---
234079_at	RGNEF	-0.024	intracellular signaling cascade	---	---	---
241007_at	---	-0.024	---	---	---	---
243402_at	MGC35023	-0.024	---	---	---	---
1556613_s_at	LOC203107	-0.023	---	---	---	---

220041_at	SMP3	-0.023	---	RNA binding /// ribonuclease H activity /// transferase activity, transferring glycosyl groups	---	---	---
220880_at	---	-0.023	---	---	---	---	---
1556238_at	FLJ22313	-0.022	protein modification	---	---	---	---
231693_at	FABP1	-0.022	organ morphogenesis/// fatty acid metabolism/// transport/// cell-cell signaling	lipid binding/// lipid transporter activity	cytoplasm	---	---
233874_at	KIAA1458	-0.022	---	---	---	---	---
238506_at	LOC116064	-0.022	---	---	---	---	---
1563945_at	LOC284100	-0.021	---	---	---	---	---
219265_at	MOBKL2B	-0.021	---	---	---	---	---
237634_at	C1QTNF3	-0.021	phosphate transport	---	---	---	---
1560906_at	HUMYZ82H07	-0.02	---	---	---	---	---
232439_at	---	-0.02	---	---	---	---	---
236948_x_at	SFRS11	-0.02	nuclear mRNA splicing, via spliceosome /// RNA splicing	RNA binding /// pre-mRNA splicing factor activity	nucleus	---	---
242114_at	LAT1-3TM	-0.02	---	---	---	---	---
1554594_at	LOC201175	-0.019	---	---	---	---	---
204184_s_at	ADRBK2	-0.019	protein amino acid phosphorylation /// signal transduction	G-protein coupled receptor kinase activity /// signal transducer activity /// ATP binding /// transferase activity /// beta-adrenergic-receptor kinase activity	---	---	---
243311_at	DEFB32	-0.019	---	---	---	---	---

1557257_at	BCL10	-0.018	induction of apoptosis /// regulation of apoptosis /// positive regulation of I-kappaB kinase/NF-kappaB cascade /// negative regulation of cell cycle	signal transducer activity /// protein binding	intracellular	---
210112_at	HPS1	-0.018	---	---	---	---
210155_at	MYOC	-0.018	visual perception /// morphogenesis	structural molecule activity /// latrotoxin receptor activity	non-muscle myosin /// cilium /// membrane	---
224084_at	---	-0.018	---	---	---	---
233509_at	HERC4	-0.018	ubiquitin cycle	ubiquitin-protein ligase activity	intracellular	---
1552490_at	LACE1	-0.017	---	---	---	---
215312_at	---	-0.017	---	---	---	---
236581_at	---	-0.017	---	---	---	---
239008_at	---	-0.017	---	---	---	---
209910_at	SLC25A16	-0.016	transport	binding /// solute:solute antiporter activity	mitochondrion /// mitochondrial inner membrane /// integral to membrane	---
222363_at	---	-0.016	---	---	---	---
239949_at	FLJ10916	-0.016	metabolism	catalytic activity	---	---
240929_at	---	-0.016	---	---	---	---
204205_at	APOBEC3G	-0.015	RNA metabolism /// innate immune response /// negative regulation of retroviral genome replication	RNA binding /// cytidine deaminase activity /// zinc ion binding /// hydrolase activity /// protein homodimerization activity	nucleus	---
215196_at	LOC91316	-0.015	carbohydrate metabolism	hydrolase activity, hydrolyzing O-glycosyl compounds	---	---

229443_at	ITPR3	-0.015	cation transport /// calcium ion transport	receptor activity /// inositol 1,4,5-triphosphate-sensitive calcium-release channel activity /// calcium channel activity	endoplasmic reticulum /// integral to membrane	Calcium regulation in cardiac cells /// Smooth muscle contraction
239897_at	BCLAF1	-0.015	regulation of transcription, DNA-dependent /// induction of apoptosis	DNA binding /// transcriptional repressor activity	nucleus	---
243700_x_at	FAM47A	-0.015	---	---	---	---
208159_x_at	DDX11	-0.014	mitotic sister chromatid segregation /// regulation of cell cycle /// S phase of mitotic cell cycle /// G2/M transition of mitotic cell cycle /// nucleobase, nucleoside, nucleotide and nucleic acid metabolism /// nucleotide-excision repair /// positive regulation of cell proliferation /// ATP synthesis coupled proton transport	DNA binding /// ATP-dependent DNA helicase activity /// ATP binding /// hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides /// hydrogen-transporting ATP synthase activity, rotational mechanism /// hydrogen-transporting ATPase activity, rotational mechanism	nucleus /// nucleolus /// proton-transporting two-sector ATPase complex	---
233531_at	MGC9564	-0.014	transport	transporter activity	membrane /// integral to membrane	---
243223_at	---	-0.014	---	---	---	---
243856_at	---	-0.014	---	---	---	---
229015_at	LOC286367	-0.013	---	---	---	---
229776_at	SLCO3A1	-0.013	ion transport	transporter activity	integral to membrane	---
233366_at	FBXO4	-0.013	ubiquitin cycle /// protein ubiquitination	ubiquitin-protein ligase activity	ubiquitin ligase complex	---

1557631_at	SLC25A4	-0.012	generation of precursor metabolites and energy/// mitochondrial genome maintenance/// mitochondrial transport/// transport	adenine transporter activity	integral to plasma membrane/// mitochondrial inner membrane	---
205067_at	IL1B	-0.012	regulation of cell cycle /// apoptosis /// inflammatory response /// signal transduction /// cell cell signaling /// cell proliferation /// negative regulation of cell proliferation /// antimicrobial humoral response (sensu Vertebrata)	signal transducer activity /// interleukin-1 receptor binding	extracellular space	Smooth muscle contraction
205881_at	ZNF74	-0.012	regulation of transcription, DNA-dependent /// development	nucleic acid binding /// DNA binding /// RNA binding /// zinc ion binding	nucleus	---
213416_at	ITGA4	-0.012	cell adhesion/// integrin-mediated signaling pathway	identical protein binding/// calcium ion binding/// receptor activity	integral to membrane/// integrin complex	cell adhesion molecules (CAMs)/// ECM-receptor interaction/// focal adhesion/// hematopoietic cell lineage/// leukocyte transendothelial migration/// regulation of actin cytoskeleton
1555322_at	---	-0.011	---	---	---	---
1559485_at	---	-0.011	---	---	---	---
239732_x_at	FAM47B /// LOC44244 4	-0.011	---	---	---	---

1554008_at	OSMR	-0.01	cell surface receptor linked signal transduction /// cell proliferation	receptor activity /// oncostatin-M receptor activity	oncostatin-M receptor complex	---
209856_x_at	ABI2	-0.01	actin polymerization and/or depolymerization/// cell migration/// cytoskeleton organization and biogenesis	cytoskeletal adaptor binding/// kinase binding/// SH3/SH2 adaptor binding/// DNA binding	cytoplasm/// cytoskeleton/// filopodium/// lamellipodium/// nucleus	regulation of actin cytoskeleton
214087_s_at	MYBPC1	-0.01	striated muscle contraction /// cell adhesion /// muscle development	actin binding /// protein binding /// structural constituent of muscle	striated muscle thick filament	Striated muscle contraction
230152_at	WDR52	-0.01	---	---	---	---
236268_at	SEC22L3	-0.01	ER to Golgi transport /// vesicle-mediated transport	---	endoplasmic reticulum /// integral to membrane	---
1559826_a_at	LOC401074	-0.009	---	---	---	---
1560180_at	CAPN14	-0.009	---	---	---	---
215864_at	INPP4B	-0.009	signal transduction	hydrolase activity/// phosphatidylinositol-3,4-bisphosphate 4-phosphatase activity	---	inositol phosphate metabolism/// phosphatidylinositol signaling system
224174_at	TTTY11	-0.009	---	---	---	---
230897_at	FLJ20972	-0.009	---	---	---	---
240530_at	SLC25A16	-0.009	transport	solute:solute antiporter activity	integral to membrane/// mitochondrial inner membrane/// mitochondrion	---
243172_at	---	-0.009	---	---	---	---
1552910_at	SIGLEC11	-0.008	cell adhesion	protein binding /// sugar binding	integral to membrane	---

1553831_at	APOBEC3D	-0.008	metal ion transport	zinc ion binding /// hydrolase activity /// hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines /// metal ion binding	---	---
1557495_at	---	-0.008	---	---	---	---
230880_at	KIAA1652	-0.008	---	---	---	---
1569465_at	LOC391705	-0.007	---	---	---	---
1570065_at	LOC400933	-0.007	---	---	---	---
1562250_at	SEMA4D	-0.006	anti-apoptosis /// immune response /// cell adhesion /// development /// neurogenesis	receptor activity	integral to membrane	---
1563117_at	LOC388456	-0.006	---	---	---	---
1561895_at	ANK2	-0.005	signal transduction /// metabolism	structural constituent of cytoskeleton /// protein binding /// oxidoreductase activity	actin cytoskeleton /// membrane	Ribosomal Proteins
203492_x_at	PIG8	-0.005	---	---	nucleus	---
205542_at	STEAP	-0.005	---	channel or pore class transporter activity	early endosome /// integral to plasma membrane /// intercellular junction /// integral to Golgi membrane /// vesicular fraction	---
223756_at	FLJ10081	-0.005	---	---	---	---

239608_at	LOC254531	-0.005	metabolism /// phospholipid biosynthesis	acyltransferase activity /// transferase activity	integral to membrane	---
1552639_at	MGC16635	-0.004	---	---	---	---
219819_s_at	MRPS28	-0.004	---	RNA binding /// structural constituent of ribosome	mitochondrion /// mitochondrial small ribosomal subunit	---
229865_at	FNDC3B	-0.004	---	---	---	---
241770_x_at	SLC22A9	-0.004	transport	transporter activity	integral to membrane	---
1558401_at	---	-0.003	---	---	---	---
231976_at	WINS1	-0.003	---	---	---	---
244513_at	MGC33214	-0.003	---	---	---	---
1557602_at	LOC201617	-0.002	---	---	---	---
208477_at	KCNC1	-0.002	cation transport /// potassium ion transport	voltage-gated potassium channel activity /// protein binding	membrane fraction /// voltage-gated potassium channel complex /// integral to membrane	---
230667_at	---	-0.002	---	---	---	---
232685_at	ETV6	-0.002	regulation of transcription, DNA-dependent	transcription factor activity	nucleus	Circadian Exercise
235326_at	FLJ12529	-0.002	nuclear mRNA splicing, via spliceosome	nucleic acid binding	---	---
240046_at	FLJ25778	-0.002	---	---	---	---
226718_at	AMIGO	-0.001	---	---	integral to membrane	---

234705_at	NCK2	-0.001	signal complex formation /// regulation of epidermal growth factor receptor activity /// intracellular signaling cascade /// negative regulation of cell proliferation /// positive regulation of actin filament polymerization /// positive regulation of T-cell proliferation /// T-cell activation	protein binding /// cytoskeletal adaptor activity /// receptor signaling complex scaffold activity	cytoplasm	---
240220_at	ELMO2	-0.001	phagocytosis /// apoptosis	---	cytoskeleton /// membrane	---

[00080] Thus, during the early postnatal weeks, supplementation at levels of 0.33% DHA/0.67% ARA (L) and 1.00% DHA/0.67% ARA (L3) altered gene expression across diverse biological processes when compared to an unsupplemented control group. The expression of 1108 genes was altered as a result of DHA/ARA supplementation in the brain tissue, most genes showing less than two-fold changes. When comparing the L group to the C group, 534 genes were upregulated and 574 genes were downregulated. When comparing the L3 group to the C group, 666 genes were upregulated and 442 genes were downregulated.

[00081] Probe sets with ≥1.4 fold expression change are presented in Table 10. Expression change is shown for the L group (third column) as well as the L3 group (fourth column). The L/C comparison corresponds to inclusion of DHA and ARA at current levels near the worldwide breastmilk mean, while the L3 group corresponds to DHA supplementation which is near the worldwide high.

Table. 10. Probe sets showing ≥ 1.4 fold changes in gene expression.

Affymetrix Probe ID No.	Gene Symbol	Expression change (Fold Changes):	Expression change (Fold Changes):
		L/C	L3/C
231628_s_at	SERPINB6	-1.45	4.59
231655_x_at	SERPINB6		1.81
1552719_at	H63		1.64
1564654_at	COL4A6		1.61
208137_x_at	ZNF611		1.58
210800_at	TIMM8A		1.56
233399_x_at	---		1.54
226134_s_at	MSI2	1.54	
224105_x_at	---		1.52
238895_at	TEBP/// PTGES3		1.52
1560276_at	LOC283403		1.51
234788_x_at	FLJ13611		1.51
241867_at	PARP6		1.50
230867_at	LOC131873		1.50
212179_at	C6orf111		1.49
205745_x_at	ADAM17		1.49

233808_at	STK3		1.48
242273_at	---		1.48
216051_x_at	---		1.48
1553844_a_at	C10orf67		1.47
214768_x_at	---		1.47
215604_x_at	---		1.47
215208_x_at	RPL35A		1.46
242391_at	---		1.45
224143_at	TTTY8		1.45
239199_at	---		1.45
238269_at	FBXL7		1.44
231538_at	C11orf1		1.44
244310_at	---		1.44
208844_at	VDAC3		1.43
221304_at	UGT1A10		1.42
235767_x_at	PHAX		1.42
234652_at	---		1.41
1554583_a_at	MGC50559		1.41
216600_x_at	ALDOB		1.41
235425_at	SGOL2		1.41
242016_at	LOC284409	1.40	
216202_s_at	SPTLC2		1.40
234594_at	C14orf85		1.40
233868_x_at	ADAM33		1.40
227149_at	TNRC6C	1.40	
1553641_a_at	TSGA13		-1.40
218575_at	ANAPC1		-1.41
234006_s_at	RP4-622L5		-1.41
229023_at	MGC5391		-1.41
203023_at	HSPC111		-1.41
216300_x_at	RARA		-1.41
221418_s_at	THRAP5		-1.41
244858_at	TGIF		-1.42
210764_s_at	CYR61		-1.42
223852_s_at	MGC4796		-1.42
206681_x_at	GP2		-1.42
222349_x_at	RNF126P1		-1.43
230117_at	LOC285878	-1.44	
229118_at	PRRG3		-1.44
219088_s_at	ZNF576		-1.44
241399_at	FAM19A2		-1.44
209364_at	BAD		-1.45
202862_at	FAH		-1.47
244128_x_at	GLIS1		-1.48

205839_s_at	BZRAP1		-1.49
211534_x_at	PTPRN2		-1.49
221256_s_at	HDHD3		-1.49
223018_at	NOB1P		-1.50
204647_at	HOMER3		-1.50
224451_x_at	ARHGAP9		-1.54
205440_s_at	NPY1R	-1.56	
237847_at	---		-1.56
238996_x_at	ALDOA		-1.62
203395_s_at	HES1		-1.63
220551_at	SLC17A6	-3.21	-1.87

[00082] Nine genes were tested by quantitative real time PCR to confirm the array results, as shown in Table 11. All were qualitatively consistent with the gene array results.

Table 11. Comparison of microarray versus QRT-PCR gene expression values (Fold-changes)

Gene Name	Microarray	QRT-PCR	Microarray	QRT-PCR
	L/C	L/C	L3/C	L3/C
Lumicam (LUM)	1.03	4.18	1.30	6.04
Translocase of inner mitochondrial membrane 8 homolog A (TIMM8A)	1.04	1.33	1.57	1.76
ATPase, Class I, type 8B, member 1 (ATP8B1)	1.28	1.13	1.36	1.20
ADAM metallopeptidase domain 17 (ADAM17)	1.37	1.95	1.50	2.66
Neurofibromin 1 (NF1)	1.03	2.07	1.20	2.16
Frizzled homolog 3 (FZD3)	1.13	1.80	1.20	2.58
Zinc finger protein 611 (ZNF611)	1.10	1.46	1.60	3.25
Uncoupling protein 2 (UCP2)	1.16	2.18	1.30	3.82
Epidermal growth factor receptor (EGFR)	-1.08	-1.20	1.17	1.40

[00083] Functional characterization by gene ontology of these differentially regulated genes assigns them to diverse biological processes including lipid and other metabolism, ion channel and transport, development, visual perception, G-protein and signal transduction, regulation of transcription, cell cycle, cell proliferation, and apoptosis.

Several categories of gene ontogeny which were influenced by DHA and ARA supplementation are discussed below.

Lipid (fatty acid and cholesterol) Metabolism

[00084] Table 12 presents results from genes related to lipid metabolism that are regulated by dietary LCPUFA.

Table 12. Lipid and energy metabolism gene modulation in expression profiles.

Metabolism	Gene Symbol	Unigene ID	L1	L3
Lipid	*ATP8B1*	Hs.569910	1.28	1.36
	PDE3A	Hs.386791	1.08	1.30
	ELOVL5	Hs.520189	-1.02	1.11
	ACSL3	Hs.471461	-1.13	1.08
	HNF4A	Hs.116462	1.06	-1.16
	CLPS	Hs.1340	1.02	-1.16
	ALDH3B2	Hs.87539	1.05	-1.16
	PLCE1	Hs.20022	-1.10	-1.19
Fatty acid oxidation	*ACADSB*	Hs.81934	-1.10	1.38
	ACAD10	Hs.331141	-1.08	1.10
	GLYAT	Hs.274336	1.01	1.30
	ADH5	Hs. 78989	1.03	1.22
	CPT2	Hs.145384	1.10	-1.22
Energy	*LEP*	Hs.194236	-1.01	1.17
Ceramide	*NSMAF*	Hs.372000	-1.04	1.31
	LASS5	Hs.270525	1.06	1.11
Glycosphingolipid	*SPTLC2*	Hs.435661	1.27	1.40
Steroid	*OSBP2*	Hs.517546	-1.17	1.35
	UGT2B15	Hs.150207	1.04	1.21
	SULT2B1	Hs.369331	1.04	-1.38
Phospholipid	*DGKE*	Hs.546318	-1.10	1.17
	PLA2G6	Hs.170479	-1.09	-1.20
Prostaglandin and Leukotriene	*TEBP*	Hs.50425	1.02	1.52
	ANXA3	Hs.480042	1.26	-1.04
	LTC4S	Hs.456	-1.33	-1.24
Cholesterol	*DHCR24*	Hs.498727	-1.18	1.17
	PRKAG2	Hs.131133	-1.07	1.09
	PRKAA1	Hs.43322	1.09	-1.02
	SOAT1	Hs.496383	-1.09	-1.12
	FDFT1	Hs.546253	1.01	-1.13

[00085] Genes related to phospholipids biosynthesis (*PLA2G6* and *DGKE*) were differentially expressed. *PLA2G6* was downregulated in both groups. This gene codes for the Ca-independent cytosolic phospholipase A2 Group VI. Alterations in this gene have very recently been implicated as a common feature of neurodegenerative disorders involving iron accumulation, Morgan, N.V., *et al.*, PLA2G6, *Encoding a Phospholipase*

A2, is Mutated in Neurodegenerative Disorders with High Brian Iron, Nat. Genet. 38(7): 752-54 (2006), as well as the underlying factor in infantile neuroaxonal dystrophy, a neurodegenerative disorder caused by accumulation of iron in the globus pallidus and resulting in death by age 10. Khateeb, S., *et al.*, *PLA2G6 Mutation Underlies Infantile Neuroaxonal Dystrophy*, Am. J. Hum. Genet. 79(5): 942-48 (2006). PLA2 are a superfamily of enzymes that liberate fatty acids from the sn-2 position of phospholipids; in the globus pallidus DHA and ARA are the most abundant acyl groups at this site. Thus, the present invention has shown to be useful in downregulating PLA2G6, thereby preventing or treating neurodegerative disorders.

[00086] Remarkably, among the elongation and desaturation enzymes associated with LCPUFA synthesis, only a single elongation enzyme was differentially expressed. The human *ELOVL5* transcript was downregulated slightly in the L/C group and upregulated in the L3/C group. This enzyme, also called *HELO1*, catalyzes the two carbon elongation of polyunsaturated 18 and 20 carbon fatty acids. Leonard, A.E., *et al.*, *Cloning of a Human cDNA Encoding a Novel Enzyme Involved in the Elongation of Long-Chain Polyunsaturated Fatty Acids*, Biochem. J. 350 Pt. 3: 765-70 (2000); Leonard, A.E., *et al.*, *Identification and Expression of Mammalian Long-Chain PUFA Elongation Enzymes*, Lipids 37(8): 733-40 (2002).

[00087] The inventors also found that *DGKE* was upregulated in the L3/C comparison. Genes involved in ceramide metabolism (*NSMAF*, *LASS5*), glycosphingolipid metabolism (*SPTLC2*) and steroid metabolism (*OSBP2*, *UGT2B15*) showed increased expression in L3/C group, whereas *NSMAF* and *OSBP2* were downregulated in L/C group.

[00088] A further gene modulated by DHA and ARA supplementation was serine palmitoyltransferase, long-chain base subunit 2 (SPTLC2). Serine palmitoyl-CoA transferase (SPT) is the key rate-limiting enzyme in

the biosynthesis of sphingolipids. Sphingolipids play a very important role in cell membrane formation, signal transduction, and plasma lipoprotein metabolism. SPT is considered to be a heterodimer of two subunits of Sptlc1 and Sptlc2. A SPTLC2 deficiency causes a significant decrease in plasma Ceramide levels. Ceramide is a well known second messenger and plays an important role in apoptosis. Strategies elevating cellular Ceramide are employed for therapies aimed at arresting growth or promoting apoptosis. M. R. Hojjati, *et al.*, Serine Palmitoyl-CoA Transferase (SPT) Deficiency and Sphingolipid Levels in Mice, Biochim Biophys Acta. 1737(1):44-51 (2005); Y.A. Hannun, *et al.*, *Enzymes of Sphingolipid Metabolism: From Modular to Integrative Signaling*, Biochemistry 40(16):4893-903 (2001).

[00089] A SPTLC2 deficiency causes a significant decrease of plasma S1P (sphingosine-1-phosphate) levels. In human plasma, 65% of S1P is associated with lipoproteins, where HDL is the major carrier. The S1P in HDL has been shown to bind to S1P/Edg receptors on human endothelial cells, and for this reason is believed to mediate many of the anti-inflammatory actions of HDL on endothelial cells. F. Okajima, *Plasma Lipoproteins Behave as Carriers of Extracellular Sphingosine 1-Phosphate: Is this an Atherogenic Mediator or an Anti-Atherogenic Mediator?* Biochim Biophy. Acta. 1582:132–137 (2002); T. Kimura, *et al.*, *High-Density Lipoprotein Stimulates Endothelial Cell Migration and Survival Through Sphingosine 1-Phosphate and its Receptors.* Arterioscler Thromb Vasc Biol. 23:1283-1288 (2003).

[00090] A SPTLC2 deficiency also causes dramatically decreased plasma LysoSM (lysosphingomyelin) levels. LysoSM is a putative second messenger important in several intracellular and intercellular events, and has been implicated in regulation of cell growth, differentiation, and apoptosis. It increases intracellular calcium concentration and nitric oxide production in endothelial cells, causing endothelium-dependent

vasorelaxation of bovine coronary arteries. Y. Xu. *Sphingosylphosphorylcholine and Lysophosphatidylcholine: G Protein-Coupled Receptors and Receptor-Mediated Signal Transduction.* Biochim Biophys Acta. 1582:81–88 (2002); K. Mogami, *et al.*, *Sphingosylphosphorylcholine Induces Cytosolic Ca(2+) Elevation in Endothelial Cells in Situ and Causes Endothelium-Dependent Relaxation through Nitric Oxide Production in Bovine Coronary Artery.* FEBS Lett. 457:375–380 (1999).

[00091] As shown in Table 9, SPTLC2 was upregulated in both the L group and the L3 group in the present study. It is believed that supplementation with DHA and ARA can increase plasma LysoSM levels and plasma S1P levels.

[00092] The best studied role of ARA is as a precursor for eicosanoids including prostaglandins, leukotrienes, and thromboxanes. One of the genes derived from membrane-bound ARA, which catalyze the first step in the biosynthesis of cysteinyl leukotrienes, Leukotriene C4 synthase (*LTC4S*), was downregulated in both DHA/ARA groups. *LTC4S* is a potent proinflammatory and anaphylactic mediator. Welsch, D.J., *et al*, *Molecular Cloning and Expression of Human Leukotriene-C4 Synthase*, Proc. Natl. Acad. Sci. 91(21): 9745-49 (1994). Thus, it is believed that DHA and ARA supplementation may have anti-inflammatory effects due to its downregulation of LTC4S.

[00093] An elevated level of mRNA for *PGES3* (prostaglandin E synthase 3) was observed in both of the feeding groups. *PGES3* is also known as *TEBP* (telomerase-binding protein p23) or inactive progesterone receptor, 23-KD (*p23*). A ubiquitous highly conserved protein which functions as a co-chaperone for the heat shock protein, *HSP90*, *p23* participates in the folding of a number of cell regulatory proteins. Buchner, J., *Hsp90 & Co. – A Holding for Folding*, Trends Biochem. Sci. 24(4): 136-41 (1999); Weaver, A.J., *et al.*, *Crystal Structure and Activity of Human*

p23, a Heat Shock Protein 90 Co-Chaperone, J. Bio. Chem. 275(30): 23045-52 (2000). It has been demonstrated to bind to human telomerase reverse transcriptase (hTERT) and contribute to telomerase activity. Holt, S.E., *et al.*, *Functional Requiremetn of p23 and Hsp90 in Telomerase Complexes*, Genes Dev. 13(7): 817-26 (1999). Decreased levels of Annexin A3 (*ANXA3*) also known as Lipocortin III was observed with increasing DHA.

[00094] Genes involved in fatty acid oxidation (*ACADSB*, *ACAD10* and *GLYAT*) were overexpressed and carnitine palmitoyltransferase II (*CPT2*) downregulated in the L3/C group. The upregulation of both the ACADs family members *ACADSB* and *ACAD10* in the L3/C group was consistent with greater energy production in the high DHA group. ACADs (acyl-CoA dehydrogenases) are a family of mitochondrial matrix flavoproteins that catalyze the dehydrogenation of acyl-CoA derivatives and are involved in the β-oxidation and branched chain amino-acid metabolism. Rozen, R. *et al.*, *Isolation and Expression of a cDNA Encoding the Precursor for a Novel Member (ACADSB) of the acyl-CoA Dehydrogenase Gene Family*, Genomics 24(2):280-87 (1994); Ye, X., *et al.*, *Cloning and Characterization of a Human cDNA ACAD10 Mapped to Chromosome 12q24.1*, Mol. Bio. Rep. 31(3): 191-95 (2004). ACADSB deficiency causes isolated 2-methylbutyrylglycinuria, a defect in isoleucine catabolism. Isolated excretion of 2-methylbutyrylglycine (2-MBG), a recently identified defect in the proximal pathway of L-isoleucine oxidation, is caused by ACADSB deficiency.

[00095] Mitochondrial-specific *GLYAT* (glycine-N-acyltransferase) also known as acyl CoA:glycine N-acyl transferase (*ACGNAT*), conjugates glycine with acyl-CoA and participates in detoxification of various drugs and xenobiotics. Mawal, Y.R. & Qureshi, I.A., *Purification to Homogeneity of Mitochondrial Acyl coa:glycine n-acyltransferase from Human Liver*, Biochem. Biophys. Res. Commun. 205(2): 1373-79 (1994); Mawal, Y.R.,

et al., *Developmental Profile of Mictochondrial Glycine N-Acyltransferase in Human Liver*, J. Pediatr. 130(6): 1003-7 (1997). Mawal, *et al.* also suggested that delayed development of *GLYAT* might impair detoxification process in children.

[00096] Genes involved in cholesterol biosynthesis, *DHCR24*, *PRKAG2*, *PRKAA1*, *SOAT1*, and *FDFT1* showed significant associations with LCPUFA levels. Increasing DHA upregulated *DHCR24* and *PRKAG2* and downregulated *PRKAA1*, *SOAT1* and *FDFT1*. *DHCR24* (24-dehydrocholesterol reductase), also known as selective AD indicator 1 (*SELADIN1*), catalyzes the reduction of the Δ-24 double bond of sterol intermediates during cholesterol biosynthesis. Waterham, H.R., *et al.*, *Mutations in the 3beta-Hydroxysterol Delta-Reductase Gene Cause Desmosterolosis, An Autosomal recessive Disorder of Cholesterol Biosynthesis*, Am. J. Hum. Genet. 69(4): 985-94 (2001). *SELADIN1* may activate estrogen receptors in the brain and protect from beta-amyloid-mediated toxicity. Peri, A.G., *et al.*, *Seladin-1 as a Target of Estrogen Receptor Activation in the Brain: A New Gene for a Rather Old Story?* J. Endocrin. Invest. 28(3): 285-93 (2005). Decreased expression of *SELADIN1* was observed in brain regions of patients with Alzheimer's disease. Benvenuti, S., *et al.*, *Estrogen and Selective Estrogen Receptor Modulators Exert Neuroprotective Effects and Stimulate the Expression of Selective Alzheimer's Disease Indicator-1, A Recently Discovered AntiApoptotic Gene, in Human Neuroblast Long-Term Cell Cultures*, J. Clin. Endocrin. Metab. 90(3): 1775-82 (2005). *PRKAG2* (protein kinase, AMP-activated, gamma 2) is a member of AMP-activated protein kinase (AMPK) family. AMPKs perform multifunctional roles in calcium signaling, weight loss, regulation of energy metabolism in heart. Evans, A.M., *AMP-Activated Protein Kinase and the Regulation of Ca2+ Signalling in O2-Sensing Cells*, J. Physiol. (2006); Watt, M.J., *et al.*, *CNTF Reverses Obesity-Induced Insulin Resistance by Activating Skeletal Muscle AMPK*,

Nat. Med. 12(5): 541-48 (2006); Dyck, J.R., *et al.*, *AMPK Alterations in Cardiac Physiology and Pathology: Enemy or Ally?* J. Physiol. (2006).

[00097] *SOAT1* (sterol O-acyl transferase) or Acyl-coenzyme A:cholesterol acyl transferase (*ACAT*) is an intracellular protein which catalyzes the formation of cholesterol esters in endoplasmic reticulum and is involved in lipid droplets that are characteristic of foam cells of atherosclerotic plaques. Miyazaki, A., *et al.*, *Inhibitors of Acyl-CoEnzyme A:Cholesterol Acyltransferase*, Curr. Drug Targets Cardio. Haematol. Disorder, 5(6): 463-69 (2005); Stein, O. & Stein, Y., *Lipid Transfer Protein (LTP) and Atherosclerosis*, Pharm. Res. 22(10) 1578-88 (2005); Leon, C., *et al.*, *Potential Role of Acyl-Coenzyme A:Cholesterol Transferase (ACAT) Inhibitors as Hypolipidemic and Antiatherosclerosis Drugs*, Pharm. Res. 22(10) 1578-88 (2005).

[00098] Increased expression was detected for *ATP8B1* and *PDE3A* in both groups, comparatively more in L3/C, while transcripts involving *HNF4A* (Hepatic nuclear factor-4α), *CLPS,* and *ALDH3B2* showed decreased expression with increasing DHA. *ATP8B1* expression was confirmed by real time PCR.

[00099] Intrahepatic cholestasis, or impairment of bile flow, is an important manifestation of inherited and acquired liver disease resulting in hepatic accumulation of the toxic bile acids and progressive liver damage. Bile acids enhance efficient digestion and absorption of dietary fats and fat-soluble vitamins, and are the main route for excretion of sterols. Expression of *ATP8B1* is high in the small intestine, and mutations in the *ATP8B1* gene have been linked to intrahepatic cholestasis. Bull, L.N., *et al.*, *A Gene Encoding a P-Type ATPase Mutated in Two Forms of Hereditary Cholestasis*, Nat. Genet. 18(3): 219-24 (1998); Mullenbach, R., *et al.*, *ATP8B1 Mutations in British Cases with Intrahepatic Cholestasis of Pregnancy*, Gut. 54(6): 829-34 (2005). ATP8B1 may function as a bile salt transporter. The knockout mouse phenotype of ATP8B1 revealed a

disruption in bile salt homeostasis without impairment of bile secretion. Calcium malabsorption, magnesium deficiency and vitamin D deficiency are often associated with osteoporosis and hypocalcemia in cholestatic liver diseases. It has been suggested that the ATP8B1 gene is involved in gene calcium regulation via the parathyroid hormone.

[000100] *PDE3A* (phosphodiesterase 3A, cGMP-inhibited) is a 120 kDa protein found in myocardium and platelets. Liu, H., *Expression of Cyclic GMP-Inhibited Phosphodiesterases 3A and 3B (PDE3A and PDE3B) in Rat Tissues: Differential Subcellular Localization and Regulated Expression by Cyclic AMP*, Br. J. Pharm. 125(7): 1501-10 (1998). Ding, *et al.* showed significantly decreased expression of *PDE3A* in the left ventricles of failing human hearts. Ding, B., *et al.*, *Functional Role of Phosphodiesterase 3 in Cardiomyocyte Apoptosis: Implication in Heart Failure*, Circulation 111(19): 108-14 (2000). Genetic evidece indicates that resumption of meiosis in vivo and in vitro requires PDE3A activity. Complete sterility was noted in female PDE3A-/- mice. *PDE3A* expression also is required for the regulation of penile erection in humans. Kuthe, A., *et al.*, *Gene Expression of the Phosphodiesterase 3A and 5A in Human Corpus Cavernosum Penis*, Eur. Urol. 38(1): 108-14 (2000).

[000101] Leptin (*LEP*), which has a role in energy metabolism, was overexpressed in the brain tissue of the L3/C group. Leptin is a secreted adipocyte hormone that plays a pivotal role in the regulation of food intake and energy homeostasis. Zhang, Y., *et al.*, *Positional Cloning of the Mouse Obese Gene and Its Human Homologue*, Nature 372(6549):543-46 (1995); Halaas, J.L., *et al.*, *Weight-Reducing Effects of the Plasma Protein Encoded by the Obese Gene*, Science 269(5223): 543-46 (1995). Leptin suppresses feeding and decreases adiposity in part by inhibiting hypothalamic Neuropeptide Y synthesis and secretion. Stephens, T.W., *et al.*, *The Role of Neuropeptide Y in the Antiobesity Action of the Obese Gene Product*, Nature 377(6549) 530-32 (1995); Schwartz, M.W., *et al.*,

Identification of Targets of Leptin Action in Rat Hypothalamus, J. Clin. Invest. 98(5): 1101-06 (1996). In diabetic mice, administration of LEP reduced hyperphagia, hyperglycemia, and Ghrelin mRNA levels. Decreased mRNA levels of LEP were detected in obese mice.

[000102] Based on the modulation of the above-noted genes, the inventors have shown that DHA and ARA are useful in altering lipid metabolism. More specifically, DHA and ARA supplementation may provide greater energy production, regulation of energy metabolism, suppression of appetite, and weight loss. Accordingly, in an embodiment, the present invention is directed to a method for improving body composition in a subject by administering a therapeutically effective amount of DHA and ARA to that subject.

Ion Channel and Transport

[000103] Expression levels of transcripts involved in ion channel and transporter activity were altered by dietary LCPUFA. Uncoupling protein 2 LOC131873 (hypothetical protein) and *ATP11C*, which have ion channel activity, are upregulated in both the groups but more so in L3/C. Other transcripts with ion channel activity, including *VDAC3*, *FTH1*, *KCNK3*, *KCNH7*, and *TRPM1* were overexpressed in L3/C group and underexpressed in L/C. *GLRA2*, *TRPV2* and *HFE* are overexpressed in L/C and repressed in L3/C. *P2RX2*, *GRIA1* and *CACNA1S* are repressed in both the groups.

[000104] One of the significant observations in the present invention is the overexpression of uncoupling protein 2 (*UCP2*), a mitochondrial proton carrier. The data shows an increased expression of *UCP2* in neonatal cerebral cortex associated with dietary LCPUFA; increased expression was observed in both the groups but more so in L3/C. QRT-PCR confirmed the array results. Nutritional regulation and induction of mitochondrial uncoupling proteins resulting from dietary n3-PUFA in skeletal muscle and white adipose tissue have been observed. Baillie,

R.A., *et al.*, *Coordinate Induction of Peroxisomal Acyl-CoA Oxidase and UCP-3 by Dietary Fish Oil: A Mechanism for Decreased Body Fat Deposition*, Prostaglandins Leukot. Essent. Fatty Acids, 60(5-6): 351-56 (1999); Hun, C.S., *et al.*, *Increased Uncoupling Protein2 mRNA in White Adipose Tissue, and Decrease in Leptin, Visceral Fat, Blood Glucose, and Cholesterol in KK-Ay Mice Fed with Eicosapentaenoic and Docosahexaenoic Acids in Addition to Linolenic Acid*, Biochem. Biophys. Res. Commun. 259(1): 85-90 (1999). Increased *UCP2* expression is beneficial in diseases associated with neurodegeneration, cardiovascular and type-2 diabetes. Mattiasson, G. & Sullivan, P.G., *The Emerging Functions of UCP2 in Health, Disease, and Therapeutics*, Antixoid. Redox Signal, 8(1-2) 1-38 (2006). Dietary fats in milk increased the expression and function of *UCP2* in neonatal brain and protected neurons from excitotoxicity. Sullivan, P.G., *et al.*, *Mitochondrial Uncoupling Protein-2 Protects the Immature Brain from Excitotoxic Nueronal Death*, Ann. Neurol. 53(6): 711-717 (2003).

[000105] *VDAC3* (voltage-dependent anion channel 3) belongs to a group of pore forming proteins found in the outer mitochondrial membrane and in brain synaptic membranes. Blachly-Dyson, E., *et al.*, *Human Genes Encoding the Voltage-Dependent Anion Channel (VDAC) of the Outer MitoChondrial Membrane: Mapping and Identification of Two New Isoforms*, Geomics 20(1): 62-67 (1994); Shafir, I., *et al.*, *Voltage-Dependent Anion Channel Proteins in Synaptosomes of the Torpedo Electric Organ: Immunolocalization, Purification, and Characterization*, J. Bioenerg. Biomembr. 30(5): 499-510 (1998). Massa, *et al.* observed a significant reduction of *VDAC3* mRNA levels in the skeletal muscle and brains of dystrophin-deficient mdx mice during postnatal development. Massa, R., *et al.*, *Intracellular Localization and Isoform Expression of the Voltage-Dependent Anion Channel (VDAC) in Normal and Dystrophic Skeletal Muscle*, J. Muscle Res. Cell. Motil. 21(5): 433-42 (2000). Mice

lacking *VDAC3* exhibit infertility. Sampson, M.J., *et al.*, *Immotile Sperm and Infertility in Mice Lacking Mitochondrial Voltage-Dependent Anion Channel Type 3*, J. Biol. Chem. 276(42): 39206-12 (2001). All the transcripts (*VDAC3*, *KCNK3* and *KCNH7*) having voltage-gated anion channel porin activity were overexpressed with increasing DHA.

[000106] The present invention has shown that FTH1 (ferritin heavy chain 1) is upregulated by DHA and ARA supplementation in infancy. *FTH1* is the primary iron storage factor and is required for iron homeostasis. It has been previously shown to be expressed in the human brain. Percy, M.E., *et al.*, *Iron Metabolism and Human Ferritin Heavy Chain cDNA from Adult Brain with an Elongated Untranslated Region: New Findings and Insights*, Analyst 123(1): 41-50 (1998). It has been identified as an essential mediator of the antioxidant and protective activities of NF-κB. A reduced expression of FTH1 may be responsible for abnormal accumulation of ferritin and may be responsible for human cases of hyperferritenemia. Abnormal accumulation of ferritin was found to be associated with an autosomal dominant slowly progressing neurodegenerative disease clinically characterized by tremor, cerebellar ataxia, Parkinsonism, pyramidal signs, behavioral disturbances, and cognitive decline. FTH1 was downregulated in the L group by 8%, but was upregulated in the L3 group by 37%, as compared to the control group. Thus, it is believed that the upregulation of FTH1 by DHA and ARA supplementation in infancy can improve iron absorption and/or can prevent the onset of various iron related disorders.

[000107] Genes encoding small molecule transporters were differentially expressed, including carriers of glucose (*SLC2A1*, *SLC5A4*), chloride (*SLC12A6*), sodium (*SLC13A3*), monoamine (*SLC18A2*) and others (*SLC26A4*, *SLC17A6*). These transporters might help in exchange of nutrients and metabolites. Members of the cytochrome P and B family of proteins were also differentially expressed. Transcripts encoding *VDP*,

RSAFD1, *C1QG* and *OXA1L* were significantly repressed by increasing DHA.

[000108] Based upon the above results, the present invention has shown that DHA and ARA can positively influence the transport and exchange of important nutrients and metabolites in the body. This may be important in biological processes ranging from nervous system function to muscle contraction to insulin release.

G-Proteins and Signaling

[000109] Numerous genes encoding G-protein activity were differentially regulated. The majority of those were induced by high levels of DHA. For example, *GNA13*, *GNA14*, *PTHR2*, *RCP9* and *FZD3* showed increased expression in both DHA groups. *EDG7*, *SH3TC2*, *GNRHR*, *ADRA1A*, *BLR1*, *GPR101*, *GPR20* and *OR8G2* were downregulated in L/C and upregulated in L3/C.

[000110] DHA regulates G-protein signaling in the brain and retina. Salem, N., *et al.*, *Mechanisms of Action of Docosahexaenoic Acid in the Nervous System*, Lipids 36(9): 945-59 (2001). G-proteins are membrane-associated proteins which promote exchange of GTP for GDP and regulate signal transduction and membrane traffic. Bomsel, M., & Mostov, K., *Role of Heterotrimeric G Proteins in Membrane Traffic*, Mol. Biol. Cell. 36(9): 945-59 (2001). *GNA13* deficiency impairs angiogenesis in mice while *GNA14* activates the NF-κB signaling cascade. Offermanns, S., *et al.*, *Vascular Systme Defects and Impaired Cell Chemokinesis as a Result of Galpha13 Deficiency*, Science 275(5299): 533-36 (1997); Liu, A.M. & Wong, Y.H., *Activation of Nuclear Factor κB by Somatostatin Type 2 Receptor in Pancreatic Acinar AR42J Cells Involves Gα14 and Multiple Signaling Components: A Mechanism Requiring Protein Kinase C, Calmodiulin-Dependent Kinase II, ERK, and c-Src*, J. Biol. Chem. 280(41): 34617-25 (2005). Parathyroid hormone receptor 2 (*PTHR2*) is activated by parathyroid hormone and is relatively abundant in the CNS. Usdin,

T.B., *et al.*, *New Members of the Parathyroid Hormone/Parathyroid Hormone Receptor Family: the Parathyroid Hormone 2 Receptor and Tuberoinfundibular Peptide of 39 Residues*, Front Neroendocrin. 21(4): 349-83 (2000); Harzenetter, M.D., *et al.*, *Regulation and Fucntino of the CGRP Receptor Complex in Human Granulopoiesis*, Exp. Hematol. 30(4): 306-12 (2002). *RCP9*, also known as calcitonin gene-related peptide-receptor component protein, may have a role during hematopoiesis.

[000111] Another gene modulated by DHA and ARA supplementation includes FZD3 (frizzled, drosophilia, homolog of, 3). The *FZD3* array results were confirmed by SYBR green real time PCR assay. G-Proteins are involved in the signaling mechanism, which uses the exchange of GDP for GTP as a molecule "switch" to allow or inhibit biochemical reactions inside the cell. Members of the FZD family are receptors for secreted WNT glycoproteins, which are involved in developmental control. RT-PCR and quantitative TaqMan analysis detected wide expression of *FZD3*, with highest levels in the limbic areas of the CNS and significant levels in testis, kidney, and uterus, as well as in a neuroblastoma cell line. C. F. Sala, et al., *Identification, Gene Structure, and Expression of Human Frizzled-3 (FZD3)*, Biochem. Biophys. Res. Commun. 273(1):27-34 (2000). Tissir and Goffinet showed expression of *FZD3* during postnatal CNS development in mice. Tissir, F. & Goffinet, A.M., *Expression of Planar Cell Polarity genes During Development of the Mouse CNS*, Eur. J. Neurosci. 23(3): 597-607 (2006).

[000112] The frizzled 3 (FZD3) gene is located on chromosome 8p21, a region that has been implicated in schizophrenia in genetic linkage studies. A strong association has been shown between the FZD3 locus and schizophrenia in Chinese population. Y. Zhang, et al., *Positive Association of the Human Frizzled 3 (FZD3) Gene Haplotype with Schizophrenia in Chinese Han Population.* Am. J. Med. Genet. B. Neuropsychiatr. Genet. 129(1):16-9 (2004); J. Yang, et al., *Association*

Study of the Human FZD3 Locus with Schizophrenia, Biol. Psychiatry 54(11):1298-301 (2003).

[000113] Frizzled 3 (FZD3) can be a candidate tumor suppressor gene as loss of heterozygosity at chromosome 8p21 is detected in human breast and ovarian cancers. FZD3 has also been proposed as an important gene implicated in the neurogenesis of the CNS during embryogenesis. H. Kirikoshi, *et al.*, *Molecular Cloning and Genomic Structure of Human Frizzled-3 at Chromosome 8p21* Biochem. Biophys. Res. Commun. 271(1):8-14 (2000). As shown in Table 4, FZD3 has been upregulated in baboon infants in the L and L3 groups via DHA and ARA supplementation. Thus, it is believed that DHA and ARA supplementation has a beneficial effect on the incidence of schizophrenia or tumor suppression, among other things.

[000114] Neuropeptide Y is a 36-amino acid peptide with strong orexigenic effects *in vivo*. Tatemoto, K., *Neuropeptide Y: Complete Amino Acid Sequence of the Brain Peptide*, Proc. Natl. Acad. Sci. 79(18): 5485-89 (1982). Two major subtypes of NPY (Y1 and Y2) have been defined by pharmacologic criteria. *NPY1R* was suggested to be unique for the control of feeding. Gehlert, D.R., *Multiple Receptors for the Pancreatic Polypeptide (PP-fold) Family: Physiological Implications*, Proc. Soc. Exp. Biol. Med. 218(1): 7-22 (1998). Pedrazzini, *et al.* observed a moderate but significant decrease in food intake in mice lacking the *NPY1R* gene. Pedrazzini, T., *et al.*, *Cardiovascular Response, Feeding Behavior and Locomotor Activity in Mice Lacking the NPY Y1 Receptor*, Nat. Med. 4(6): 722-26 (1998). Leptin suppresses feeding and decreases adiposity in part by inhibiting hypothalamic Neuropeptide Y sythesis and secretion.

[000115] *EDG7* (endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7) mediates calcium mobilization. Bandoh, K., *et al.*, *Molecular Cloning and Characterization of a Novel Human G-Protein-Coupled Receptor, EDG7, for Lysophosphatidic Acid*, J. Biol.

Chem. 274(39): 277776-85 (1999). Mutation in the *SH3TC2* gene causes childhood-onset of a neurodegenerative disorder affecting motor and sensory neurons. Senderek, J., *et al.*, *Mutations in a Gene Encoding a Novel SH3/TPR Domain Protein Cause Autosomal Recessive Charcot-Marie-Tooth Type 4C Neuropathy*, Am. J. Hum. Genet. 73(5): 1106-19 (2003).

[000116] Several signaling proteins (*NF1*, *WSB1*, *SOCS4*, *RIT1*, *CD8B1*, *OR2A9P* and *RERG*) were upregulated in both groups. Genes that are upregulated in L3/C and downregulated in L/C were also observed. For example, *PDE4D*, *KRAS*, *ITGA2*, *PLCXD3*, *WNT8A*, *ARHGAP4*, *RAPGEF6*, *OR2F1/OR2F2*, *CCM1* and *SFRP2* were upregulated in L3/C and downregulated in L/C. Several genes (*WNT10A*, *ADCY2*, *OGT*, *DDAH1* and *BCL9*) were upregulated in L/C and downregulated in L3/C. *IQGAP3*, *GCGR*, *APLN*, *CYTL1*, *GRP*, *LPHN3*, *CNR1*, *VAV3* and *MCF2* were downregulated in both the groups.

[000117] Another of the genes upregulated in the cerebral cortex by DHA and ARA supplementation was NF1. *NF1* expression levels were confirmed by QRT-PCR. Neurofibromatosis type 1 (NF1) is a disorder characterized particularly by "café-au-lait" spots and fibromatous tumors of the skin with an incidence of approximately 1 in 3000 people worldwide. Half of all patients present osseous manifestations, such as congenial pseudarthrosis. T. Kuorilehto, *et al.*, *NF1 Gene Expression in Mouse Fracture Healing and in Experimental Rat Pseudarthrosis*, J Histochem. Cytochem. 54(3):363-370 (2005).

[000118] NF1 gene expression and function are required for normal fracture healing. *Id.* Individuals with germline mutations in NF1 are predisposed to the development of benign and malignant tumors of the peripheral and central nervous system. Y. Zhu, *et al.*, *Inactivation of NF1 in CNS Causes Increased Glial Progenitor Proliferation and Optic Glioma Formation*. Development. 132(24):5577-88 (2005). Loss of neurofibromin

expression have been observed in a variety of NF1-associated tumors, including astrocytomas. D. H. Gutmann, *et al.*, *Loss of Neurofibromatosis 1 (NF1) Gene Expression in NF1-Associated Pilocytic Astrocytomas*, Neuropathol. Appl. Neurobiol. 26:361 -367 (2002); L. Kluwe, *et al.*, *Loss of NF1 Alleles Distinguish Sporadic from NF1-Associated Pilocytic Astrocytomas*, J. Neuropathol. Exp. Neurol. 60:917-920 (2001).

[000119] In the L group, the NF1 gene was upregulated by only 2%, but in the L3 group, the gene was upregulated 27%, as compared to the control group. It is believed, therefore, that the upregulation of NF1 by DHA and ARA supplementation in infancy can prevent the later development of various tumors.

[000120] *WSB1* is a SOCS-box-containing WD-40 protein expressed during embryonic development in chicken. Vasiliauskas, D.S., *et al.*, *SwiP-1: Novel SOCS Box Containing WD-Protein Regulated by Signalling Centres and by Shh During Development*, Mech. Dev. 82(1-2):79-94 (1999). RAS and RAS related gene families of small GTPases (*RIT1*, *KRAS*, *RERG* and *RAPGEF6*) were upregulated by increasing DHA.

[000121] Diets deficient in n-3 PUFA induce substitution of n-6 DPA (22:5n-6) in neural membranes, and impairment of functions mediated by G protein mediated signaling, such as visual perception, learning and memory, and olfactory discrimination. Evidence indicates that this results in reduced rhodopsin activation, and signaling in rod outer segments compared to DHA-replete animals.

[000122] The results of the invention have illustrated that DHA and ARA supplementation may positively affect the signaling of G-proteins by allowing them to properly regulate cell processes. A malfunction in G-protein signaling may lead to diseases or disorders such as schizophrenia, tumors, or overweight. Thus, supplementation with DHA and ARA may aid in preventing or treating schizophrenia or tumors, may suppress appetite, and may aid in fracture healing.

Development

[000123] Table 13 shows differential expression of 24 genes related to development.

Table 13. Development gene modulation in expression profiles.

Development	Gene Symbol	Unigene ID	L1	L3
Nervous system	*TIMM8A*	Hs.447877	1.04	1.57
	NRG1	Hs.453951	1.02	1.21
	SEMA3D	Hs.201340	1.10	1.14
	NUMB	Hs.585653	1.01	1.10
	HES1	Hs.250666	-1.30	-1.63
	SIM1	Hs.520293	-1.16	-1.16
	GDF11	Hs.591023	-1.18	1.09
	SMA3///SMA5	Hs.482414/484969/	-1.08	1.06
	SH3GL3	588240	-1.16	1.04
	FGF5	Hs.270055/458285	1.08	-1.20
	FGF14	Hs.37055	1.01	-1.10
		Hs.591206		
Muscle	C6orf97	Hs.130239	-1.03	1.34
	CALD1	Hs.490203	1.09	1.14
Skeletal	*BAPX1*	Hs.105941	1.05	1.08
Heart	*GATA4*	Hs.243987	-1.02	1.22
Epidermis	*S100A7*	Hs.112408	-1.06	1.27
	FGF7	Hs.122006	1.14	1.02
	SCEL	Hs.115166	-1.01	-1.13
Ectoderm/ Mesoderm	*SMURF1*	Hs.189329	1.15	1.32
	TCF21	Hs.78061	-1.12	-1.18
Gametogenesis	*OTEX*	Hs.196956	1.09	1.24
	TCP11	Hs.435371	-1.02	1.08
	CDV1	Hs.528382	-1.001	-1.10
	SPAG6	Hs.527698	-1.03	-1.22

[000124] The products of 11 transcripts play a role in nervous system development. The expression of *TIMM8A*, *NRG1*, *SEMA3D* and *NUMB* genes were upregulated in both L/C and L3/C groups. *HES1* and *SIM1* were downregulated in both the groups. *GDF11*, *SMA3/SMA5*, *SH3GL3* were downregulated in L/C and upregulated in L3/C. The mRNA levels of growth factors *FGF5* and *FGF14* displayed increased abundance in L/C and decreased abundance in L3/C.

[000125] *TIMM8A*, also known as Deafness/Dystonia Peptide 1 (*DDP1*), is a well conserved protein organized in mitochondrial intermembrane space. It belongs to a family of evolutionary conserved proteins that are organized in the mitochondrial intermembrane space. These proteins mediate the import and intersection of hydrophobic membrane proteins into the mitochondrial inner membrane. It is a homolog of yeast translocase of the inner mitochondrial membrane 8.

[000126] Loss of function in the TIMM8A gene causes Mohr-Tranebjaerg syndrome, a progressive neurodegenerative disorder resulting in deafness, blindness, dystonia and mental deficiency. Loss of function in the TIMM8A gene can also cause Jensen syndrome, a disorder which results in optocoacoustic nerve atrophy with dementia. L. Tranebjærg, *et al., A De Novo Missense Mutation in a Critical Domain of the X-linked DDP Gene Causes the Typical Deafness-Dystonia-Optic Atrophy Syndrome*. Eur J Hum Genet. 8(6):464-67 (2000); S. Hofmann, *et al., The C66W Mutation in the Deafness Dystonia Peptide 1 (DDP1) Affects the Formation of Functional DDP1·TIM13 Complexes in the Mitochondrial Intermembrane Space,* J. Biol. Chem. 277(26):23287-93 (2002); L. Tranebjaerg, *et al., Neuronal Cell Death in the Visual Cortex is a Prominent Feature of the X-linked Recessive Mitochondrial Deafness-Dystonia Syndrome Caused by Mutations in the TIMM8a Gene,* Ophthalmic Genet. 22(4):207-23 (2001).

[000127] In the present study, TIMM8A was upregulated in the cerebral cortex. Specifically, it was upregulated by 4% in the L group and 57% in the L3 group as compared to the control group. TaqMan assay confirmed the array results. Thus, it is believed that upregulation of the TIMM8A gene through DHA and ARA supplementation in infancy can prevent the later onset of Mohr-Tranebjaerg syndrome, Jensen syndrome and other neurodegenerative disorders.

[000128] TIMM23, which is also known as TIM23, is a mitochondrial inner membrane protein and is essential for cell viability. Lohret TA, *et al., Tim23, a Protein Import Component of the Mitochondrial Inner Membrane, is Required for Normal Activity of the Multiple Conductance Channel, MCC*, J. Cell. Biol. 21;137(2):377-86 (1997). TIM23 mRNA content per cell clearly increases during the late stage of pregnancy and the mammary gland function is activated at this stage and may trigger lactogenesis. Sun Y, *et al., Hormonal Regulation of Mitochondrial Tim23 Gene Expression in the Mouse Mammary Gland*, Mol. Cell. Endocrinol. 172(1-2):177-84 (2001). Impaired biogenesis of the human *TIMM23* complex causing severe pleiotropic mitochondrial dysfunction may be involved in the neurodegenerative disease Mohr-Tranebjaerg syndrome. Rothbauer, U., *et al., Role of the Deafness Dystonia Peptide 1 (DDP1) in Import of Human Tim23 into the Inner Membrane of Mitochondria*, J. Biol. Chem. 276(40):37327-34 (2001).

[000129] Thus, because TIMM23 was upregulated in infant baboon thymus tissue and TIMM23 is involved in Mohr-Tranebjaerg syndrome, it is believed that DHA and ARA supplementation can prevent and/or treat Mohr-Tranebjaerg syndrome.

[000130] *NRG1* is essential for the development and function of the CNS facilitating the neuronal migration and axon guidance. Bernstein, H.G., *et al., Localization of Neuregulin-1Alpha (Heregulin-Alpha) and One of its Receptors, ErbB-4 Tyrosine Kinase, in Developing and Adult Human Brain*, Brain Res. Bull. 69(5): 546-59 (2006). *NUMB* negatively regulates notch signaling and plays a role in retinal neurogenesis, influencing the proliferation and differentiation of retinal progenitors and maturation of postmitotic neurons. Dooley, C.M., *et al., Involvement of Numb in Vertebrate Retinal Development: Evidence for Multiple Roles of Numb in Neural Differentiation in the Central-Nervous-System*, J. Neuro. 54(2): 313-325 (2003). *HES1* (Hairy/Enhancer of Split, Drosophila, Homolog of,

1), a basic helix-loop-helix protein, was downregulated. Decreased expression of *HES1* is observed as neurogenesis proceeds; in case of persistent expression, differentiation of neuronal cells are blocked in the CNS. Ishibashi, M., *et al.*, *Persistent Expression of Helix-Loop-Helix Factor Hes-1 Prevents Mammalian Neural Differentiation in the Central-Nervous-System*, Embo. J. 13(8): 1799-1805 (1994).

[000131] In an embodiment, therefore, the invention is directed to a method for regulating the development of a subject comprising administering to that subject a therapeutically effective amount of DHA and ARA. These LCPUFAs may be effective in preventing various neurodegenerative disorders via their ability to modulate development-related genes.

Visual Perception

[000132] Nine transcripts having a role in visual perception were differentially expressed (Table 14).

Table 14. Visual perception gene modulation in expression profiles

Gene Product	Unigene ID	L	L3
Lumican (LUM)	Hs.406475	1.03	1.30
Interphotoreceptor matrix proteoglycan 1 (IMPG1)	Hs.590893	-1.03	1.18
Echinoderm microtubule associated protein like 2 (EML2)	Hs.24178	1.07	1.15
TIMP metallopeptidase inhibitor 3 (TIMP3)	Hs.297324	1.28	1.05
Tetratricopeptide repeat domain 8 (TTC8)	Hs.303055	1.10	1.01
IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1)	Hs.534808	-1.20	-1.12
Tubby like protein 2 (TULP2)	Hs.104636	1.07	-1.15
Retina and anterior neural fold homeobox (RAX)	Hs.278957	-1.10	-1.24
Regulator of G-protein signalling 16 (RGS16)	Hs.413297	1.01	-1.26

[000133] Genes coding for *LUM*, *EML2*, *TIMP3* and *TTC8* were overexpressed in both the supplemental groups. TaqMan assay showed a 5-fold greater upregulation of *LUM* than that shown in the microarray data.

IMPG1 was upregulated in L3/C and downregulated in L/C. *RGS16* and *TULP2* were upregulated in L/C and downregulated in L3/C. *RAX* and *IMPDH1* were downregulated in both the supplemental groups.

[000134] Lumican (LUM), a member of the small-leucine-rich-proteoglycan (SLRP) family, is an extracellular matrix glycoprotein widely distributed in mammalian connective tissues. E.C. Carlson, *et al.*, *Keratocan, a Cornea-specific Keratan Sulfate Proteoglycan, Is Regulated by Lumican*, J. Biol. Chem. 280(27): 25541-47 (2005). It is present in large quantities in the corneal stroma and in interstitial collagenous matrices of the heart, aorta, skeletal muscle, skin, and intervertebral discs. S. Chakravarti & T. Magnuson, *Localization of Mouse Lumican (Keratan Sulfate Proteoglycan) to Distal Chromosome 10*, Mamm. Genome. 6(5):367-68 (1995). Lumican helps in the establishment of corneal stromal matrix organization during neonatal development in mice. Those lacking lumican exhibit several corneal related defects. Beecher, N., *et al.*, *NeoNatal Development of the Corneal Stroma in Wild-Type and Lumican-Null Mice*, Invet. Opthalmol. Vis. Sci. 42(8): 1750-1756 (2006). It is important for corneal transparency in mice. Mutations in *TIMP3* gene result in autosomal dominant disorder, Sorsby's fundus dystrophy, an age-related macular degeneration of retina. Li, Z., *et al.*, *TIMP3 Mutation in Sorsby's Fundus Dystrophy: Molecular Insights*, Expert Rev. Mol. Med. 7(24) 1-15 (2005). It has been suggested that a possible mechanism for retinal degeneration in Sorsby's fundus dystrophy was traceable to nutrition. Clarke, M., *et al.*, *Clinical Features of a Novel TIMP-3 Mutation Causing Sorsby's Fundus Dystrophy: Implications for Disease Mechanism*, Br. J. Opthamol. 85(12): 1429-1431 (2001).

[000135] Lumican-null mice exhibit altered collagen fibril organization and loss of corneal transparency. Carlson, et al., J. Biol. Chem. 280(27):25541-47. Lumican also significantly suppressed subcutaneous tumor formation in syngenic mice and induced and/or enhanced the

apoptosis of these cells. Z. Naito, *The Role of Small Leucine-rich Proteoglycan (SLRP) Family in Pathological Lesions and Cancer Cell Growth.* J. Nippon. Med. Sch. 72(3):137-45 (2005). In breast cancer, decreased mRNA expression levels of Lumican are associated with rapid disease progression and a poor survival rate. *Id.* Lumican has been implicated as an apoptotic gene in breast, pancreatic and colorectal cancers. S. Troup, *et al.*, *Reduced Expression of the Small Leucine-rich Proteoglycans, Lumican, and Decorin Is Associated with Poor Outcome in Node-negative Invasive Breast Cancer*, Clin. Cancer Res. 9(1):207-14 (2003); Y. P. Lu, *et al.*, *Lumican Expression in Alpha Cells of Islets in Pancreas and Pancreatic Cancer Cells*, J. Pathol. 196(3):324-30 (2002); Y. P. Lu, *et al.*, *Expression of Lumican in Human Colorectal Cancer Cells*, Pathol. Int. 52(8):519-26 (2002).

[000136] LUM was upregulated in both the L and L3 group in brain tissue. Thus, DHA and ARA supplementation has a beneficial effect in upregulating LUM expression and it is believed that such upregulation can slow disease progression and provide a higher survival rate among individuals with breast, pancreatic, or colorectal cancers. It is believed that DHA and ARA supplementation also aids in tumor suppression.

[000137] *IMPG1* is a proteoglycan which participates in retinal adhesion and photoreceptor survival. Kuehn, M.H. & Hageman, G.S., *Expression and Characterization of the IPM 150 Gene (IMPG1) Product, A Novel Human Photoreceptor Cell-Associated Chondroitin-Sulfate Proteoglycan*, Matrix Bio. 18(5): 509-518 (1999). Higher amounts of DHA in the infant formula increased the expression of *IMPG1*. Expression of *RAX* transcript was decreased in both the supplemental groups. Increased *RAX* expression is seen in the retinal progenitor cells during the vertebrate eye development and is downregulated in the differentiated neurons. Mathers, P.H. & Jamrich, M., *Regulation of Eye Formation by the Rx and Pax6 Homeobox Genes*, Cell. Mol. Life Sci. 57(2): 186-194 (2000); Furukawa,

T., *et al.*, *Rax, Hes1 and Notch1 Promote the Formation of Muller Glia by Postnatal Retinal Progenitor Cells*, Neuron. 26(2): 383-394 (2000). DHA is well known to promote neurite growth in the brain; this could be the possible reason for *RAX* downregulation in the present study.

[000138] Based upon the above results, DHA and ARA supplementation modulate genes which aid in preserving or developing visual heath. Supplementation may prevent or treat the development of visual diseases or disorders or may improve the development of visual components.

Integral to Membrane/Membrane Fraction

[000139] Transcripts that are integral parts of biological membranes or within the membrane fractions were differentially expressed in the present invention. For example, *EVER1*, *PERP*, *Cep192*, *SSFA2*, *LPAL2*, *TMEM20*, *TM6SF1* were upregulated in both the groups. *ORMDL3*, *SEZ6L*, *HYDIN*, *TA-LRRP*, *PKD1L1* were upregulated in L3/C and downregulated in L/C. *MFAP3L* was upregulated in L/C and downregulated in L3/C. Transcripts of *GP2* and *SYNGR2* were downregulated in both the groups.

[000140] Numbers of transcripts were upregulated by increased DHA in the formulas. LCPUFA supplementation can affect biological membrane functions by influencing membrane composition and permeability, interactions with membrane proteins, membrane-bound receptor functions, photoreceptor signal transduction, and/or transport. Liefert, W.R., *et al.*, *Membrane Fluidity Changes are Associated with the Antiarrhythmic Effects of Docosahexaenoic Acid in Adult Rat Cardiomyocytes*, J. Nutr. Biochem. 11(1): 38-44 (2000); Stillwell, W. & Wassall, S.R., *Docosahexaenoic Acid: Membrane Properties of a Unite Fatty Acid*, Chem. Phys. Lipids 126(1): 1-27 (2003); SanGiovanni, J.P. & Chew, E.Y., *The Role of Omega-3 Long-Chain Polyunsaturated Fatty Acids in Health and Disease of the Retina*, Prog. Retinal Eye Res. 24(1): 87-138 (2005). Mutations in *EVER1* or transmembrane channel-like 6

(*TMC6*) gene cause epidermodysplasia verruciformis, a type of skin disorder. Ramoz, N., *et al.*, *Mutations inTwo Adjacent Novel genes are Associated with Epidermodysplasia Verruciformis*, Nat. Genet. 32(4): 579-81 (2002). *HYDIN* is a novel gene and nearly-complete loss of its function due to mutations causes congenital hydrocephalus in mice. Davy, B.E. & Robinson, M.L., *Congenital Hydrocephalus in Hy3 Mice is Caused by a Frameshift Mutation in Hydin, a Large Novel Gene*, Hum. Mol. Gen. 12(10): 1163-1170 (2003). The exact function of *GP2* is unknown, but it has been associated with the secretory granules in the pancreas. Yu, S., *et al.*, *Effects of GP2 Expression on Secretion and Endocytosis in Pancreatic AR4-2J Cells*, Biochem. & Biophys. Res. Comm. 322(1): 320-325 (2004).

[000141] PERP (p53 Effector Related to PMP22) was expressed in the brain via DHA and ARA supplementation. PERP is a putative transmembrane receptor and a tumor suppressor gene. PERP knockout mice die after birth due to compromised adhesion and dramatic blistering in stratified epithelia. Loss of PERP might be associated with ectodermal dysplasia syndromes or an enhanced spontaneous risk of cancer by impairing the tumor suppression activity of both the p53 and p63 pathways. During normal zebrafish development, *PERP* is required for the survival of notochord and skin cells.

[000142] Thus, DHA and ARA supplementation may affect membrane/membrane functions by influencing (1) membrane composition and permeability, (2) interactions with membrane proteins, (3) membrane-bound receptor functions, (4) photoreceptor signal transduction, and/or (5) transport.

Programmed Cell Death/Apoptosis

[000143] Transcripts with apoptotic activity were differentially expressed. Seven out of nine transcripts in the present study were upregulated with increasing DHA, including *CARD6*, *TIA1*, *BNIP1*, *FAF1*, *GULP1*, *CASP9*

and FLJ13491. Programmed cell death (PCD) plays an important role during the development of immune and nervous systems. Kuida, K., *et al.*, *Decreased Apoptosis in the Brain and Premature Letharlity in CPP32-Deficient Mice*, Nature 384(6607): 368-372 (1996). Jacobson, *et al.* proposed PCD as an important event in eliminating unwanted cells during development. Mice with targeted deletion of *CASP3* die perinatally due to vast excesses of cells deposition in their CNS as a result of decreased apoptotic activity. Jacobson, M.D., *et al.*, *Programmed Cell Death in Animal Development*, Cell 88(3): 347-354 (1997). *CARD6* (caspase recruitment domain protein 6) was upregulated in both the groups. It is a microtubule-interacting protein that activates NF-KB and takes part in the signaling events leading to apoptosis. Dufner, A.S., *et al.*, *Caspase Recruitment Domain Protein 6 is a Microtubule-interacting Protein that Positively Modulates NF-KB Activation*, Proc. Natl. Acad. Sci 103(4): 988-93 (2006). *TIA1* was upregulated in L3/C and downregulated in L/C in the present invetion. *TIA1* is a member of RNA-binding protein family with pro-apoptotic activity, and it silences the translation of cyclooxygenase-2 (*COX2*). Narayanan, *et al.* suggested that DHA indirectly increases the expression of genes which downregulate *COX2* expression. Narayanan, B.A., *et al.*, *Docosahexaenoic Acid Regulated Genes and Transcription Factors Inducing Apoptosis in Human Colon Cancer Cells*, Int. J. Oncol. 19(6): 1255-62 (2001). The COX2 enzyme catalyzes the rate-limiting step for prostaglandin production, which influence many processes including inflammation. Dixon, D.A., *et al.*, *Regulation of Cyclooxygenase-2 Expression by the Translational Silencer TIA-1*, J. Exp. Med. 198(3): 475-481 (2003). Downregulation of *TIA1* in L/C could be due to the influence of ARA, the major *COX2* substrate, rather than that of DHA, which is a competitive inhibitor. *GULP1* assists in efficient removal of the apoptotic cells by phagocytosis. Su, H.P., *et al.*, *Interaction of CED-6/GULP, an Adapter Protein Involved in Englufment of Apoptotic Cells with CED-1 and*

CD91/Low Density Lipoprotein Receptor-Related Protein (LRP), J. Bio. Chem. 277(14): 11772-11779 (2002). *CASP9* activates caspase activation cascade and is an important component of mitochondrial apoptotic pathway. Brady, *et al.*, *Regulation of Caspase 9 Through Phosphorylation by Protein Kinase C Zeta in Response to Hyperosmotic Stress*, Mol. Cell Bio. 25(23): 10543-55 (2005).

[000144] The results discussed above indicate that the modulation of these genes may assist in the elimination of unwanted cells as a part of programmed cell death or apoptosis. This result is important in the development of a healthy immune and nervous system. The modulation caused by DHA and ARA supplementation may also be useful in preventing or treating inflammation in a subject.

Cytoskeleton and Cell adhesion

[000145] In the present invention, dietary LCPUFAs regulated expression of a number of transcripts involved in cytoskeleton and cell adhesion. In fact, the expression of 27 ps involved in cytoskeleton was altered. Genes encoding Myosin isoforms *MYO1A*, *MYO5A* and *MYO1E* were changed. *MYO1A* and *MYO5A* were upregulated with increasing amounts of DHA whereas *MYO1E* showed decreased expression. Myosin-1 isoforms are membrane associated molecular motors which play essential roles in membrane dynamics, cytoskeletal structure and signal transduction. Sokac, *et al..*, *Regulation and Expression of Metazoan Unconventional Myosins*, in *International Review of Cytology – A Survey of Cell Biology*, Vo. 200: 197-304 (2000).

[000146] Expression of Collagen types IV and IX were altered by dietary LCPUFA. *COL4A6* and *COL9A3* showed increased expression whereas *COL4A2* and *COL9A2* showed decreased expression with increasing DHA. Type IV collagen is the major component of the basement membrane. Mild forms of Alport nephropathy are associated with deletion in *COL4A6* gene and eye abnormalities are common in people afflicted

with Alport syndrome. Mothes, *et al.*, *Alport Syndrome Associated with Diffuse Leiomyomatosis: COL4A5-COL4A6 Delection Associated with a Mild Form of Alport Nephrophathy*, Nephrol. Dial. Transplant, 17(1): 70-74 (2002); Colville, *et al.*, *Ocular Manifestation of Autosomal Recessive Alport Syndrome*, Ophtalmic Gen. 18(3): 119-128 (1997). Loss of the *COL4A6* in epithelial basement membrane occurs in the early stage of cancer invasion. The expression of the *COL4A6* was down-regulated in colorectal cancer. Leiomyomata of the esophagus is also associated with deletion in *COL4A6* gene.

[000147] *WASL*, also known as neural WASP (*WASP*), was upregulated in both the groups. Actin cytoskeleton regulation is vital for brain development and function. *WASL* is an actin-regulating protein and mediates filopodium formation. Miki, *et al.*, *Induction of Filopodium Formation by a WASP Subcellular Localization and Function*, Nature 391(6662): 93-96 (1998); Wu, *et al.*, *Focal Adhesion Kinase Regulation of N-WASP Subcellular Localization and Function*, J. Bio. Chem. 279(10): 9565-76 (2004); Suetsugu; *et al.*, *Regulation of Actin Cytoskeleton by mDab1 through N-WASP and Ubiquitination of mDab1*, Biochem. J. 384: 1-8 (2004). *HIP1* (huntingtin interacting protein 1) and *HOOK2* (hook homolog 2) were downregulated in both the groups.

[000148] The expression levels of 15 transcripts involved in cell adhesion changed as a result of dietary LCPUFA. For example, *BTBD9*, *CD44*, *ARMC4*, *CD58*, LOC389722 and *PCDHB13* showed increased expression in both the groups. Glycoprotein *CD44* is a cell-surface adhesion molecule that is involved in cell-cell and cell-matrix interactions while *PCDHB13* is a member of protocadherin beta family of transmembrane glycoproteins. Wu, *et al.*, *A Striking Organization of a Large Family of Human Neural Cadherin-like Cell Adhesion Genes*, Cell 97(5) 779-790 (1999). *NLGN3* and *CYR61* were downregulated in both groups.

[000149] The proper function of cytoskeletal and cell adhesion is important for the normal functioning of living organisms. Cell adhesion proteins hold together the components of solid tissues. They are also important for the function of migratory cells like white blood cells. Certain cancers involve mutations in genes for adhesion proteins that result in abnormal cell-to-cell interactions and tumor growth. Cell adhesion proteins also hold synapses together, which may affect learning and memory. In Alzheimer's disease there is abnormal regulation of synaptic cell adhesion. The results have shown that DHA and ARA can modulate genes involved with proper cytoskeletal and cell adhesion. Thus, a method of the present invention involves supplementing a subject with DHA and ARA in order to treat or prevent cancer or Alzheimer's disease, improve memory, or allow the migration of white blood cells.

Peptidases

[000150] Several transcripts having peptidase activity were differentially expressed. *SERPINB6* was significantly upregulated in L3/C and downregulated in L/C. Of note, the ADAM families of proteins (*ADAM17*, *ADAM33*, *ADAM8*, and *ADAMTS16*) were upregulated and *ADAMTS15* was downregulated in both the supplemental groups. ADAM proteins are membrane-anchored glycoproteins named for two of the motifs they carry: an adhesive domain (disintegrin) and a degradative domain (metalloprotease). These proteins are involved in several biological processes including cell-cell interactions, heart development, neurogenesis and muscle development. *ADAM17* is required for proteolytic processing of other proteins and has been reported to participate in the cleaving of the amyloid precursor protein. Loss of *ADAM17* is reported in abnormalities associated with heart, skin, lung and intestines. Real time PCR confirmed the array results of *ADAM17*.

[000151] *ADAM17* is also known as Tumor Necrosis Factor-Alpha Converting Enzyme (*TACE*). *ADAM17* plays a neuroprotective role by

cleaving of the amyloid precursor protein (APP) within the amyloid-beta (Aβ) sequence and thus play a key role in Alzheimer's disease process by preventing the formation of toxic amyloid-beta peptides. Buxbaum JD, *et al., Evidence that Tumor Necrosis Factor Alpha Converting Enzyme is Involved in Regulated Alpha-Secretase Cleavage of the Alzheimer Amyloid Protein Precursor*, J. Biol. Chem. 273:27765-27767 (1998); Endres K, *et al., Shedding of the Amyloid Precursor Protein-Like Protein APLP2 by Disintegrin-Metalloproteinases*, FEBS J. 272 (22):5808-5820 (2005). Additionally, aspirin induces platelet receptor shedding via *ADAM17*. Aktas B, *et al., Aspirin Induces Platelet Receptor Shedding via ADAM17 (TACE)*, J. Biol. Chem. 280(48):39716-22 (2005).

[000152] A lack of *ADAM17* leads to developmental abnormalities in mice, including defects in epithelial structures such as skin and intestines, as well as in morphogenesis of the lung. Peschon JJ, *et al., An Essential Role for Ectodomain Shedding in Mammalian Development*, Science 282(5392):1281-4 (1998); Zhao J, *et al., Pulmonary Hypoplasia in Mice Lacking Tumor Necrosis Factor-Alpha Converting Enzyme Indicates an Indispensable Role for Cell Surface Protein Shedding During Embryonic Lung Branching Morphogenesis*. Dev. Biol. 232(1):204-18 (2001). Thus, it is believed that the upregulating effect of DHA and ARA on ADAM17 can prevent abnormalities in epithelial structures and heart development and can prevent or treat Alzheimer's.

[000153] *ADAM17* mediates regulated ectodomain shedding of the severe-acute respiratory syndrome-coronavirus (SARS-CoV) Receptor, Angiotensin-converting enzyme-2 (*ACE2*). Lambert, D.W., *et al., Tumor Necrosis Factor-Alpha Convertase (ADAM17) Mediates Regulated Ectodomain Shedding of the Severe-Acute Respiratory Syndrome-Coronavirus (SARS-CoV) Receptor, Angiotensin-Converting Enzyme-2 (ACE2)*. J. Biol. Chem. 280(34):30113-9 (2005). It has also been shown that mice lacking *ADAM17* and *ADAM19* have exacerbated defects in

heart development. Horiuchi K, *et al.*, *Evaluation of the Contributions of ADAMs 9, 12, 15, 17, and 19 to Heart Development and Ectodomain Shedding of Neuregulins Beta1 and Beta2*, Dev. Biol. 283(2):459-71 (2005). The heart abnormalities observed in mice lacking functional ADAM17 are thickened and misshapen semilunar valves (aortic and pulmonic valves) and atrioventricular valves. Jackson, L.F., *et al.*, *Defective Valvulogenesis in HB-EGF and TACE-Null Mice is Associated with Aberrant BMP Signaling*, EMBO J. 22(11):2704-16 (2003).

[000154] *ADAM33* is a member of the 'disintegrin and metalloprotease domain' family of proteins and has been recently implicated in asthma and bronchial hyperresponsiveness by positional cloning. Van Eerdewegh, P., *et al.*, *Association of the ADAM33 Gene with Asthma and Bronchial Hyperresponsiveness*, Nature 418:426-30 (2002).

[000155] *ADAM33* occurs in smooth muscle bundles and around embryonic bronchi, strongly suggesting that it might play an important role in smooth muscle development and function. Haitchi HM, *et al.*, *ADAM33 Expression in Asthmatic Airways and Human Embryonic Lungs*, Am. J. Respir. Crit. Care Med. 171(9):958-65 (2005). ADAM33 protein in both differentiated and undifferentiated embryonic mesenchymal cells suggests that it may be involved in airway wall "modeling" and may additionally be involved in determining lung function throughout life. *Id.*; Holgate, ST, *et al.*, *ADAM33: a Newly Identified Protease Involved in Airway Remodeling*, Pulm. Pharmacol. Ther. 19(1):3-11 (2006). In murine models *ADAM33* mRNA expression increases during embryonic lung development and remains into adulthood. *Id.* High-level expression in smooth muscles and fibroblasts suggest that ADAM33 plays a role in airway remodeling in asthmatics. Lee, JY, *et al.*, *A Disintegrin and Metalloproteinase 33 Protein in Asthmatics : Relevance to Airflow Limitation*, Am. J. Respir. Crit. Care Med. (Dec 30, 2005).

[000156] Because ADAM33 was upregulated in both the L group and the L3 group of neonatal baboons, the inventors believe that DHA and ARA supplementation aids in airway wall "modeling" and smooth muscle development and function.

[000157] *ADAM8* (a disintegrin and metalloproteinase domain 8) was expressed in the liver via DHA and ARA supplementation. *ADAM8*, also known as CD156, is highly expressed in monocytes, neutrophils, and eosinophils. It plays an important role in asthma disease. Recently, it was discovered that *ADAM8* significantly inhibited experimentally induced asthma in mice. Thus, *ADAM8* may also play a role in allergic diseases. *ADAM8* plays a role in regulating monocyte adhesion and migration. Peroxisome proliferator-activated receptor-γ activation could also lead to increased expression of *ADAM8*.

[000158] *CTSB* (Cathepsin B), also known as amyloid precursor protein secretase (*APPS*), was upregulated. It is involved in the proteolytic processing of amyloid precursor protein. Felbor, *et al.* reported deficiency of *CTSB* results in brain atrophy and loss of nerve cells in mice. Felbor, *et al.*, *Neuronal Loss and Brain Atrophy in Mice Lacking Cathepsis V and L*, Proc. Natl. Acad. Sci. 99(12) 7883-7888 (2002). *CTSC* (cathepsin C) was downregulated in the L/C group and upregulated in the L3/C group. Loss of function mutations in *CTSC* gene are associated with tooth and skin abnormalities. Toomes, *et al.*, *Loss-of-Function Mutations in the Cathepsin C Gene Result in Periodontal Disease and Palmoplantar Keratosis*, Nat. Genet. 23(4): 421-424 (1999).

[000159] Cathepsin B (CTSB) was shown to be expressed in the brain due to DHA and ARA supplementation. Cathepsin B is also known as amyloid precursor protein secretase (APPS) and is involved in the proteolytic processing of amyloid precursor protein (APP). Incomplete proteolytic processing of APP has been suggested to be a causative factor in Alzheimer's disease. CTSB localization in placental and decidual

macrophages suggests a role in the physiological function of these cells in mediating villous angiogensis and decidual apoptosis. CTSB deficient mice show a reduction in premature intrapancreatic trypsinogen activation. It has been reported that combined deficiency of CTSB and CTSL results in neuronal loss and brain atrophy, suggesting that CTSB and CTSL are essential for maturation and integrity of the CNS.

[000160] *NAALAD2* was upregulated while *PAPLN, RNF130, TMPRSS2, PGC, CPZ, FURIN* were downregulated. *CPZ* interacts with WNT proteins and may regulate embryonic development; however, its expression in adult tissues is less abundant. *TPP2* and *SPPL2B* showed increased expression in L/C and decreased expression in L3/C. *PAPPA, GZMA, SERPINA1, QPCTL* transcripts were downregulated in L/C and upregulated in L3/C. Several hypothetical proteins (FLJ10504, FLJ30679, FLJ90661, FLJ25179, DKFZp686L1818) were differentially expressed.

[000161] Based upon the above results, the inventors have shown that DHA and ARA supplementation are effective in modulating peptidase genes. Accordingly, DHA and ARA are useful in prevention or treating abnormalities in the skin, heart, lung and/or intestines. As part of the method of the present invention, DHA and ARA may be especially useful in aiding the maturation and integrity of the lungs and/or CNS. DHA and ARA may also be useful in preventing or treating asthma or allergic disease.

Cell Cycle, Cell Growth and Cell Proliferation

[000162] Fifteen transcripts having a role in cell cycle regulation, growth and proliferation were differentially expressed. Four of the transcripts *SESN3, RAD1, GAS1* and *PARD6B* involved in cell cycle regulation were upregulated in both the groups.

[000163] *SESN3* (sestrin 3) was expressed in the brain by DHA and ARA supplementation. Sestrins are cysteine sulfinyl reductases whose expression is modulated by p53. Budanov, *et al.* showed that sestrins are

required for regeneration of peroxiredoxins which help in reestablishing the antioxidant properties. Budanov, *et al.*, *Regeneration of Peroxiredoxins by p53-Regulated Sestrins, Homologs of Bacterial AhpD*, Sci. 304(5670): 596-600 (2004). The exact function of *SESN3* is still not known.

[000164] Cell growth factors, *INHBC* and *OGN* were induced in both the groups. *FGFR1OP* is a positive regulator of cell proliferation and showed increased expression. *KAZALD1*, *CDC20* and *CDKN2C* were downregulated.

[000165] Growth arrest specific gene 1 (*GAS1*) expression is positively required for postnatal cerebellum development. Mice lacking *GAS1* had significantly reduced cerebellar size compared to wild type mice. Liu, *et al.* proposed that *GAS1* perform dual roles in cell cycle arrest and in proliferation in a cell autonomous manner. Liu, *et al.*, *Growth Arrest Specific Gene 1 is a Positive Growth Regulator for the Cerebellum*, Dev. Biol. 236(1): 30-45 (2001). *PARD6B* has a role in axonogenesis. Brajenovic, *et al.*, *Comprehensive Proteomic Analysis of Human Par Protein Complexes Reveals an Interconnected Protein Network*, J. Bio. Chem. 279(13): 12804-11 (2004).

[000166] *INHBC* is a member of transforming growth factor-beta (TGF-β) superfamily and is involved cell growth and differentiation. Osteoglycin (*OGN*) is also known as Mimecan and Osteoinductive factor (*OIF*). Mimecan is a member of small-leucine rich proteoglycan gene family and is a major component of cornea and other connective tissues. It has a role in bone formation, cornea development and regulation of collagen fibrillogenesis in corneal stroma. *CDC20* regulates anaphase-promoting complex.

[000167] The inventors have shown in the present invention that DHA and ARA can modulate genes related to cell cycle, cell growth, and cell proliferation. As such, a method of the present invention comprises

supplementing the diet of a subject with a therapeutically effective amount of DHA and ARA in order to enhance cell growth and proliferation and improve the cell cycle in general.

Response to Stress

[000168] *MSRA*, *SOD2*, *GSTA3* and *GSR* genes were differentially expressed. *MSRA* (peptide methionine sufoxide reductase) was upregulated in both the supplemental groups. *SOD2* was downregulated in L/C and upregulated in L3/C. *GSR* was upregulated in the L/C and downregulated in the L3/C. *GSTA3* was downregulated in both the groups.

[000169] Oxidative damage to proteins by reactive oxygen species is associated with oxidative stress, aging, and age-related diseases. MSRA is expressed in the retinal pigmented epithelial cells, neurons, and throughout the nervous system. Knock-outs of the *MSRA* gene in mice result in shortened life-spans both under normoxia and hyperoxia (100% oxygen) conditions. *MSRA* also participates in the regulation of proteins. *MSRA* plays an important role in neurodegenerative diseases like Alzheimer's and Parkinson's by reducing the effects of reactive oxygen species. Overexpression of *MSRA* protects human fibroblasts against H_2O_2-mediated oxidative stress.

[000170] Reactive oxygen species (ROS) can oxidize methoionine (Met) to methionine sulfoxide (MetO). The oxidized product, methinine sulfoxide, can be enzymatically reduced back to methionine by peptide methionine sulfoxide reductase. Overexpression of MSRA under elevated oxidative stress conditions predominantly in the nervous system markedly extended the life span of the Drosophilia. Methionine sulfoxide reductase is a regulator of antioxidant defense and life span in mammals.

[000171] *SOD2* belongs to the iron/manganese superoxide dismutase family. It encodes a mitochondrial protein and helps in the elimination of reactive oxygen species generated within mitochondria. In the present

study, increased amounts of DHA reduced the expression of glutathione-related proteins *GSR* and *GSTA3*.

[000172] The data in the present invention has shown that DHA and ARA supplementation are effective in modulating genes associated with stress response. Based upon these results, DHA and ARA supplementation are useful in preventing or treating oxidative stress, age-related disorders, and neurodegenerative diseases. In addition, DHA and ARA supplementation may aid in proper development and integrity of the retina, neurons, and nervous system. Supplementation of a therapeutically effective amount of DHA and ARA may also lengthen the life span of a subject.

Kinases and Phosphatases

[000173] Phosphorylation and dephosphorylation of proteins control a multitude of cellular processes. Several proteins having kinase activity were altered in the present invention as a result of DHA and ARA supplementation. Of note, transcripts involving *STK3*, *STK6*, *HINT3*, *TLK1*, *DRF1*, *GUCY2C* and *NEK1* were significantly upregulated with increasing DHA. A number of MAP kinases were downregulated in L3/C group, including *MAP4K1*, *MAPK12*, *MAP3K2* and *MAP3K3*. Other transcripts which showed significantly decreased expression were *CKM*, *LMTK2*, *NEK11*, *TNK1*, *BRD4* and MGC4796.

[000174] Transcripts having dephosphorylation activity, including *ACPL2*, KIAA1240, *PPP2R3A*, *PPP1R12B*, *PTPRG*, *PPP3CA* and *ACPP* were upregulated in L3/C group. *MTMR2*, *PPP1R7*, *PTPRN2* and *HDHD3* were significantly downregulated with increasing DHA.

Transcription Factors

[000175] Several transcription factors are differentially expressed by dietary LCPUFA. Zinc finger proteins, Homeo box proteins and RNA Pol II transcription factors were among them. Several of the Zinc finger proteins were overexpressed in L3/C, which include *ZNF611*, *ZNF584*, *ZNF81*,

ZNF273, *ZNF547*, *MYNN*, *ZBTB11*, *PRDM7*, *JJAZ1*, *ZNF582*, *MLLT10*, *ZNF567*, *ZNF44*, *ZNF286*, *ZFX*, *NAB1*, *ZNF198*, *ZNF347* and *ZNF207*, while *PCGF2*, *ZBTB9*, *ZNF297*, *WHSCIL1*, *SALL4*, *ZNF589*, *ZFY*, *ZNF146*, *ZNF419* and *ZNF479* were repressed in L3/C group. Zinc finger proteins exhibit varied biological functions in eukaryotes including activation of transcription, protein folding, regulation of apoptosis, and lipid binding. Homeobox transcription factors, *TGIF2*, *PHTF1*, *OTP* and *HHEX* were induced whereas *PHOX2A*, *IRX1* and *MITF* were repressed in L3/C. RNA Pol II transcription factors (*BRCA1*, *TFCP2*, *CHD2*, *THRAP3*, *SMARCD2* and *NFE2L2*) showed increased expression in L3/C. However, transcripts for *UTF1*, *POU2F2*, *ELL*, *POLR2C*, *THRAP5*, *TGIF* and *GLIS1* showed decreased expression in L3/C. *SOX7* and *SOX12*, high mobility group (HMG) box proteins, were also differentially expressed. *ZNF611* array expression results were confirmed by real time PCR.

[000176] *BRCA1* is a tumor suppressor gene. *BRCA1* was the first identified and cloned breast and ovarian cancer susceptibility gene. Miki Y., *et al.*, *A Strong Candidate for the Breast and Ovarian Cancer Susceptibility Gene BRCA1*, Science 266(5182):66-71 (1994). Both hereditary and sporadic breast and ovarian tumors frequently have decreased *BRCA1* expression. Wilcox CB, *et al.*, *High-Resolution Methylation Analysis of the BRCA1 Promoter in Ovarian Tumors*, Cancer Genet. Cytogenet. 159(2):114-22 (2005). *BRCA1* may contribute to its tumor suppressor activity, including roles in cell cycle checkpoints, transcription, protein ubiquitination, apoptosis, DNA repair and regulation of chromosome segregation. Venkitaraman AR. *Cancer Susceptibility and the Functions of BRCA1 and BRCA2*, Cell 108:171-182 (2002); Rosen EM, *et al.*, *BRCA1 Gene in Breast Cancer*, J. Cell. Physiol. 196:19-41 (2003); Lou Z, *et al.*, *BRCA1 Participates in DNA Decatenation*, Nat. Struct. Mol. Biol. 12:589-93 (2005); Zhang, J. & Powell, S.N., *The Role of*

the BRCA1 Tumor Suppressor in DNA Double-Strand Break Repair. Mol. Cancer Res. 3(10):531-9 (2005).

[000177] The emerging picture is that *BRCA1* plays an important role in maintaining genomic integrity by protecting cells from double-strand breaks (DSB) that arise during DNA replication or after DNA damage. Zhang & Powell, 2005. *BRCA1* mutation carriers have a significantly increased risk of pancreatic, endometrial, and cervical cancers as well as prostatic cancers in men younger than age 65. Thompson, D. & Easton, D.F., *Cancer Incidence in BRCA1 Mutation Carriers,* J. Natl. Cancer Inst. 94:1358-1365 (2002).

[000178] BRCA1 was upregulated in both the L group and the L3 group, and, thus, it is believed that DHA and ARA supplementation lowers the risk of pancreatic, endometrial, cervical, and prostatic cancers and can suppress tumors.

Receptor Activity

[000179] Transcripts performing receptor activities were differentially expressed. While increasing levels of DHA were associated with decreased expression of *CD40, ITGB7, IL20RA, CD14, DOK3, MR1, BZRAP1, RARA, CD3D, IL1R1, MCP,* and *HOMER3* transcripts, increased expression was detected for *FCGR2B, IL31RA, MRC2, SCUBE3, CR2, NCR2, CRLF2, SLAMF1, EGFR* and *KIR3DL2.* Interestingly, retinoic acid receptor α (*RARA*) activity was decreased in both the groups. *EGFR* expression levels were confirmed by QRT-PCR.

Ubiquitin Cycle

[000180] Twenty-five probe sets having a role in the ubiquitination process were differentially expressed. Interestingly, five members of F-box protein family (*FBXL7, FBXL4, FBXL17, FBXW4* and *FBXW8*) showed increased expression in L3/C group. F-Box proteins participate in varied cellular processes such as signal transduction, development, regulation of transcription, and transition of cell cycle. They contain

protein-protein interaction domains and participate in phosphorylation-dependent ubiquitination. Proteins associated with anaphase-promoting complex (*CDC23* and *ANAPC1*) were downregulated in L3/C group.

Others

[000181] Transcripts involved in 1) calcium ion binding (MGC33630, *UMODL1*, FLJ25818, *S100Z*, MGC12458, *ITSN2* and *PRRG3*), 2) zinc ion binding (*FGD5*, *ZFYVE28*, *PDLIM4*, *ZCCHC6*, *ZNF518* and *INSM2*), 3) ATP binding (*MMAA* and C6orf102), 4) GTP binding (*DOCK5*, *DOCK6*, *DOCK10*, *MFN1* and *GTP*), 5) nucleic acid binding (*IFIH1*, C13orf10, *DDX58*, *TNRC6C*, *RSN*, *ZCCHC5*, DJ467N11.1, MGC24039 and LOC124245), 6) DNA binding (KIAA1305, *HP1-BP74*, *H2AFY*, C17orf31, *HIST1H2BD* and *HIST1H1E*) 7) protein binding (*ABTB1*, MGC50721, *RANBP9*, *STXBP4*, *BTBD5* and *KLHL14*) and 8) protein folding (*HSPB3*, *DNAJB12*, *FKBP11* and *TBCC*) were all differentially expressed. Also, several transcripts which play a role in RNA processing events were differentially expressed. For example, *SFRS2IP*, LOC81691, *EXOSC2*, *SFPQ*, *SNRPN* and *SFRS5* showed increased expression with increasing DHA whereas *NOL5A*, *RBM19*, *NCBP2* and *PHF5A* showed decreased expression with increasing DHA. Transcripts related to immune response were also differentially expressed. For example, *HLA-DPB1*, *MX2* and *IGHG1* were overexpressed and *PLUNC* was underexpressed with increasing DHA.

[000182] A gene known as FOXP2 (Forkhead box P2), was upregulated in the cerebral cortex of baboons supplemented with DHA and ARA. In the L group, the gene was downregulated by 8%, but in the L3 group the gene was upregulated by 38%, as compared to the control group. FOXP2 is a putative transcription factor that plays an important role in neurological development. A mutation in FOXP2 can cause severe speech and language deficits. Recent studies in songbirds show that during times of song plasticity FOXP2 is upregulated in a striatal region essential for song

learning. The gene has also been implicated in speech development. Therefore, the inventors believe that upregulation of FOXP2 through DHA and ARA supplementation aids neurological and speech development.

[000183] Other genes that were upregulated by DHA and ARA supplementation include XLC1 and 2. They are chemokines, C motif, ligands 1 & 2. Chemokines are a group of small (approximately 8 to 14 kD), mostly basic structurally related molecules that regulate cell trafficking of various types of leukocytes through interactions with a subset of 7-transmembrane G protein-coupled receptors. Chemokines also play fundamental roles in the development, homeostasis, and function of the immune system, and they have effects on cells of the central nervous system as well as on endothelial cells involved in angiogenesis or angiostasis. They are considered to be mediators of the immune response. Therefore, the inventors believe that upregulation of XLC1 or 2 via DHA and ARA supplementation improves function of the immune system.

[000184] Yet another gene that was upregulated by DHA and ARA supplementation was RNASE3. RNASE3, also known as Eosinophil Cationic protein, is a ribonuclease of the "A" family. It is localized to the granule matrix of the eosinophil and possess neurotoxic, helminthotoxic, and defense responses to bacteria and ribonucleolytic activities. It has been implicated in connection with cellular immunity. It is believed, therefore, that the upregulation of RNASE3 via DHA and ARA supplementation improves the function of the immune system.

[000185] *NRF1* is a transcription factor that acts on nuclear genes encoding respiratory subunits and components of the mitochondrial transcription and replication machinery. *NRF1* is well known to regulate mitochondrial DNA transcription and replication in various tissues. Knocking out the *NRF1* gene leads to embryonic death around the time of the implantation in a mouse. May-Panloup P., *et al.*, *Increase of*

Mitochondrial DNA Content and Transcripts in Early Bovine Embryogenesis Associated with Upregulation of mtTFA and NRF1 Transcription Factors, Reprod. Biol. Endocrinol. 3:65 (2005).

[000186] It has been shown that *NRF1* expression is down-regulated in the skeletal muscle of diabetic and prediabetic insulin-resistant individual. Patti, M.E., *et al.*, *Coordinated Reduction of Genes of Oxidative Metabolism in Humans with Insulin Resistance and Diabetes: Potential Role of PGC1 and NRF1*, Proc. Natl. Acad. Sci. 100(14):8466-71 (2003). It has also been shown that *NRF1* has a protective function against oxidative stress and that mice with somatic inactivation of *NRF1* in the liver developed hepatic cancer. Parola, M. & Novo, E., *Nrf1 Gene Expression in the Liver: a Single Gene Linking Oxidative Stress to NAFLD, NASH and Hepatic Tumours*, J. Hepatol. 43(6):1096-7(2005).

[000187] Intake of EPA and DHA increase the expression of *NRF1*. Flachs P, *et al.*, *Polyunsaturated Fatty Acids of Marine Origin Upregulate Mitochondrial Biogenesis and Induce Beta-Oxidation in White Fat*, Diabetologia. 48(11):2365-75 (2005). It has also been suggested that *NRF1* plays an important role in neuronal survival after acute brain injury. Hertel M, *et al.*, *Upregulation and Activation of the Nrf-1 Transcription Factor in the Lesioned Hippocampus*, Eur. J. Neurosci. 15(10):1707-11 (2002).

[000188] Over-expression of *NRF1* increases the intracellular glutathione level. Gamma-glutamylcysteinylglycine or glutathione (GSH) performs important protective functions in the cell through maintenance of the intracellular redox balance and elimination of xenobiotics and free radicals. Myhrstad MC, *et al.*, *TCF11/NRF1 Overexpression Increases the Intracellular Glutathione Level and Can Transactivate the Gamma-Glutamylcysteine Synthetase (GCS) Heavy Subunit Promoter*, Biochim. Biophys. Acta. 1517(2):212-9 (2001).

[000189] It is believed that the upregulation of *NRF1* through DHA and ARA supplementation in the present invention can be a method for improving brain development, health, and function.

[000190] *STK3* is a gene which is also known as Mammalian Sterile 20-Like 2 *(MST2)* or Kinase Responsive to Stress 1 *(KRS1).* It is a member of the germinal center kinase group II (GCK II) family of mitogen-activated protein kinases. Dan I., *et al., The Ste20 Group Kinases as Regulators of MAP Kinase Cascades*, Trends Cell. Biol. 11:220–30 (2001). Emerging evidence suggests that the proapoptotic kinase *MST2* acts in a novel tumor suppression pathway. O'Neill EE, *et al., Mammalian Sterile 20-Like Kinases in Tumor Suppression: An Emerging Pathway*, Cancer Res. 65(13):5485-7 (2005). Overexpression of *MST2* induces apoptosis. O'Neill E, *et al., Role of the Kinase MST2 in Suppression of Apoptosis by the Proto-Oncogene Product Raf-1*, Science 306:2267-2270 (2004). STK3 was upregulated in both the L and L3 formula groups in the present study. Thus, it is believed that DHA and ARA supplementation is effective in tumor suppression via the upregulation of STK3.

[000191] *RNASE3* is also known as Eosinophil cationic protein (ECP). It is a highly basic protein of the ribonuclease-A family that is released from matrix of eosinophil granules. *RNASE3* possesses antiviral, antibactericidal, neurotoxic, helminthotoxic, and ribonucleolytic activities. Rosenberg, H.F., *Recombinant Human Eosinophil Cationic Protein: Ribonuclease Activity is not Essential for Cytotoxicity*, J. Biol. Chem. 270(14):7876-81 (1995); Kreuze, J.F., et al., *Viral Class 1 RNase III Involved in Suppression of RNA Silencing*, J. Virol. 79(11):7227-38 (2005). RNA silencing is a eukaryotic cellular surveillance mechanism that defends against viruses, controls transposable elements, and participates in the formation of silent chromatin. RNA silencing is also involved in post-transcriptional regulation of gene expression during developmental processes. RNASE3 enhances the suppression of RNA silencing.

Kreuze, *et al.*, 2005. It has also been shown that only human RNASE 3, among five human pancreatic-type RNASES, excels in binding to the cell surface and has a growth inhibition effect on several cancer cell lines. Maeda T, *et al.*, *RNase 3 (ECP) is an Extraordinarily Stable Protein Among Human Pancreatic-Type RNases*, J. Biochem. 132(5):737-42 (2002).

[000192] *RNASE2* is also known as Eosinophil-derived neurotoxin (*EDN*). It has been demonstrated that remarkable similarities exist between Eosinophil-derived neurotoxin and Eosinophil cationic protein. Hamann KJ, *et al.*, *Structure and Chromosome Localization of the Human Eosinophil-Derived Neurotoxin and Eosinophil Cationic Protein Genes: Evidence for Intronless Coding Sequences in the Ribonuclease Gene Ssuperfamily*, Genomics 7(4):535-46 (1990). *EDN* inactivates retroviruses in vitro. Rosenberg, H.F., Domachowske, J.B., *Eosinophils, Eosinophil Ribonucleases, and their Role in Host Defense Against Respiratory Virus Pathogens*, J. Leukoc. Biol. 70(5):691-8 (2001). *EDN* possesses antiviral, antibactericidal, cytotoxic, neurotoxic, helminthotoxic, dendritic cell chemotactic activities, and ribonucleolytic activities. *Id.*; Yang D, *et al.*, *Eosinophil-Derived Neurotoxin (EDN), an Antimicrobial Protein with Chemotactic Activities for Dendritic Cells*, Blood 102(9):3396-403 (2003). *EDN* has also been shown to be responsible in part for the HIV-1 inhibitory activities in the supernatant of allogeneic mixed lymphocyte reaction. Rugeles MT, *et al. Ribonuclease is Partly Responsible for the HIV-1 Inhibitory Effect Activated by HLA Alloantigen Recognition*, AIDS 17:481-486 (2003).

[000193] Both RNASE2 and RNASE3 were upregulated in the baboon thymus in the presence of either 1.00% DHA or 0.33% DHA and 0.67% ARA supplementation. Thus, the present invention has shown that DHA and ARA supplementation can be effective in providing antiviral, antibactericidal, neurotoxic, helminthotoxic, and ribonucleolytic properties,

cytotoxic, and dendritic cell chemotactic activities via the upregulation of RNASE2 and RNASE3.

[000194] TNNC1, also known as Troponin C, Cardiac (TNC), was shown in the present invention to be expressed in the liver. Contractions in striated muscles are regulated by the calcium-ion-sensitive, multiprotein complex troponin and the fribrous protein tropomysoin. The first mutation of the TNNC1 gene was identified in a patient with hypertrophic cardiomyopathy. This mutation is associated with a reduction in calcium sensitivity. The amino acid substitution TNNC1 (G159D) is localized in a domain of the protein contitutively occupied by Ca^{2+}. This may change the affinity for Ca^{2+} and, thereby, alter the ability of the troponin complex to regulate myocardial contractility. Idiopathic dilated cardiomyopathy (DCM) is the most common cause of heart failure and cardiac transplantation in the young. The condition is characterized by unexplained left ventricle dilation, impaired systolic function, and nonspecific histologic abnormalities dominated by myocardial fibrosis. Patients may experience severe disease complications including arrhythmia, thromboembolic events, and sudden death. It has been proposed that DCM mutations in the troponin complex may induce a profound reduction in force generation leading to impaired systolic function and cardiac dilation. In addition, it is possible that the myocardium of mutation carriers may be more susceptible to environmental influences such as viruses and toxic agents.

[000195] Thus, it is believed that an increased expression of TNNC1 via DHA and ARA supplementation may prevent or treat malfunctions, diseases, or disorders of the heart, such as arrhythmia, thromboembolic events, and even heart failure.

[000196] ASB1 (ankyrin repeat- and socs box-containing protein) has been shown to be expressed in the liver due to DHA and ARA supplementation. ASB1 belongs to the suppressor of cytokine signaling (SOCS) box protein superfamily. The ankyrin-repeats are compatible with a role in protein-protein interactions. It has been shown that mice lacking

the ASB1 gene display a dimunition of spermatogenesis with less complete filling of seminiferous tubules. However, overexpression of ASB1 had no apparent effects. It is believed, then, that DHA and ARA supplementation according to the method of the present invention may modulate the expression of ASB1 and aid in the proper development and activity of the reproductive system.

[000197] Cathepsin D (CTSD) is a lysosomal aspartic proteinase that has been shown to be expressed in the liver in the present invention. It plays an important role in the degradation of proteins and in apoptotic processes induced by oxidative stress, cytokines, and aging. Reduced activity of CTSD has been found in congenital ovine neuronal ceroid lipofuscinosis (CONCL), a type of neurodegenerative disease. CONCL is caused by a point mutation in the CTSD gene and is characterized by small brain size, pronounced neuronal loss, reactive astrocytosis, and infiltration of macrophages. CTSD cleaves beta-amyloid precursor protein near the beta secretase sites. It has been shown CTSD may play an important role in processing mutant Huntingtin protein (mHtt) in Huntington's disease. The inactive form of CTSD in the retinal pigment epithelium (RPE) in a transgenic mice model showed RPE atrophy, photoreceptor outer segment (POS) shortening and loss and accelerated debris accumulation. It has been shown that decreased CTSD expression levels in renal cell cancer specimens is associated with increased likelihood for the development of metastatic disease. CTSD deficiencies cause massive neuronal death in the central nervous system and may be the cause for lysosomal storage, stroke and age-related neurodegenerative diseases including Alzheimer's. Thus, the method of the present invention is useful in modulating CTSD expression and preventing or treating neurodegenerative and/or metastatic diseases through DHA and ARA supplementation.

[000198] *LMX1B* (LIM Homeobox Transcription Factor 1, beta) was expressed in the thymus upon DHA and ARA supplementation. Loss of

function mutations in *LMX1B* causes nail patella syndrome (NPS). NPS is an autosomal dominant disorder affecting development of the limbs, kidney, eyes and neurologic functions. *Lmx1b* may have a unique role in neuronal migration in the developing spinal cord. The diminished pain responses in NPS patients may be due to the inability of afferent sensory neurons to migrate. *Lmx1b* is required for the development of 5-hydroxytryptamine neurons in the central nervous system in mice. Dreyer, *et al.* showed expression of *LMX1B* during joint and tendon formation. Dreyer, *et al.*, *Lmx1b Expression During Joint and Tendon Formation: Localization and Evaluation of Potential Downstream Targets*, Gene Exp. Patterns 4(4): 397-405 (2004). *LMX1B* regulates the expression of multiple podocyte genes critical for podocyte differentiation and function.

[000199] Supplementation with DHA and ARA according to the method of the invention has been shown to modulate LMX1B expression and thereby prevent or treat autosomal disorders. In addition, DHA and ARA supplementation aids in proper development of the limbs, kidney, eyes, neurological system, and spinal cord via LMX1B modulation.

[000200] *BHMT* (betaine-Homocysteine methyltransferase) was expressed in the liver upon DHA and ARA supplementation. *BHMT* is an important zinc metalloenzyme in the liver. The expression of BHMT is confined mainly to the liver and its expression is reduced in cases of liver cirrhosis and liver cancer. *BHMT* is expressed abundantly in the nuclear region of the monkey eye lens and is developmentally regulated. As *BHMT* is abundantly present in the eye lens, it can be considered as an enzyme crystallin. Hyperhomocysteinemia is considered to be a risk factor for a number of important diseases like kidney failure, cardiovascular disorders, stroke, neurodegenerative diseases (including Alzheimer's) and neural tube defects. *BHMT* catalyzes the transfer of methyl groups from betaine to homocysteine to form dimethylglycine and methionine and helps in reducing the levels of homocysteine. Therefore,

the present invention is useful in modulating the expression of BHMT in the liver and thereby promoting healthy liver function.

[000201] *PPARD* (peroxisome proliferator-activated receptor-Δ) was expressed in the liver upon DHA and ARA supplementation. C18 unsaturated fatty acids are known to activate human and mouse *PPARD*. Syndrome X or metabolic syndrome is a collection of obesity related disorders. PPARs are transcription factors and are involved in the regulation of genes in response to fatty acids. *PPARD* knockout mice were observed to be metabolically less active and glucose intolerant, whereas receptor activation improved insulin sensitivity. This suggests that *PPARD* ameliorates hyperglycemia and could suggest a therapeutic approach to treat type II diabetes. *PPARD* plays beneficial roles in cardiovascular disorders by inhibiting the onset of oxidative stress-induced apoptosis in cardiomyoblasts. Ligand activation of *PPARD* can induce terminal differentiation of keratinocytes. Burdick, *et al.* reviewed the literature on *PPARD* and reported from several recent studies that ligand activation of *PPARD* can induce fatty acid catabolism in skeletal muscle and is associated with improved insulin sensitivity, attenuated weight gain and elevated HDL levels. Burdick, *et al.*, *The Role of Peroxisome Proliferator-Activated Receptor-Beta/Delta in Epithelial Cell Growth and Differentiation*, Cell Signal 18(1): 9-20 (2006). This suggests that *PPARD* can be used as target for treating obesity, dyslipidemias and type-2 diabetes. Increased expression of *PPARD* is observed during first and third trimester of pregnancy, indicating an important role in placental function.

[000202] Therefore, DHA and ARA supplementation according to the method of the present invention can modulate PPARD expression, improving insulin sensitivity, improving glucose intolerance, improving hyperglycemia, and treating obesity, dyslipidemias and type-2 diabetes.

[000203] Other genes that were affected by DHA and ARA supplementation are listed in Tables 15 and 16, respectively.

Table 15. Cerebral Cortex Genes Affected by DHA and ARA Supplementation.[1]

Gene	Biological Activity	L group (% regulation as compared to control group)	L3 group (% regulation as compared to control group)
TIMM8A	Homolog of yeast translocase of inner mitochondrial membrane 8	4	57
NF1	Neurofibromatosis, type 1	2	27
ADAM17	Distintegrin and metalloproteinase domain 17	37	50
BRCA1	Breast cancer 1 gene	4	35
LUM	Lumican	3	30
FOXP2	Forkhead box P2	-8	38
SPTLC2	Serine palmitoyltransferase, LC base subunit 2	26	40
FTH1	Ferritin heavy chain 1	-8	37
OSBP2	Oxysterol-binding protein 2	-16	35
NSMAF	Neural sphingomyelinase activation-asso factor	-4	31
PDE3A	Phophodiesterdase, 3A cgmp-inhibited	8	30
SOD	Superoxide dimutase 2	-7	29
ACADSB	Acyl-coa dehydrogenase, short/branched chain	-11	38
SFTPB	Surfactant, pulmonary associated protein B	3	35

[1] Positive values indicate upregulation; negative values indicate downregulation.

Table 16. Thymus Genes Affected by DHA and ARA Supplementation.

Gene	Biological Activity	L group (% regulation as compared to control group)	L3 group (% regulation as compared to control group)
TOB1	Transducer of ERBB2, 1	30	110
XCL1 & XCL2	Chemokine, C motif, ligands 1 & 2	40	32
RNASE3	Ribonuclease A family 3	60	43
SULT1C1	Sulfotransferase family 1C, member 1	35	35
HSPCA	Heat-shock, 90KD protein 1, alpha	-2	25
CD44	CD44 antigen	37	30
CD24	CD24 antigen	43	28
OSBPL9	Oxysterol-binding protein-like protein 9	3	20
FCER1G	FC fragment of IGE, receptor subunit 1	44	23
KIR2DS1	Killer cell immunoglobin-like receptor, two domains, short cytoplasmic tail, 1	30	10

[000204] Finally, 406 transcripts with no known gene ontology functions were differentially expressed. Several of these transcripts were among the most differentially expressed, among these, *H63*, LOC283403, FLJ13611, *PARP6*, C6orf111, C10orf67, *TTTY8*, C11orf1 and *PHAX* were upregulated, whereas transcripts for *CHRDL2*, *TSGA13*, *RP4-622L5*, MGC5391, *RNF126P1*, *FAM19A2* and *NOB1P* were repressed considerably.

Ingenuity Network Analysis

[000205] The inventors explored relationships among sets of genes using Ingenuity Systems network analysis. Out of 1108 differentially expressed probe sets in the present data, 387 probe sets (34.93%) were found in the Ingenuity Pathway Analysis (IPA) knowledge database, and are labeled "focus" genes. Based on these focus genes, IPA generated 41 biological networks, which are shown in Table 17.

Table 17: Ingenuity Functional Network Analysis
Brain Networks: L/C

ID	Modulated Genes in Network	Decreased Expression	Score	Focus Genes	Top Categories
1	ACTL6A, ADAM17, CD44, CTSB, DDAH1, FGF7, HAP1, IFITM2, LETMD1, LUM, MAP4K1, NF1, NRG1, NUMB, PDE3A, PERP, PPP3CA, RGS16, SFTPB, SMARCE1, TIMP3	ADRA1A, EDG7, EGFR, GNRHR, HES1, MDM2, PLCE1, SFTPC, SH3D19, SMARCA4, SMARCD2, SOAT1, UBE2D2, VAV3	49	35	Cellular Development, Nervous System Development and Function, Cellular Growth and Proliferation
2	BAD, BRCA1, GSR, HHEX, HNF4A, PHLDA1, POU2F1, PRKAA1, PTPRB, SHMT2, SLC2A1, STC1, TCF2, TIE1, VMD2, WASL	ALDOB, BLR1, CASP9, CD40, COL4A2, CR2, CYR61, FTH1, GATA4, GH1, GHRHR, GRP, GSTA3, LEP, NFE2L2, NSMAF, RARA, RPS6SB1, SERPINA1	49	35	Organismal Injury and Abnormalities, Organismal Survival, Cell Death
3	CRSP7, MCP, MYCN, NEIL1, PARD6B, PRKAA1,PRKAG2, RPL35A, TERF2	ALDOA, BCLAF1, CRAMP1L, ITGA2, KIAA0992, MCF2, NUDCD3, TARS, TCF3, THRAP5	18	20	Gene Expression, Cell Cycle, Cellular Assembly and Organization
4	CAMK2G, COL9A2, ESRRBL1, GNA14, PLAG1, RNASEH1, SOCS4, TIMP3, UGT2B15	APLN, COL9A3, GRIA1, HIP1, IL20RA, MAP3K2, MAP3K3, MAPK12, PLEC1	15	18	Cell Death, Cardiovascular System Development and Function, Cell Morphology
5	ACPP, CMIP, EEA1, FGF5, MAP4K1, PTPRG	ALPP, ASB6, CRLF2, LTC4S, RBM14, SFRS5, STX6, TGIF, UGTA10, ZFYVEP	14	17	Cellular Growth and Proliferation, Cardiovascular System Development and Function, Cellular Development
6	C20orf14, CDK9, JUB, ORC5L, PDIA2, POU2F2, PSMD10, PVRL2, UTF1	BRF1, CDKN2C, DOK3, GLCCI1, NCR2, TBN, TCF3, TCP10	14	17	DNA Replication, Recombination, and Repair, Gene Expression, Cell Cycle
7	ANAPC1, BAPX1, CYP1A2, HBQ1, MLLT10, SOSTDC1, SS18, YEATS4	ARHGAP4, BICD1, CDC23, CHRDL2, ETV6, FLII, PHOX2A, TCF21, TP73L	14	17	Cell Signaling, Cell Morphology, Skeletal and Muscular System Development and Function
8	ARHGDIA, BUB3, CDK9, FCGR2B, OGN, RGS16, SMOX, STXBP4	ABTB1, CDC20, CORO2B, FBXW8, NEK1, RAX, STK6, TLE2	13	16	Cell Cycle, Cancer, DNA Replication, Recombination, and Repair
9	CD58, CHD2, FCGR2A, MAOA, SLC26A4, TFCP2, TNK1	C19orf10, CD14, CATM, IGHM, ITGB7, MRPS10, SERPINB6, SYNGR2	11	15	Cell-To-Cell Signaling and Interaction, Immunological Disease, Cellular Growth and Proliferation

10	CKM, MPP6, PLAGL1, SATB2,	ACSL3, DCTN2, ELL, EPS8L2, FAT2, GART, KRAS, MDM2, MTMR2, TBL1X, TP73L	11	15	Gene Expression, Cancer, Cell Death
11	CYB561, CYP24A1, GNA13, IL1R1, IL31RA, MX2, OTP, PTHR2, TLR7	AKAP13, NPY1R, SIGLEC11, SLAMF1, UBE2E1, ZFX	11	15	Tissue Morphology, Connective Tissue Development and Function, Skeletal and Muscular System Development and Function
12	CALD1, CPT2, DNTT, FUBP1,PHF5A, TPD52, TPP2	BZRAP1, EDIL3, NOL5A, PSMD6, RARA, SCEL, SFRP2, SNRPN	11	15	Gene Expression, Cancer, Cell Morphology
13	CKM, DCK, INHBC, UCP2	CFC1, CYB5, HBP1, IRX1, MYO5A, PAPPA, PLA2G6, SFPQ, SOX7,TCF3, UQCRC2	11	15	Gene Expression, Cellular Development, Reproductive System Development and Function
14	BAD, ITSN2, PDK3, RSN, SLC18A2,TGIF2	C1QG, CDGAP, GRP, KRIT1, NEXN, PPP2R3A, RICS, RPS6KB1, ZNF198	11	15	Cell Cycle, Cellular Growth and Proliferation, Cellular Assembly and Organization
15	CUL2, IFIH1, OAS2, OASL, RCP9, SCUBE3, SEMA3D, SLC12A6	CCL1, EXT1, TGIF, WTAP, ZBTB11	10	14	Cellular Function and Maintenance, Immune Response, Cellular Movement
16	WNT10A, AP3S2,LISCH7, LRRC17, MECT1, PHLDB2, TBC1D4	AKAP13, C8G, MITF, NCBP2, PPP1R7, TIA1, TM4SF8, TRPM1	10	14	Cellular Assembly and Organization, Nervous System Development and Function, Developmental Disorder
17	ARNTL2, BAD, CARD6, HOMER3, IL1R1, RAD1, RAD17, SPRR2B, SSA2, TLK1	BRD4, CD14, ELP4, GZMA	10	14	Cellular Development, Hematological System Development and Function, Immune and Lymphatic System Development and Function
18	HFE, NOX1, PPP1R12B, TEBP	BNIP1, CIAPIN1, CTSC, CYR61, GDF11, MFN1, PPIL5, S100A7, VDAC3, ZNF207	10	14	Cell Cycle, Cancer, Cell Death
19	CDK9, EZH2, PTPRG, STK3, SUZ12, TBC1D22A, ZNF611	FAM19A2, MBP, PCGF2, PLEKHE1, RPH3AL, RSAFD1,	9	13	Gene Expression, Cancer, Cell Cycle
20	DHX8, KL, PBX2, PTPRN2, TRPV2, TUBGCP2, TUBGCP3, WSB1	AKAP8, ANK1, CACNA1S, PDE4D, TROAP	9	13	Cellular Assembly and Organization, Cellular Function and Maintenance, Cell Death
21	ADCY2, AMBP, GAS1, MRC2, OGT, POLR3F, SCIN	BRF1, FLJ30655, FURIN, GCGR, MTA3,	8	12	Cancer, Skeletal and Muscular Disorders, Tumor Morphology

22	ANXA3, FDFT1, PACRG, PDIA6, TIMP3, WWP2	FAF1, IPO9, M-RIP, MAPK12, RAVER1, UBE2G2	8	12	Cardiovascular Disease, Genetic Disorder, Respiratory Disease
23	CD84, CD8B1, DNAH1, EXOSC2, GAB2, GLRA2, H2AFY, NAB1, POLR2C	MR1 (H2ls), P2RX2, PTPN5	8	12	Cellular Development, Hematological System Development and Function, Immune and Lymphatic System Development and Function
24	CD3D, DPYD, GUCY2C, NAALAD2, NXT2, RBM8A	CENTG2, KCNK3, NXF2, PDLIM4, SIM1, TRA@,	8	12	Gene Expression, Molecular Transport, RNA Trafficking
25		DERL1	1	1	Protein Degradation, Protein Synthesis, Cellular Assembly and Organization
26	COCH		1	1	Auditory Disease, Cell-To-Cell Signaling and Interaction, Digestive System Development and Function
27	CLPS		1	1	Lipid Metabolism, Small Molecule Biochemistry, Vitamin and Mineral Metabolism
28	EMP2,		1	1	Cell Death, Renal and Urological Disease, Cell-To-Cell Signaling and Interaction
29	SPTLC2		1	1	Genetic Disorder, Neurological Disease, Lipid Metabolism
30		MYO1A	1	1	Cellular Assembly and Organization, Cell Morphology
31		ARL6IP2	1	1	Developmental Disorder, Genetic Disorder, Neurological Disease
32	HSPB3		1	1	Cellular Compromise, Renal and Urological Disease, Cell-To-Cell Signaling and Interaction
33		NEK11	1	1	Cancer, Cell Cycle, Cell Morphology
34	CLK4		1	1	Post-Translational Modification, Amino Acid Metabolism, Small Molecule Biochemistry

35		S100Z	1	1	Cancer, Cellular Movement, Respiratory Disease
36	DRF1		1	1	Cell Cycle, Cellular Assembly and Organization, Cellular Development
37	FNTB		1	1	Amino Acid Metabolism, Post-Translational Modification, Small Molecule Biochemistry
38		CSHL1	1	1	Gene Expression, Cell Signaling
39		GP2	1	1	Cellular Function and Maintenance
40	HDAC8		1	1	Cellular Development, Hematological System Development and Function, Immune and Lymphatic System Development and Function
41		FOXP2	1	1	Gene Expression, Cardiovascular System Development and Function, Cellular Compromise

Brain Networks: L3/C

1	ADAM17, ADRA1A, CD44, CTSB, EDG7, EGFR, FGF7, GNRHR, LUM, NF1, NRG1, NUMB, PDE3A, PERP, PPP3CA, SFTPB, SFTPC, SH3D19, SMARCD2, SMARCE1, TIMP3, UBE2D2	ACTL6A, DDAH1, HAP1, HES1, IFITM2, LETMD1, MAP4K1, MDM2, PLCE1, RGS16, SMARCA4, SOAT1, VAV3	49	35	Cellular Development, Nervous System Development and Function, Cellular Growth and Proliferation
2	ALDOB, BLR1, BRCA1, CASP9, CR2, FTH1, GATA4, HHEX, LEP, NFE2L2, NSMAF, PHLDA1, POU2F1, RPS6KB1, SERPINA1, TCF2, WASL	BAD, CD40, COL4A2, CYR61, GH1, GHRHR, GRP, GSR, GSTA3, HNF4A, PRKAA1, PTPRB, RARA, SHMT2, SLC2A1, STC1, TIE1, VMD2	49	35	Organismal Injury and Abnormalities, Organismal Survival, Cell Death
3	BCLAF1, CRAMP1L, ITGA2, KIAA0992, MYCN, PARD6B, RPL35A, TARS, VIL2	ALDOA, CRSP7, MCF2, MCP, NEIL1, NUDCD3, PRKAA1, PRKAG2, TCF3, TERF2, THRAP5	18	20	Gene Expression, Cell Signaling, Cell Cycle
4	GLCCI1, NCR2	BRF1, C20orf14,CDK9, CDKN2C, DOK3, ITGB7, JUB, ORC5L, PDIA2, POU2F2, PSMD10, PVRL2, TBN, TCF3, TCP10, UTF1	15	18	Gene Expression, DNA Replication, Recombination, and Repair, Cell Cycle
5	ACPP, ALPP, CRLF2, CTSB, EEA1, PTPRG, RBM14, SFRS5, STX6, UGT1A8, UGT1A10, ZFYVE9	ASB6, CMIP, FGF5, LTC4S, TGIF,	14	17	Cellular Growth and Proliferation, Hepatic System Development and Function, Tissue Morphology
6	COL9A3, ESRRBL1, GNA14, PLAG1, SOCS4, UGT2B15	APLN, CAMK2G, COL9A2, GRIA1, HIP1, IL20RA, MAP3K2, MAP3K3, MAPK12, PLEC1, RNASEH1	14	17	Gene Expression, Cardiovascular Disease, Hematological System Development and Function
7	ARHGAP4, BAPX1,CYP1A2, ETV6, MLLT10, SOSTDC1, TP73L, YEATS4	ANAPC1, BICD1, CDC23, CHRDL2, FLII, HBQ1, PHOX2A, SS18, TCF21	14	17	Cell Cycle, Cell Signaling, Renal and Urological System Development and Function
8	ABTB1, CORO2B, FBXW8, FCGR2B, NEK1, OGN, STK6	ARHGDIA, BUB3, CDC20, CDK9, RAX, RGS16, SMOX, STXBP4, TLE2	13	16	Cell Cycle, Cellular Assembly and Organization, Cancer
9	CD58, CHD2, GATM, IGHM, MRPS10, SERPINB6, SLC26A4, TFCP2	C19orf10, CD14, FCGR2A, ITGB7, MAOA, SYNGR2, TNK1	11	15	Cell-To-Cell Signaling and Interaction, Immunological Disease, Cellular Development

10	CYP24A1, FCGR2B, GNA13, IL31RA, MX2, OTP, PTHR2, SIGLEC11, SLAMF1, TLR7, UBE2E1, ZFX	AKAP13, CYB561, NPY1R	11	15	Immunological Disease, Inflammatory Disease, Cellular Growth and Proliferation
11	CALD1, DNTT, EDIL3, FUBP1, PSMD6, SFRP2, SNRPN	BZRAP1, CPT2, NOL5A, PHF5A, RARA, SCEL, TPD52, TPP2	11	15	Cellular Development, Cellular Growth and Proliferation, Cancer
12	CYB5, DCK, HBP1, INHBC, MYO5A, PAPPA, SFPQ, SOX7, UCP2, UQCRC2	CFC1, CKM, IRX1, PLA2G6, TCF3	11	15	Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry
13	CCL1, CUL2, EXT1, IFIH1, RCP9, SCUBE3, SEMA3D, WTAP, ZBTB11	OAS2, OASL, SLC12A6, TGIF, WNT10A	10	14	Cardiovascular System Development and Function, Organismal Development, Organismal Survival
14	ACSL3, DCTN2, EPS8L2, FAT2, GART, KRAS, MPP6, SATB2, TBL1X	CKM, ELL, MDM2, MTMR2, PLAGL1	10	14	Cancer, Cell Death, Skeletal and Muscular Disorders
15	LRRC17, PHLDB2, TIA1, TM4SF8, TRPM1	AKAP13, AP3S2, C8G, LISCH7, MECT1, MITF, NCBP2, PPP1R7, TBC1D4	10	14	Cellular Assembly and Organization, Nervous System Development and Function, Developmental Disorder
16	BNIP1, CIAPIN1, CTSC, GDF11MFN1, NOX1, PPP1R12B, S100A7, TEBP, VDAC3, ZNF207	CYR61, HFE, PPIL5	10	14	Cancer, Cell Cycle, Cell Death
17	CDGAP, KRIT1, NEXN, PDK3, PPP2R3A, RICS, RPS6KB1, RSN, SLC18A2, TGIF2, ZNF198	BAD, C1QG, ITSN2	10	14	Cell Cycle, Cellular Assembly and Organization, Cancer
18	PTPRG, STK3, SUZ12, ZNF611	CDK9, EZH2, FAM19A2, MBP, PCGF2, PLEKHE1, RPH3AL, RSAFD1, TBC1D22A	9	13	Gene Expression, Cell Cycle, Neurological Disease
19	KL, PDE4D, WSB1	AKAP8, ANK1, CACNA1S, DHX8, PBX2, PTPRN2, TROAP, TRPV2, TUBGCP2, TUBGCP3	9	13	Cellular Assembly and Organization, Cellular Function and Maintenance, Cell Death
20	AMBP, FLJ30655,GAS1, MRC2, MTA3, SCIN	ADCY2, BRF1, FURIN, GCGR, OGT, POLR3F	8	12	Cancer, Skeletal and Muscular Disorders, Tumor Morphology
21	CARD6, GZMA, IL1R1, RAD1, SSA2, TLK1	ARNTL2, BRD4, ELP4, HOMER3, RAD17, SPRR2B	8	12	Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Response

22	FAF1, RAVER1, TIMP3, UBE2G2	ANXA3, FDFT1, IPO9, M-RIP, MAPK12, PACRG, PDIA6, WWP2	8	12	Post-Translational Modification, Protein Folding, Cell Death
23	CD84, CD8B1, DNAH1, EXOSC2, GAB2, H2AFY, NAB1, PTPN5	GLRA2, MR1 (H2ls), P2RX2, POLR2C	8	12	Cellular Development, Hematological System Development and Function, Immune and Lymphatic System Development and Function
24	CENTG2, DPYD, GUCY2C, KCNK3, NAALAD2, NXT2, TRA@	CD3D, NXF2, PDLIM4, RBM8A, SIM1	8	12	Lipid Metabolism, Small Molecule Biochemistry, Cellular Development
25	DERL1		1	1	Protein Degradation, Protein Synthesis, Cellular Assembly and Organization
26		COCH	1	1	Auditory Disease, Cell-To-Cell Signaling and Interaction, Digestive System Development and Function
27		CLPS	1	1	Lipid Metabolism, Small Molecule Biochemistry, Vitamin and Mineral Metabolism
28		EMP2	1	1	Cell Death, Renal and Urological Disease, Cell-To-Cell Signaling and Interaction
29	SPTLC2		1	1	Genetic Disorder, Neurological Disease, Lipid Metabolism
30	MYO1A		1	1	Cellular Assembly and Organization, Cell Morphology
31	ARL6IP2		1	1	Developmental Disorder, Genetic Disorder, Neurological Disease
32	HSPB3		1	1	Cellular Compromise, Renal and Urological Disease, Cell-To-Cell Signaling and Interaction
33		NEK11	1	1	Cancer, Cell Cycle, Cell Morphology
34	CLK4		1	1	Post-Translational Modification, Amino Acid Metabolism, Small Molecule Biochemistry
35	S100Z		1	1	Cancer, Cellular Movement, Respiratory Disease

36	DRF1		1	1	Cell Cycle, Cellular Assembly and Organization, Cellular Development
37	FNTB		1	1	Amino Acid Metabolism, Post-Translational Modification, Small Molecule Biochemistry
38		CSHL1	1	1	Gene Expression, Cell Signaling
39		GP2	1	1	Cellular Function and Maintenance
40		HDAC8	1	1	Cellular Development, Hematological System Development and Function, Immune and Lymphatic System Development and Function
41	FOXP2		1	1	Gene Expression, Cardiovascular System Development and Function, Cellular Compromise

[000206] Among these 41 networks, 24 had scores of >8 and the top 2 networks with 35 genes had scores of 49. The top network identified by IPA is associated with nervous system development and function, cellular growth, and proliferation (Figure 1). Epidermal growth factor receptor (*EGFR*) is the most outstanding interaction partner found within the network. *EGFR* interacts with *TIMP3*, *NRG1*, *ADAM17*, *EDG7* and *FGF7*; all are overexpressed, and involved in neural or visual perception development. *EGFR* signaling is implicated in early events of epidermal, neural and eye development. Loss of *EGFR* signaling results in reduced brain size and loss of larval eye and optic lobe in *drosophila*. *EGFR* expression is required for postnatal forebrain and astrocytes development in mice. Functional pathway analysis conducted on this network using the IPA tool set identified three genes, *ADAM17*, *NUMB* and *HES1*, involved in the Notch signaling pathway which regulates nervous system and eye development. *ADAM17* and *NUMB* were overexpressed while *HES1* was repressed in both the groups. This analysis suggests that LCPUFAs influence many processes with influences that converge on *EGFR*. It further illustrates that DHA and ARA supplementation, according to the method of the present invention, can improve cellular growth and proliferation and nervous system, epidermal, and eye development and function. Thus, a method of the present invention is directed to improving at least one of these areas via a therapeutically effective amount of DHA and ARA supplementation.

[000207] LCPUFA are known to directly interact with nutrient sensitive transcription factors such as peroxisome proliferator-activated receptors (PPARs), liver X receptors, hepatic nuclear factor-4α, sterol regulatory binding proteins, retinoid X receptors and NF-KB. Upon ingestion, LCPUFA can elicit a transcriptional response within minutes. Microarray studies on LCPUFA-supplemented animals have identified several tissue-

specific pathways regulated by LCPUFA, particularly involving the liver, adipose, and brain tissue transcriptome. Using murine 11K Affymetrix oligoarrays, Berger, *et al.* showed increased hepatic expression of lipolytic and decreased expression of lipogenic genes. Berger, *et al.*, *Unraveling Lipid Metabolism with Microarrays: Effects of Arachidonate and Docosaheaenoate Acid on Murine Hepatic and Hippocampal Gene Expression*, Genome Bio. 3(7): preprint0004 (2002); Berger, *et al.*, *Dietary Effects of Arachidonate-Rich Fungal Oil and Fish Oil on Murine Hepatic and Hippocampal Gene Expression*, Lipids Health Dis. 1(2): 2 (2002).

[000208] However, in the hippocampus brain region, increased expression of *HTR4* and decreased expression of *TTR* and *SIAT8E*, genes involved in the regulation of cognition and learning, as well as *POMC*, a gene associated with appetite control, was identified. The first paper published on the brain gene transcriptome with respect to LCPUFA supplementation by Kitajka, *et al.* demonstrated that feeding fish oil (DHA 26.9%) to rats increased expression of genes involved in lipid metabolism (*SPTLC2*, *FPS*), energy metabolism (ATP synthase subunit d, ATP synthase H^+, cytochromes, *IDH3G*), cytoskeleton (Actin related protein 2, *TUBA1*), signal transduction (Calmodulins, *SH3P4*, *RAB6B* small GTPase), receptors, ion channels and neurotransmission (Vasopressin V1b receptor, Somatostatin), synaptic plasticity (Synucleins) and regulatory proteins (protein phosphatases). Kitijka, *et al.*, *The Role of n-3 Polyunsaturated Fatty Acids in Brain: Modulation of Rat Brain Gene Expression by Dietary n-3 Fatty Acids*, Proc. Natl. Acad. Sci. 99(5): 2619-24 (2002).

[000209] In the same study, fish oil supplementation also significantly reduced the expression of phospholipase D and Transthyretin. In related work, Kitajka, *et al.*, using rat cDNA microarrays with 3,200 spots, found results similar to those previously reported. Kitajka, *et al.*, *Effects of Dietary Omega-3 Polyunsaturated Fatty Acids on Brain Gene Expression*,

Proc. N. Acad. Sci. 101(30): 10931-10936 (2004). Barcelo-Coblijn, *et al.* were the first to report moderation of age-induced changes in gene expression in rat brain as a result of diets rich in fish oil (DHA 11.2%). Barcelo-Coblijn, *et al.*, *Modification by Docosahexaenoic Acid of Age-Induced Alterations in Gene Expression and Molecular Composition of Rat Brain Phospholipids*, Proc. Natl. Acad. Sci. 100(20): 11321-26 (2003). In this study, 2 month old rats showed increased expression of *SNCA* and *TTR*, however, 2-year old rats exhibited no significant changes. *Id.*

[000210] In addition, Puskas, *et al.* demonstrated that administration of omega-3 fatty acids from fish oil (5% EPA and 27% DHA; total fat content: 8%) for 4 weeks in 2-year old rats induced expression of transthyretin and mitochondrial creatine kinase and decreased expression of *HSP86*, *ApoC-I* and Makorin RING zinc-finger protein 2, genes in hippocampus brain region. Puskas, *et al.*, *Short-Term Administration of Omega 3 Fatty Acids from Fish Oil Results in Increased Transthyretin Transcription in Old Rat Hippocamus,* Proc. Natl. Acad. Sci 100(4): 1580-85 (2003). Finally, Flachs, *et al.* showed increased expression of genes for mitochondrial proteins in adipose tissue. Flachs, *et al.*, *Polyunsaturated Fatty Acids of Marine Origin Upregulate Mitochondrial Biogenesis and Induce Beta-Oxidation in White Fat*, Diabetologia 48(11): 2365-2375 (2005).

[000211] In comparison with previous brain transcriptome analyses, the present study employing the use of high-density Affymetrix oligoarrays (>54,000 ps) revealed genes differentially regulated by LCPUFA at ranges mimicking breast milk. The present data indicate that LCPUFA supplementation within the ranges of breast milk will induce global changes in gene expression across numerous biological processes.

[000212] Conclusions

[000213] The impact of DHA and ARA on infant baboons was both significant and widespread. Several novel differentially-expressed transcripts were identified in 12-week old baboon cerebral cortexes

modulated by dietary LCPUFA. The majority of probe sets showed subtle changes in gene transcription. In the cerebral cortex, increased expression of mitochondrial proton carrier, *UCP2* (uncoupling protein 2) was observed in both groups, but more in L3/C. *PLA2G6*, implicated in childhood neurodegeneration, was differentially expressed. *TIA1*, a silencer of the *COX2* gene translation was upregulated in L3/C. Increased expression was observed for *TIMM8A*, *NRG1*, *SEMA3D* and *NUMB*, genes involved in neural development. *LUM*, *EML2*, *TIMP3* and *TTC8* genes with roles in visual perception were overexpressed. Hepatic nuclear factor-4α (*HNF4A*) showed decreased expression with increasing DHA. *RARA* was repressed in both the groups.

[000214] A network involving 35 genes attributed to neural development and function was identified using Ingenuity network analysis, emphasizing *EGFR* as the most outstanding interaction partner in the network. In this network *EGFR* interacts with genes involved in neural or visual perception, *TIMP3*, *NRG1*, *ADAM17*, *EDG7* and *FGF7*. Although subtle, the upregulation of *NUMB* and downregulation of *HES1* in the Notch signaling pathway, not previously shown to interact with fatty acids, supports the involvement of LCPUFA, particularly DHA, in neural development. Interestingly, no known desaturases and only one elongase, LCPUFA biosynthetic enzymes, were differentially expressed in cerebral cortex.

[000215] In a study of liver gene expression, fatty acid desaturases *SCD* and *FADS1* were significantly downregulated. A multifunctional protein, *TOB1*, was significantly overexpressed in the liver. TOB1 is a gene that was affected by DHA and ARA supplementation. It is a transducer of ERBB2, 1 and was upregulated in the liver and thymus by 30% in the L group and by 110% in the L3 group, as compared to the control group. TOB1 is a novel multifunctional anti-proliferative protein involved in hippocampus-dependent learning and memory. Jin, *et al.*, *The Negative Cell Cycle Regulator, Tob (Transducer of Erb-2), is a Multifunctional*

Protein Involved in Hippocampus-Dependent Learning and Memory, Neurosc. 131(3):647-59 (2005). The gene has also been linked with the regulation of quiescence in lymphocytes, tumor suppression, and decreased incidences of osteoarthritis. Yusuf and Fruman, *Regulation of Quiescence in Lymphocytes*, Trends Immunol. 24(7):380-86 (2003); Yoshida, *et al.*, *Mice Lacking a Transcriptional Corepressor Tob are Predisposed to Cancer*, Genes Dev. 17(10):1201-06 (2003); Gebauer, *et al.*, *Repression of Anti-Proliferative Factor Tob1 in Osteoarthritic Cartilige*, Arthritis Res. Ther. 7(2):R274-R284 (2005). Thus, because the gene is indicated in connection with learning, memory, tumor suppression, and osteoarthritis, it is believed that upregulation of TOB1 through DHA and ARA supplementation prevents and/or treats each of these functions or disorders.

[000216] These data represent the first comprehensive transcriptome analysis in primates and have identified widespread changes in cerebral cortex genes that are modulated by increases in DHA, induced by dietary means. Importantly, the range of DHA used herein is within limits of human and primate breast milks, the natural food for infants, and indicate that CNS gene expression responds to LCPUFA concentrations.

[000217] The inventors have determined that increasing levels of DHA and ARA induces the regulation of global changes in gene expression across diverse biological processes. For example, in an embodiment of the present invention, DHA and ARA supplementation is effective in increasing plasma Ceramide and LysoSM levels, tumor suppression, preventing iron related disorders, improving neurological development such as speech, learning and memory, mediating an immune response, increasing lung function and development, and preventing heart, skin, intestinal, and lung abnormalities. The inventors also believe that an embodiment of the present invention is effective in preventing or treating various neurodegenerative disorders, various cancers, such as breast,

pancreatic, colorectal, ovarian, endometrial, and prostatic, as well as osteoarthritis, schizophrenia and Alzheimer's disease.

[000218] In addition, regulation at the transcription and/or translational levels of genes involved in the lipid machinery, such as absorption, transport, and metabolism, can lead to lower plasma triglyceride levels, lower accumulation of lipids in adipocytes, increased utilization and hydrolysis of triglycerides, and increased fatty acid oxidation in adipocytes and muscles. These actions can orchestrate lowering adiposity, weight gain, and the occurrence of obesity and atherosclerosis in infants and children.

[000219] All references cited in this specification, including without limitation, all papers, publications, patents, patent applications, presentations, texts, reports, manuscripts, brochures, books, internet postings, journal articles, periodicals, and the like, are hereby incorporated by reference into this specification in their entireties. The discussion of the references herein is intended merely to summarize the assertions made by their authors and no admission is made that any reference constitutes prior art. Applicants reserve the right to challenge the accuracy and pertinence of the cited references.

[000220] Although embodiments of the invention have been described using specific terms, devices, and methods, such description is for illustrative purposes only. The words used are words of description rather than of limitation. It is to be understood that changes and variations may be made by those of ordinary skill in the art without departing from the spirit or the scope of the present invention, which is set forth in the following claims. In addition, it should be understood that aspects of the various embodiments may be interchanged both in whole or in part. For example, while methods for the production of a commercially sterile liquid nutritional supplement made according to those methods have been exemplified, other uses are contemplated. Therefore, the spirit and scope

of the appended claims should not be limited to the description of the versions contained therein.

WHAT IS CLAIMED IS:

1. Use of an amount of DHA and ARA in the preparation of a composition for modulating the expression of one or more genes in a subject, wherein the gene is selected from the group consisting of those genes listed in Tables 4-9 under the "Gene Symbol" column.

2. The use according to claim 1, wherein the subject is one that is in need of such modulation.

3. The use according to claim 1, wherein the composition contains ARA and the DHA in a ratio of from about 10:1 to about 1:10 by weight.

4. The use according to claim 1, wherein the composition contains ARA and the DHA in a ratio of from about 2:1 to about 1:2 by weight.

5. The use according to claim 1, wherein the composition contains ARA and DHA in a ratio of about 1:1.5 by weight.

6. The use according to claim 1, wherein the subject is an infant.

7. The use according to claim 6, wherein the DHA and ARA are administered to an infant during the time period from birth until the infant is about one year of age.

8. The use according to claim 6, wherein the composition is an infant formula.

9. The use according to claim 8, wherein the infant formula comprises DHA in an amount of from about 15 mg to about 60 mg per 100 kcal infant formula.

10. The use according to claim 8, wherein the infant formula comprises ARA in an amount of from about 25 mg to about 40 mg per 100 kcal infant formula.

11. Use of an amount of DHA and ARA in the preparation of a composition for upregulating the expression of one or more genes in a subject, wherein the gene is selected from the group consisting of those genes listed in Tables 4 and 6 under the "Gene Symbol" column.

12. The use according to claim 11, wherein the subject is one in need of such upregulation.

13. The use according to claim 11, wherein the subject is a human infant.

14. The use according to claim 13, wherein the composition contains ARA and DHA in a ratio of ARA:DHA of between about 1:2 to about 2:1 by weight.

15. Use of an amount of DHA and ARA in the preparation of a composition for downregulating the expression of one or more genes in a subject, wherein the gene is selected from the group consisting of those genes listed in Tables 5 and 7 under the "Gene Symbol" column.

16. The use according to claim 15, wherein the subject is one in need of such downregulation.

17. The use according to claim 15, wherein the subject is a human infant.

18. The use according to claim 15, wherein the composition contains ARA and DHA in a ratio of ARA:DHA of between about 1:2 to about 2:1 by weight.

19. Use of an amount of DHA and ARA in the preparation of a composition for upregulating the expression of one or more genes in a subject, wherein the gene is selected from the group consisting of TIMM8A, TIMM23, EGFR, NF1, SFTPB, ACADSB, SOD, PDE3A, NSMAF, OSBP2, FTH1, SPTLC2, FOXP2, LUM, BRCA1, ADAM17, ADAM33, TOB1, XCL1, XCL2, RNASE2, RNASE3, SULT1C1, HSPCA, CD44, CD24, OSBPL9, FCER1G, FXD3, NRF1, STK3, KIR2DS1, and any combination thereof.

20. The use according to claim 19, wherein the subject is one in need of such upregulation.

21. The use according to claim 19, wherein the subject is a human infant.

22. The use according to claim 19, wherein the composition contains ARA and DHA in a ratio of ARA:DHA of between about 1:2 to about 2:1 by weight.

23. Use of an amount of DHA and ARA in the preparation of a composition for modulating the expression of one or more genes in a subject, wherein the gene is selected from the group consisting of TIMM8A, TIMM23, NF1, LUM, BRCA1, ADAM17, TOB1, RNASE2, RNASE3, NRF1, STK3, FZD3, ADAM8, PERP, COL4A6, PLA2G6, MSRA, CTSD, CTSB, LMX1B, BHMT, TNNC1, PDE3A, PPARD, NPY1R, LEP, and any combination thereof.

24. Use of an amount of DHA and ARA in the preparation of a composition for treating or preventing tumors in a subject, the use comprising modulating the expression of a gene selected from the group consisting of TOB1, NF1, FZD3, STK3, BRCA1, NRF1, PERP, and COL4A6 in the subject.

25. The use according to claim 24, wherein the subject is in need of such modulation.

26. The use according to claim 24, wherein the subject is a human infant.

27. The use according to claim 24, wherein the composition contains ARA and DHA in a ratio of ARA:DHA of between about 1:2 to about 2:1 by weight.

28. Use of an amount of DHA and ARA in the preparation of a composition for treating or preventing neurodegeneration in a subject, the use comprising modulating the expression of a gene selected from the group consisting of PLA2G6, TIMM8A, ADAM17, TIMM23, MSRA, CTSD, CTSB, LMX1B, and BHMT in the subject.

29. The use according to claim 28, wherein the neurodegenerative condition treated or prevented is selected from the group consisting of Mohr-Tranebjaerg syndrome, Jensen syndrome, Alzheimer's disease, Parkinson's disease, nail patella syndrome, and congenital ovine neuronal ceroid lipofuscinosis.

30. Use of an amount of DHA and ARA in the preparation of a composition for improving vision in a subject, wherein DHA and ARA modulate the expression of the LUM gene in the subject.

31. Use of an amount of DHA and ARA in the preparation of a composition for treating or preventing macular degeneration in a subject, wherein DHA and ARA modulate the expression of the LUM gene in the subject.

32. The use according to claim 31, wherein the macular degeneration is Sorsby's fundus.

33. Use of an amount of DHA and ARA in the preparation of a composition for stimulating an immune response in a subject, wherein DHA and ARA modulate the expression of a gene selected from the group consisting of RNASE2, RNASE3, and ADAM8 in the subject.

34. Use of an amount of DHA and ARA in the preparation of a composition for improving lung function in a subject, wherein DHA and ARA modulate the expression of the ADAM33 gene in the subject.

35. The use according to claim 34 comprising the treatment or prevention of a disorder selected from the group consisting of asthma, and bronchial hyperresponsiveness.

36. Use of an amount of DHA and ARA in the preparation of a composition for improving cardiac function in a subject, wherein DHA and ARA modulate the expression of a gene selected from the group consisting of TNNC1 and PDE3A in the subject.

37. The use according to claim 36, wherein the idiopathic dilated cardiomyopathy is treated or prevented.

38. Use of an amount of DHA and ARA in the preparation of a composition for treating or preventing obesity in a subject, wherein DHA and ARA modulate the expression of a gene selected from the group consisting of PPARD, NPY1R, and LEP in the subject.

39. The use according to claim 38, wherein the use treats or prevents a disorder selected from the group consisting of hyperglycemia and type II diabetes.

40. Use of an amount of DHA in the preparation of a composition for modulating the expression of one or more genes in an infant, wherein the gene is selected from the group consisting of those genes listed in Tables 4-9 under the "Gene Symbol" column.

41. The use according to claim 40, wherein the expression is upregulated in a gene selected from the group consisting of those genes listed in Tables 4 and 6 under the "Gene Symbol" column.

42. The method according to claim 40, wherein the expression is downregulated in a gene is selected from the group consisting of those genes listed in Tables 5 and 7 under the "Gene Symbol" column.

43. Use of an amount of ARA in the preparation of a composition for modulating the expression of one or more genes in an infant, wherein the gene is selected from the group consisting of those genes listed in Tables 4-9 under the "Gene Symbol" column.

44. Use of an amount of DHA in the preparation of a composition for modulating the expression of one or more genes in a child, wherein the gene is selected from the group consisting of those genes listed in Tables 4-9 under the "Gene Symbol" column.

45. The use according to claim 44, wherein the child is between the ages of one and six years of age.

46. The use according to claim 44, wherein the child is between the ages of about seven and twelve years of age.

47. The use according to claim 44 additionally comprising administering ARA to the child.

48. Use of an amount of DHA in the preparation of a composition for modulating the expression of one or more genes in a child, wherein the gene is selected from the group consisting of TIMM8A, TIMM23, NF1, LUM, BRCA1, ADAM17, TOB1, RNASE2, RNASE3, NRF1, STK3, FZD3, ADAM8, PERP, COL4A6, PLA2G6, MSRA, CTSD, CTSB, LMX1B, BHMT, TNNC1, PDE3A, PPARD, NPY1R, LEP, and any combination thereof.

49. The use according to claim 48, wherein the child is between the ages of one and six years of age.

50. The use according to claim 48, wherein the child is between the ages of about seven and twelve years of age.

51. The use according to claim 48, wherein the composition additionally comprises ARA.

52. Use of an amount of ARA in the preparation of a composition for modulating the expression of one or more genes in a child, wherein the gene is selected from the group consisting of those genes listed in Tables 4-9 under the "Gene Symbol" column.